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DOCTORAL THESIS

In Life and Health Sciences

Characterization of extracellular vesicles in heart and in the circulation of patients with heart failure

Defended on December 12th, 2022 by

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- Longwood Extracellular Vesicles Symposium – 2020 (online)
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Abstract

Acute decompensation of previously stable chronic heart failure (ADHF) is a major cause of mortality worldwide. ADHF is associated with re-appearance of symptoms of heart failure and requires immediate medical attention. Experiments performed on a rat model of ADHF showed that treatment with Thiamet G (TG), a molecule increasing global intracellular O-GlcNAcylation, promotes cardiac recovery following ADHF and increases survival. The aim of this thesis project was to investigate whether cardiac extracellular vesicles (EVs)–a class of secreted membrane-bound particles carrying proteins, nucleic acids, and lipids–play a role in mediating the therapeutic effect of TG.

We have shown that cardiac EVs display distinct markers that differ from classical EV markers. Through a comparative proteomic approach, we found that cardiac EVs are specifically loaded with the sarcomeric protein LIM domain binding 3 (LDB3). We then validated LDB3 as a marker of cardiac EVs after their isolation using different techniques in both rat and human cardiac tissue samples.

Additionally, we found that cardiac LDB3 levels change during HF, but its level in EVs remains unchanged. We also found no change in cardiac LDB3 levels between ADHF rats treated or not with TG. However, intracellular LDB3 displayed higher O-GlcNAcylation in TG-treated animals.

These data suggest that LDB3 is a potential marker of cardiac EVs, and its secretion into EVs is not influenced by HF. Furthermore, LDB3 O-GlcNAcylation can be further studied for its downstream effect on cardiac function and as a therapeutic target during ADHF.

Key words: Heart failure; O-GlcNAcylation; extracellular vesicles

Résumé

La décompensation aiguë suite à une insuffisance cardiaque chronique précédemment stable (ADHF) est une cause majeure de mortalité dans le monde. L'ADHF est associée à la réapparition des symptômes d'insuffisance cardiaque et nécessite une prise en charge médicale immédiate. Des expériences réalisées sur un modèle de rat d'ADHF ont montré que le traitement par le Thiamet G (TG), une molécule augmentant le taux de O-GlcNAcylation intracellulaire global, favorise la récupération cardiaque suite à l'ADHF et augmente la survie. L'objectif de ce projet de thèse était d'étudier si les vésicules extracellulaires (VE) cardiaques - une classe de particules membranaires sécrétées transportant des protéines, des acides nucléiques et des lipides - jouent un rôle dans la médiation de l'effet thérapeutique bénéfique du TG.

Nous avons montré que les VE cardiaques présentent des marqueurs distincts qui diffèrent des marqueurs classiques des VE. Grâce à une approche protéomique comparative, nous avons découvert que les VE cardiaques expriment spécifiquement la protéine sarcomérique LIM domain binding 3 (LDB3). Nous avons ensuite validé LDB3 comme un marqueur des VE cardiaques après leur isolement/purification en utilisant différentes techniques à partir de tissus cardiaques humains et de rats.

De plus, nous avons constaté que les niveaux de LDB3 cardiaque changent au cours du développement de l'insuffisance cardiaque, mais que son niveau dans les VE reste inchangé. Nous avons également constaté qu'il n'y avait pas de changement dans les niveaux de LDB3 cardiaques entre les rats ADHF traités ou non par TG. Cependant, la protéine LDB3 intracellulaire présentait une O-GlcNAcylation plus élevée chez les animaux traités par TG.

Ces données suggèrent que LDB3 est un marqueur potentiel des VE cardiaques, et que sa sécrétion dans les VE n'est pas influencée par l'insuffisance cardiaque. En perspectives, les modulations des taux d'O-GlcNAcylation de LDB3 sur la fonction cardiaque devront être caractérisés comme comme cible thérapeutique pendant l'ADHF.

Mots clés : Insuffisance cardiaque ; O-GlcNAcylation ; vesicules extracellulaires

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Abbreviations

Symbols

⌀: diameter

°C: degrees Celsius

A

A: amperes

ADAM10: A Disintegrin and metalloproteinase domain-containing protein 10

ACE-I: angiotensin converting enzyme inhibitor

ADHF: acute decompensated heart failure

AGO2: argonaut 2

ALIX: ALG-2 interacting protein X

AP: action potential

APS: ammonium persulfate solution

ARF: ADP-ribosylation factor

ARMM: ARRDC1-mediated microvesicle

ARNI: angiotensin receptor-neprilysin inhibitor

ARRDC1: arrestin domain-containing protein 1

B

BBB: blood-brain barrier

BP: blood pressure

C

CD: cluster of differentiation

CHMP: charged multivesicular body protein

CO: cardiac output

CRYAB: alpha-B crystallin

Ct: cycle threshold

cUC: cushioned ultracentrifugation

D

d^2: diameter of the particle

DBP: diastolic blood pressure

DGUC: density gradient ultracentrifugation

DMEM: Dulbecco's modified eagles medium

DPBS: Dulbecco's phosphate-buffered saline

DTT: Dithiothreitol

dUC: differential ultracentrifugation

E

ECL: enhanced chemiluminescence

ECM: extracellular matrix

EDTA: Ethylenediaminetetraacetic acid

EF: ejection fraction

ER: endoplasmic reticulum

ESC: European Society of Cardiology

ESCRT: endosomal sorting complex required for transport

EV: extracellular vesicle

EVtrap: EV total isolation and recovery

F

FBS: fetal bovine serum

Fru-6P: fructose-6-phosphate

G

g: centrifugal force

g: gram

GAPDH: Glyceraldehyde 3-phosphate dehydrogenase

GFAT1: Glutamine–fructose-6-phosphate amidotransferase 1

Glc: glucose

GlcN: glucosamine-6-phosphate

GlcNAc-6P: N-acetylglucosamine-6-phosphate

GLUT: glucose transporter

GTP: Guanosine-5'-triphosphate

H

H_2O_2: hydrogen peroxide

H9c2: rat embryo cardiac myoblast cells

HBP: hexosamine biosynthetic pathway

HD-PTP: His domain protein tyrosine phosphatase

HF: heart failure

HFpEF: heart failure with preserved ejection fraction

HFrEF: heart failure with reduced ejection fraction

hnRNPA2B1: heterogenous nuclear ribonucleoprotein A2B1

HRS: hepatocyte growth factor-regulated tyrosine kinase substrate

HSC70: Heat shock cognate 71 kDa protein

HSP70: Heat shock protein 70 kDa

I

ILV: intraluminal vesicle

INSERM: Institut national de la santé et de la recherche médicale

IP: intraperitoneal

IP: intraperitoneal

ISG15: interferon-stimulating gene 15

L

L: density of the solution

LA: left atrium

LBPA: lysobisphosphatidic acid

LC-MS: liquid chromatography mass spectrometry

LDB3: LIM domain binding 3

LDL: low density lipoprotein

LDS: Lithium Dodecyl Sulfate

lEV: large EV

lncRNA: long non-coding RNA

LV: left ventricle

LVR: left ventricular remodeling

M

M199: Medium 199

MSC: mesenchymal stem cells

MHC: major histocompatibility complex

MI: myocardial infarction

min: minute

miRNA: micro-ribonucleic acid

MISEV18: Minimal information for studies of extracellular vesicles 2018

MLC: myosin light chain

mM: millimolar

mmHg: millimeter of mercury

MRA: mineralocorticoid receptor antagonists

mRNA: messenger ribonucleic acid

MV: microvesicle

MVB: multivesicular body

MVB12: multivesicular body subunit 12

MVE: multivesicular endosome

MVP: major vault protein

MW: molecular weight

MYH7: Myosin heavy chain 7

N

n: viscosity of the solution

NRVF: neonate ventricular fibroblasts

NRVM: neonate rat ventricular myocytes

nSMase2: neutral sphingomyelinase 2

NUP62: Nucleoporin p62

O

OGA: O-GlcNAcylase

O-GlcNAc: O-linked-N-acetylglucosamine

OGT: O-GlcNAc transferase

P

P/S: penicillin/streptomycin

p: particle density

PAGE: polyacrylamide gel electrophoresis

PDLIM5: PDZ and LIM domain 5

PdtIns3P: phosphatidylinositol 3-phosphate

PEG: polyethylene glycol

PMA: phorbol 12-myristate 13-acetate

PTM: post-translational modification

PTS: phase-transfer surfactant

PUGNAc: O-(2-acetamido-2-deoxy-D-glucopyranosylidene)amino-N-phenylcarbamate

R

RA: right atrium

RAAS: renin-angiotensin-aldosterone system

Rho: Ras homologous

RISC: RNA-induced silencing complex

ROCK: Rho-kinase

ROS: reactive oxygen species

RPM: rotations per minute

RT: room temperature

RT-qPCR: Quantitative reverse transcription PCR

RV: right ventricle

S

SA: sinoatrial

SBP: systolic blood pressure

SDS: sodium dodecyl sulfate

SEC: size exclusion chromatography

SEM: standard error of the mean

sEV: small EV

SMAD7 : mothers against DPP homologues 7

SNARE: soluble N-ethylmaleimide-sensitive factor attachment proteins receptor

SNS: sympathetic nervous system

SORBS2: SH3 domain-containing protein 2

STAM: signal transducing adaptor molecule

SV: stroke volume

SVR: systemic vascular resistance

SYNCRIP: synaptotagmin-binding cytoplasmic RNA-interacting protein

T

TBST: 1X Tris-Buffered Saline, 0.1% Tween® 20 Detergent

TEMED: tetramethylethylenediamine

TFA: trifluoroacetic acid

TSG101: tumor susceptibility gene 101

U

UDP: uridine diphosphate

UF: ultrafiltration

V

v/v: volume per volume

v: sedimentation rate

V: volts

VPS: vacuolar protein sorting

VSMC: vascular smooth muscle cell

W

w/v: weight per volume

Y

YBX-1: Y-box binding protein

Introduction

I. THE HEART

1. Healthy hearts

1.1. Anatomy

The heart is a muscular organ that serves the role of a pump, distributing blood to all organs. It is located in the cavity between the lungs, or the "**mediastinum**" (Figure 1) (Saladin et al., 2021). Surrounding the heart is a sac-like structure with two walls called the **pericardium**. The outer wall of the pericardium, called the **fibrous pericardium**, surrounds the heart and is connected to the diaphragm below, while the inner pericardial membrane, called the **serous pericardium**, is in contact with the heart. The serous pericardium is itself made up of two layers, the *parietal layer* lining the fibrous pericardium, and the *visceral layer*, which lines the heart and is considered the outermost layer of the heart (also known as the **epicardium)**. The space between the serous pericardium layers, known as the **pericardial cavity**, is filled with **pericardial fluid** (5 to 30 mL) secreted by the serous pericardium. The pericardium serves to maintain the heart in a suspended position and minimize friction during contraction.

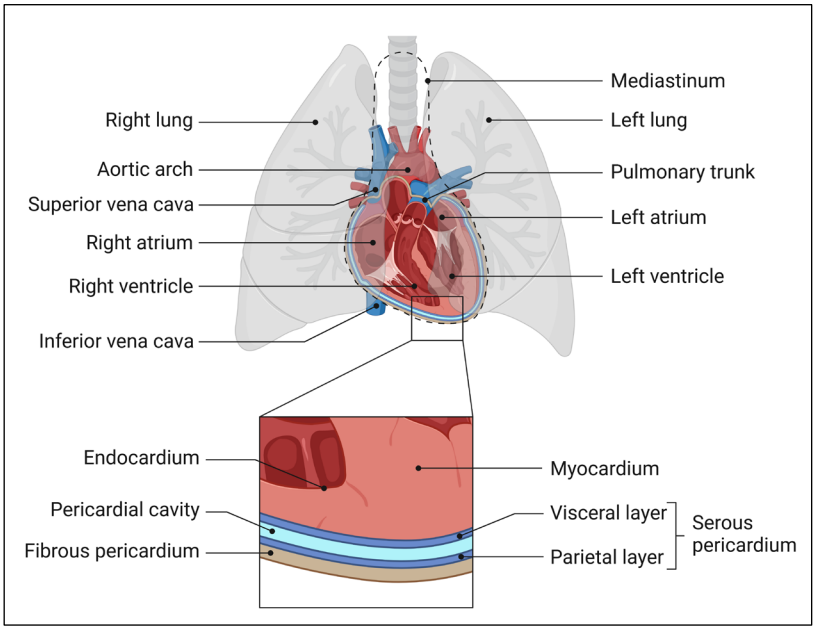


Figure 1. The heart and its surrounding structures (created with BioRender.com).

The heart itself is divided into four chambers: two atria on the top and two ventricles on

the bottom (Figure 1). The left (LA) and right atrium (RA) are separated by the *interatrial septum*, while the left (LV) and right ventricle (RV) are separated by the *interventricular septum*. Between the atria and the ventricles are *atrioventricular valves* (tricuspid on right side, mitral on left).

Cardiac tissue made up of three layers, from the outside in: the **epicardium**, the **myocardium**, and the **endocardium**. The epicardium and endocardium are composed of a thin, single layer of cells resting on connective tissue, while the myocardium, made up primarily of contractile and mesenchymal cells, forms the largest part of heart tissue. Myocardium is thicker in the LV, and thinner in the RA.

1.2. Histology

Epithelial cells line the epicardial and endocardial heart layers, while the myocardial layer is populated by various cell types. The primary cell types in the heart are contractile **cardiomyocytes**. Cardiomyocytes constitute 49.2% of cells in the ventricles, while **vascular smooth muscle cells (VSMC)** are 21.2%, **fibroblasts** are 15.5%, **endothelial cells** are 7.8%, and various **immune cells** 5.3% (Litviňuková et al., 2020) (Figure 2).

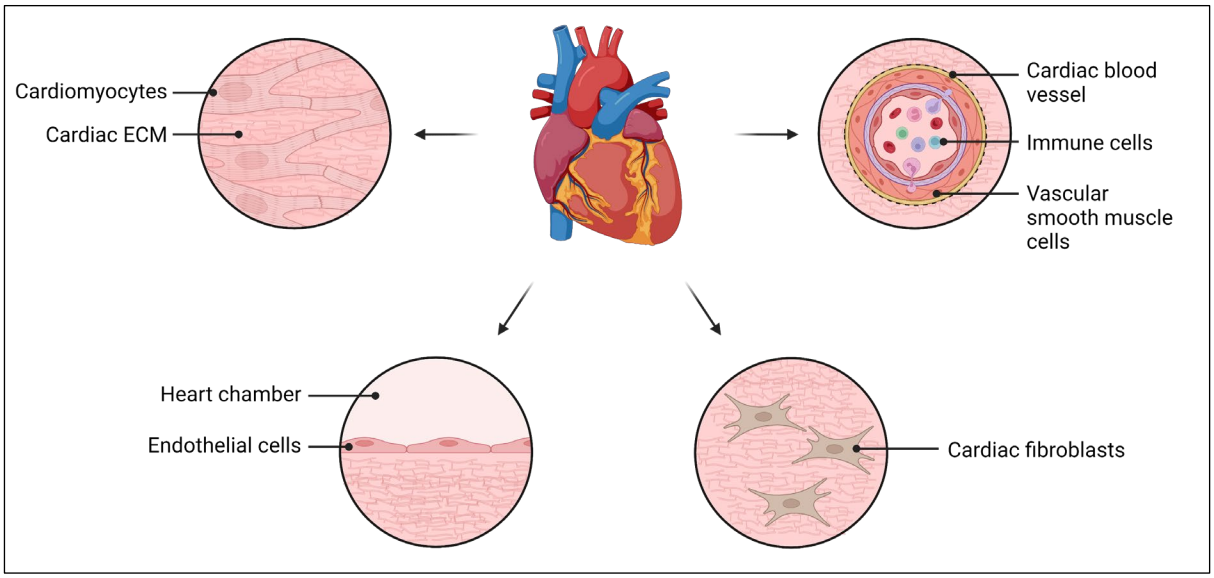


Figure 2. The main cardiac cell types. ECM: extracellular matrix (created with BioRender.com).

Cardiomyocytes are one of the three muscle cell types in vertebrates, the other two being skeletal and smooth muscle cells. Cardiomyocytes drive the contractile force of the heart. These

cells function as a unit, transmitting the contractile signal, known as *action potential* (AP) in a manner that allows the heart to beat for optimal blood ejection. This synchronization is possible due to the presence of *intercalated discs* connecting cardiomyocytes through cell junctions (Figure 3).

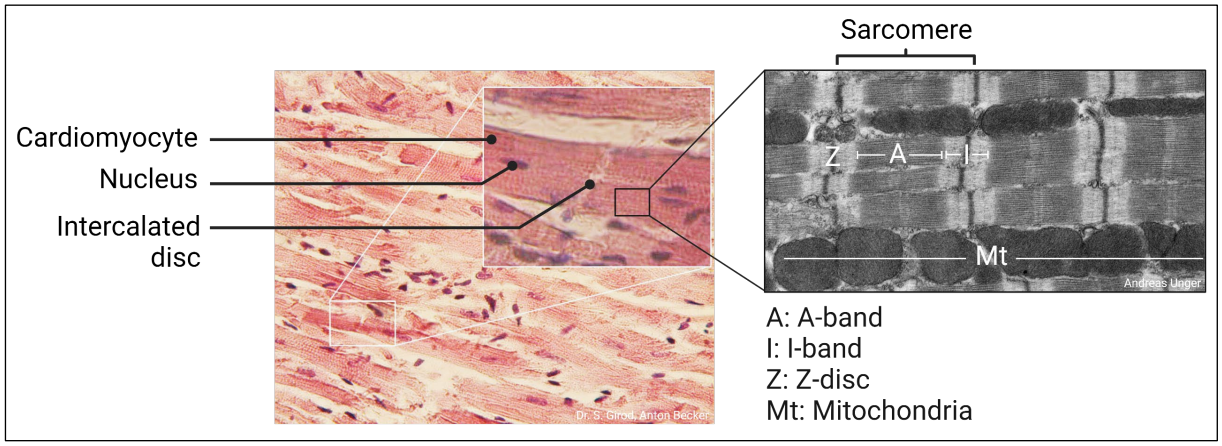


Figure 3. Cardiomyocyte organization in heart tissue showing intercalated discs and sarcomere striations (Wikimedia Commons; Innovations Report [accessed 24/10/2022])

Cardiomyocytes contain contractile organelles called *myofibrils*. Myofibrils are tube-like bundles of long proteins organized in a structure called a *sarcomere*.

The sarcomere is composed mainly of *actin* and *myosin* filaments which interact to produce contractile force. Many other proteins are necessary to maintain sarcomeric structural integrity during contraction (Figure 4). *Titin* is an essential, giant protein anchoring sarcomeric proteins and maintaining myosin in a central position with respect to actin. It acts as a spring and allows for sarcomeric elasticity. It is the largest known protein, with a molecular weight between 3000 to 4000 kDa depending on its isoform (Labeit and Kolmerer, 1995). *α-actinin* is a Z-disc protein that connects actin filaments of adjacent sarcomeres (Sjöblom et al., 2008). *Myotilin* and *LIM domain binding 3* (LDB3) maintain sarcomeric structural integrity by anchoring actin to α-actinin (Lin et al., 2014). LDB3 was also shown to be essential for sarcomere and integrin adhesion site assembly (Jani and Schöck, 2007). *Tropomyosin* and cardiac *Troponins* (Troponin I, T and C) are regulators that surround actin filaments and mainly function to prevent actin-myosin interaction when the heart is not contracting. This functional inhibition is calcium-dependent. When cellular calcium levels rise, these proteins

undergo a conformational change exposing actin interaction sites (Marques and de Oliveira, 2016). *Tropomodulin* and *CapZ* are actin filament capping proteins that control the filament's elongation and anchor it to the Z-disc (Hishiya et al., 2010, p. 3; Rao et al., 2014). *Desmin* is mainly present surrounding the Z-disc region of the sarcomere. It is essential for connecting the contractile structures with the cytoskeleton, including the nucleus, the subsarcolemmal cytoskeleton, and adjacent sarcomeres (Paulin and Li, 2004). *αB-crystallin* (CRYAB) is a small heat shock-related protein that binds to desmin and cytoplasmic actin. It may act as a chaperone under conditions of stress, during which it translocates to the cytoskeleton (Barbato et al., 1996; Bennardini et al., 1992).

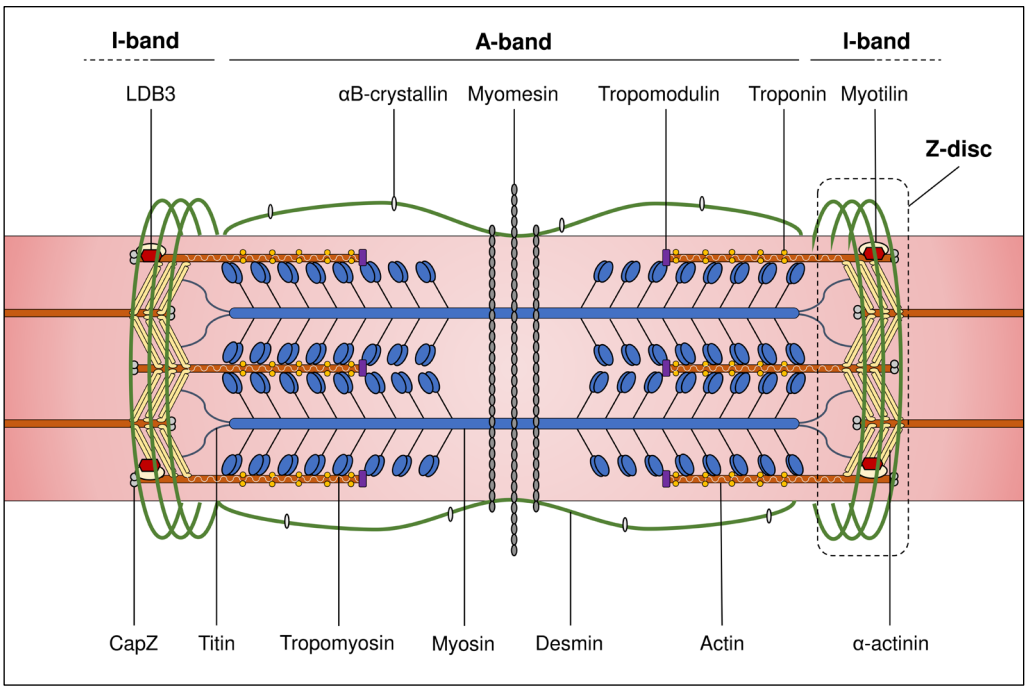


Figure 4. A schematic representation the main sarcomeric proteins. LDB3: LIM domain binding 3. Figure was adapted from (Lambert et al., 2020).

When an AP arrives, ionic changes take place in the cell, inducing the interaction of sarcomeric proteins that shorten the sarcomere, and as a result shorten the entire cell (see more in section 1.3.4). Cardiac contraction takes place when cardiomyocytes shorten during the transmission of the AP throughout cardiac tissue.

Cardiac cells in the myocardium are surrounded by an extracellular matrix (ECM) consisting of proteins which can be structural (collagen, elastin), or non-structural

(proteoglycans) (del Monte-Nieto et al., 2020). Fibroblasts produce the collagen network of the ECM, which plays an essential role in the conduction of contractile signals and rhythmicity of cardiac function, as well as providing strength to the heart wall (Ivey and Tallquist, 2016; Tallquist and Molkentin, 2017).

Endothelial cells line the inner layer of the heart (endocardium) and blood vessels. In the heart, they are the first interface between blood and cardiac tissue, allowing the diffusion of oxygen and nutrients into the heart, and carbon dioxide and waste into the circulation. Endothelial cells also function by releasing endocrine, paracrine, and autocrine factors that play essential roles in immune activation and penetration into cardiac tissue, blood vessel constriction/relaxation, and blood coagulation (Amersfoort et al., 2022; Lowe and Anderson, 2015).

1.3. Function

The heart beats at a resting rate of about 70 to 80 beats per minute in adults. During the heart's function, both atria contract at the same time, pushing blood into the ventricles. Ventricles then contract to push blood either to the **systemic** (LV) or **pulmonary circulation** (RV) (Figure 5), respectively carrying oxygenated blood to organs, including the heart itself, or deoxygenated blood to the lungs. As both circulations are running at the same time, the heart acts as a double pump. In both circulations, blood leaving the heart is always carried by the *arterial network*, which is composed of blood vessels of varying size and thickness called **arteries**, while blood returning to the heart is carried by the *venous network* made up of **veins** that are similarly variable in size, but overall thinner than arteries.

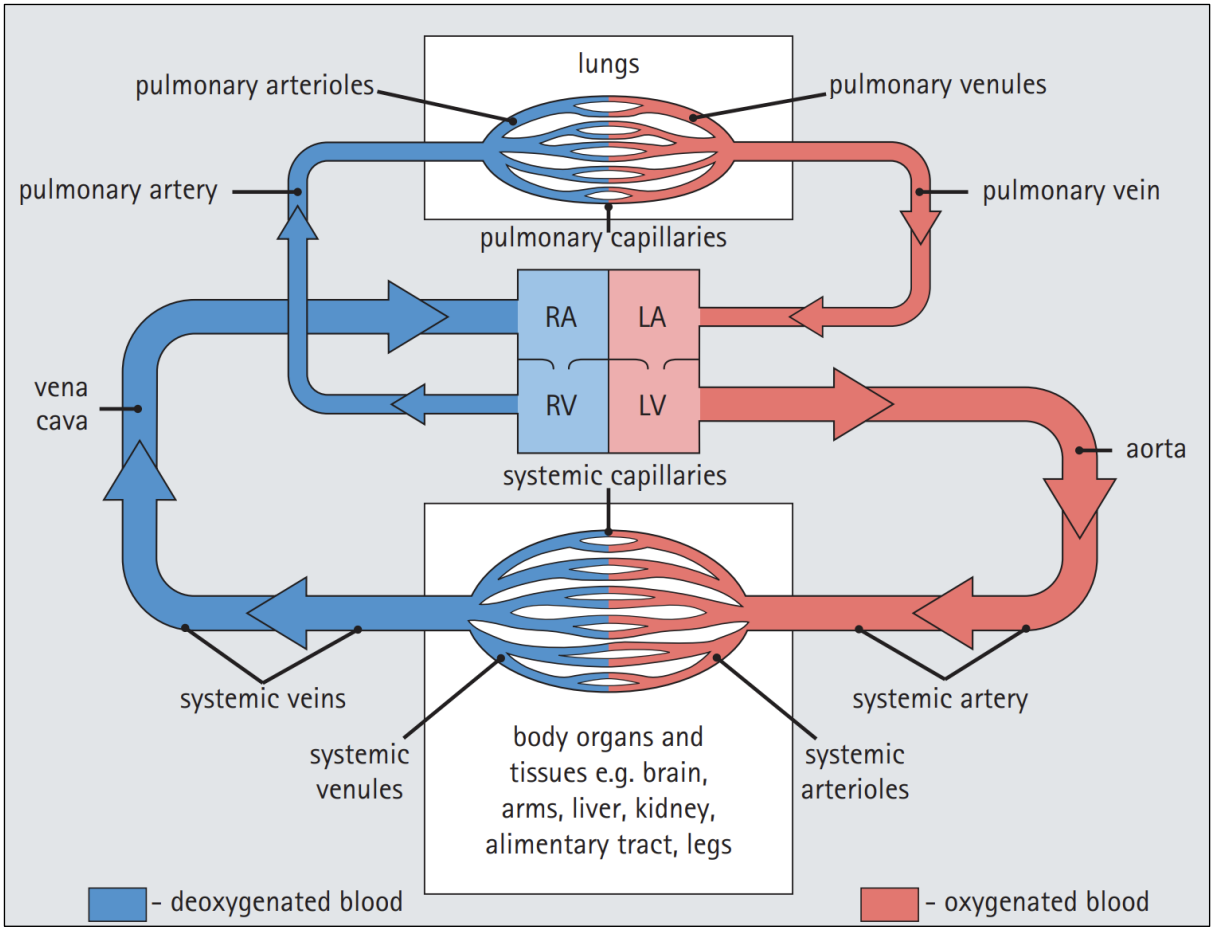


Figure 5. The systemic and pulmonary circulations. RA: right atrium. LA: left atrium. RV: right ventricle. LV: left ventricle (Lowe and Anderson, 2015, fig. 9.1).

1.3.1. Systemic circulation

Oxygenated blood passes from the LA to LV through the mitral valve. When ventricles contract, oxygenated blood exits the LV through the aortic valve to the aorta, which then branches off into smaller arteries throughout the organs. Oxygen and nutrient exchange takes place in the smallest and most permeable vessels called capillaries. After deoxygenation, blood continues into the venous circulation back towards the heart. Eventually, blood passes through superior and inferior vena cava and empties in the RA.

Coronary circulation

When ventricles relax, a portion of oxygenated blood leaving the aorta flows backwards towards the heart. However, the structure of the aortic valve prevents this backflow and closes the valve. Due to this backward pressure and the closure of the aortic valve, blood escapes into the coronary arteries which supply the heart tissue itself. These arteries similarly branch off to

provide oxygen and nutrient exchange, eventually returning through coronary veins into the RA with the rest of the body's deoxygenated blood.

1.3.2. Pulmonary circulation

Deoxygenated blood that empties into the RA is then pushed into the RV, passing through the tricuspid valve. When the ventricles contract, deoxygenated blood is pushed out through the pulmonary valve into the pulmonary trunk, which branches off into pulmonary arteries that lead to the two lungs. Blood in the pulmonary circulation passes through capillaries in the lungs to be reoxygenated and eventually returned to the heart through pulmonary veins, emptying in the LA.

1.3.3. The cardiac conduction system

Cardiac muscle contraction is a process involving the generation of an AP and its transmission across cardiac tissue (Figure 6) by specialized cardiac cells called the **cardiac conduction system**. The signal is first generated by *pacemaker cells* located in the **sinoatrial (SA) node**, at the entrance of the superior vena cava. Next, the signal spreads across the atria, inducing atrial contraction and the complete transfer of blood into the ventricles. During atrial contraction, the signal is transmitted into the **atrioventricular (AV) node**. The AV node then transmits the signal to the ventricles through conductive cells called the **bundle of His**, which branch further into ventricular tissue to become **Purkinje fibers**. The transmission of the signal through Purkinje fibers induces ventricular contraction and the ejection of blood from the ventricles to the systemic and pulmonary circulations.

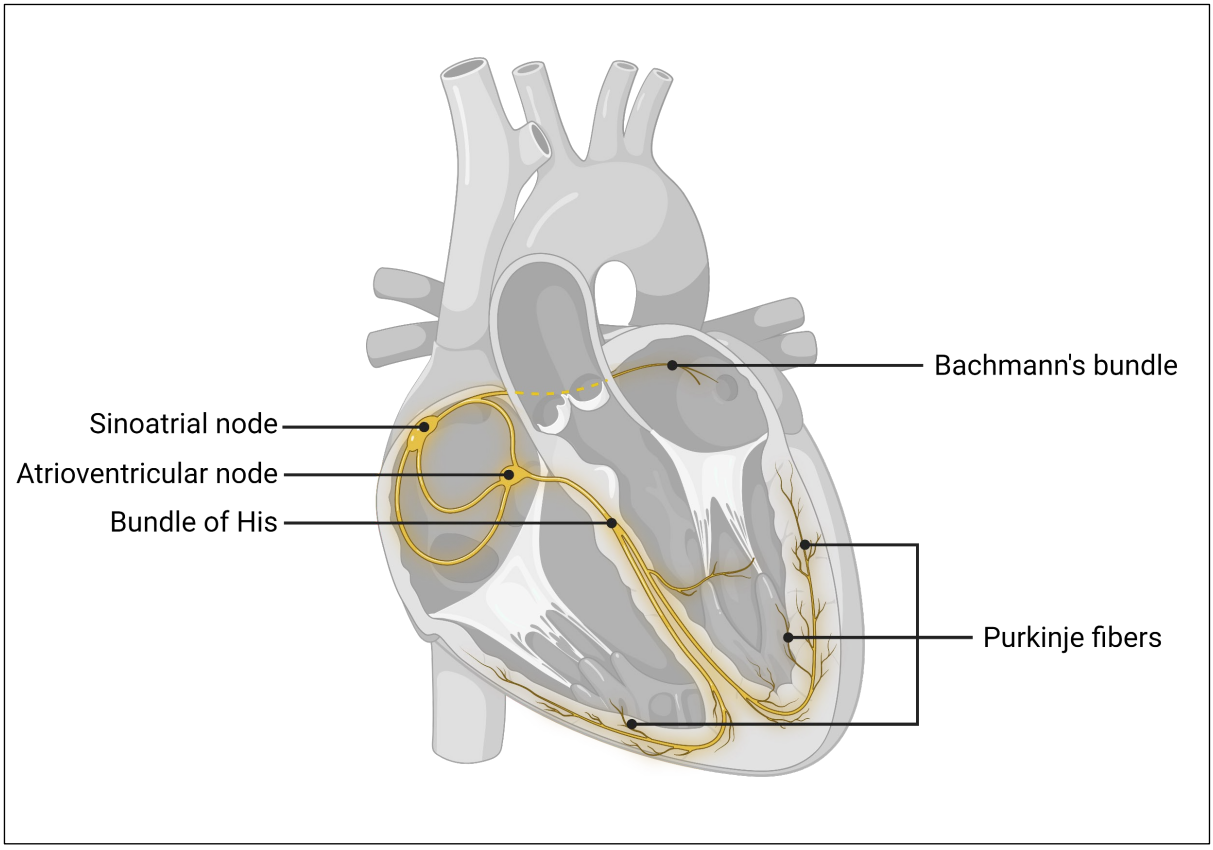


Figure 6. Schematic representation of the cardiac conduction system (created with BioRender.com).

1.3.4. Physiology of cardiomyocyte contraction

At the base of cardiac contraction are individual cardiomyocytes that must function as a unit. This is possible due to the histological structure of cardiac of tissue, where cardiomyocytes are interconnected by intercalated discs. Once a myocardial region receives the AP carried by Purkinje fibers, it is rapidly distributed among the cardiomyocytes in that region with little resistance. The AP induces a rapid influx of sodium and calcium ions into the cytosol of cardiomyocytes. This increase in intracellular calcium induces a restructuring of the sarcomere, where sarcomeric proteins actin and myosin are pushed together, shortening the cardiomyocytes (Figure 7). The period of cardiomyocyte contraction is known as **cardiac systole**. This continues until calcium levels return to normal by the action of calcium pumps, restoring the sarcomere to its original conformation and resulting in cardiomyocyte relaxation, known as **cardiac diastole**.

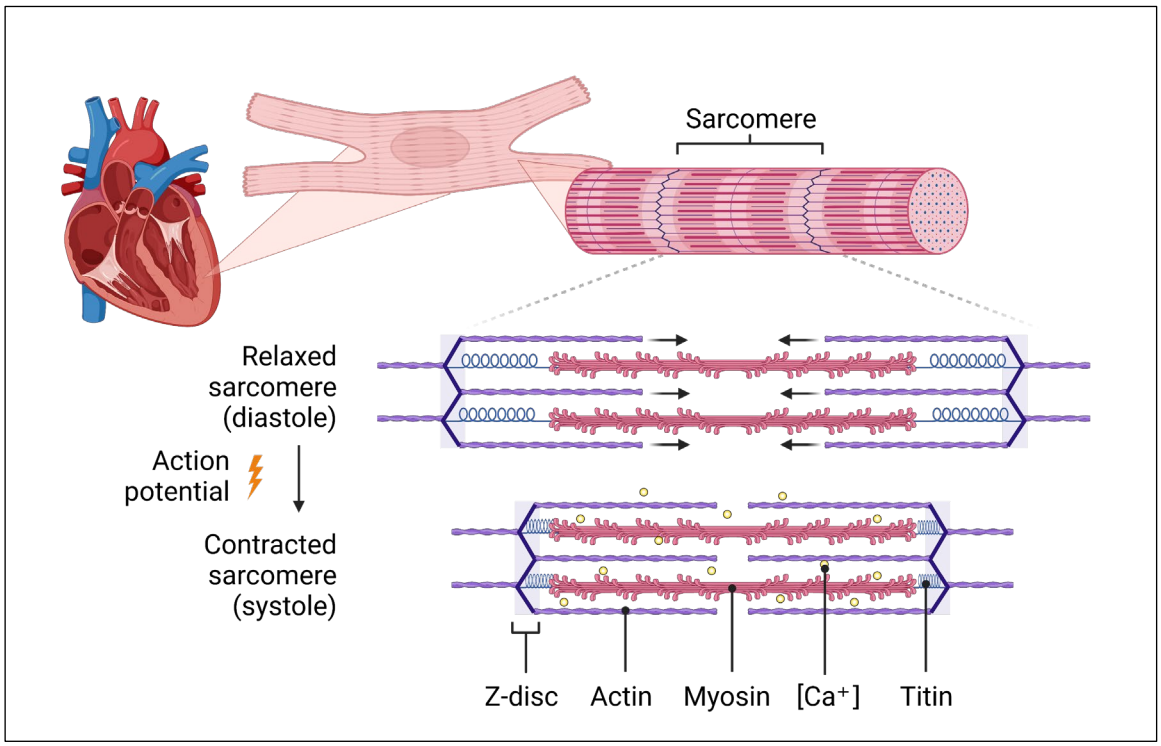


Figure 7. Change of sarcomeric conformation during cardiomyocyte contraction (created with BioRender.com).

2. Heart failure (HF)

2.1. Pathophysiology

It is estimated that heart failure (HF) has 17 primary causes which are not mutually exclusive (Ziaeian and Fonarow, 2016). Of these, ischemic heart disease, hypertension, chronic obstructive heart disease, and rheumatic heart disease account for two-thirds of all cases.

2.1.1. Ischemic heart disease

In order to ensure continuous cardiac function, the heart is irrigated by a network of blood vessels called the coronary circulation. These vessels penetrate cardiac tissue and are essential for the constant transfer of oxygen and nutrients to the heart. Ischemia is defined as an inadequate supply of oxygen to meet metabolic demands. In the heart, this can be caused by a partial or complete obstruction of a coronary artery (Figure 8). Coronary artery obstruction most commonly occurs during **atherosclerosis** due to the formation of an atherosclerotic plaque, but may also be caused by a blood clot or a constriction of the artery (Institute of Medicine (U.S.) et al., 2010; Steenbergen and Frangogiannis, 2012). Partial (<50%) obstruction

of a coronary artery does not produce symptoms. However, if left untreated, atherosclerotic plaques develop and cause significant blood flow reduction. Symptoms normally appear during high oxygen-demand states, such exercise or elevated stress. The principal symptom of ischemia is *angina pectoris*, or localized chest pain that may extend to the shoulders, arms, back, or jaw. Complete coronary artery obstruction leads to muscle death, a condition known as a *myocardial infarction* (MI).

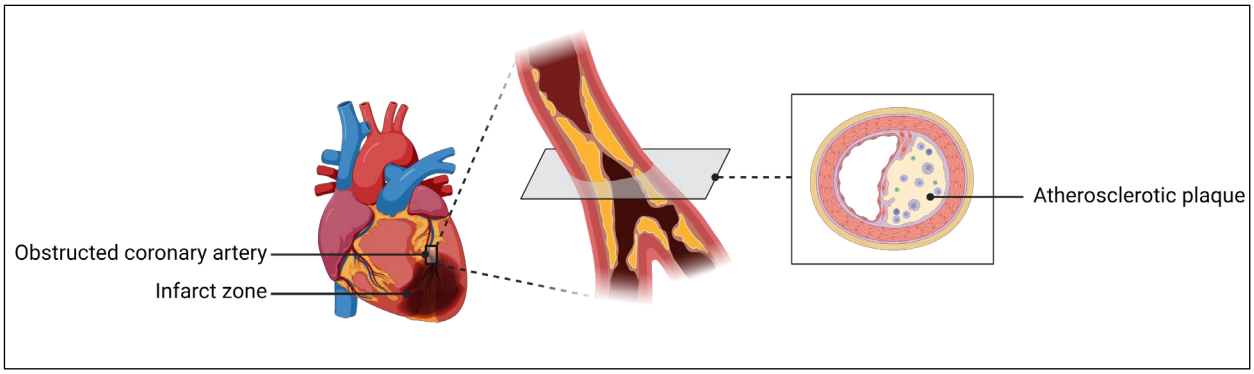


Figure 8. Anatomical properties of cardiac ischemic injury caused by atherosclerosis (created with BioRender.com).

Atherosclerosis occurs due to a combination of environmental and hereditary risk factors. Low-density lipoprotein (LDL) concentration in plasma plays a central role in the development of atherosclerosis, with increased risk being associated with hypertension, diabetes, and smoking ("Pathogenesis of Atherosclerosis," 2006). However, it should be noted that the participation of LDL in the induction of atherosclerosis is not completely proven or understood (Libby, 2021). Atherosclerosis develops over three phases: initiation, progression, and complications. In the first phase, excess LDL levels in the blood (higher than 30 mg/dL) penetrate the wall of coronary arteries due to inefficient endothelial barrier function caused by damage to the endothelium. LDL molecules then induce a cycle of inflammatory activation and *reactive oxygen species* (ROS) production. Accumulation of ROS in the sub-endothelial layer results in LDL oxidation, followed by their uptake by macrophages. When macrophages are overloaded by oxidized LDL particles, they transform into foam cells. The presence of foam cells is a hallmark sign of atherosclerotic lesions. Once established, atherosclerosis develops by the accumulation of LDL and foam cells, accompanied by a migration of VSMCs into the

subendothelial layer of coronary artery wall where the atherosclerotic lesion is developing. The resulting mix of impaired immune cells and VSMCs forms the core of the atheroma. Accumulation of calcium may also take place in atherosclerotic plaques, leading to localized calcification. The progression of atherosclerosis is summarized in Figure 9.

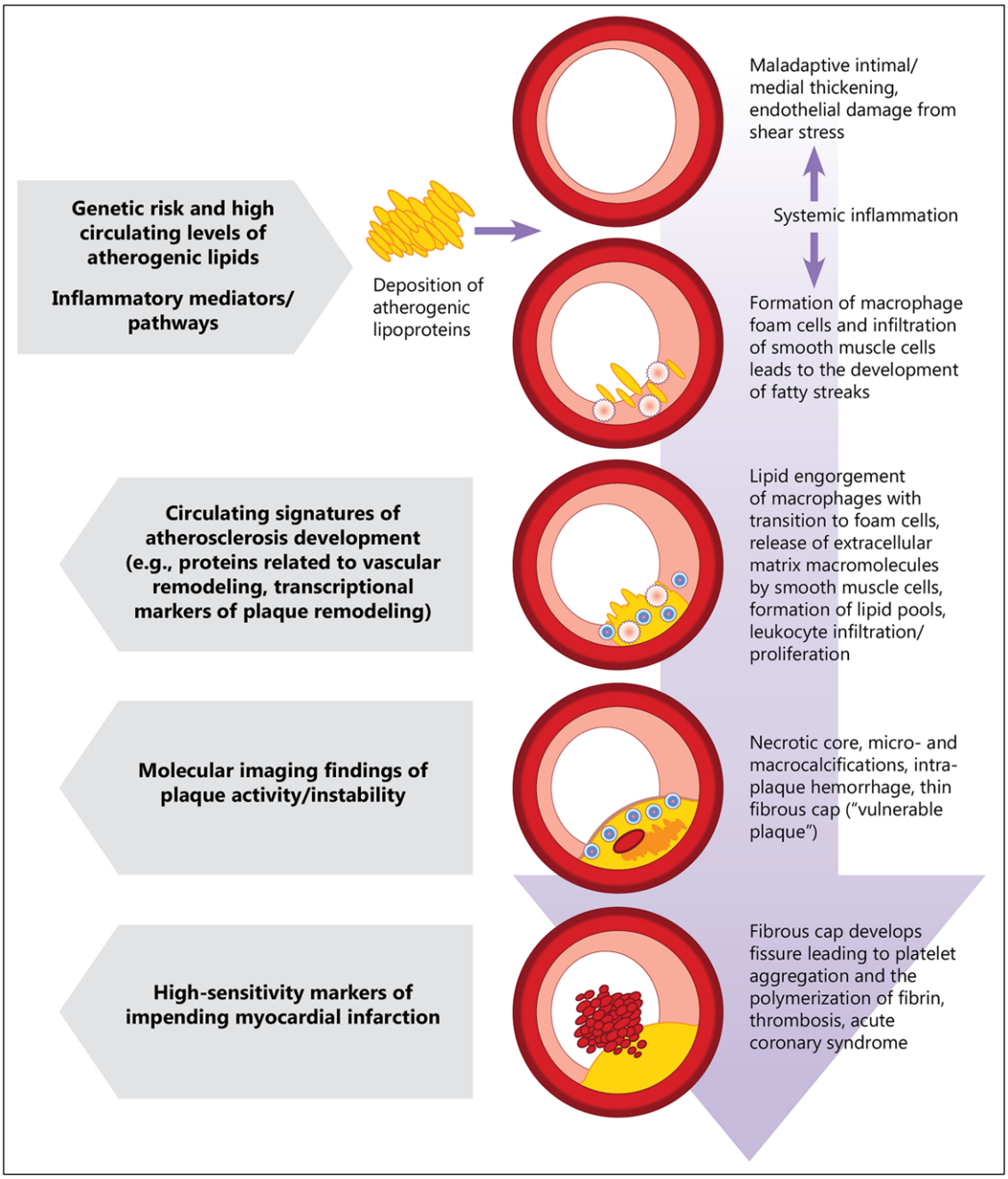


Figure 9. The progression of atherosclerosis (Nayor et al., 2021, fig. 1).

Complications of atherosclerosis occur as the atherosclerotic plaque enlarges sufficiently to restrict blood flow through the coronary artery. Enlarged plaques become

vulnerable to rupture, exposing their contents to the circulation, and inducing acute thrombosis. Ultimately, the detachment of the formed thrombus causes a complete obstruction of the coronary artery downstream, resulting in MI (Libby et al., 2019). The zone of cardiac tissue whose blood supply is cut off is called the infarct zone. Cells in the infarct zone undergo inflammation due to increased immune cell infiltration, in addition to necrosis, apoptosis, and autophagy (Prabhu and Frangogiannis, 2016).

The stress induced by MI causes resident fibroblast activation. Fibroblasts respond to the inflammatory signals and, when activated, transform into *myofibroblasts* (Figure 10). While fibroblasts in healthy tissue are quiescent, myofibroblasts exhibit novel contractile, proliferative, and secretory features that are essential for infarct wound healing. These cells migrate towards the infarct zone and produce ECM proteins (mostly collagen, fibronectin, and laminin) which replace the necrotic cells that are eliminated by infiltrating immune cells (Figure 11). Initially, fibroblast activation and ECM deposition are necessary for wound healing. The tensile strength of collagen fibers serves to compensate for lost contractility. However, maladaptive collagen deposition may take place in non-infarcted areas of the heart, stiffening ventricular tissue and causing its dysfunction (Pfeffer, M.D., Ph.D, 1995; van den Borne et al., 2010).

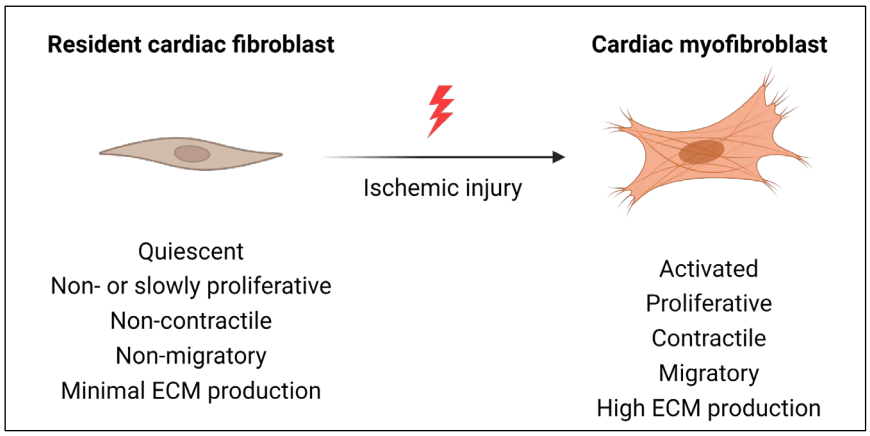


Figure 10. Fibroblast activation and transformation into myofibroblast (created with BioRender.com).

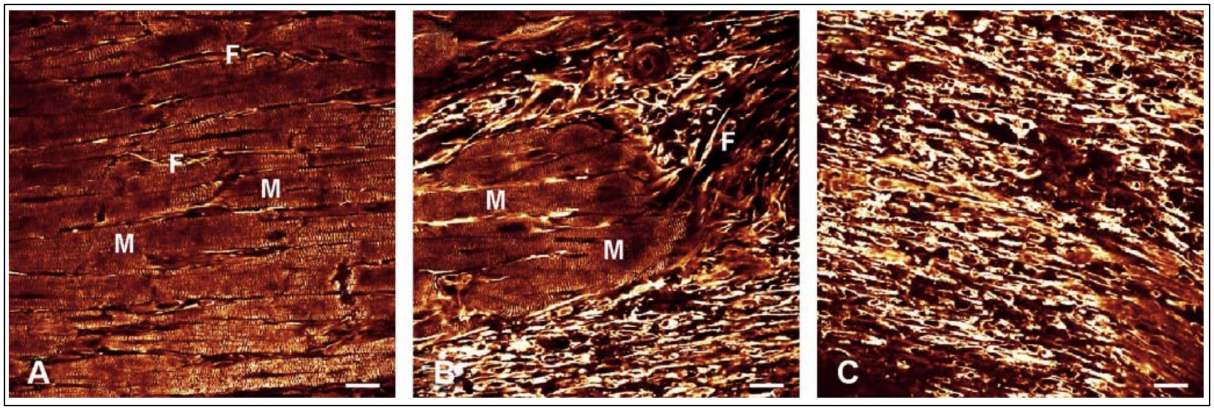


Figure 11. Ventricular tissue at the normal myocardium (A), infarct zone border (B), and infarct center (C) Fibroblasts are stained with anti-vimentin (F, bright cells), and myocytes are stained with anti-myomesin (M, striated cells). Scale bars = 20 μm (Camelliti et al., 2005, fig. 4).

The cascade of events following MI lead to structural and functional changes in the heart. This is known as **cardiac remodeling.** Most commonly, the heart undergoes *left ventricular remodeling* (LVR), as the left ventricle is most impacted by ischemic injury (Turkoglu et al., 2008) (Figure 12). The progression of LVR is dependent on multiple factors, such the size and location of the infarct zone, the depth of its penetration into cardiac tissue, and the duration of ischemia. Initially, infarct expansion takes place in the first hours to days following MI. This is characterized by a thinning of the infarcted zone due to the loss of cardiomyocytes and their dispersion, and to the mechanical force applied to the ventricular wall during ventricular filling and contraction. Cardiomyocyte loss also results in loss of contractile function, leading to a reduction in the efficiency of heart contraction as measured by the *ejection fraction* (EF), or the fraction of blood ejected from the ventricles out of the total volume before contraction (Pfeffer, M.D., Ph.D, 1995). In order to compensate for the reduced EF, the non-infarcted myocardium undergoes dilatation coupled with compensatory cardiomyocyte hypertrophy, allowing more blood to enter the ventricles. Increased blood volume stretches the ventricular wall, and the resulting tension force created by this stretch will push more blood out of the heart (*Frank-Starling Law*). Therefore, dilatation allows for increased *stroke volume* (SV) in an attempt to recover cardiac function and eject sufficient blood to the organs. However, increased ventricular dilatation causes increased wall stress, which induces further enlargement of the ventricle creating a cycle that aggravates ventricular dysfunction over time (Pfeffer, M.D., Ph.D, 1995). Eventually, when ventricular dilatation reaches a point where it no longer

compensates for the lost cardiac function, HF presents as a progressive reduction in EF (HF with reduced EF; HFrEF), and an increase the volume of blood remaining in the ventricle after contraction (*end systolic volume*) (Cohn et al., 2000).

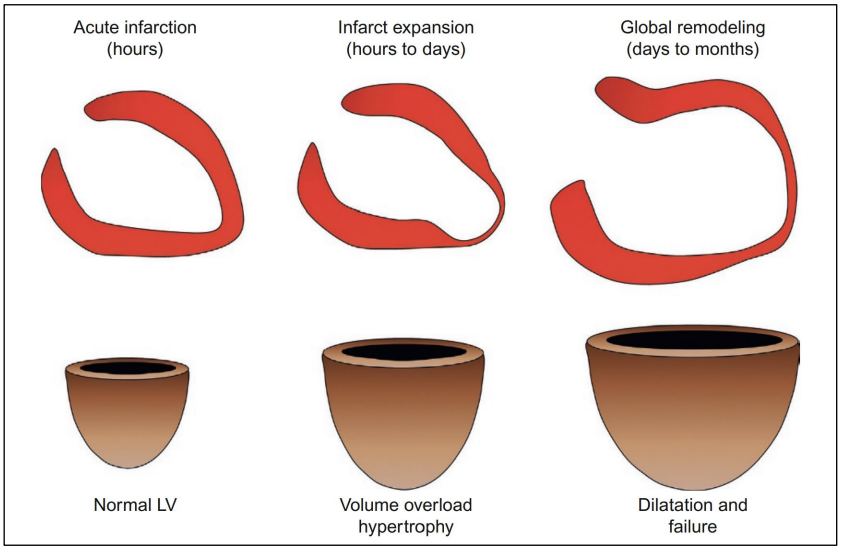


Figure 12. Stages of left ventricular remodeling (LVR) following myocardial infarction (MI) (Flotats et al., 2015, fig. 10.3).

2.1.2. Hypertensive heart disease

Hypertension is characterized by increased blood pressure (BP) against vessel walls during ventricular (systolic blood pressure; SBP) and/or atrial contraction (diastolic blood pressure; DBP). Although BP fluctuates throughout the day due to various stimuli, it is considered hypertension when the average BP is increased for a long duration. Hypertension is considered a major risk factor of HF, accounting in men for 39% of HF cases, and in women for 59% of cases (Messerli et al., 2017). The European Society of Cardiology (ESC) defines hypertension as SBP exceeding 140 mmHg and/or DBP exceeding 90 mmHg, and the gravity of hypertension can be categorized into 3 levels (Table 1) (Williams et al., 2018).

Table 1. Grades of hypertension and their corresponding blood pressure measurements.

Category	**Systolic (mmHg)**		**Diastolic (mmHg)**
Optimal	<120	and	<80
Normal	120–129	and/or	80–84
High normal	130–139	and/or	85–89
Grade 1 hypertension	140–159	and/or	90–99
Grade 2 hypertension	160–179	and/or	100–109
Grade 3 hypertension	≥180	and/or	≥110
Isolated systolic hypertension	≥140	and	<90

Hypertension is a complex condition caused by a combination of genetics and environment. Although it tends to cluster in families with inherited biochemical abnormalities, the severity and onset of hypertension is influenced by many factors, including psychological and nutritional imbalances, secondary medical conditions (e.g. diabetes), and increased sympathetic nervous system activity (Oparil et al., 2003). Under normal conditions, blood pressure regulation occurs in relationship to the volume of blood ejected by the heart every minute, known as *cardiac output* (CO), and the resistance imposed by the blood vessels in the body, known as the *systemic vascular resistance* (SVR). At least 8 control systems regulate BP in the body, acting through different mechanisms and duration of activation (Guyton, 1991).

Resistance occurs as blood vessels constrict and relax due to the force of the vascular smooth muscle cell population in the vessel walls. This is essential for controlling blood flow to specific organs according to their requirements. The constriction/relaxation of blood vessels is controlled by hormones collectively known as *vasoactive substances.* A key role in the release and regulation of vasoactive substances is played by *sympathetic nervous system* (SNS) activation. Necessary for maintaining normal blood pressure, the SNS may be pathologically overactive, one of the main signs of hypertension (Esler and Kaye, 2000). Increased SNS activation results in increased blood pressure through the release of *vasoconstrictive* hormones,

such as *norepinephrine,* which increase SVR and consequently raise BP.

The transition from sustained hypertension to HF occurs as the increased vascular resistance induces cardiac hypertrophy. The increased work load imposed by this resistance forces the heart muscle to adapt and increase in size. Hypertrophy may be *concentric* (cardiomyocytes increase in width, growing towards the inside of the heart), or *eccentric* (cardiomyocytes increase in length, growing adjacently and expanding the heart chamber) (Figure 13). Hypertension primarily results in concentric hypertrophy (Bornstein et al., 2022).

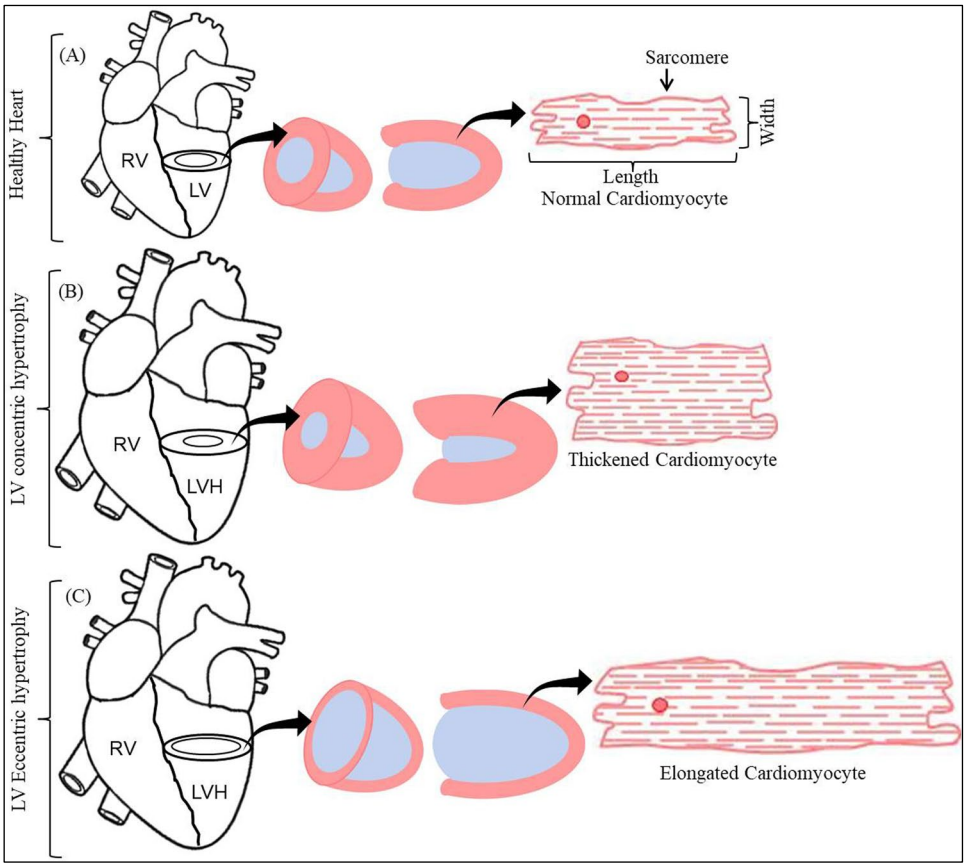


Figure 13. Schematic representation of ventricular hypertrophy and its effect on heart chamber size with the corresponding cardiomyocyte morphology. RV: right ventricle. LV: left ventricle. LVH: left-ventricular hypertrophy (Singh et al., 2021, fig. 2).

The main outcome of concentric hypertrophy is a significant reduction of LV chamber size. This reduction, in addition to the stiffness imposed by the thickened myocardial layer, prevents the ventricle from properly filling with blood during diastole. This is known as *diastolic dysfunction*. As less blood enters the left ventricle, less blood is ejected from the heart to the organs. In this situation, as opposed to HF induced by ischemic injury, the EF is preserved (HF

with preserved EF; HFpEF), while stroke volume is reduced. Patients with HFpEF may be asymptomatic at rest, with signs appearing during physical or psychological effort. The hypertrophied ventricular tissue additionally has an increased oxygen demand, which increases the risk for ischemic injury as described earlier, despite the absence of an atherosclerotic plaque (Janardhanan et al., 2009).

2.2. Treatment options

One of the primary causes of hospitalization due to HF, regardless of EF, is congestion (Rossignol et al., 2019). Congestion is defined as the accumulation of excess fluid in the vasculature and the interstitial compartments (Boorsma et al., 2020). Treatment of congestion most commonly relies on the use of diuretics, which are drugs that promote the release of fluid from the body by the kidneys through urine.

Patients with HFrEF may be given inhibitors of the renin-angiotensin-aldosterone system (RAAS), such as angiotensin-converting enzyme inhibitors (ACE-I) or angiotensin receptor-neprilysin inhibitor (ARNI) and mineralocorticoid receptor antagonists (MRA). Additionally, inhibitors of SNS such as beta-blockers are administered. A combination of these treatments is often recommended for optimal results (McDonagh et al., 2021).

In patients with HFpEF, treatment options are more limited. Although decongestion treatments remain helpful, there is small evidence to support the use of RAAS-targeting medications for HFpEF, but their use remains recommended (McDonagh et al., 2021; Rossignol et al., 2019). Ideally, treatment should start before HF development in people with above-normal BP in order to reduce their risk of major cardiac remodeling and LV dysfunction.

2.3. Acute decompensated heart failure (ADHF)

Patients with HF remain at risk for rehospitalization if their symptoms return and overpower their compensatory processes. The majority of patients admitted to hospitals for acute HF experience a worsening of pre-existing HF (Joseph et al., 2009). ADHF is characterized by the re-appearance of signs of congestion such as dyspnea, edema, exercise intolerance, and fatigue, necessitating emergency medical attention (Njoroge and Teerlink, 2021). ADHF is

caused primarily by a re-occurrence of a cardiac incident (ischemic injury, arrhythmia), hypertension, non-adherence to diet or medication, and worsening renal function (Fonarow, 2008), although an estimated up to 40% of hospitalization may have no known cause (Opasich et al., 2001). ADHF remains a significant cause of mortality worldwide. A US cohort revealed that patients admitted for ADHF have a 30-day mortality of 11% and a 1-year mortality of 28% in men, while in women it is 10% and 24%, respectively (Levy et al., 2002). Therapy is mainly by the administration of diuretics, vasodilators, and calcitropes (molecules that increase cardiac contraction force while modulating intracellular calcium concentrations) (Njoroge and Teerlink, 2021).

2.4. Post-translational modifications (PTMs) during HF

PTM changes have been reported during cardiovascular diseases. Notably, O-linked-N-acetylglucosaminylation (O-GlcNAcylation) signaling was shown to be increased during hypertrophy and HF (Facundo et al., 2012; Gélinas et al., 2018; Lunde et al., 2012). This PTM is fueled by the *hexosamine biosynthetic pathway* (HBP) (Figure 14). It involves the reversible addition of O-linked N-acetylglucosamine (O-GlcNAc) to a *serine* or *threonine* residue on the target protein. The addition of O-GlcNAc is mediated by *O-GlcNAc transferase* (OGT), while its removal is mediated by *O-GlcNAcylase* (OGA). In the case of ischemia-reperfusion injury, increased protein O-GlcNAcylation through the administration of glucosamine or OGA inhibitor O-(2-acetamido-2-deoxy-D-glucopyr-anosylidene)amino-N-phenylcarbamate (PUGNAc) significantly improved cardiac functional recovery after 20 minutes of ischemia (Liu et al., 2007). As O-GlcNAcylation and phosphorylation share amino acid targets (serine and threonine), there is complex interplay between the two PTMs (Hart et al., 2011). Indeed, cardiac sarcomeric proteins such as *troponin T* and *desmin* display modifications in these PTMs during ischemic HF (Dubois-Deruy et al., 2015; Mercier et al., 2018).

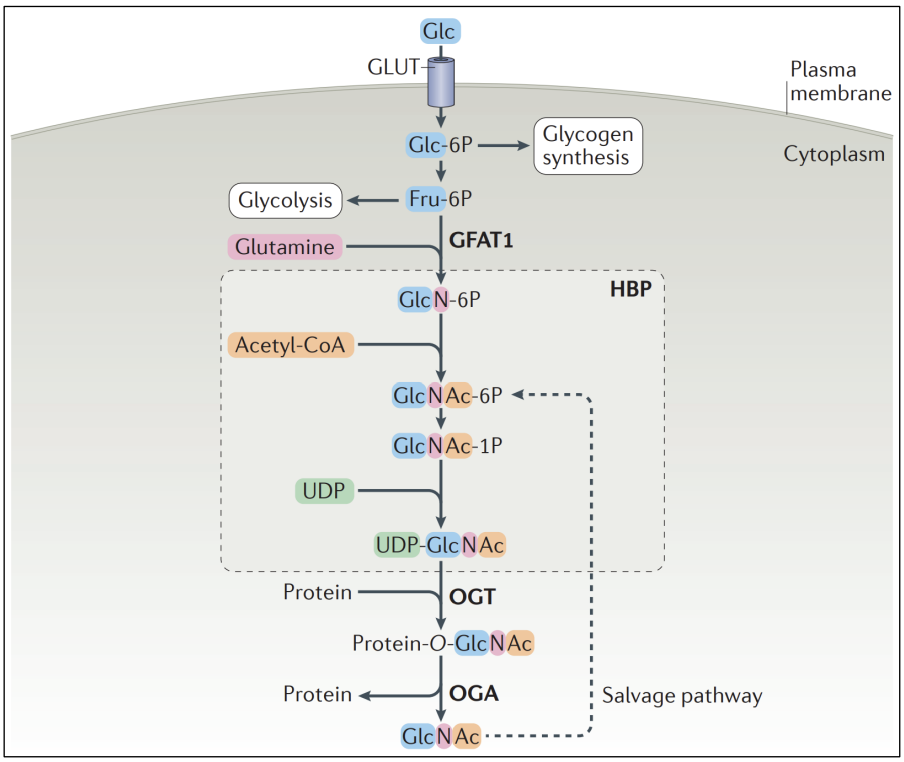


Figure 14. O-GlcNAcylation pathway. Glc: glucose. GLUT: glucose transporter. Fru-6P: fructose-6-phosphate. GFAT1: Glutamine–fructose-6-phosphate amidotransferase 1. GlcN: glucosamine-6-phosphate. GlcNAc-6P: N-acetylglucosamine-6-phosphate. UDP: uridine diphosphate. O-GlcNAc: O-linked N-acetylglucosamine. OGT: O-GlcNAc transferase. OGA: O-GlcNAcylase (Yang and Qian, 2017, fig. 1).

II. EXTRACELLULAR VESICLES (EVS)

1. Definition

Extracellular vesicles (EVs) are lipid bilayer-bound particles containing cytosolic material and secreted by both eukaryotic and prokaryotic cells (Yáñez-Mó et al., 2015). Biologically active EVs were first described in 1967 as "platelet dust" which are released by—and are distinct from—intact platelets (Wolf, 1967). More studies later on showed membrane vesicles present in connective tissue, such as cartilage (Anderson, 1969) and biological fluids, including blood (COLE et al., 1978; Schrier et al., 1971) and semen (Stegmayr et al., 1982).

2. Types and biogenesis

2.1. Exosomes

Exosomes are relatively small EVs (⌀ 50-150 nm) produced by intracellular endosomal trafficking (Figure 15). Exosome biogenesis begins when cells internalize molecules and membrane receptors through various endocytic pathways, which are primarily divided into *clathrin-dependent* and *clathrin-independent*. These molecules are then sorted through the endosomal pathway by early endosomes (Grant and Donaldson, 2009). Endosomal trafficking is mediated by cytoplasmic proteins, notably members of the Rab family of GTPases (Gorvel et al., 1991). Rab5 associates with early endosomes as they are transported within the cell. Early endosome maturation into late endosomes involves a "Rab switch", where Rab5 is replaced by Rab7 (Poteryaev et al., 2010). Endosome trafficking takes place via the cytoskeletal network of microtubules and is driven by dynein and kinesins -1 and -2. Early endosomes start near the plasma membrane, and may either get recycled back towards the membrane, or move progressively closer to the nucleus as they develop. Late endosomes are generally found in perinuclear area (Loubéry et al., 2008; Villari et al., 2020). During their maturation, endosomes take up proteins through the formation of *intraluminal vesicles* (ILV), which is facilitated by *endosomal sorting complex required for transport* (ESCRT) proteins (Figure 16) (Henne et al., 2011). Late endosomes containing ILVs, also known as *multivesicular bodies* (MVB) or

multivesicular endosomes, are then directed to either fuse with a lysosome and degrade their cargo, or to fuse with the cellular plasma membrane, thereby releasing the ILVs into the extracellular medium as exosomes (Raposo et al., 1996). It was also shown that late endosomes may fuse with *autophagosomes*, which are the main organelles involved in autophagy, producing *amphisomes* destined for either release or lysosomal degradation (Liang et al., 2008). It is unclear what determines late endosome/MVB fate (lysosomal degradation vs. plasma membrane fusion), but evidence suggests that PTMs of MVB-membrane proteins may play a role. For example, the conjugation of interferon-stimulating gene 15 (ISG15) to *tumor susceptibility gene 101* (TSG101), known as ISGylation, induces TSG101 aggregation and degradation, thereby inhibiting exosome release (Villarroya-Beltri et al., 2016). Similarly, TSG101 ubiquitination facilitates the fusion of MVBs to lysosomes (Majumder and Chakrabarti, 2015).

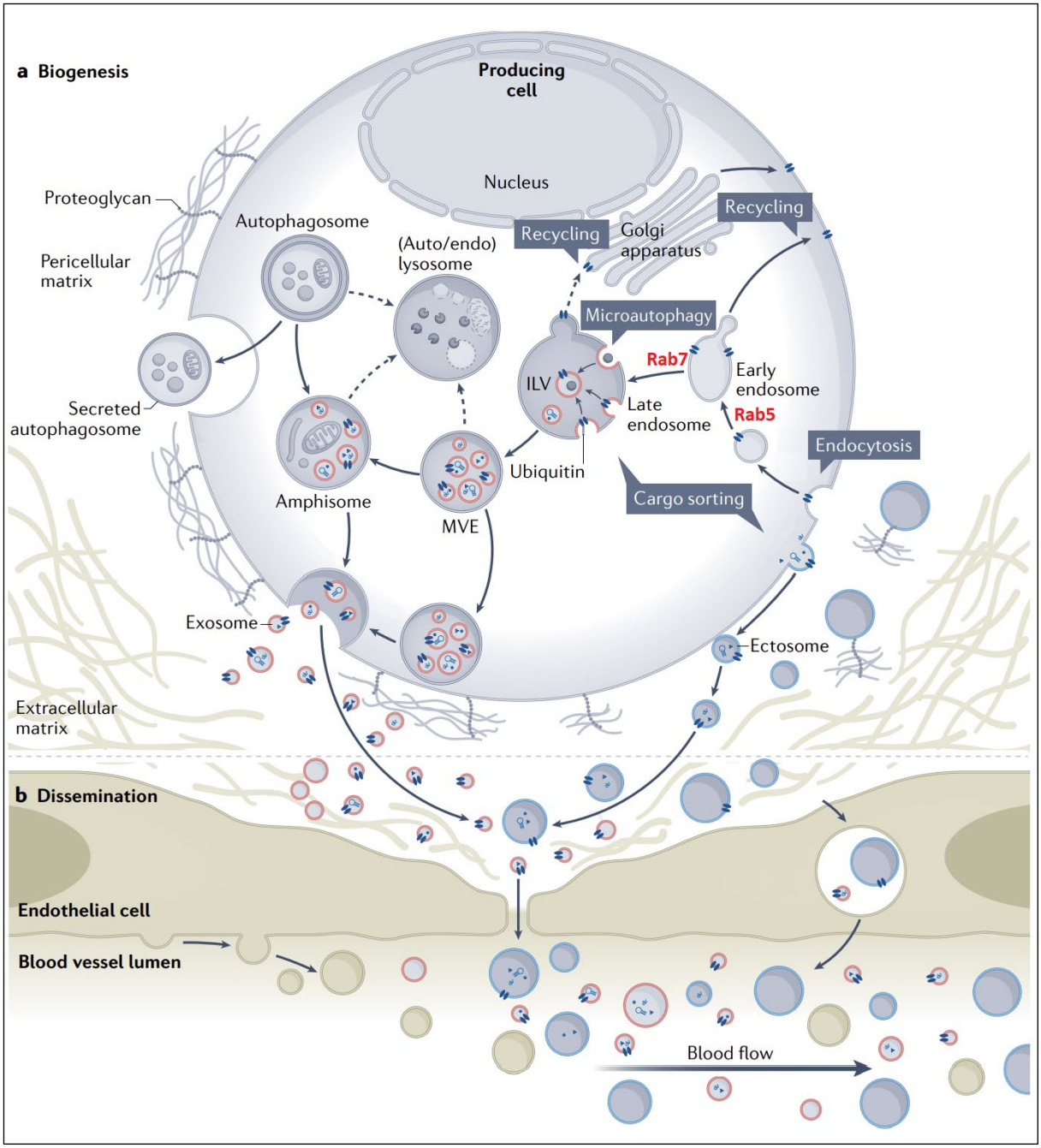


Figure 15. The endosomal pathway showing the steps of exosome biogenesis, secretion, and distribution. ILV: intraluminal vesicle. MVE: multivesicular endosome (van Niel et al., 2022, fig. 1).

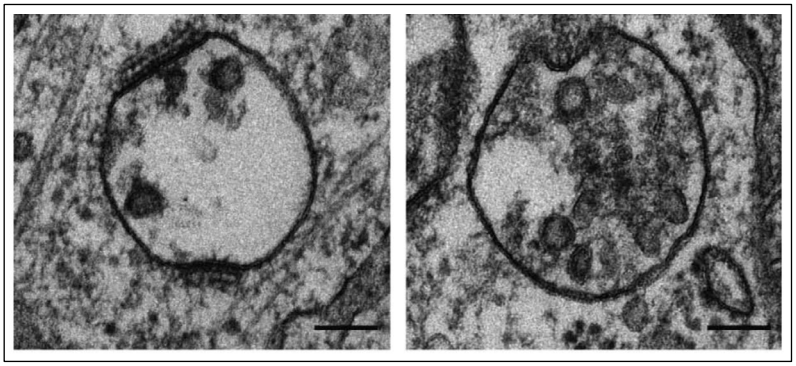


Figure 16. Early (left panel) and late endosome (right panel) showing the presence of intraluminal vesicles. Scale bars = 100 nm (Huotari and Helenius, 2011, fig. 3).

It was also shown that ILVs form through ESCRT-independent mechanisms, with processes involving localized sphingolipid ceramide and lysobisphosphatidic acid (LBPA) organization at the endosomal membrane, tetraspanins such as *cluster of differentiation 63* (CD63), the syndecan-syntenin-Alix pathway, LAMP2A, Tsg101, and Hsc70 (Babst, 2011; Babst et al., 2000; Baietti et al., 2012; Ferreira et al., n.d.; Ghossoub et al., 2014; Sahu et al., 2011; van Niel et al., 2011) (Figure 17).

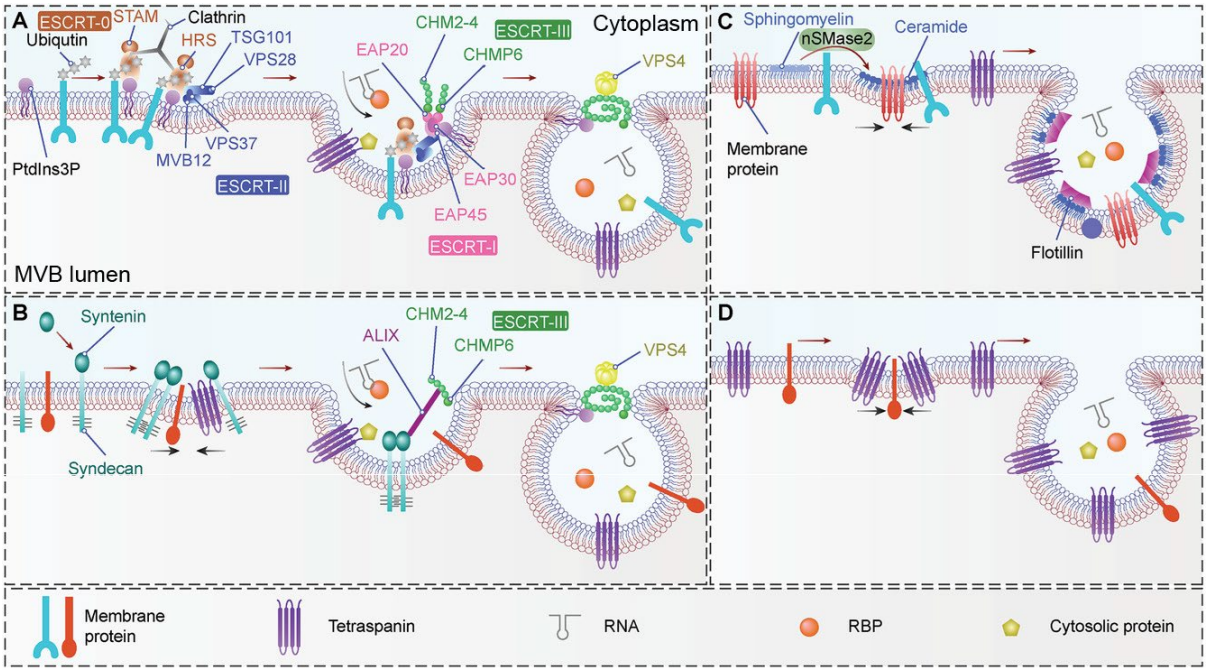


Figure 17. Protein and RNA sorting during ILV formation via four prominent mechanisms. The canonical ESCRT-dependent pathway (A), the sydencan-syntenin-ALIX pathway (B), the ceramide-dependent pathway (C), and the tetraspanin (CD63, CD9, CD81)-dependent pathway (D). MVB: multivesicular body. ILV: intraluminal vesicle. ESCRT: endosome sorting complex required for transport. PdtIns3P: phosphatidylinositol 3-phosphate. STAM: signal transducing adaptor molecule. HRS: hepatocyte growth factor-regulated tyrosine kinase substrate. TSG101: tumor susceptibility gene 101 protein. VPS: vacuolar protein sorting. MVB12: multivesicular body subunit 12. CHMP: charged multivesicular body protein. HD-PTP: His domain protein tyrosine phosphatase. ALIX: ALG-2

interacting protein X. nSMase2: neutral sphingomyelinase 2 (Teng and Fussenegger, 2021, fig. 2).

In addition to proteins, ILVs can carry nucleic acids. Thus far, the majority of work on exosomal nucleic acid content describes RNA sorting, specifically of microRNAs (miRNA) and mRNAs (Valadi et al., 2007). RNA sorting into ILVs is a complex process that may involve more than one pathway. miRNA loading into exosomes does not depend on the ESCRT proteins (Kosaka et al., 2010). *RNA-induced silencing (RISC) complex* proteins Argonaut 2 (AGO2) and GW182 colocalized to MVBs have been shown to be implicated in miRNA sorting into ILVs (Gibbings et al., 2009). The DNA- and RNA-binding protein Y-box binding protein (YBX-1) forms condensates that bind miRNA and sort them selectively into exosomes (Liu et al., 2021). Other proteins involved in exosomal miRNA sorting include heterogeneous nuclear ribonucleoprotein A2B1 (hnRNPA2B1), major vault protein (MVP), and synaptotagmin-binding cytoplasmic RNA-interacting protein (SYNCRIP) (Santangelo et al., 2016; Teng et al., 2017; Villarroya-Beltri et al., 2013).

MVB fusion with the plasma membrane and exosome secretion has been shown to involve other members of the Rab family, namely Rab27a and Rab27b (Ostrowski et al., 2010, p. 27). These proteins are necessary for MVB docking to the plasma membrane, and their inhibition caused significant increase in MVB size and their redirection towards the nucleus. Other Rab proteins have been indirectly associated with exosome secretion, like Rab11 and Rab35 (Sato et al., 2008). Once at the plasma membrane, fusion takes place via a *Soluble N-ethylmaleimide-Sensitive Factor Attachment Proteins Receptor (SNARE)*-dependent mechanism. Two types of SNAREs interact to generate the fusion event: v-SNAREs, located on the MVB membrane, and t-SNAREs, located on the plasma membrane (Zylbersztejn and Galli, 2011). The interaction of v-SNAREs (such as VAMP7 (Fader et al., 2009, p. 7)) and t-SNAREs and the formation of a SNARE complex drives the fusion process.

2.2. Microvesicles

Microvesicles (MV) are a subpopulation of EVs that form by a budding of a section of the plasma membrane and its detachment from the cell (Figure 18). These vesicles are

collectively called *ectosomes*, and include MVs, apoptotic bodies, oncosomes, and others (Cocucci and Meldolesi, 2015). MV size ranges from 100–1000 nm. MV secretion was shown to rely on external conditions, and was thought to be implicated in metastatic invasion and tumor progression (Muralidharan-Chari et al., 2010). Wang *et al.* (Wang et al., 2014) showed that oxygen deprivation increased MV shedding in a Rab22a-dependent manner in breast cancer cells. Changes in cell tumorigenicity were also associated with increased MV production (Lima et al., 2011). Exposure of tumor cells to the carcinogenic phorbol 12-myristate 13-acetate (PMA) induced the release of the metastatic transmembrane glycoprotein CD147 via MV shedding (Sidhu et al., 2004). Similarly, platelet activation by α-thrombin stimulation induced the release of both CD63-enriched exosomes and membrane protein-enriched MVs (integrins αIIb-β3 and -β1, glycoprotein Ibα, and P-selectin) (Heijnen et al., 1999).

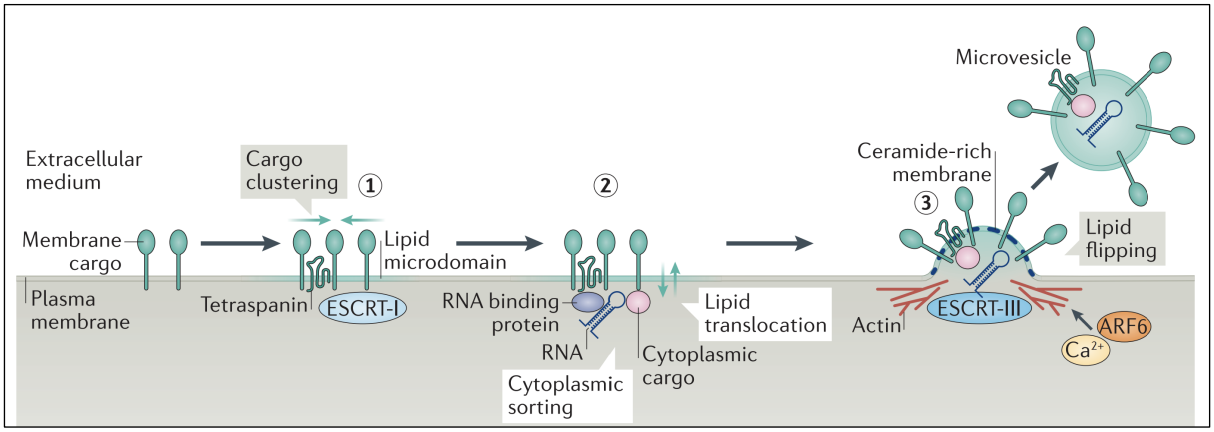


Figure 18. Formation of microvesicles (MVs) involving the interaction of plasma membrane components and cytosolic proteins (van Niel et al., 2018, fig. 2).

Although less studied than exosomes, cargo loading into MVs is believed to involve integrin-β1 and major histocompatibility complex (MHC) class I molecules (Muralidharan-Chari et al., 2009). ADP-ribosylation factor 6 (ARF6) was shown to play an important role in MV formation and in miRNA loading by interacting with miRNA processing protein Ran-GTP (Clancy et al., 2019; Muralidharan-Chari et al., 2009, p. 6). Interestingly, MV cargo included miRNA processing proteins Exportin-5, Dicer, and AGO2 (Clancy et al., 2019). Another member of the ARF family, ARF1, was shown to regulate Ras homologous (Rho) proteins A and B, which activate Rho-kinases (ROCK) that phosphorylate myosin light chain (MLC). MLC phosphorylation leads to actomyosin interactions at the neck of MVs which are necessary for

their detachment from the cell membrane (Schlienger et al., 2014).

A subset of MVs is released by the recruitment of TSG101 to the plasma membrane, followed by its interaction with membrane protein *arrestin domain-containing protein 1* (ARRDC1) to produce what is known as ARRDC1-mediated microvesicles (ARMMs). ARMMs play a role in intercellular NOTCH signaling (Nabhan et al., 2012; Wang and Lu, 2017).

2.3. Apoptotic bodies

Apoptosis is a process of cell death that is orchestrated by the dying cell itself. Unlike necrotic cell death, apoptosis is a controlled process that takes place when cells undergo irreparable damage. Most commonly, apoptosis is driven by a group of serine proteases called *caspases* (Hengartner, 2000; Xu et al., 2019). A morphological hallmark of apoptosis is the occurrence of membrane blebs, which are plasma membrane deformations formed by a similar process as MVs. Apoptotic blebs are formed as dying cells fragment, facilitating their engulfment by phagocytes. Cell contents, such as endoplasmic reticulum (ER) fragments and nuclear content were found to be translocated into membrane blebs in late apoptotic cells (Cocca et al., 2002; Lane et al., 2005). These blebs eventually detach from the plasma membrane of apoptotic cells as large EVs called *apoptotic bodies* (⌀ 1–5 μm). The mechanism of bleb formation and release involves a cleavage of ROCK1 by caspase-3 in a Rho-independent manner, leading to the constitutive activation of ROCK1 and increased MLC phosphorylation (Figure 19) (Coleman et al., 2001; Shi and Wei, 2007; Tixeira et al., 2020, p. 1).

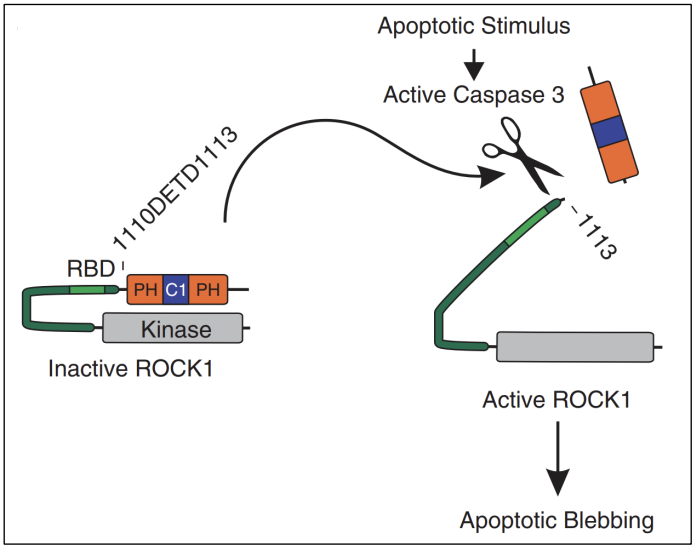


Figure 19. ROCK1 cleavage during apoptosis. This process is independent from the canonical Rho-mediated activation of ROCK1.

2.4. Novel extracellular vesicles

A newly discovered type of EVs are *exophers*, which are large (⌀ 3.5–4 μm) vesicles released by membrane budding and are possibly involved in autophagy, where cells release large organelles in response to cellular stresses (not due to apoptosis or tumor spreading). Exophers were first discovered in muscle and neuronal cells in *Caenorhabditis elegans* (Melentijevic et al., 2017; Turek et al., 2021), then were well elaborated in murine cardiomyocyte models by Nicolás-Ávila *et al.* in two articles describing the role of exophers as an autophagic mechanism for adult cardiomyocytes to dispose of defective mitochondria in association with cardiac resident macrophages, as well as a detailed method for isolating these exophers for downstream analysis (Nicolás-Ávila et al., 2020, 2021).

Robert Coffey's lab has additionally elaborated two subpopulations of small particles (non-membrane bound), *exomeres* and *supermeres* (supernatant of exomeres), which are particles normally left over in the supernatant of exosomal isolations. Although the nature of these particles is not completely understood, they were shown to contain distinct proteomic and miRNA profiles (Zhang et al., 2021a, 2021b, 2019).

3. Isolation

Many EV isolation techniques have been developed since their introduction as

biologically active components, with detailed descriptions for sample handling, storage, isolation, and downstream analysis. Various reviews have been published, with great contributions culminating in standardized guidelines, primarily the *Minimal information for studies of extracellular vesicles 2018* (MISEV2018) by Théry & Witwer *et al*, published in the *Journal of Extracellular Vesicles* (Théry et al., 2018; Van Deun et al., 2014; Witwer et al., 2013).

EV isolation typically involves classic methods, most commonly differential centrifugation, followed by density gradient, ultrafiltration, size exclusion, polymeric precipitation, and immunoaffinity. Many studies combine more than one technique to ameliorate their EV purity (Gardiner et al., 2016; Witwer et al., 2013).

Differential ultracentrifugation (dUC): This technique relies on the different sedimentation forces of particles in a solution. In the example of EVs, different particles in the sample solution will pellet according to Stokes' law:

$$v = \frac{d^2(\mathrm{p} - \mathrm{L}) \times g}{18n}$$

v: sedimentation rate

d^2*:* diameter of the particle

p: particle density

L: density of the solution

g: centrifugal force

n: viscosity of the solution

Based on this law, larger, more dense particles pellet faster than small, less dense particles. When a centrifugal force (*g*) is applied to a solution containing a mixture of cellular debris and EVs, the debris pellets before large EVs (lEVs), and lEVs pellet before small EVs (sEVs). Consequently, with dUC a series of centrifugations are performed at gradually increasing speeds to pellet different constituents of the original sample. Regardless of sample origin, dUC typically involves a low-speed centrifugation to pellet large debris and apoptotic

bodies. The supernatant is recuperated and centrifuged once again at medium speed to pellet lEVs, whose supernatant is again centrifuged at high speed to pellet sEVs.

Density gradient ultracentrifugation (DGUC): A modified version of dUC, where non-purified EV samples (after elimination of debris and lEVs) of usually 2–3 mL are layered on top of (or sometimes below) fractions of increasing concentration of sucrose or iodixanol. This technique also utilizes Stokes' law, where instead of pelleting EVs to the bottom of the centrifugation tube, centrifugal force pushes EVs into a fraction of the density gradient where they reach an equilibrium. Small EVs tend to float at densities between 1.05–1.15 g/ml, and fractions obtained from this technique are usually taken individually, diluted, and ultracentrifuged normally to pellet their EV content (Jeppesen et al., 2019).

Cushioned ultracentrifugation (cUC): Similar to dUC, cUC involves placing a fraction, usually 1–3 mL, of sucrose or iodixanol at the bottom of the centrifugation tube, then placing the sample on top of the fraction. During ultracentrifugation, the EVs enter the cushion fraction, which would finally be taken and diluted to be ultracentrifuged. Addition of a cushion was shown to improve sample purity (Brennan et al., 2020; Gupta et al., 2018).

Size exclusion chromatography (SEC): This method relies on the separation of EVs by size. Samples are eluted by gravity through a column containing porous beads. Small particles (non-vesicular, proteins, etc.) that are small enough enter the pores, while EVs pass between the beads. This allows EVs to elute faster out of the column, and can therefore be collected separately from non-vesicular matter (Böing et al., 2014; Gámez-Valero et al., 2016).

Ultrafiltration (UF): UF also takes advantage of particle size differences to enrich EVs, where samples are passed through multiple filtration steps with specific molecular weight cut-offs to separate sample particles (Parimon et al., 2018).

Precipitation: Due to the similarity of EVs to viruses in dimensions and mode of secretion from donor cells (Nguyen et al., 2003), some studies took advantage of this similarity and employed techniques normally used for virus isolation to isolate EVs (García-Romero et al., 2019; Ludwig et al., 2018; Rider et al., 2016; Vajda, 1978). Samples are usually left overnight

with a concentration of a polymeric agent, most commonly *polyethylene glycol* (PEG), which sediments soluble particles including EVs as a precipitate. The EV-containing precipitate is then collected by a low speed centrifugation. Typically, an ultracentrifugation is performed after diluting the precipitate to eliminate PEG from the samples.

Immunocapture: This method relies on incubating samples in the presence of magnetic beads labelled with antibodies specific to a known membrane EV marker, typically tetraspanins (CD63, CD81, CD9). After the incubation period, beads are collected using a magnetic rack, and the supernatant is discarded. EVs are recovered off the beads using a solvent or a lysis buffer (Chen et al., 2020).

4. Role of EVs in intercellular signalling

4.1. EV release and uptake

Once released from cells, EVs must then move across the ECM and endothelial cells to enter into the circulation. The mode of EV crossing into the circulation has not been fully explored. Once released into the circulation, EVs seem to be mainly taken up by endothelial cells and macrophages (Verweij et al., 2019). Evidence for specific organ targeting is scarce, with a majority of studies indicating that EVs work in the local environment of their release, transferring functional protein and RNA cargo (Ghoroghi et al., 2021; Ridder et al., 2015). Exogenous EV administration revealed that EV uptake is highest in the liver, spleen, and gastrointestinal tract, but the proportion of uptake changed when EV cellular origin, route of administration, and quantity were changed (Wiklander et al., 2015).

EVs enter recipient cells through different routes (Figure 20). Research has been performed to investigate how EVs cross the blood-brain barrier (BBB) (Banks et al., 2020; Chen et al., 2016; Morad et al., 2019). In an *in vitro* model mimicking the BBB, Chen *et al.* (Chen et al., 2016) showed that EVs rely on *transcytosis* of endothelial cells through clathrin- and caveolin-dependent mechanisms. A similar experiment was performed by Morad *et al.* (Morad et al., 2019), showing that EVs are additionally endocytosed by clathrin-independent mechanism involving endosomal pathway proteins (Rabs, SNAREs). The majority of studies

indicate that EV uptake involves their entry into the endosomal pathway. The extent that these mechanisms represent EV uptake by recipient cells is unclear. Other mechanisms, such as direct membrane fusion or receptor-mediated entry may also be involved (Mathieu et al., 2019). Similarly, the proportion of EV cargo that is used by recipient cells versus the proportion that is recycled out of the cell and/or degraded remains to be fully discovered.

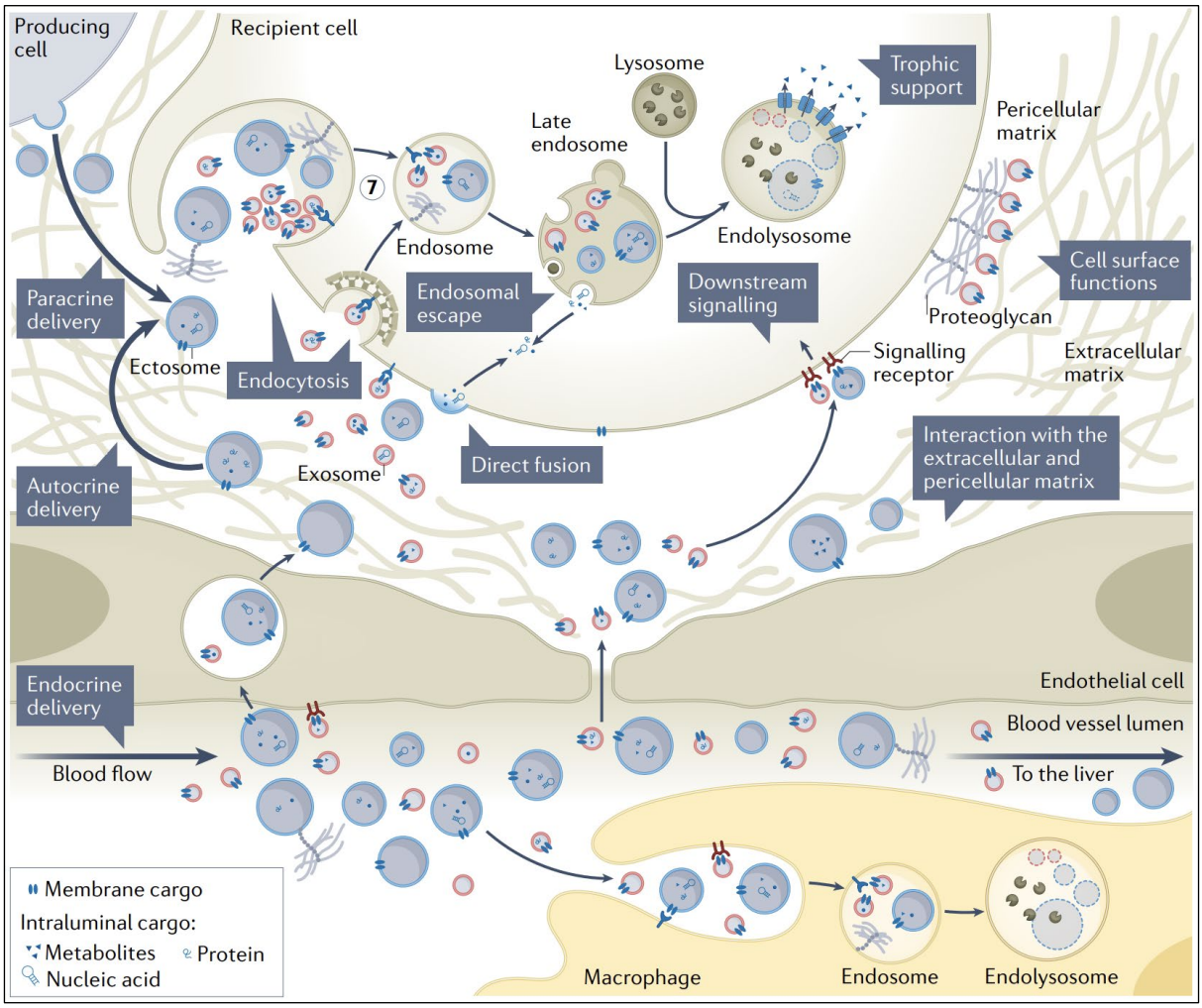


Figure 20. A representation of the different mechanisms of EV uptake by recipient cells (van Niel et al., 2022, fig. 2).

4.1. Functional effects of EVs

EVs are released into all body fluids. In addition to blood, they were found in urine, saliva, bile, breast milk, faeces, cerebrospinal-, bronchoalveolar-, synovial-, nasal-, uterine-, seminal-, and amniotic-fluid (Balbi et al., 2017; Barranco et al., 2019; Burns et al., 2014; Chiasserini et al., 2014; Foers et al., 2018; Kim and Yi, 2020; Lee et al., 2019; Li et al., 2014;

Merchant et al., 2017; Park et al., 2018; Winck et al., 2015; Wu et al., 2015). The main function of EVs in these fluids is thought to be the disposal of non-functional cellular content. However, there is rising evidence that EVs carry other functional roles, particularly in pathological conditions. Consequently, research interest in EVs has expanded exponentially in recent decades (Figure 21).

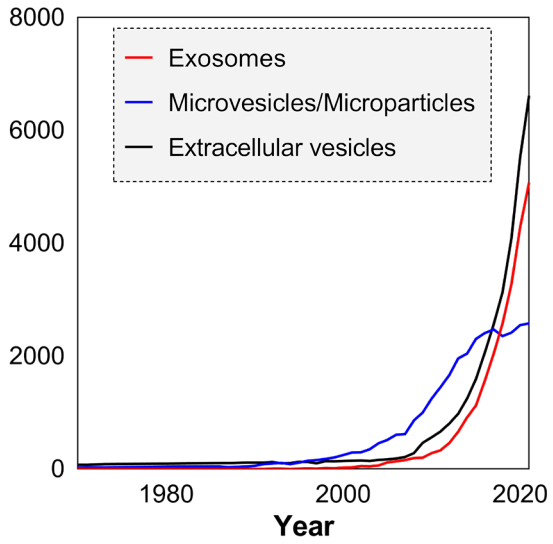


Figure 21. Research interest in extracellular vesicles by number of publications over time (PubMed).

The earliest evidence for EV function was demonstrated in platelets, where coagulating properties were retained by platelet-free plasma due to the presence of platelet-derived EVs (Chargaff and West, 1946; O'Brien, 1955).

EVs are also implicated in immune system function, where they can play both immunostimulatory and immunosuppressive roles. EVs were shown to activate T cells through direct and indirect antigen presentation (Lindenbergh and Stoorvogel, 2018; Robbins and Morelli, 2014). Additionally, B cells release and exchange CD24-containing EVs in a process helping their differentiation (Buzas, 2022). Microbial EVs may help host immune system activation, while in the cases of viruses, host EV production mechanisms may be used to hide viruses from immune defences (Johnston et al., 2021; van der Grein et al., 2018). EVs may also function in inhibiting the immune response when it is detrimental, as in the case of pregnancy and in the respiratory tract (Stenqvist et al., 2013; Wan et al., 2018).

Cancer research implicates EV in the transfer of oncogenic cargo between cancer cells

within the tumour microenvironment or pre-metastatic niche, as well as the communication between cancer and non-cancer cells. The role of EVs in cancer also includes facilitating tumorigenicity and the metastatic process, and dampening the host's immune response (Becker et al., 2016; Nigri et al., 2022; Xie et al., 2022). As the proteomic profile of EVs released by different cancer types is unique, EVs cargo have been proposed as potential biomarkers for the presence and progression (Lai et al., 2017; Melo et al., 2015; Möller and Lobb, 2020; Signore et al., 2021).

5. EVs in cardiovascular diseases

Boulanger *et al.* (Boulanger et al., 2017) outlined the role of EVs in coronary artery disease, where the authors summarized the effect of EVs on endothelial cell function in atherosclerotic conditions. The effect of EVs varies based on cellular origin and the condition during their production. Circulating EVs may increase inflammation and immune cell penetration into atherosclerotic lesions. EVs of endothelial origin were found to promote endothelial dysfunction, although the same EVs produced during physiological conditions did not produce this effect. EVs from different cells induced increased lipid retention in macrophages, leading to increased foam cell production. The resulting stress caused by EVs induces more EV production by monocytes and macrophages, promoting further lesion progression. Transfer of miRNAs from EVs of endothelial/circulation origin to VSMCs may control the rate of VSMC proliferation in the atherosclerotic plaque, which can significantly impact plaque size. However, transfer of miRNAs between endothelial cells and VSMCs can also be mediated by non-EV components such as Argonaut proteins. Moreover, changes in the environment of the atherosclerotic lesion (such as increased pro-inflammatory stimuli and changes in mineral concentrations) can induce the release of pro-calcification EVs from VSMCs, endothelial cells, and macrophages. In more advanced stages of atherosclerosis, EVs may play a mixed role depending on their cellular origin and type. Microvesicles of leukocyte, erythrocyte, and VSMC origin are highly pro-coagulant and may facilitate plaque rupture, while exosomes of platelet origin inhibited platelet aggregation. Similarly, EV-mediated transfer of specific miRNAs and proteins promoted plaque stability during atherosclerosis and

neovascularization in infarcted hearts. It is not clear whether the overall effect of EVs during atherosclerosis *in vivo* is beneficial or deleterious.

Fibroblast-derived EVs carrying the miR-21-3p induced cardiomyocyte hypertrophy by influencing sorbin and SH3 domain-containing protein 2 (SORBS2) and PDZ and LIM domain 5 (PDLIM5) expression (Bang et al., 2014). EVs were found to be involved in the recruitment of immune cells and the modulation of inflammation following MI (Cheng et al., 2019; Loyer et al., 2018). Cardiomyocyte-derived EVs also impact fibroblast behaviour through RNA transfer. Transfer of long non-coding RNAs (lncRNA) ENSMUST00000122745 and Neat1 to fibroblasts via EVs during ischemia induced a pro-fibrotic behaviour (Kenneweg et al., 2019), while cardiomyocyte EVs carrying miR-92a induced fibroblast activation and transformation into myofibroblasts via transcriptional regulation of *mothers against DPP homologues 7* (SMAD7) (Wang et al., 2020). Circulating, pro-inflammatory EVs are significantly increased following MI. Inhibiting the production of these EVs resulted in an improved functional recovery of the heart (Biemmi et al., 2020). In a heart-on-chip model, Yadid *et al.* (Yadid et al., 2020) showed that endothelial cell EVs may play a therapeutic role against ischemic injury by supplying cardiomyocytes with metabolic salvaging and homeostasis proteins. At the same time, cardiomyocytes supply endothelial cells with active glucose transporters and glycolytic enzymes to facilitate glucose uptake from the circulation (Garcia et al., 2016). Epicardial-derived EVs were shown to induce myocardial regeneration after ischemic injury through the transfer of miR-30a, miR-100, miR-27a, and miR-30e (del Campo et al., 2022).

Objectives

Objectives

Previously, the lab has identified three miRNAs (miR-21-5p, miR-23a-3p and miR-222-3p) as potential biomarkers of LVR and HF in the circulation. We were interested in understanding how these miRNAs were transported into the blood stream.

Our primary hypothesis was that miRNA were carried by EVs. EVs were shown to transport regulatory molecules such as proteins and nucleic acids in both physiological and pathological conditions. Additionally, EV cargo was proven to be influenced by some pathological conditions, such as cancer.

Experiments performed in our lab to isolate EVs suggest that that cardiac EVs may not display the conventional markers that are usually detected in cancer cell-derived EVs, such as tetraspanins (CD81, CD9, CD63). Therefore, we were interested in characterizing cardiac EVs from different types of samples (LV samples or culture medium from primary cardiac cell cultures of neonate or adult rat origin) by developing and testing new isolation techniques.

Mass spectrometry analysis was performed to identify cardiac EV markers by detecting proteins differentially expressed in EVs of LV origin versus EVs of plasma origin from neonate rats.

Our aim was to use the cardiac EV markers identified to characterize EVs from a rat model of acutely decompensated HF. This model was treated by Thiamet G, an O-GlcNAcylase inhibitor, and the purpose was to study whether recovery of Thiamet G-treated ADHF rats was mediated by EVs.

Materials & methods

1. Human samples

Human heart tissue biopsies were obtained from the cardiovascular biobank of Bichat Hospital in Paris (BB-0033-00029, coordinator Dr JB Michel) with approval by the INSERM Institutional Review Board. Explanted heart tissues were obtained from patients undergoing heart transplantation for end-stage ischemic heart failure and from patients who died of noncardiac causes. Samples were quick-frozen and stored at −80°C. All materials from patients were recovered as surgical waste with informed consent of the donors and with approval of the local ethical boards ("Centre Hospitalier et Universitaire de Lille", Lille, according to the Declaration of Helsinki).

2. Animal models

2.1. Rat model of heart failure (HF)

Rats with HF were produced after MI as previously described (Mulder et al., 1997) in a collaboration with Pr. Paul Mulder (INSERM U1096, Rouen). Animal experimentation was performed following the regulations for care and use of laboratory animals (National Institute of Health, USA, NO1-OD-4-2-139, revised in 2011). Ten-week-old male Wistar rats (Charles River) were sedated by intraperitoneal (IP) injections of 50 mg/kg sodium methohexital and 5 mg/kg xylazine. MI was induced by ligation of the descending branch of the left coronary artery. Control animals were subjected to the same experimental protocol but without the ligation. After surgery, animals were given IP xylazine at 50 mg/kg. To validate HF, echocardiographic and morphometric parameters of the animals were recorded after anesthesia with 50 mg/kg IP sodium methohexital. Animals were sacrificed 2 months after surgery using IP sodium pentobarbital at 500 mg/kg. Hearts were harvested and washed with Krebs-Henseleit buffer (120 mM NaCl, 4.7 mM KCl, 1.2 mM KH_2PO_4, 1.2 mM $MgSO_4$, 25 mM $NaHCO_3$, 11 mM D-Glucose, 2.5 mM $CaCl_2$). After removing necrotic areas, LV was separated and stored at −80°C.

2.2. Rat model of acute decompensated HF (ADHF)

Rats with acute decompensated heart failure were produced as described previously

(Peschanski et al., 2021) in a collaboration with Pr. Paul Mulder (INSERM U1096, Rouen). Briefly, Wistar rats with established chronic HF (3 months after coronary ligation) were given a gavage of salt water (1.8 g/kg in 2 mL of tap water) to induce acute decompensation. After 12 hours, ADHF rats were administered OGA inhibitor Thiamet G (TG, 25 mg/kg IP) as described in Figure 22. Left ventricular (LV) hemodynamics and structure as well as LV coronary function were assessed 24 hours after salt induction, followed by animal sacrifice.

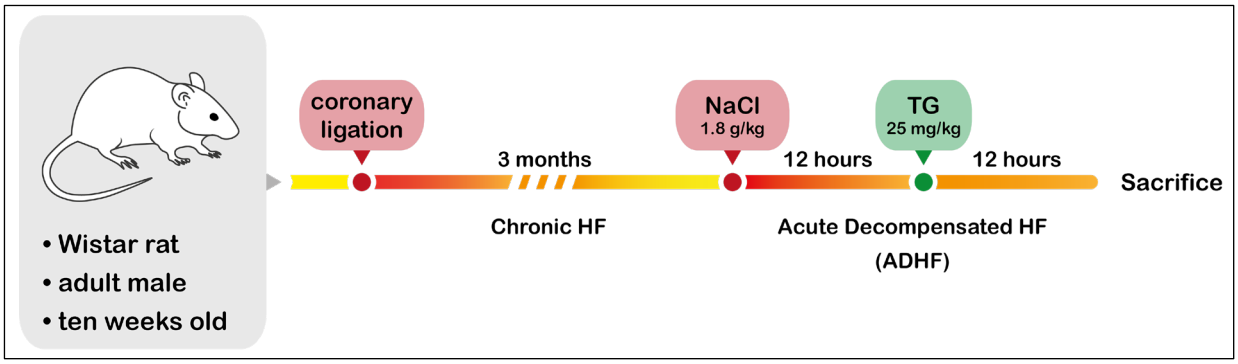


Figure 22. Timeline for the production of Wistar rat ADHF model.

2.3. Neonatal rats

One- to two- day old Wistar rat neonates (Janvier Labs) were anesthetized by hypothermia, then sacrificed by rapid decapitation. Blood was collected from the neck via EDTA-coated capillary blood collection tubes (16.444.100, Sarstedt). Hearts were harvested and washed directly in ADS conservation buffer (6.8 g/L NaCl, 1 g/L glucose, 0.12 g/L NaH_2PO_4, 0.4 g/L KCl, 0.1 g/L $MgSO_4$, 4.76 g/L HEPES, pH 7.4). Atria were removed, and ventricles were minced using fine scissors on a clean 100 mm culture dish. Minced ventricular tissue was transferred to an Erlenmeyer flask, and 100 µL conservation buffer per heart was added. The ventricular tissue was then used to isolate neonatal ventricular myocytes and fibroblasts (section II.3.1 and 3.2).

To obtain plasma, blood collection tubes were centrifuged at 2,000*g* for 5 min at 4°C without brake. About 100 µL of plasma supernatant were obtained per animal.

3. Cellular models

3.1. Neonate rat ventricular myocytes (NRVM)

NRVM were isolated from ventricular tissue obtained in section II.2.3. ADS buffer was first removed using a micropipette (kept for EV isolation, discussed in section II.4.1.1). Tissue was pre-digested by adding 6 mL of enzyme solution containing 0.044% (w/v) collagenase type II (LS004176, Worthington) and 0.055% (w/v) pancreatin (P3292-25G, Sigma), and incubating for 8 min at 37°C with shaking (180 rotations per minute [RPM]). Resulting supernatant was discarded, and a new digestion was performed by adding 6 mL of enzyme solution and incubating in similar conditions for 15 min. Once digestion was complete, the supernatant containing released cells is transferred to a new 15-mL tube (62.554.502, Sarstedt) containing 1 mL fetal bovine serum (FBS) to stop the digestion. The tube was centrifuged at 133 *g* for 1 min, and the pelleted cells were resuspended in 4 mL NRVM complete culture medium (Dulbecco's modified eagles medium [DMEM], Medium 199 [M199] [4:1 (v/v)], 10% [v/v] horse serum, 5% [v/v] FBS, and 1% [v/v] penicillin/streptomycin [P/S]). The resuspended cells were stored at 37°C and 5% CO_2 until the end of digestion. Undigested tissue remaining in the flask was re-incubated with 6 mL of enzyme solution and the process was repeated. Six successive digestions were performed in total. The resulting cell suspensions were then pooled (three 15-mL tubes were pooled into one) and re-centrifuged at 133*g* for 7 min. The supernatants were discarded, and the cell pellets were resuspended in 2 mL NRVM complete culture medium.

Cell suspensions obtained from this digestion contain several cardiac cell types, including NRVM and fibroblasts. In order to separate these cells, a discontinuous Percoll gradient was constructed by layering 4 mL of 58.5% (v/v) Percoll (P4937, Sigma) followed by 3 mL of 40.5% Percoll (v/v) into a 15-mL tube. The cell suspensions were carefully layered on top of the Percoll gradient, then centrifuged at 1,600*g* for 30 minutes without brake. Fibroblasts remain in the top gradient layer due to their lower density, while NRVM stabilize between the two gradient layers. NRVM are recovered and diluted in complete culture medium. Cells are counted using a Malassez cell counting chamber (0640610, Marienfeld).

For EV isolation, 5 million cells were seeded on 100-mm culture dishes (353003, Falcon) pre-coated with collagen (C8919, Sigma). Cells were incubated at 37°C with 5% CO_2 in 10 mL of complete culture medium, with media change 24 and 48 hours after seeding. To induce EV release, NRVM were incubated in reduced media volume (5 mL, serum-free) 96 hours after seeding. Cells were incubated for another 96 hours in these conditions without media change.

3.2. Neonate rat ventricular fibroblasts (NRVF)

NRVF were obtained from the Percoll gradient used for NRVM separation. NRVF were similarly counted using a Malassez chamber.

For EV isolation, obtained NRVF were seeded on a non-coated 100-mm culture dish. Cells were incubated at 37°C with 5% CO_2 in complete NRVF culture medium (DMEM GlutaMAX, 10% [v/v] FBS) with media change after 2 hours to eliminate non-attached cells, and again after 24 hours. Cells were trypsinized using 0.05% Trypsin-EDTA (25300-054, Gibco) 48 hours after seeding, re-counted, and seeded again at 5 million cells per 100-mm non-coated culture dish. To induce EV release, NRVF were incubated in reduced media volume (5 mL, serum-free) 96 hours after seeding. Cells were incubated for another 96 hours in these conditions without media change.

4. EV isolation

4.1. Sample sources

4.1.1. Neonate rat cardiac EVs

ADS buffer used to conserve minced neonate rat ventricular tissue was recovered (without taking tissue fragments), and centrifuged at 400*g* for 10 min, then 2,000*g* for 20 min (both at 4°C). Pellets were discarded, and the final supernatant was used as a pre-cleared sample for neonate rat cardiac EV isolation (stored at −20°C).

4.1.2. Neonate rat plasma EVs

Plasma from blood collection tubes was pooled, clarified by a 3,000*g* centrifugation for 15 min (4°C), and stored at −20°C.

4.1.3. Adult rat cardiac EVs

Adult heart tissue was minced using a scalpel into small pieces, which were then immersed in collagenase II solution (0.1%) for enzymatic digestion at 37°C for 30 minutes with agitation. After digestion, remaining tissue and cellular debris were discarded by passing the sample through a 70-µm mesh filter, followed by centrifugation at 400*g* for 10 minutes, then 2,000*g* for 20 minutes (both at 4°C) to produce a pre-cleared sample.

4.2. Isolation techniques

4.2.1. Differential ultracentrifugation (dUC)

Pre-cleared samples were transferred to 17-mL ultraclear UC tubes (344061, Beckman Coulter) and diluted with 1X Dulbecco's phosphate-buffered saline (DPBS) (14200075, Thermo Fisher Scientific), then centrifuged at medium speed (10,000-30,000*g*) to pellet large EVs (enriched in microvesicles). Supernatants were transferred to a new tube, then centrifuged at high speed (100,000*g* or higher) to pellet smaller vesicles (enriched in exosomes) in a SW32.1 Ti rotor using an Optima XE-90 ultracentrifuge. Pellets were recuperated in 30 µL of either DPBS or radioimmunoprecipitation assay (RIPA) lysis buffer (100 mM Tris, 300 mM NaCl, 2% [v/v] Igepal NP40, 1% [w/v] sodium deoxycholate, 0.2% [w/v] sodium dodecyl sulfate [SDS], cOmplete™ Protease Inhibitor Cocktail [11697498001, Sigma], 2 mM sodium orthovanadate, 2% [v/v] Phosphatase Inhibitor Cocktail 2 [P5726, Sigma], 2% [v/v] Phosphatase Inhibitor Cocktail 3 [P0044, Sigma]) and stored at −20°C.

4.2.2. Cushioned ultracentrifugation (cUC)

This technique was reported to provide a more pure EV pellet compared to dUC (Gupta et al., 2018; Langevin et al., 2019; Matejovič et al., 2021). cUC relies on the same centrifugal force to pellet vesicles of different size. After performing medium-speed centrifugation, a "cushion" (1 mL of 30% sucrose) fraction was placed at the bottom of the ultracentrifugation tube. The supernatant was then placed gently above the cushion and ultracentrifuged at high speed. EVs typically collect in the sucrose fraction, thus the supernatant was discarded and the sucrose fraction was taken and diluted in approximately 15 mL DPBS. The diluted fraction was

ultracentrifuged again at high speed to pellet EVs. The final pellet was resuspended in 30 µL RIPA or DPBS and stored at −20°C.

4.2.3. Polyethylene glycol precipitation (PEG)

Precipitation using a volume excluding polymer, most commonly polyethylene glycol (PEG), was initially used for virus enrichment (Vajda, 1978). PEG was eventually adopted as a method for EV isolation in large amounts (Ludwig et al., 2018; Rider et al., 2016; Weng et al., 2016). PEG aggregates vesicles together into a precipitate that can easily be pelleted with low speed centrifugation. Pre-cleared samples were incubated overnight with PEG 6000 (P0903, TCI) at a final concentration of 10%. Resulting precipitate was pelleted at 1,500*g* for 30 minutes, and the supernatant was discarded. Precipitates were resuspended in 30 µL RIPA or DPBS and stored at −20°C.

4.2.4. Density gradient ultracentrifugation (DGUC), alone or with UC

Density gradients (chiefly made from diluted sucrose or iodixanol) employ the different floating densities of particles in a given sample. In order to avoid contamination of exosomes with HIV, Cantin *et al.* (Cantin et al., 2008) used an iodixanol gradient and found that the two types of particles float at densities sufficiently different for their separation. A gradient was made by layering iodixanol fractions prepared from Optiprep solution (07820, Stem Cell Technologies) diluted in DPBS. 3 mL of 40% iodixanol was added to the bottom of an ultracentrifugation tube, then 3 mL of each fraction of 20%, 10%, and 5% were carefully layered on top. Pre-cleared sample (2–3 mL) was placed gently on top of the gradient, then ultracentrifuged at high speed (100,000*g* or higher) for 18 hours. The contents of the sample pass through the gradient and stop at the equilibrium density of their floatation. The volume at the top of the tube (2–3 mL) was discarded, then 12 fractions of 1 mL were collected starting from the top. Fractions were either analyzed directly, or diluted in approximately 16 mL DPBS to be centrifuged again at high speed (100,000*g* or higher), with the final pellets resuspended in 30 µL RIPA and stored at −20°C.

4.2.5. Size exclusion chromatography (SEC)

Size exclusion was suggested as an alternative to ultracentrifugation and density gradient centrifugation, avoiding the issues of protein contamination, vesicle aggregation, and loss of function encountered by the former methods (Böing et al., 2014). A column (qEV original Size Exclusion Column, SP1) filled with Sepharose beads (agarose beads with pores of 70 nm diameter) was used. Pre-cleared sample was concentrated to 500 µL using Vivaspin 2 column at 10K molecular weight cut-off (Sartorius; VS0201). The concentrate was then added at the top of the SEC column, then wash buffer (DPBS) was continuously added as the sample passed through the column. The particles in the sample travel with the buffer at different speeds based on their size. Proteins are small enough to enter the pores, thus have to make a longer distance, while the larger vesicles cannot enter and pass between the beads, thus are eluted first. Fractions of 500 µL were collected (F1-6 void volume pooled, F7-15 collected individually, then F16-30 protein fractions pooled).

4.2.6. EV total isolation and recovery (EVtrap)

Unpurified EVs from plasma and minced ventricles were captured and processed using magnetic EVtrap beads as previously described (Wu et al., 2018). Briefly, unpurified EV solution from ventricles (3,000*g* supernatant) was filtered using a 100,000 Da Amicon filter (UFC9100, Millipore) allowing the removal of free molecules with small molecular mass. Samples were then washed and diluted 1:10 with 1X phosphate buffered saline (PBS). In order to isolate EVs, magnetic EVtrap beads were added to the filtered solution at 1:10 v/v ratio, followed by shaking for 1 hr. The beads were then captured using a magnetic separator rack, and the supernatant was removed. Beads were washed using PBS.

5. Sample analysis

5.1. Western blot

5.1.1. Protein extraction

Cells and ventricular tissue samples were lysed mechanically using a potter (neonate rat organs) or Ultra-Turrax homogenizer in the presence of sample lysis buffer RIPA. EV samples

were resuspended and incubated with RIPA lysis buffer. All samples were incubated with RIPA for 1 hour at 4°C with rotation, followed by a centrifugation at 12,000*g* for 15 min. The resulting supernatant containing soluble proteins was taken and stored at −20°C until use.

5.1.2. Protein quantification

Samples were quantified for their protein concentration using the Bradford assay method. *Bovine serum albumin* (BSA) was used as standard by depositing a gradually increasing volume of BSA 1 mg/mL (0, 1, 2, 5, 10, 15, and 20 µL) into a 96-well plate (655101, Greiner Bio-One) in two replicates. Sample (2-5 µL) was deposited in two replicates. Bio-Rad Protein Assay Dye Reagent (5000006, Bio-Rad) was diluted to 1X concentration, and 1 mL was added to each well containing BSA or sample. Absorbance was measured at 595 nm using a PowerWave XS2 microplate reader (BioTek). Results were analyzed using Gen5 software (BioTek).

Alternatively, Pierce™ Bicinchoninic Acid (BCA) Protein Assay (23225, Thermo Fisher Scientific) was used according to manufacturer instructions. Briefly, BSA (2 mg/mL) was diluted in DPBS according to Table 2. BSA standard and samples were deposited in two replicates on a 96-well plate, and BCA reagent mixture was added to each well. The plate was incubated at 37°C for 30 min allowing reduction of Cu^{2+} to Cu^{+} by proteins. A purple coloration is generated when Cu^{+} interacts with the BCA, and its absorbance was measured at 562 nm.

Table 2. Pierce BCA standard preparation (stock = 2 mg/mL BSA)

Tube	DPBS (µL)	Volume and source of BSA (µL)	Final BSA concentration (µg/mL)
A	0	300 of stock	2000
B	125	375 of stock	1500
C	325	325 of stock	1000
D	175	175 of vial B	750
E	325	325 of vial C	500
F	325	325 of vial E	250
G	325	325 of vial F	125
H	400	100 of vial G	25
I	400	0	0 = Blank

5.1.3. Gel types and buffers

Western blots were performed using SDS-polyacrylamide gel electrophoresis (SDS-PAGE). SDS-PAGE gels were either prepared (home-made gels) at a homogenous concentration (Table 3), or commercially available, precast gels (NuPAGE, Thermo Fisher Scientific) with known concentrations.

Table 3. Composition of home-made gels.

Composition	Stacking gel	Running gel
Percentage acrylamide	4%	10%
H_2O MilliQ (mL)	1.58	4.85
Acrylamide 40% (mL)	0.25	2.5
Tris-HCl 1.5 mM pH 8.8 (mL)	-	2.5
Tris-HCl 0.5 mM pH 6.8 (mL)	0.63	-
SDS 10% (µL)	25	100
APS 10% (µL)	12.5	50
TEMED (µL)	2.5	5

For home-made gels, protein samples (1-20 µg) were diluted in reducing Laemmli sample buffer (62.5 mM Tris-HCl pH 6.8, 2% [w/v] SDS, 25% [v/v] glycerol, 0.01% [w/v]

bromophenol blue, 5% [v/v] β-mercaptoethanol), then heated at 95°C for 10 min for protein denaturation. Gels were assembled in the electrophoresis tank filled with running buffer (25 mM Tris-base, 200 mM glycine, 6.57 mM SDS 10%). Samples were allowed to cool to room temperature, then loaded into the wells of the stacking gel. Protein electrophoresis was performed at 90V until samples reached the running gel, then voltage was increased to 150V and kept until the dye exited the gel.

For precast gels with 4-12% acrylamide gradients (NP0321, Thermo Fisher Scientific), protein samples (1-20 µg) were diluted in reducing sample buffer containing 4X Lithium Dodecyl Sulfate (LDS) (NP0007, Thermo Fisher Scientific) and 10X Dithiothreitol (DTT) (NP0009, Thermo Fisher Scientific), then heated at 70°C for 10 min to allow protein denaturation. For gel electrophoresis, 500 mL of 2-(N-morpholino)ethanesulfonic acid SDS (MES SDS) (NP0002, Thermo Fisher Scientific) running buffer were added outside the gels, and 200 mL were added between the gels. An antioxidant (NP0005, Thermo Fisher Scientific) was added to the running buffer between the gels at 0.25% (v/v) to prevent protein re-oxidation. Samples were ran at a constant voltage of 200V, until the dye exited the gel.

5.1.1. Immunoblotting

When electrophoresis was complete, proteins were transferred to a 0.2 µm nitrocellulose membrane (1704158, Bio-Rad) using a Trans-Blot Turbo blotting system (170-4155, Bio-Rad). Transfers were performed at 25V and 2.5A for 10 min. At the end of transfers, the membranes were stained with Ponceau red (ab146313, Abcam) to confirm protein loading homogeneity and transfer efficiency. Ponceau staining was then removed by a 10 min wash with 1X Tris-Buffered Saline, 0.1% Tween® 20 Detergent (TBST) (0.1 M Tris-HCl pH 7.4, 150 mM NaCl, 0.1% [v/v] Tween) with rolling at room temperature (RT). Membranes were then blocked with either 5% (w/v) non-fat dry milk in TBST, or with 5% (w/v) BSA (268135000, Thermo Scientific) in TBST, for 1 hour at RT. Blocking was performed in order to prevent non-specific binding of antibodies. After blocking, membranes were incubated with primary antibody (Table 4) overnight at 4°C with rolling. Following primary antibody incubation, membranes were washed with TBST for 10 minutes three times at RT, then incubated with the corresponding

horseradish peroxidase (HRP)-coupled secondary antibody (goat anti-mouse [115-035-003, Jackson Immuno Research] or goat anti-rabbit [111-035-003, Jackson Immuno Research]) for 1 hour at RT. After incubation with secondary antibody, membranes were washed again in TBST for 10 minutes three times at RT. Proteins of interest were visualized by incubating the membranes in Clarity Western ECL Substrate (1705061, Bio-Rad) containing HRP substrate. The resulting reaction between the ECL solution and HRP coupled to the secondary antibody produces a luminescence which was detected in a Chemidoc Gel Imaging System (Bio-Rad). Detected protein band intensities were analyzed and quantified using ImageLab software (Bio-Rad). Protein expression was measured by the intensity ratio of protein of interest to the normalizing protein, or that of the Ponceau stain. If more than one antibody were used on the same membrane, a stripping step was done between each antibody by incubating the membrane in 10 mL of Restore™ PLUS Western Blot Stripping Buffer (46430, Thermo Scientific) for 10 minutes with rolling at RT. This eliminates previously used antibodies. A 10 minute wash with TBST at RT was performed followed by blocking the membrane for another 1 hour at RT. The membrane was then re-incubated with the desired antibody overnight at 4°C with rolling.

Table 4. Primary and secondary antibody conditions for western blots.

Proteins	Molecular weight (kDa)	Primary antibody			Secondary antibody dilution
		Reference	Species	Dilution	
LIM domain-binding protein 3 (LDB3)	32, 78-100	Proteintech (11004-1-AP)	Rabbit	1/5000	1/10000
Syntenin-1	32	Abcam (ab19903)	Rabbit	1/2500	1/10000
Cluster of differentiation 63 (CD63)	28	Abcam (ab108950)	Mouse	1/500	1/5000
αB-Crystallin (CRYAB)	20	Enzo Life Sciences (ADI-SPA-223)	Rabbit	1/10000	1/20000
Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)	37	Santa Cruz (sc-365062)	Mouse	1/1000	1/10000
Heat shock cognate 71 kDa protein (HSC70)	70	Santa Cruz (sc-7298)	Mouse	1/20000	1/10000
Heat shock protein 70 (HSP70)	70	Abcam (ab53496)	Mouse	1/500	1/5000
A Disintegrin and metalloproteinase domain-containing protein 10 (ADAM10)	94 (precursor) 68 (mature)	Abcam (ab124695)	Rabbit	1/500	1/5000
Calnexin	75	Abcam (ab22595)	Rabbit	1/10000	1/10000
Albumin	67	Invitrogen (MA532531)	Rabbit	1/5000	1/10000
Nucleoporin p62 (NUP62)	62	BD Transduction (610498)	Mouse	1/1000	1/10000
Myosin heavy chain 7 (MYH7)	200	Sigma (M8421)	Mouse	1/1000	1/10000
Major vault protein (MVP)	100	Proteintech (16478-1-AP)	Rabbit	1/2500	1/10000
O-GlcNAc RL2	-	Novus Bio (NB300-524)	Mouse	1/2500	1/5000

5.2. Immunoprecipitation (IP)

Protein extracts (25 µg) were diluted to a volume of 30 µL in RIPA lysis buffer in the presence of O-GlcNAcylase inhibitor PUGNAc. Samples were then incubated overnight with rotation at 4°C in the presence of 1 µg LDB3 antibody, allowing for its hybridization to LDB3 present in the protein extracts. The following day, 30 µL of Pierce™ Protein A/G Magnetic Beads (88803, Thermo Scientific) were added to the samples, and the mix was incubated for 3 h with rotation at 4°C. During this time, beads attach to the antibody. Supernatants were then recovered by collecting beads to the side of tubes using a magnetic rack (89129-096P, VWR). The beads were then resuspended in a 30 µL mix of RIPA-LDS-DTT. Tubes were heated at 70°C for 10 min to detach the proteins and antibodies from the beads, then placed again on a magnetic rack to recover the protein supernatant, while beads were discarded.

5.3. Liquid chromatography-mass spectrometry (LC-MS)

EVs isolated from hearts or plasma pre-cleared samples were dried and lysed to extract proteins using a phase-transfer surfactant (PTS). Proteins were reduced and alkylated by boiling for 10 min at 95°C in 10 mM tris(2-carboxyethyl)phosphine and 40 mM chloroacetamide. Samples were diluted in 50 mM triethylammonium bicarbonate and digested with Lys-C (Wako) for 3 hours at 37°C, and with trypsin overnight at 37°C. To remove the PTS surfactants from the samples, the samples were acidified with 1% trifluoroacetic acid (TFA) in the presence of 1:1 ethyl acetate solution. Samples were vortexed for 2 min, followed by a 16,000g centrifugation for 2 min to separate aqueous and organic phases. The organic phase was removed and the aqueous phase was collected. Centrifugation was repeated to ensure full separation of phases. Samples were then dried using a vacuum centrifuge and desalted using Top-Tip C18 tips (Glygen) according to manufacturer's instructions. Samples were then fully dried and stored at -80°C. LC-MS/MS analysis was carried out as performed previously (Wu et al., 2018).

5.4. Nanoparticle tracking analysis

EV samples were diluted 1:10 to 1:100 in 1X PBS (0.22 µm-filtered) and analyzed using

a NanoSight NS300 (Malvern Panalytical) configured with a 488 nm laser and a digital camera system (sCMOS) in collaboration with Dr. Morvane Colin (INSERM U1172, Lille). Samples were injected at a flow rate of 20 μL/min, and videos of 1 min were recorded with the camera level setting at 14 and detection threshold at 4. One mL of 1X PBS was injected between samples to clear the chamber. Videos were saved and analyzed using NTA software version 3.2 (Malvern Panalytical), with videos having high noise or vibration being excluded from analysis. To visualize particle size distribution, concentration of particles at different diameters were divided to the total number of particles. To compare the concentration of particles detected from different samples, values were normalized to cell number.

6. Data analysis

Western blot images were analysed by comparing groups using a non-parametric Mann-Whitney test. Bar and column graphs were generated using GraphPad Prism (v7.0.0).

EVtrap protein abundance was analyzed using Perseus v1.6.5 software (https://maxquant.net/perseus/, accessed on 1 October 2019). Proteins not detected in at least 3/4 of the samples (EVtrap analysis) in each group were excluded. Protein abundances were transformed to Log2. Missing values were substituted by values from the normal distribution. Groups were compared by a two-tailed Student's t test ($p < 0.05$) using the Benjamini–Hochberg correction. Differences in abundance (Log2 transformed) and p values were visualized on a Volcano plot by entering Perseus data into VolcaNoseR web app (Goedhart and Luijsterburg, 2020). Gene Ontology (GO) analysis was performed on proteins identified by MALDI TOF/TOF and LC-MS/MS using PANTHER GO (Ashburner et al., 2000; Mi et al., 2019; The Gene Ontology Consortium et al., 2021). Protein names were compared to the available Rattus norvegicus reference proteome (21,585 proteins; released 2020-11-01). EVtrap proteins selected after MS identification were compared to Vesiclepedia (Kalra et al., 2012) and Exocarta (Keerthikumar et al., 2016) databases using FunRich (v3.1.3) (Fonseka et al., 2021). Overlap values between the 3 groups were visualized using the Eulerr R package (Larsson, 2021).

Results

1. Preliminary work

Information in this section appeared in Dubois-Deruy et al., 2017 (Dubois-Deruy et al., 2017) *and in Abou Zeid et al., 2022* (Abou Zeid et al., 2022).

1.1. miRNAs in HF and LVR

Previous work was performed in our lab to identify early biomarkers of left-ventricular remodelling (LVR) in a rat model of heart failure (HF). Myocardial infarction (MI) was induced by coronary artery ligation in 10-week-old Wistar rats. Plasma samples obtained 7 days and 2 months (chronic HF) after MI revealed increased levels of 3 pre-selected microRNAs (miRNAs): miR-23a-3p, -21-5p, and 222-3p in rats with HF compared to sham-operated rats at 2 months (Figure 23).

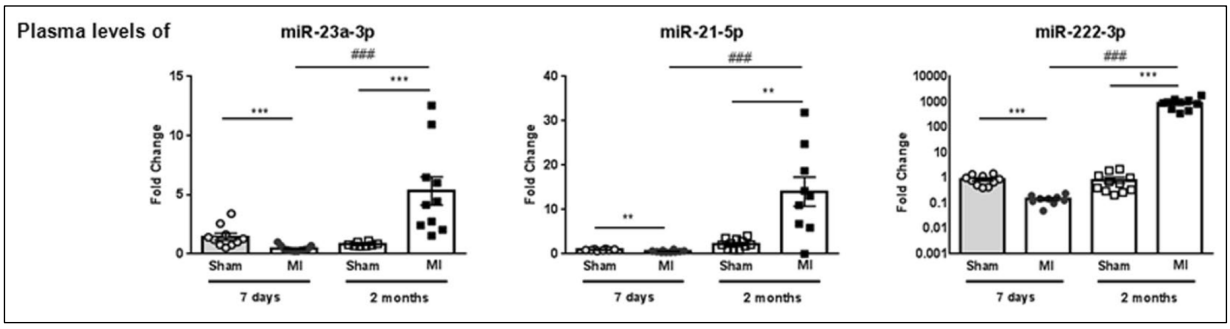


Figure 23. Reverse transcription quantitative real-time PCR (RT-qPCR) of circulating miR-23a-3p, miR-21-5p, and miR-222-3p normalized to Cel-39. Values are represented as mean ± SEM values expressed as fold change ($2^{-\Delta\Delta Ct}$). **p < 0.01; ***p < 0.001, for two groups comparison (nonparametric Mann–Whitney test) and ###p< 0.001, for multiple groups comparison (Kruskall-Wallis with Dunn's multiple comparison test).

1.2. Detection of miRNAs in EVs isolated from cultured cardiac cells

Our team was interested in identifying how these miRNAs were being transported into the circulation. Consequently, extracellular vesicles (EVs) were investigated due to their capacity to load and transport nucleic acids, including miRNA in tissues and in the blood.

In order to identify whether the miRNAs were transported by EVs, *in vitro* culture of cardiac cells was performed. Embryonic rat cardiac myoblast cells (H9c2), neonate rat ventricular myocytes (NRVM), and neonate rat ventricular fibroblasts (NRVF) were used

(Figure 24).

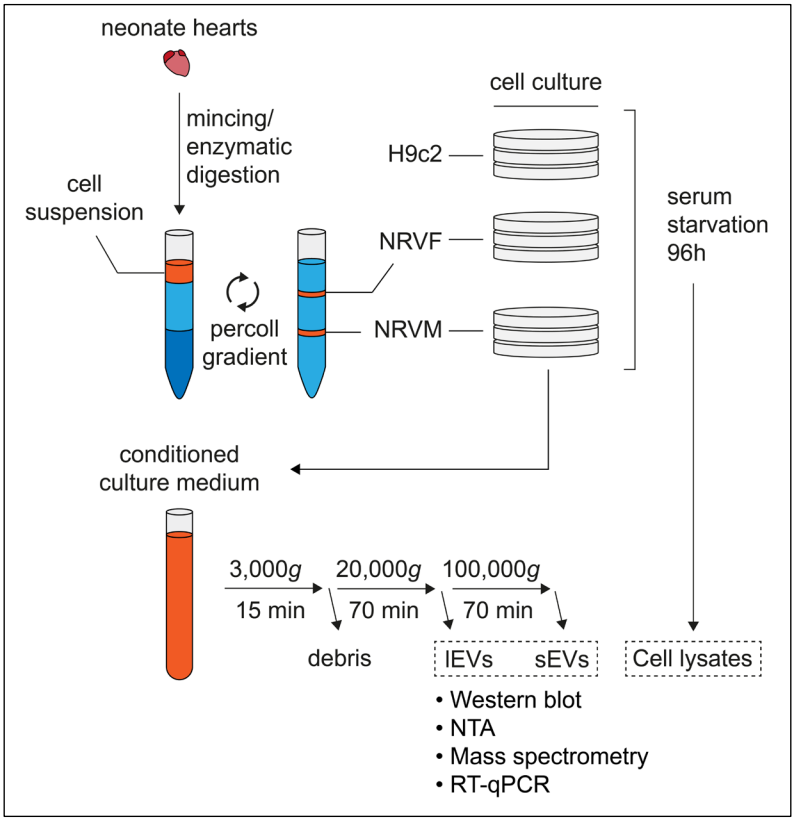


Figure 24. Procedure of neonate rat cardiac cell culture and EV isolation. Neonate rat ventricular myocytes (NRVM) and fibroblasts (NRVF) were obtained by mincing and digestion of ventricular tissue from 1-3 day old Wistar rats and separating it by Percoll gradient. Cardiac myoblast cells (H9c2) were obtained from a commercial source. NRVM, NRVF, and H9c2 cells were cultured in serum-free media for 96 hours to induce stress and EV secretion. Differential ultracentrifugation (dUC) was used to isolate large (lEVs) and small EVs (sEVs) from conditioned culture medium. NTA: nanoparticle tracking analysis.

The presence of the identified miRNAs in EVs secreted by NRVF and H9c2 cells was demonstrated by reverse transcription quantitative real-time PCR (RT-qPCR). MiR-21-5p, miR-23a-3p, and miR-222-3p were detected intracellularly (data not shown) and in secreted small EVs (sEVs) isolated by differential ultracentrifugation (dUC) (Figure 25).

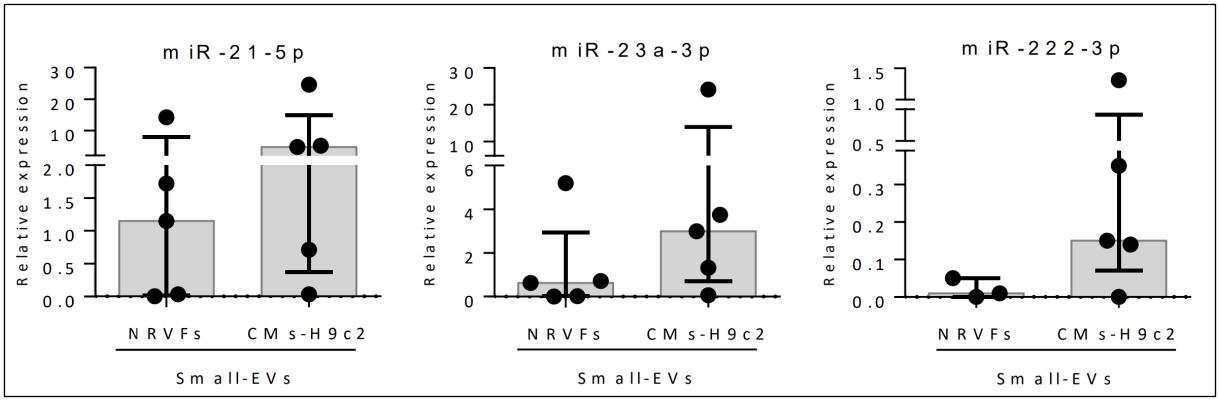


Figure 25. RT-qPCR of miR-21-5p, miR-23a-3p, and miR-222-3p in small EVs from NRVF and H9c2 cell culture media. Values were normalized to Cel-39 and represented as median ± interquartile.

1.3. Particle analysis and proteomics of cultured cardiac cell EVs

To further analyze cardiac EVs, nanoparticle tracking analysis (NTA) was performed, revealing that NRVFs produced the highest number of EVs (sEVs: 8.9E6 particles/cell; lEVs: 8.5E5 particles/cell), compared to H9c2 cells (sEVs: 1.2E5 particles/cell; lEVs: 6E4 particles/cell) and NRVMs (sEVs: 4.4E4 particles/cell; lEVs: 6E3 particles/cell). All three cell types produced more sEV than lEVs (Figure 26A). Western blot was performed to identify protein markers of cardiac EVs, and revealed that the conventional sEV marker CD63 was present in NRVF and H9c2 sEVs, while CD9 was absent (Figure 26B), suggesting a unique protein profile in cardiac sEVs. NRVM did not produce sufficient EVs for western blotting.

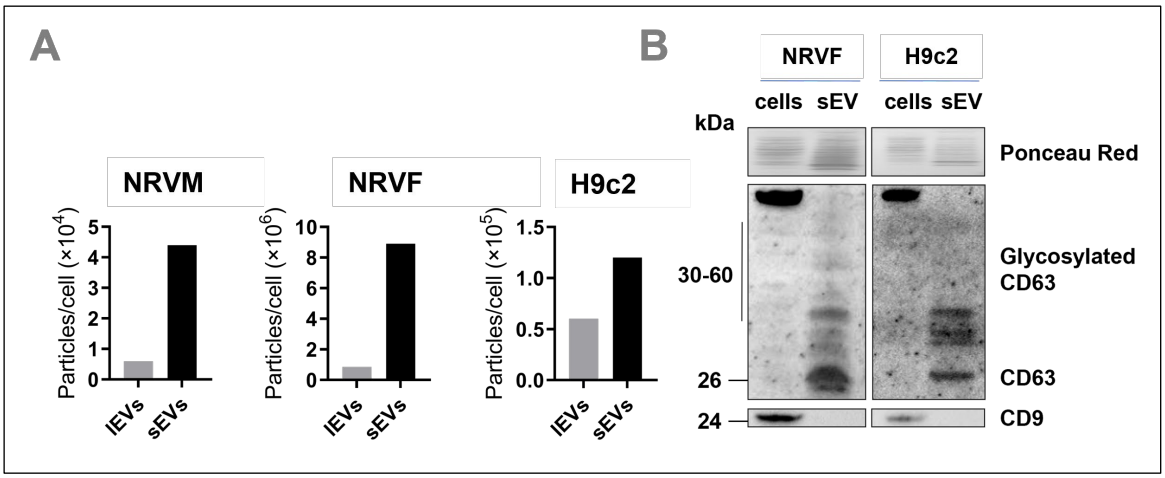


Figure 26. (A) Particle concentration in lEV and sEV pellets by nanoparticle tracking analysis (NTA) normalized to the number of producing cells. (B) Western blot of cells and corresponding sEVs to detect exosomal markers CD63 and CD9.

NRVF and H9c2 sEV proteins were then separated in a one-dimensional gel, and

protein bands revealed by Coomassie blue staining were further analyzed by mass spectrometry to identify the most enriched proteins (Figure 27A). After mass spectrometry, 63 proteins were identified from NRVF and 8 proteins from H9c2 cells. Five proteins were common (Col1a2, Fn1, Mfge8, Actb, and Actg1) (Figure 27B). When gene ontology (GO) analysis (Figure 27C) was performed for cellular component, 24 cytoskeletal proteins were revealed (such as actin and tubulin), 12 ribonucleoproteins (such as Rps2/4x/8/9 and Rpl7a/11/15), 6 extracellular matrix proteins (such as Col1a1/2 and Fn1), and 6 DNA-binding proteins (such as histones H4m/2a1e/3-3b/2aj and Morf4l2). We also identified 17 protein associated with positive regulation of protein expression (such as Hspa8, Wnt5a, and Eef1), and 15 associated with regulation of the apoptotic process (such as Hsp90aa1/a5, Grk2, Rack1, and Tcp1).

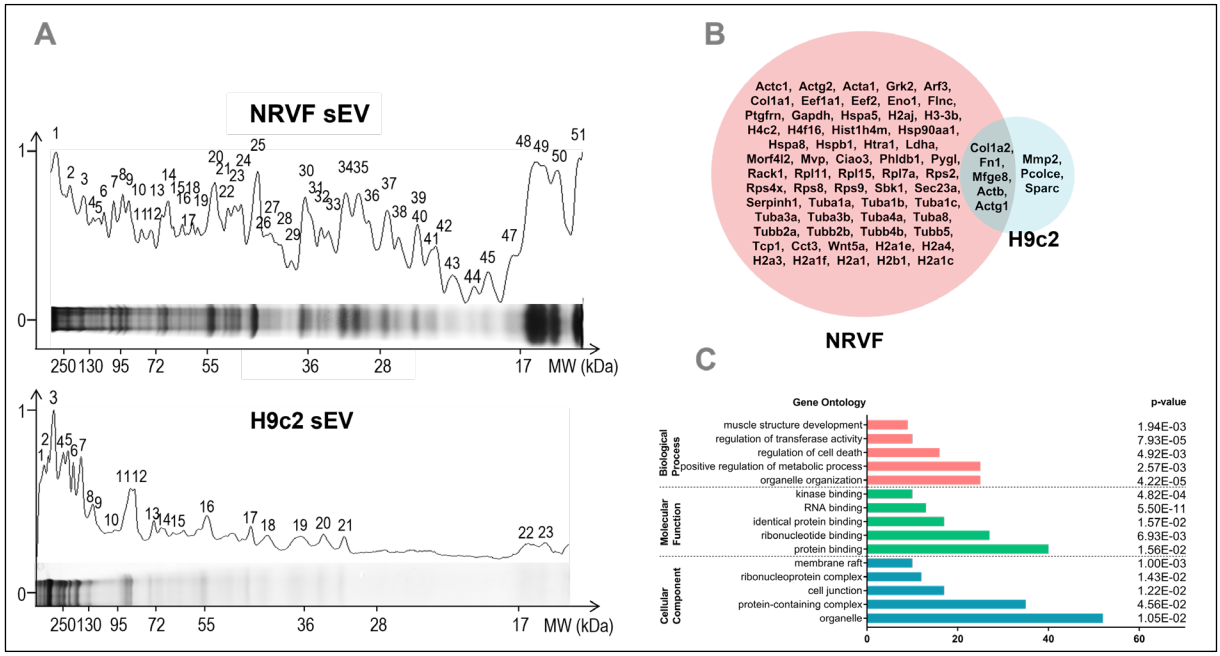


Figure 27. (A) Coomassie blue staining of NRVF (75 µg) and H9c2 (25 µg) sEV proteins separated by 1D gel. Identified bands were excised for MALDI-TOF/TOF mass spectrometry (MS). (B) A Venn diagram representing proteins detected by MS of NRVF (pink) and H9c2 (blue) sEVs. (C) GO (Gene Ontology) analysis of enriched GO terms for biological process, molecular function, and cellular component. *p* values were FDR-adjusted.

These results were limited due to the relatively low amount of EVs recovered from the starting samples. In order to get a more complete picture of the proteomic profile of cardiac EVs, a more sensitive approach was necessary to study protein abundance from small volumes of starting material. In the following section, we used EV total recovery and purification (EVtrap) to isolate EVs from the heart (identifying cardiac markers) and the plasma (comparing

cardiac markers to EVs in the circulation) of neonate rats.

2. Proteomic analysis of neonatal rat cardiac and plasma EVs isolated by EVtrap

Information in this section appeared in Abou Zeid et al., 2022 (Abou Zeid et al., 2022).

As cardiac EVs are released from cardiac cells into the circulation, they are mixed with the diverse populations of EVs released from all organs. This makes them difficult to identify, and therefore it was necessary to find markers that not only correspond to EVs, but are also specific to cardiac EVs. To do this, proteomic analysis comparing neonate rat cardiac and plasma EVs was performed. EVs isolated from neonatal rat ventricular tissue and plasma (n = 4) by EVtrap were analyzed by LC-MS (Figure 28).

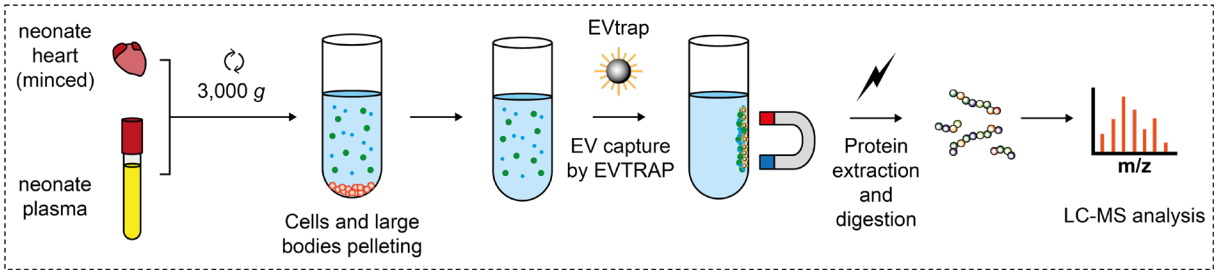


Figure 28. Experimental procedure of EV isolation from neonate rat heart and plasma (n=4) using EV total recovery and purification (EVtrap) followed by LC-MS.

A total of 3187 EV proteins were detected (Table S1), of which 2629 cardiac proteins and 1905 plasma proteins were analyzed (detected in at least 3 out of 4 samples in each group), with 1775 proteins in common (Figure 29 , Table S2).

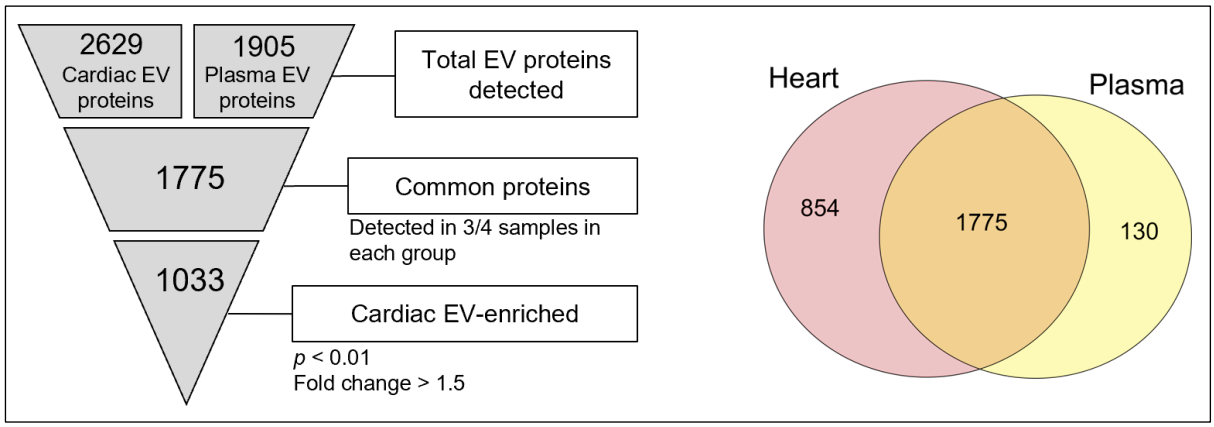


Figure 29. Selection criteria for cardiac EV-enriched proteins.

Among identified proteins, we detected most of the proteins (41 out of 66) previously identified in sEVs derived from cultured cardiac cells. Cardiac EV proteins displayed respectively 86 and 91 out of the top 100 proteins identified by public EV databases Vesiclepedia and ExoCarta (Figure 30, left panel; Table S3), indicating an enrichment of common EV proteins by EVtrap. GO analysis (Figure 30, right panel; Tables S4-6) identified conventional exosome markers (such as Sdcbp/syntenin–1, Pdcd6ip/alix, tetraspanins CD81/9, Hspa4/8, Lamp2, and Tsg101). Membrane proteins were also enriched in cardiac EVs (such as annexins, cadherins, cavins, caveolins, clusters of differentiation, and integrins), in addition to endosomal proteins (such as Chmp, Rab, EH-domain containing, vacuolar protein sorting-associated, and sorting nexin proteins), focal adhesion proteins (such as LIM domain-containing proteins), and sarcomeric proteins.

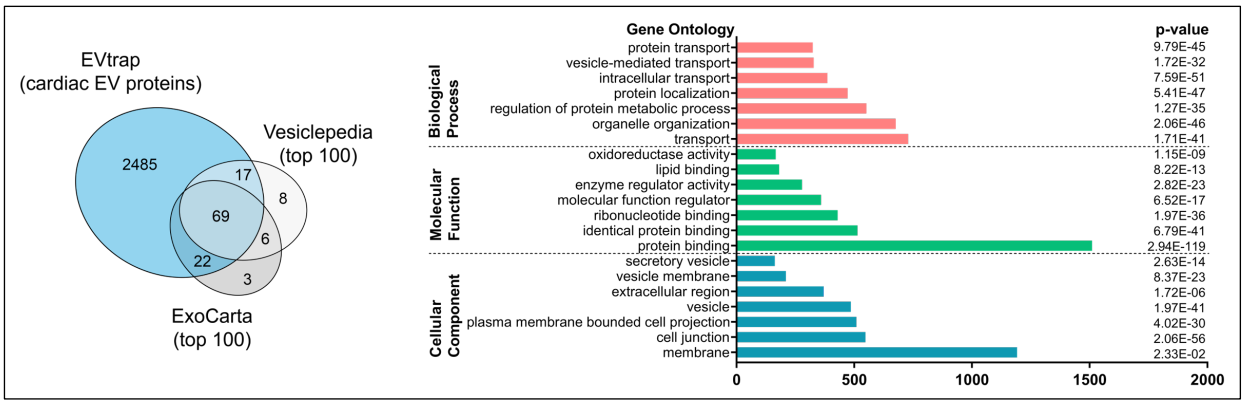


Figure 30. Venn diagram of cardiac EV proteins (blue circle) compared to the top 100 EV proteins identified in public databases Vesiclepedia and ExoCarta (left panel). GO analysis of cardiac EV proteins to identify enriched GO terms (right panel).

Cardiac and plasma EV protein abundances were compared, showing 1033 proteins enriched in cardiac EVs, while 180 proteins were enriched in plasma EVs (Figure 31A, Table S2). Compared to plasma EVs, we showed that LDB3 is the most significantly abundant protein (×160) in cardiac EVs (Figure 31B). Alpha-B crystallin (CRYAB), a previously reported marker of cardiac EVs, was also enriched in cardiac EVs (×40).

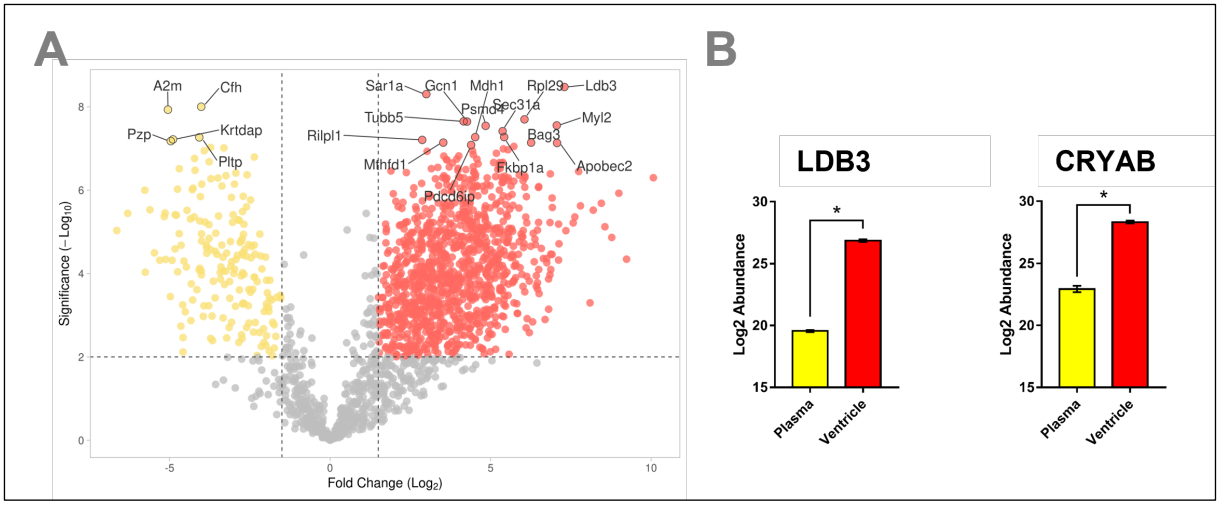


Figure 31. (A) Volcano plot comparing cardiac (red dots) and plasma (yellow dots) EV protein abundances. Proteins with P value < 0.01 and fold change > 1.5 were considered significant for the analysis. The 20 most significantly changed proteins (lowest *p* value) were labeled. (B) Bar plot of LDB3 and CRYAB abundances (log2 transformed) in plasma and heart. Error bars = SEM, $^{*}p < 0.05$.

LDB3 expression was then compared between different tissue types from neonatal rats, confirming its specific enrichment to cardiac tissue (Figure 32, left panel). Furthermore, LDB3 was confirmed to be of cardiac myocyte origin upon comparing its expression in neonate cardiac myocytes and fibroblasts (Figure 32, right panel). This indicated that LDB3 is a cardiac myocyte-specific marker. Furthermore, LDB3 was detected in two isoforms, a high molecular weight (MW) isoform (~100 kDa) and a low molecular weight isoform (~78 kDa), indicating alternative splicing.

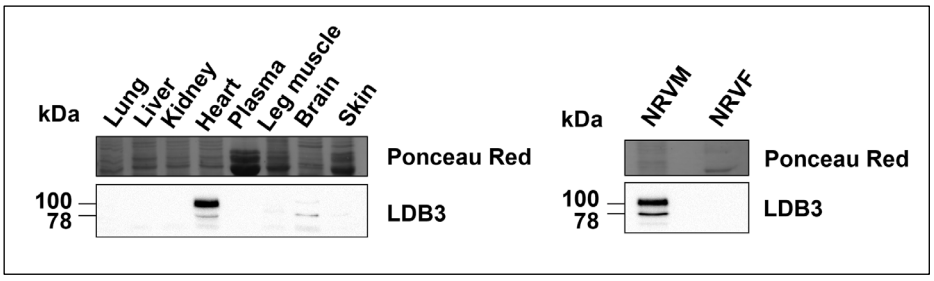


Figure 32. Western blot for LDB3 expression in neonatal rat tissues (left panel) and cultured neonatal rat cardiac cells (right panel). Equal protein amounts were loaded for each sample (20 µg left panel; 10 µg right panel). NRVM: neonate rat ventricular myocytes. NRVF: neonate rat ventricular fibroblasts.

3. EV isolation techniques

Information in this section appeared in Abou Zeid et al., 2022 (Abou Zeid et al., 2022).

Results

To validate LDB3 as a potential marker of cardiac EVs, it was necessary to first confirm its presence in cardiac tissue-derived EVs using other EV isolation techniques than EVtrap. This was necessary as different techniques may yield different EV populations with varied yield and purity.

Tissue samples were first minced (with digestion for adult tissue), then clarified from debris and cells by short speed centrifugations (400*g* to 3,000*g*). EVs were then separated into lEVs and sEVs. lEVs are generally enriched in membrane-derived ectosomes (⌀ 100–1000 nm) and were obtained by pelleting through medium-speed centrifugation (10,000*g* to 30,000*g*) centrifugation, while several isolation techniques were used to isolate sEVs (enriched in exosomes, ⌀ 50-150 nm) from an initial sample of ventricular tissue from neonate or adult rats.

Aside from cardiac markers LDB3 and CRYAB, several markers were used to identify EVs and non-EV components. These markers varied and were changed to keep up with EV literature which was actively being updated and improved during the period of my thesis project. These included exosomal markers (for sEVs) previously reported in the literature, such as syndecan-syntenin-Alix pathway member *syntenin-1*, the tetraspanin cluster of differentiation 63 (*CD63*), and A Disintegrin and metalloproteinase domain-containing protein 10 (*ADAM10*). Additionally, general EV markers which are not specific to sEVs or lEVs were used and included chaperone proteins heat shock protein 70 (*HSP70*) and heat shock cognate 71 (*HSC70*). Markers of possible EV contamination with non-EV components, including soluble secreted proteins such as *albumin*, intracellular structural proteins not associated with EVs such as myosin heavy chain 7 (*MYH7*) and *nucleoporin p62*, and proteins that may associate with intracellular vesicles as a result of cellular damage during EV isolation, such as *calnexin*. *Annexin A5* was used as a marker of apoptotic bodies that may associate with lEVs. A protein potentially involved in RNA loading into EVs, major vault protein (*MVP*), was also investigated.

3.1. Neonate rat EVs

3.1.1. Differential ultracentrifugation (dUC)

After preparing ADS solution containing unpurified EVs (Figure 33A), samples were centrifuged at different speeds to obtain corresponding pellets (Figure 33B). Exosome marker syntenin-1 was detected in the 164,000*g* pellet, indicating pelleting of exosome rich sEVs following high speed centrifugation. Syntenin-1 was also detected in the 10,000*g* pellet, implying a pelleting of a portion of exosomes at this speed. CRYAB was detected in all samples, implying low specificity to one type of EVs. Extracellular contamination marker albumin and intracellular contamination marker calnexin were detected at low- to medium-speed (2,000*g* to 30,000*g*) centrifugations, but were also detected in lower amount in sEVs. Myosin heavy chain 7 (MYH7), a central structural protein found in cardiac sarcomeres, was detected only following low- to medium-speed centrifugations, implying that it is not loaded into sEVs. The presence of albumin may be due to co-pelleting during the high centrifugation speed, while the detection of calnexin may be due to the formation of intracellular vesicles from cellular damage caused during tissue mincing. These intracellular vesicles may share certain properties with sEVs, including size and capacity to pellet.

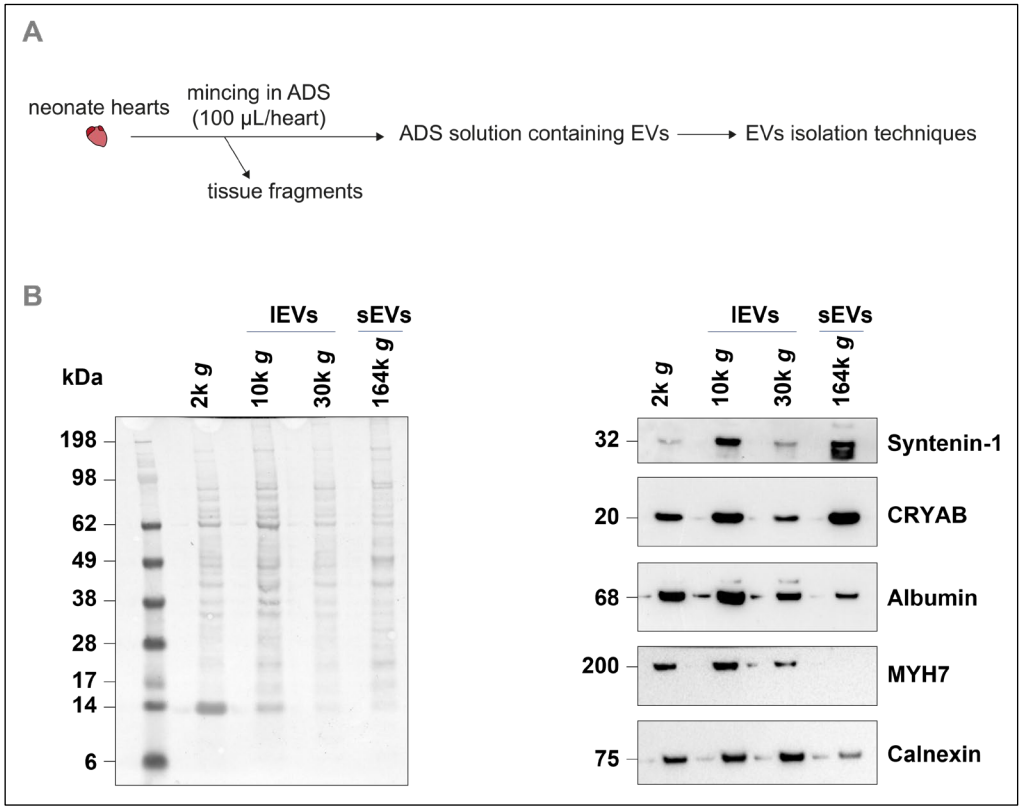


Figure 33. (A) Experimental procedure for the preparation of neonate rat heart-derived EVs via mincing of ventricles in conservation buffer (ADS). ADS containing unpurified EVs is then used for EV isolation using different techniques. (B) Ponceau Red staining (left panel) and western blot (right panel) of ADS solution centrifugation pellets obtained at different speeds. The sample corresponding to 164k was pre-cleared by a 10,000*g* centrifugation. 5µg of protein of each sample was loaded. k *g*: ×1000*g*. CRYAB: alpha B crystallin. MYH7: myosin heavy chain 7. kDa: kilodalton.

3.1.2. Cushioned ultracentrifugation (cUC)

Cushioned ultracentrifugation (cUC) was used as a modified version of dUC, where a fraction of 30% sucrose (diluted in water) is placed at the bottom of the tube before adding the sample and ultracentrifuging. The sucrose fraction has been reported to allow the passage of EVs, but excludes secreted proteins such as apolipoproteins (Langevin et al., 2019). The sucrose fraction is then taken, diluted, and ultracentrifuged again at high speed to pellet sEVs.

sEVs isolated by sucrose cushion ultracentrifugation of ADS containing unpurified EVs produced a similar protein profile compared dUC for syntenin-1, CRYAB, and calnexin (Figure 34). Heat shock cognate 71 (HSC70), a chaperone protein previously reported as a pan-EV marker (Kowal et al., 2016), was reduced in cUC-sEVs compared to dUC-sEVs.

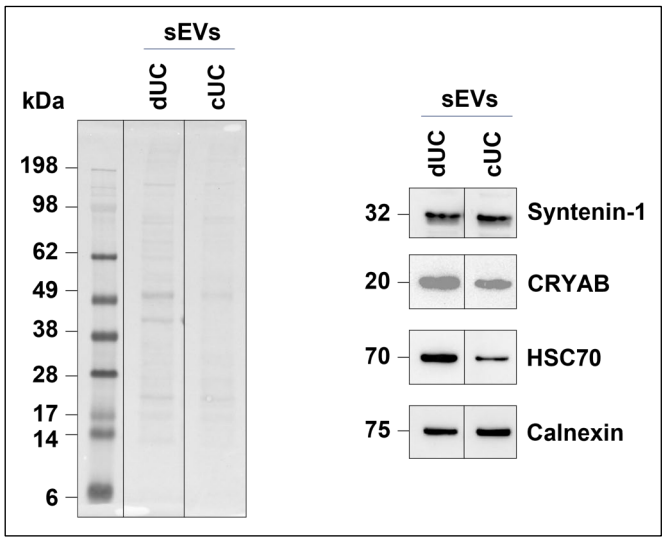


Figure 34. Ponceau Red staining (left panel) and western blot (right panel) of neonate rat cardiac sEVs isolated by dUC or cUC of ADS solution. 5µg of protein of each sample was loaded.

3.1.3. Polyethylene glycol precipitation (PEG)

Polyethylene glycol (PEG) has been used to non-specifically precipitate EVs in many sample types, and is a principal component of total EV isolation kits. It works by forming an aggregate of suspended EVs in a solution, allowing their precipitation following a relatively short incubation time. The precipitate is then easily collected by low speed centrifugation.

PEG-sEVs were compared to NRVM cell lysates and dUC-sEVs. Conventional sEV marker CD63 was not detected in sEVs isolated by both techniques (Figure 35), suggesting that conventional markers may not be enriched in these EVs. LDB3 was detected in sEVs isolated by both techniques, although only a high MW (~100 kDa) isoform was observed in dUC-sEVs, while both high and low MW (~78 kDa) isoforms were detected in PEG-sEVs. This confirms LDB3 splice variation as observed previously (Figure 32), and implies a differential loading of LDB3 isoforms into EV subtypes. CRYAB was also detected in sEVs using both techniques. Syntenin-1 was detected in higher levels in dUC-sEVs compared to PEG-sEVs, indicating higher exosomal enrichment, although this was accompanied by a higher albumin contamination. This may be due to the capacity of certain secreted proteins to pellet at high centrifugation speeds. Finally, RNA-binding protein MVP was most enriched in dUC-sEVs, suggesting a potential role of MVP in RNA loading into sEVs obtained by this technique.

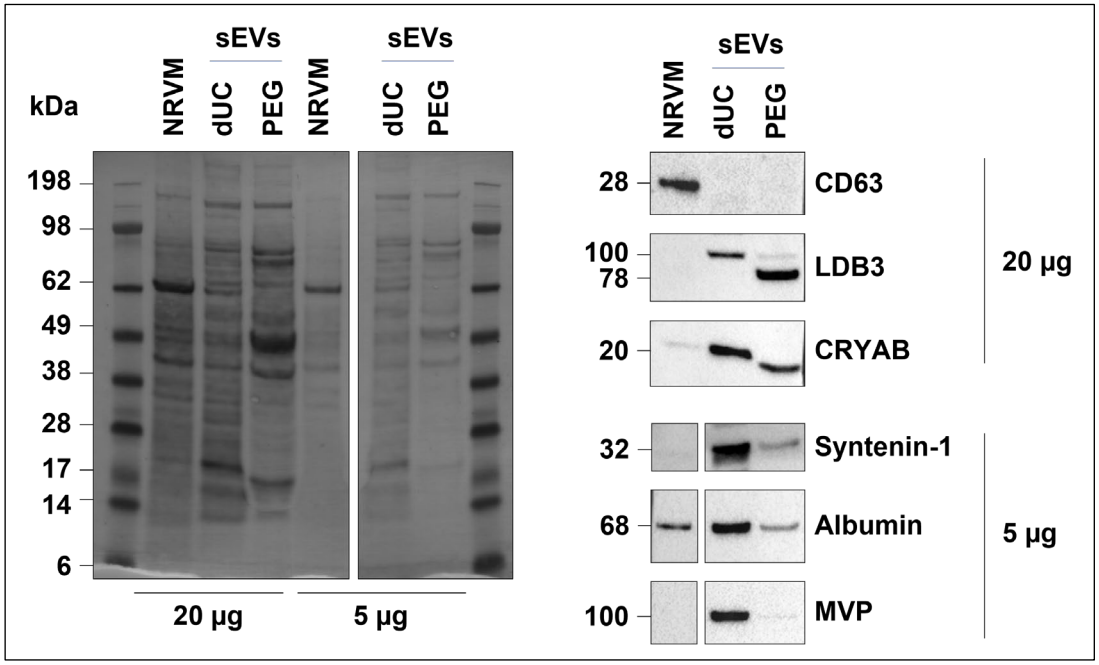


Figure 35. Ponceau Red staining (left panel) and western blot (right panel) of lysates from neonate rat ventricular myocytes (NRVM) and cardiac small EVs isolated by dUC or by PEG of ADS solution. 20µg or 5µg of protein of each sample was loaded as indicated.

3.1.4. Density gradient ultracentrifugation (DGUC)

Next, density gradient ultracentrifugation (DGUC) was used by placing ADS solution (after removing lEVs) on a discontinuous iodixanol gradient followed by high speed centrifugation. This allows the EVs to pass through the gradient until they reach an equilibrium density different from that of secreted proteins in solution.

After separating ADS solution by DGUC, 1-mL fractions were collected from the top of the ultracentrifugation tube. Pierce Bicinchoninic Acid (BCA) protein quantification revealed a high protein concentration in earlier, lower density fractions, which progressively declines in later, more dense fractions (Figure 36A). Fractions 1 to 9 were loaded either in equal volume (24 µL) or equal protein amount (2.5 µg) into a gel and migrated for a western blot (Figure 36B). In both cases, CRYAB was detected from fraction 4 to 9. The mature form of A Disintegrin and metalloproteinase domain-containing protein 10 (ADAM10), a sEV marker, and calnexin were observed in fractions 6 to 9. Albumin was concentrated in low density fractions, implying a separation of extracellular contaminants from ADAM10-positive EVs. Heat shock protein 70 (HSP70), another chaperone protein previously identified as an EV marker, similarly appeared

in the protein-rich low-density early fractions, implying that it is mainly secreted by cells as a free protein, and not in EVs. EVs may therefore be separated by DGUC, where CRYAB- and ADAM-containing EVs appear in fractions separated from soluble protein contaminants. Calnexin signal may be due to intracellular vesicles at similar density to EVs, which are therefore more difficult to distinguish from EVs.

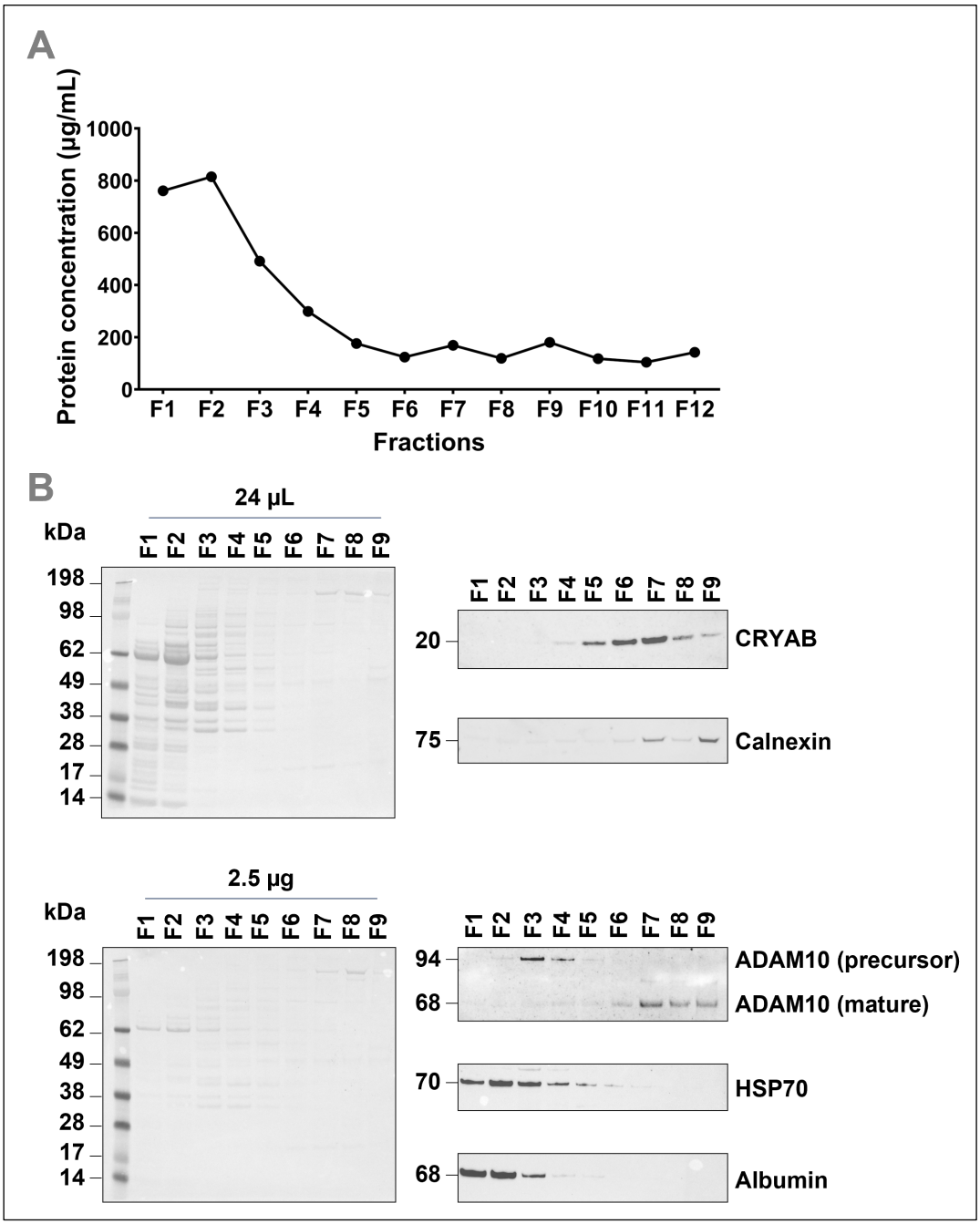


Figure 36. (A) Pierce Bicinchoninic Acid (BCA) protein quantification of DGUC-separated ADS solution fractions. (B) Ponceau Red staining (left panel) and western blot (right panel) of fractions 1-9 of DGUC-separated ADS solution, loaded in equal volume (upper panel) or equal protein amount (lower panel). ADAM10: A Disintegrin and metalloproteinase domain-containing protein 10. HSP70: heat shock protein 70.

The same samples were migrated on a different type of gel (10% acrylamide) to confirm previous results (Figure 37). As observed before, CRYAB appeared between fractions 4 and 10. Nucleoporin p62, a nuclear envelope protein which is not associated with microvesicles and exosomes (Lunavat et al., 2015), was observed in early fractions 2 and 3, implying its separation with non-EV components.

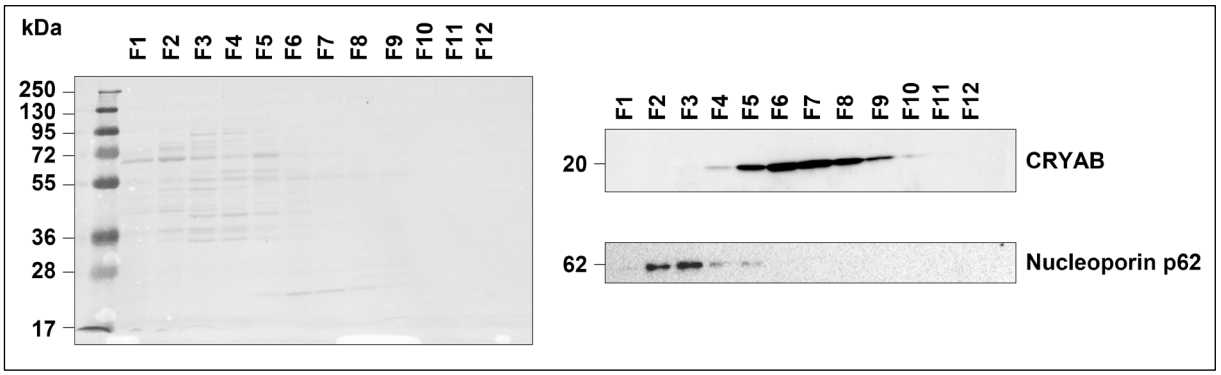


Figure 37. Ponceau Red staining (left panel) and western blot (right panel) of fractions 1-12 of DGUC-separated ADS solution, loaded in equal protein amount (2.5 µg).

In order to eliminate any remaining iodixanol from the OptiPrep solution used to construct the density gradient, a similar experiment was performed where DGUC fractions were re-diluted in DPBS and centrifuged individually at high speed. Pellets were resuspended in lysis buffer for western blotting (Figure 38). Fractions displayed a different protein profile upon Ponceau staining. Syntenin-1 was detected in fractions 7 and 8, consistent with ADAM10 signal observed previously (Figure 36B). Syntenin-1 was also observed in fraction 10, which may be caused by the presence of different sEV subtypes which were present at separate densities. Calnexin signal was also observed in fractions 7 to 10, similarly to previous results (Figure 36B). MYH7 was also detected in fractions 7 to 10, although its levels were low due to the long exposure time which was necessary to observe it. This overlap of calnexin and MYH7 signals may indicate that MYH7 is taken up by intracellular vesicles formed by damaged cells during tissue mincing. Nucleoporin p62 was not detected using this technique.

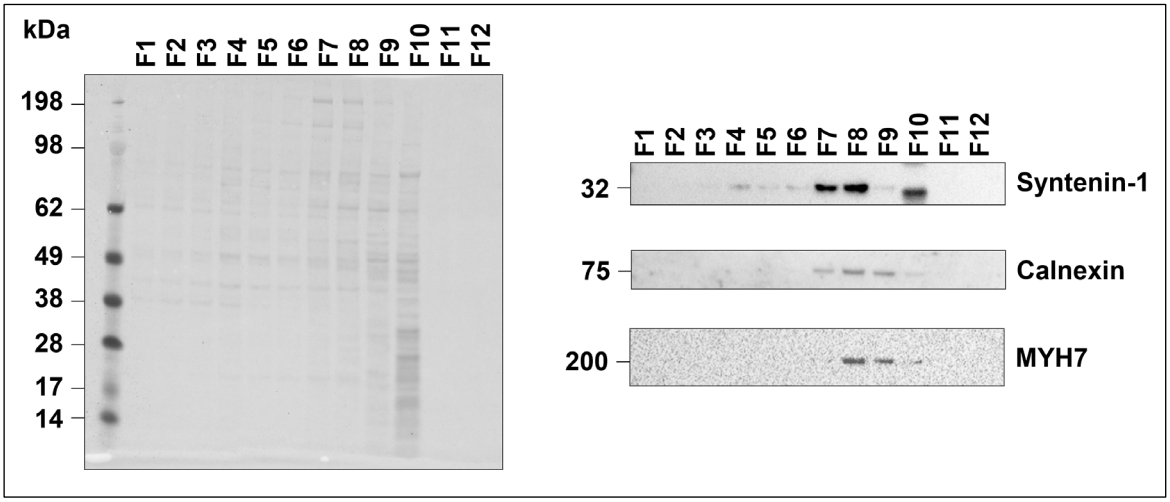


Figure 38. Ponceau Red staining (left panel) and western blot (right panel) of fractions 1-12 of DGUC-separated ADS solution pelleted by ultracentrifugation. Pellets were resuspended in RIPA lysis buffer and loaded entirely for migration.

3.2. Adult rat EVs

In order to verify whether cardiac EVs from adult rats have similar profile and can be isolated with the same capacity as those in neonate rats, some techniques were also applied to adult rat heart tissue.

3.2.1. Differential ultracentrifugation

After enzymatic digestion of adult rat left-ventricular tissue, digestion solution was used to isolate adult cardiac EVs (Figure 39A). dUC was applied to the digestion solution (after removing debris and cells by a 2,000*g* centrifugation) to obtain lEVs (15,000*g* pellet) and sEVs (164,000*g* pellet), or washed sEVs (164,000*g* followed by resuspension in DPBS, then another 164,000*g* centrifugation) (Figure 39B). Syntenin-1 was detected in both raw and washed sEV pellets. Interestingly, CRYAB was not detected in either lEVs or sEVs, implying a difference in EV cargo between neonate and adult cardiac EVs. HSC70 was detected in tissue lysate and appeared in both lEVs and sEVs, showing little selectivity to either type of EV. Calnexin was detected in lEVs, with low amount detected in the raw sEV pellet. Calnexin signal increased when sEV pellet was washed by a second centrifugation at 164,000*g*. This may be due to the elimination of protein contaminants during the wash step, while calnexin-containing intracellular vesicles remained in the solution and sedimented with the washed sEV pellet. This is supported by the detection of lower amounts of albumin following the wash step. Annexin

A5, a marker of apoptotic cells, appeared mostly in the tissue lysate and lEVs, implying that apoptotic bodies pelleted at 15,000*g* or below.

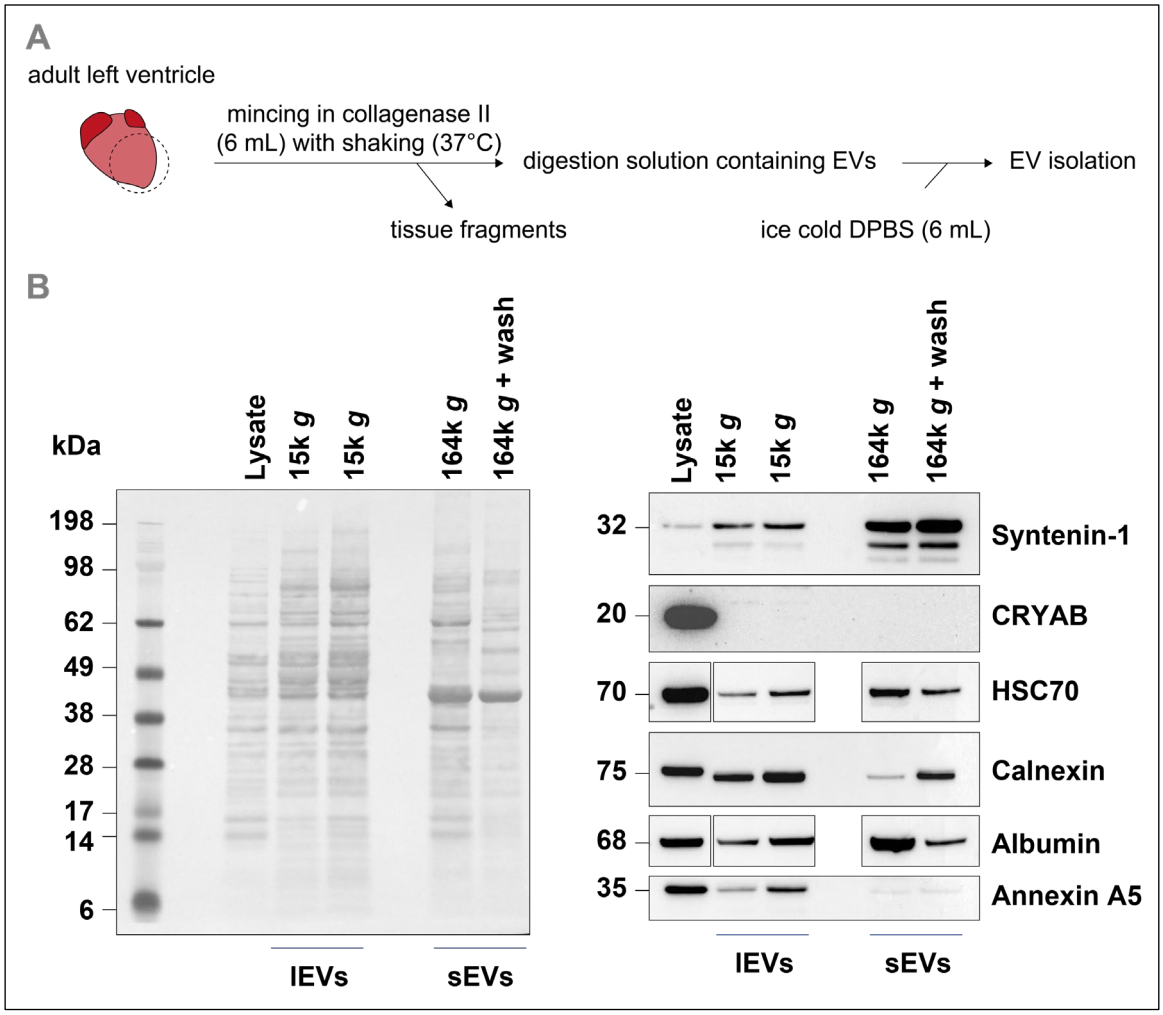


Figure 39. (A) Experimental procedure for the preparation of adult rat heart-derived EVs via mincing of ventricles in collagenase II digestion solution. Digestion solution is mixed 1:1 with ice-cold DPBS to stop the digestion. EVs are isolated from the digestion solution using different techniques. (B) Ponceau Red staining (left panel) and western blot (right panel) of adult rat left-ventricular tissue lysate, as well as centrifugation pellets of tissue digestion solution obtained at different speeds. 10µg of protein of each sample was loaded on two different gels. Ponceau of gel for HSC70 and albumin blots was not displayed. k *g*: ×1000*g*.

3.2.2. Cushioned ultracentrifugation

In order to verify whether a higher purity can be obtained by cUC, it was also applied on adult cardiac samples. Syntenin-1 was detected in the cUC-sEV pellet compared to tissue lysate and lEVs (Figure 40), indicating successful exosome enrichment. CRYAB was detected in all samples, with no specific enrichment. Similarly to dUC, HSC70 was detected in tissue lysate, lEVs and sEVs. MVP was detected in sEV pellet, consistent to dUC-sEVs of neonate rats.

MYH7 was detected in lysates and lEVs, but not in sEVs, implying that it is not associated with sEVs as shown before (Figure 33B). Calnexin was detected in all samples, and is consistent with previous results showing its association with sEV upon their isolation.

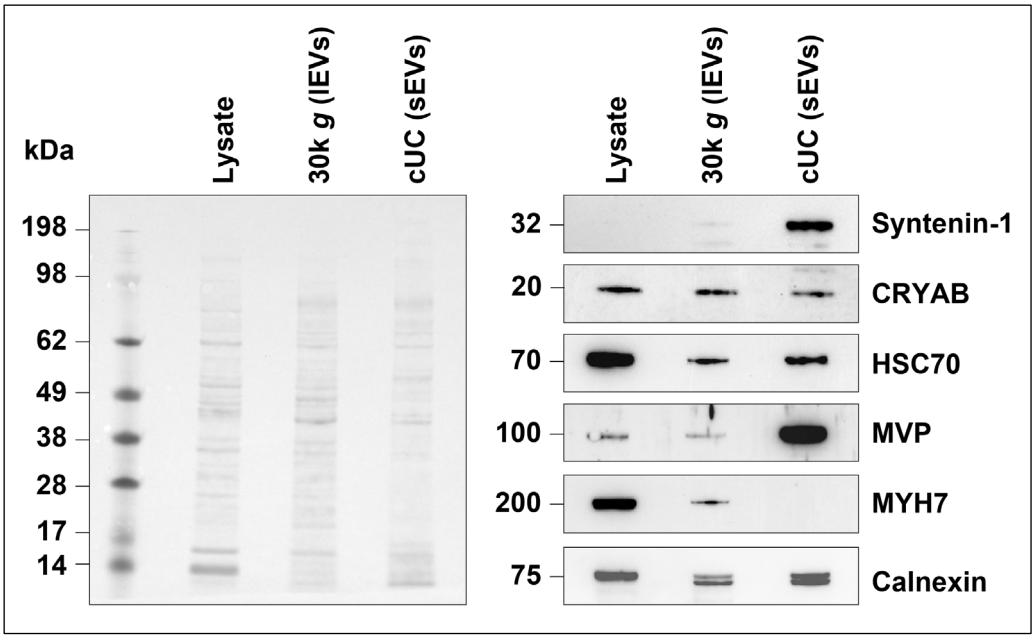


Figure 40. Ponceau Red staining (left panel) and western blot (right panel) of adult rat cardiac lEVs (30k *g*) and cUC-sEVs. 10µg of protein of each sample was loaded. k *g*: ×1000*g*.

To study possible tissue-to-tissue variability, cUC was also performed on adult rat liver tissue. The same procedure was applied to liver tissue. Syntenin-1 was detected in cUC-sEVs of both heart and liver compared to their respective tissue lysate and lEVs (Figure 41). However, syntenin-1 was notably more expressed in cardiac samples, in both tissue and EVs, than in liver samples. This is likely due to differential proteomic expression profiles between the tissue types. CRYAB enrichment was specifically observed in cardiac tissue lysate, consistent with the fact that its expression is specific to the heart. In contrast to results observed in neonate samples (Figure 34), there was low CRYAB detection in cardiac sEVs obtained from adult rats (Figure 39B, Figure 40, Figure 41), indicating that loading of CRYAB into sEVs is reduced with age. HSC70 was detected in both cardiac and liver tissue lysates in similar amounts, with lower levels in lEVs and sEVs, consistent with dUC results (Figure 39B). Calnexin expression was higher in liver compared to heart, and was detected in both lEVs and sEVs potentially due to co-isolation of intracellular vesicles similarly to previous results (Figure 34, Figure 39B). The lower detection

of calnexin in cardiac samples was likely due to its comparatively strong expression in liver samples.

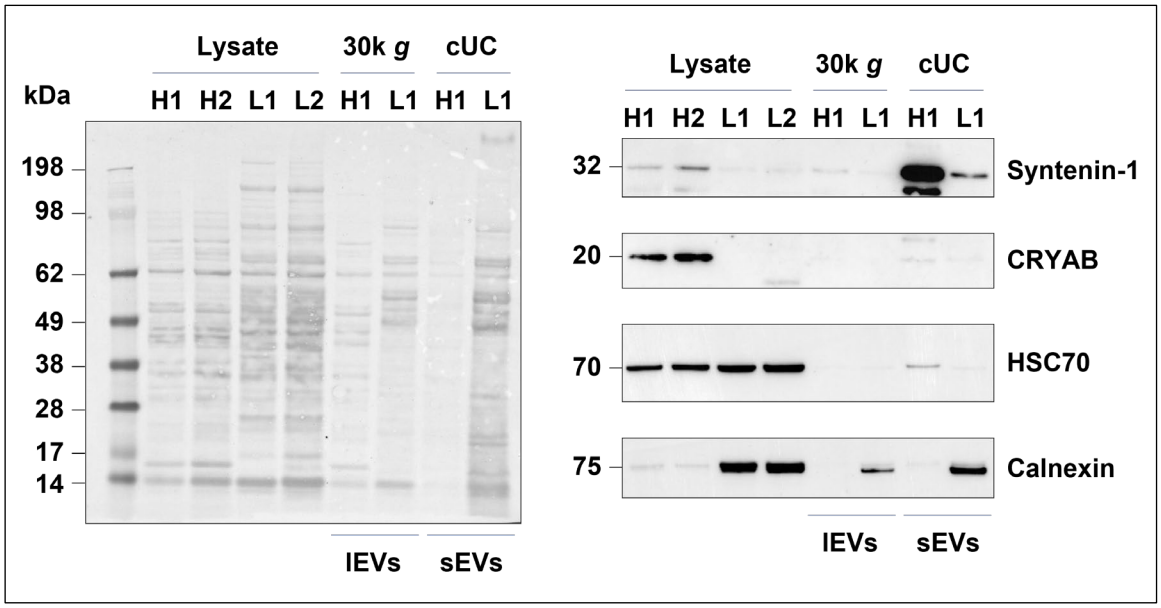


Figure 41. Ponceau Red staining (left panel) and western blot (right panel) of adult rat cardiac liver and heart lysates, lEVs (30k *g*), and cUC-sEVs. 5µg of protein of each sample was loaded. k *g*: ×1000*g*. H: heart. L: liver.

3.2.3. Density gradient ultracentrifugation

DGUC was used to purify adult rat cardiac EVs similarly to neonate EVs in Figure 38. DGUC fractions 1 to 12 revealed an enrichment of syntenin-1 from fraction 7 to 12, indicating a wide range of small EV populations containing this protein and displaying different density properties. A density shift occurred in the detection HSC70, which appeared in density fractions 7 to 10 (Figure 42). This indicates that different populations of vesicles may exist containing either syntenin-1 or HSC70, and float at different densities. Calnexin was also detected in fractions 7 and 10. The appearance of calnexin and HSC70 in similar fractions may also indicate that these proteins are both loaded inside intracellular vesicles formed due to cellular damage. Albumin was detected in fraction 8, but long exposure was necessary (135 seconds compared to 4 seconds in Figure 36B). Additionally, albumin appeared in a different fraction compared to previously observed results (Figure 36B), indicating that albumin may exist in small amounts in vesicles co-isolated in these fractions. CRYAB and nucleoporin p62 were not detected using this technique. We observed that nucleoporin contamination was also not observed in other techniques used on adult rat samples, which explains its absence from DGUC fractions.

Similarly, CRYAB was detected in much lower levels in cardiac sEVs from adult rats compared to neonate rats. Finally, the density shift of some proteins in adult rat DGUC fractions compared to neonate DGUC may either be due to a difference in EV density characteristics during aging, or due to technical aspects of the experiment such as ultracentrifugation speed (100,000*g* in neonate DGUC vs 186,000*g* in adult DGUC, leading to a general density shift of all fractions).

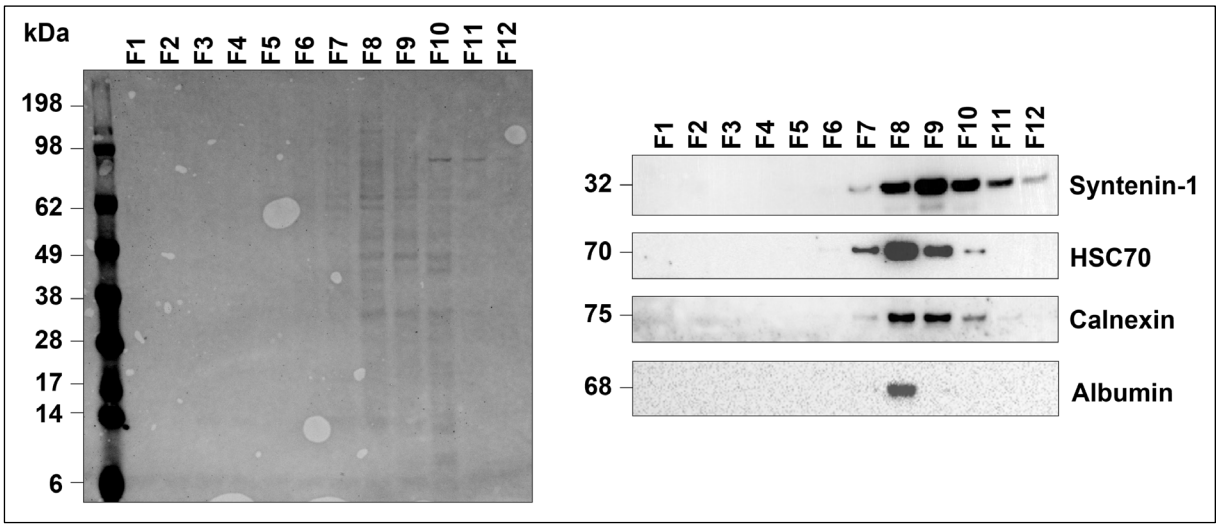


Figure 42. Ponceau Red staining (left panel) and western blot (right panel) of fractions 1-12 of DGUC-separated adult rat heart digestion solution. Fractions were collected from the top of the density gradient then pelleted by ultracentrifugation. Pellets were resuspended in RIPA lysis buffer and loaded entirely for migration.

Although the density overlap between sEVs and intracellular vesicles made it difficult to separate those vesicle populations using DGUC, it was still successful for separating sEVs from soluble proteins generally co-isolated with these EVs (such as secreted albumin, free proteins released by damaged cells such as nucleoporin p62).

3.3. Conclusion for EV isolation techniques

After using these techniques, we concluded that different EV populations exist that are separated by different methods. Large EVs can be obtained by pelleting at a medium speed centrifugation (10,000*g* to 30,000*g*) of the supernatant of an initial low speed centrifugation (2,000*g* to 3,000*g*) that eliminates cells and debris. For small EVs, results from the different isolation techniques used were summarized in Table 5. These results were similar between neonate and adult samples, however, it was not possible to use PEG with adult samples as there

was a much lower precipitation yield which was insufficient for analysis.

For neonate samples, PEG provided the highest yield, while dUC provided high yield and moderate purity. In order to improve PEG purity, PEG precipitates were resuspended in DPBS and centrifuged at high speed to eliminate some non-vesicular proteins and PEG solution present in the precipitate. This combination of the two techniques was labelled "PEG+UC". For adult samples, simple dUC was most adapted, and was therefore used for later experimentation to validate LDB3 as a marker of cardiac EVs.

Among the used markers, syntenin-1 was most reliable as a general sEV marker. This was consistent with recent findings comparing sEVs isolated from different cell lines which found syntenin-1 to be a universal exosomal marker (Kugeratski et al., 2021). A specific marker of lEVs remains difficult to establish, although general EV markers (existing in lEVs and sEVs) can be used to identify them, such as HSC70. Finally, contamination with secreted proteins was possible using albumin, and calnexin was practical in identifying intracellular damage vesicles.

Table 5. Summary of EV isolation techniques used.

	dUC	**cUC**	**PEG**	**DGUC**
Yield	•••	••	••••	•
Purity	••	••	•	••••
Ease of use	•••	••	••••	•
Time (h)	2.5	4	16	20
Hands-on time (h)	<1	<1	<0.5	1
Cost per sample (€)	11	16.5	5	17.5

Legend: •=low; ••=moderate; •••=high; ••••=very high

3.4. Validation of LDB3 as a cardiac EV marker

In order to confirm the presence of LDB3 cardiac-derived EVs, and to validate its expression at higher levels in cardiac EVs compared to similar EVs found in the circulation, dUC, PEG, and PEG+UC were used from neonate heart and plasma samples. These EVs were compared for the presence of LDB3 and sEV marker syntenin-1 (Figure 43).

LDB3, syntenin-1, and CRYAB were all detected in both lEVs and sEVs, implying that a portion of sEVs may be co-pelleted with lEVs (Figure 43, left panel). Due to the relatively high amount of these proteins in EVs compared to tissue lysate, they were not yet detected (LDB3) or detected in lower amount (syntenin-1, CRYAB) in tissue when their signal reached saturation in EVs during exposure. The three proteins were also detected in sEVs using the three techniques, but syntenin-1 and LDB3 levels were increased in PEG+UC compared to dUC or PEG alone, implying that the combined technique provides a higher proportion of LDB3-containing sEVs.

Isolation of sEVs from heart and plasma samples was confirmed by syntenin-1 (Figure 43, right panel). LDB3 was detected exclusively in cardiac EVs compared to plasma EVs, regardless of the technique used. LDB3 is present in plasma EVs, as shown in mass spectrometry of plasma EVs after EVtrap isolation (Figure 31B), however, due to the existence of EVs from different organs in the circulation, the proportion of cardiac EVs in the plasma is reduced. It is therefore possible that western blotting is not sensitive enough to visualize LDB3 in plasma EVs.

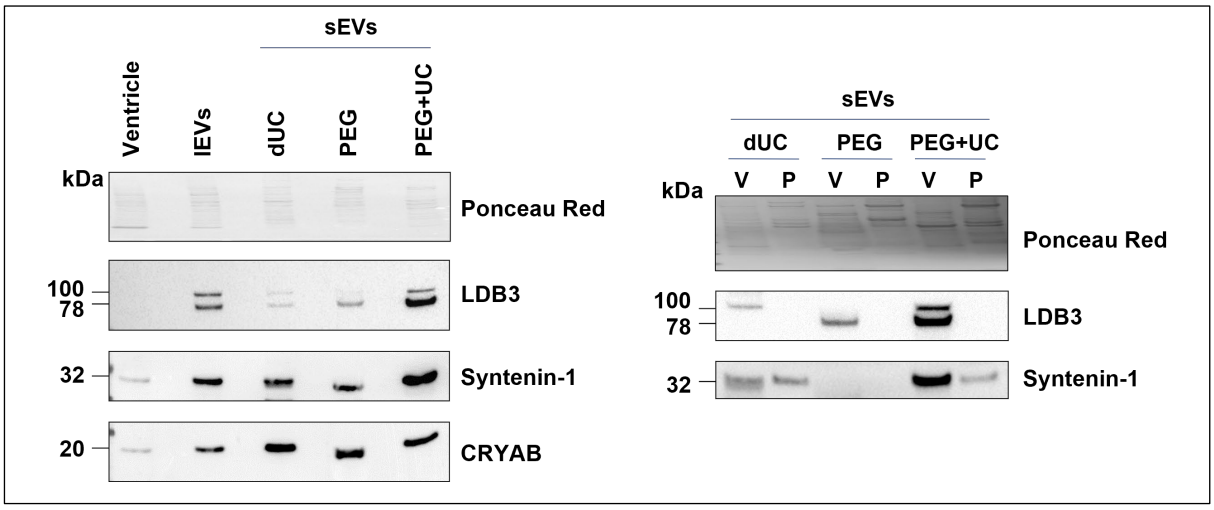


Figure 43. Ponceau Red staining (top panel) and western blot (bottom panels) of large EVs (lEVs) and sEVs isolated via dUC, PEG, and PEG+UC from neonate rat cardiac tissue detecting LDB3, syntenin-1, and CRYAB levels (left panel). The same techniques were used to compare LDB3 levels in EVs isolated from neonate rat ventricles and plasma (right panel). 10µg of protein of each sample was loaded. V: ventricle. P: plasma.

Furthermore, size exclusion chromatography (SEC) was performed on ADS solution obtained from neonate rats to separate EVs from non-vesicular components (secreted proteins) (Figure 44A). During this technique, the pre-cleared ADS sample (3,000*g* supernatant; input)

was passed through a SEC column which separates small molecules, including free proteins, from EVs, which elute earlier from the column. NTA and electron microscopy confirmed that EVs are present in earlier fractions (from fraction 7) and their concentration decreases gradually in later fractions, while Pierce BCA quantification showed that protein concentration increases starting from fraction 10 (Figure 44B). To verify whether LDB3 elutes with free proteins in ADS, a fraction of non-vesicular components (fraction 20) was compared to lEVs and sEVs obtained by dUC (Figure 44B). LDB3 was only detected in lEVs and sEVs, but not in the secreted proteins of the NV fraction. Conversely, more albumin was detected in the NV fraction compared to lEVs and sEVs. This indicates that LDB3 is not associated with non-vesicular proteins, and is contained in the cargo of EVs which elute before NVs.

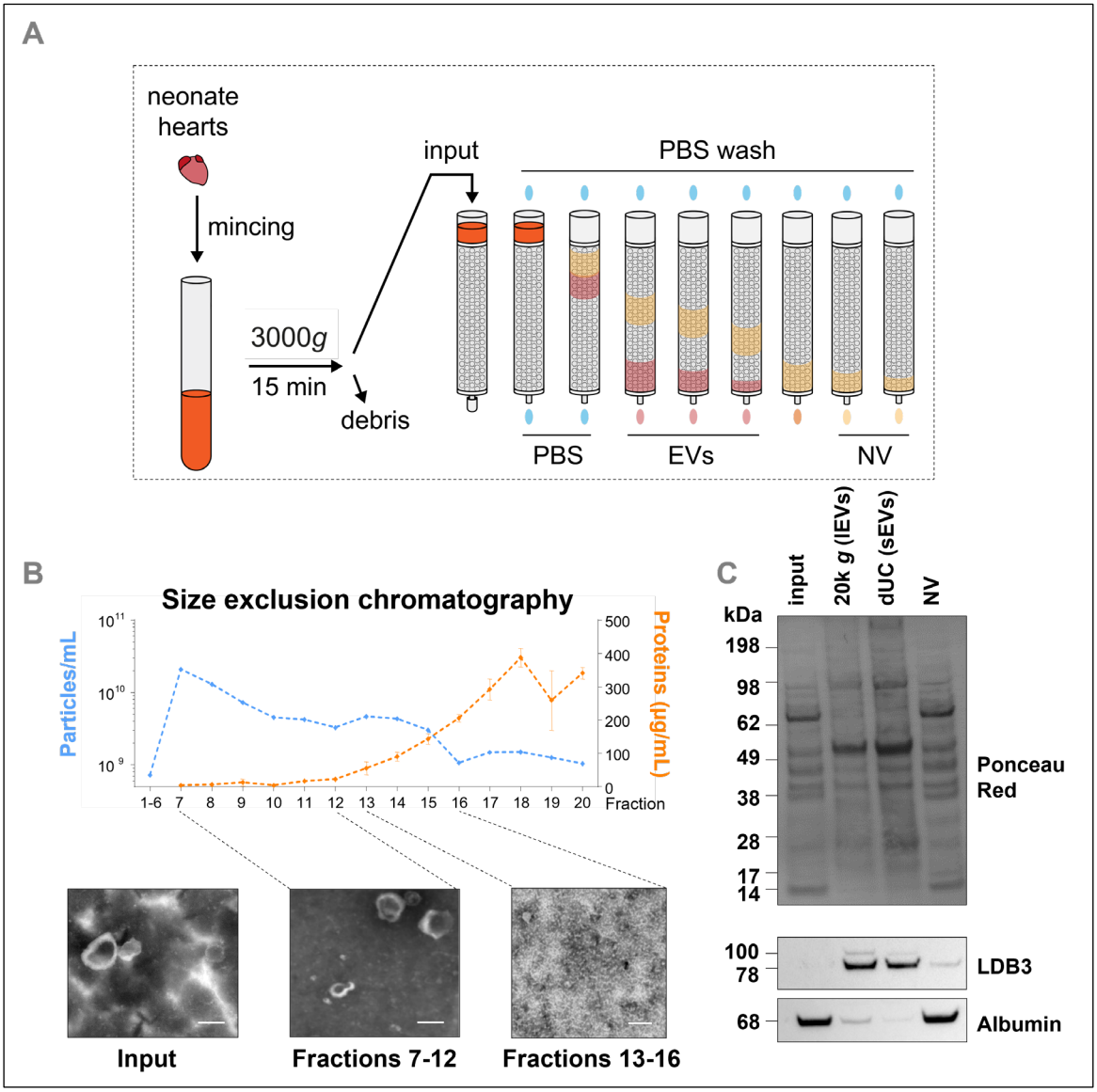


Figure 44. (A) Experimental procedure of size exclusion chromatography (SEC) on ADS solution. (B) Graph representing particle concentration (left axis; blue) as measured by nanoparticle tracking analysis (NTA) and protein concentration (right axis; orange) as measured by Pierce BCA. Fractions 7-12 (EV-rich) and 13-16 were pooled and visualized by electron microscopy. Scale bars = 150 nm. (C) Ponceau Red staining and western blot of non-purified ADS solution (input) and protein-rich non-vesicular (NV) SEC fraction 20 compared to EVs obtained by dUC (20,000g for lEVs and 100,000g for sEVs). Equal amount of protein was loaded for each sample. k *g*: ×1000*g*.

In conclusion, using different isolation techniques and EV identification using different markers, we showed that LDB3 is a viable marker contained in cardiac EVs. This protein was not associated with common contaminating factors such as free, secreted proteins.

In order to move forward in the validation of LDB3, experiments in the next section were performed to study its levels in cardiac tissue and EVs during heart failure and acute decompensated heart failure, verifying whether these disease states impact its intracellular levels

and its loading into cardiac EVs.

4. LDB3 in acute decompensated heart failure (ADHF)

Information in this section appeared in Abou Zeid et al., 2022 (Abou Zeid et al., 2022).

4.1. LDB3 expression during HF

To validate LDB3 in human HF patients, we investigated its expression in LVs from patients with HF and controls who died from non-cardiovascular reasons. In these samples we identified two LDB3 bands, a high MW of ~78 kDa band, and a low MW of ~66 kDa (Figure 45). These bands may correspond to the full-length (UniProt: O75112) and isoform 2 (UniProt: O75112-2), respectively. LDB3 expression was significantly reduced in LV of patients with HF.

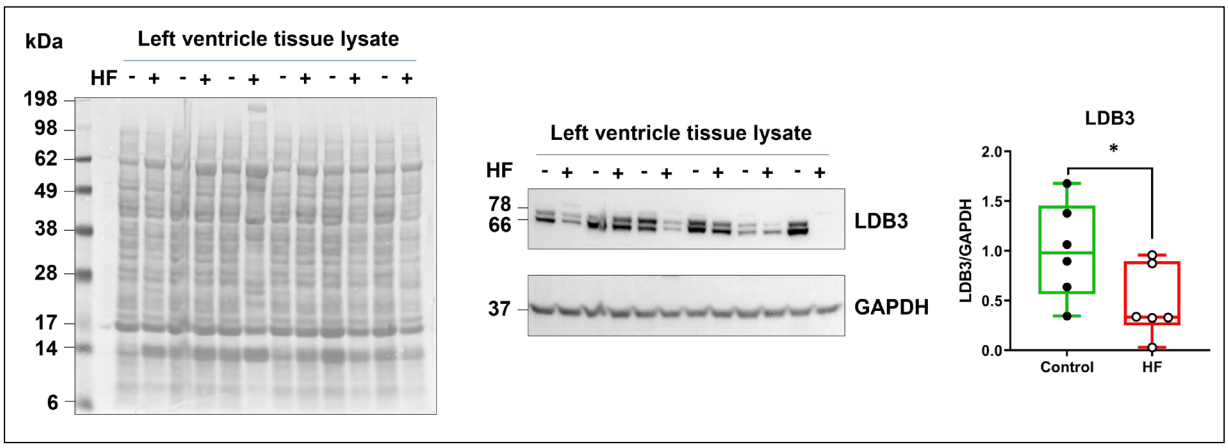


Figure 45. Ponceau Red staining and western blot of left-ventricular (LV) tissue of HF patients to detect LDB3 and quantified to GAPDH expression. 20µg of protein of each sample was loaded.

Next, human cardiac lEVs and sEVs were isolated by dUC at 20,000*g* and 100,000*g*, respectively, then analyzed by NTA (Figure 46A). In both controls and HF patients, sEVs had a mean diameter (172±3 nm in controls, 163±3 nm in HF) smaller than corresponding lEVs (213±3 nm in controls, 206±6 nm in HF). No significant change in cardiac EV concentration was observed during HF (Figure 46B). In both controls and HF patients, the amount of lEVs exceeded that of sEVs.

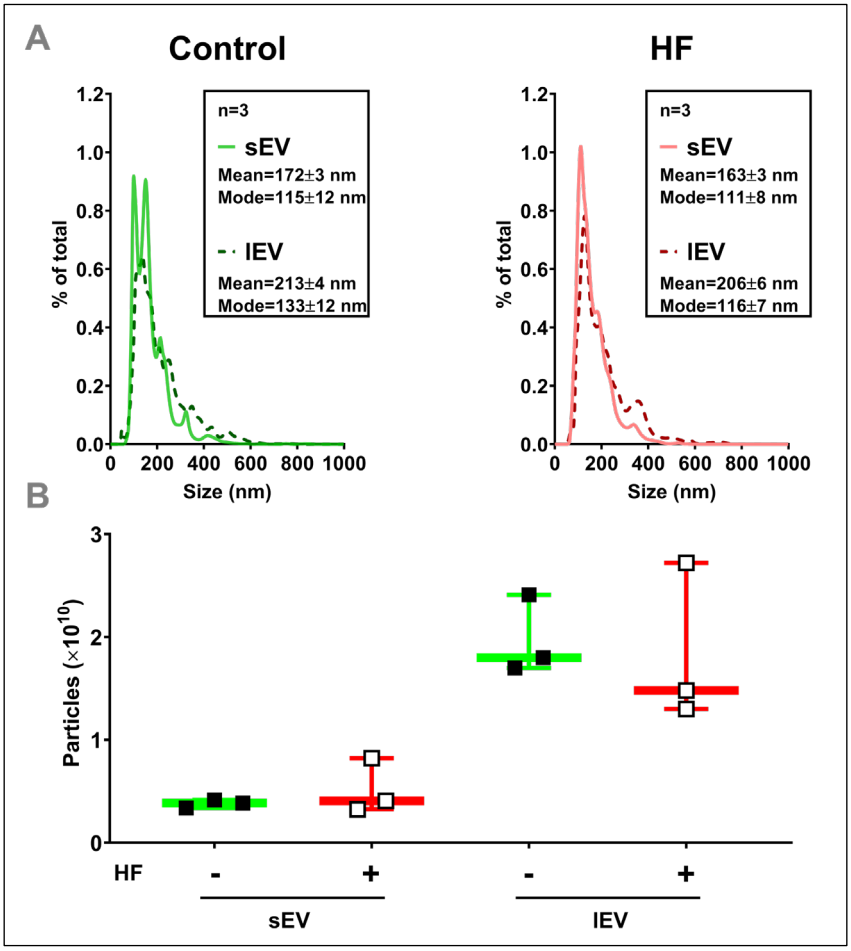


Figure 46. (A) EV size distribution and (B) total particle count of sEVs and lEVs of human cardiac sEVs and lEVs from controls or patients with HF. Size distribution was calculated as a percentage of total particles, measured using NTA.

Finally, LDB3 levels in cardiac EVs from control and HF patients were measured (Figure 47). Western blot revealed that the level of LDB3 does not change in either sEVs (left panel) or lEVs (right panel) during HF. This confirms that LDB3 may be used as a potential marker of cardiac EVs that is not influenced by disease state.

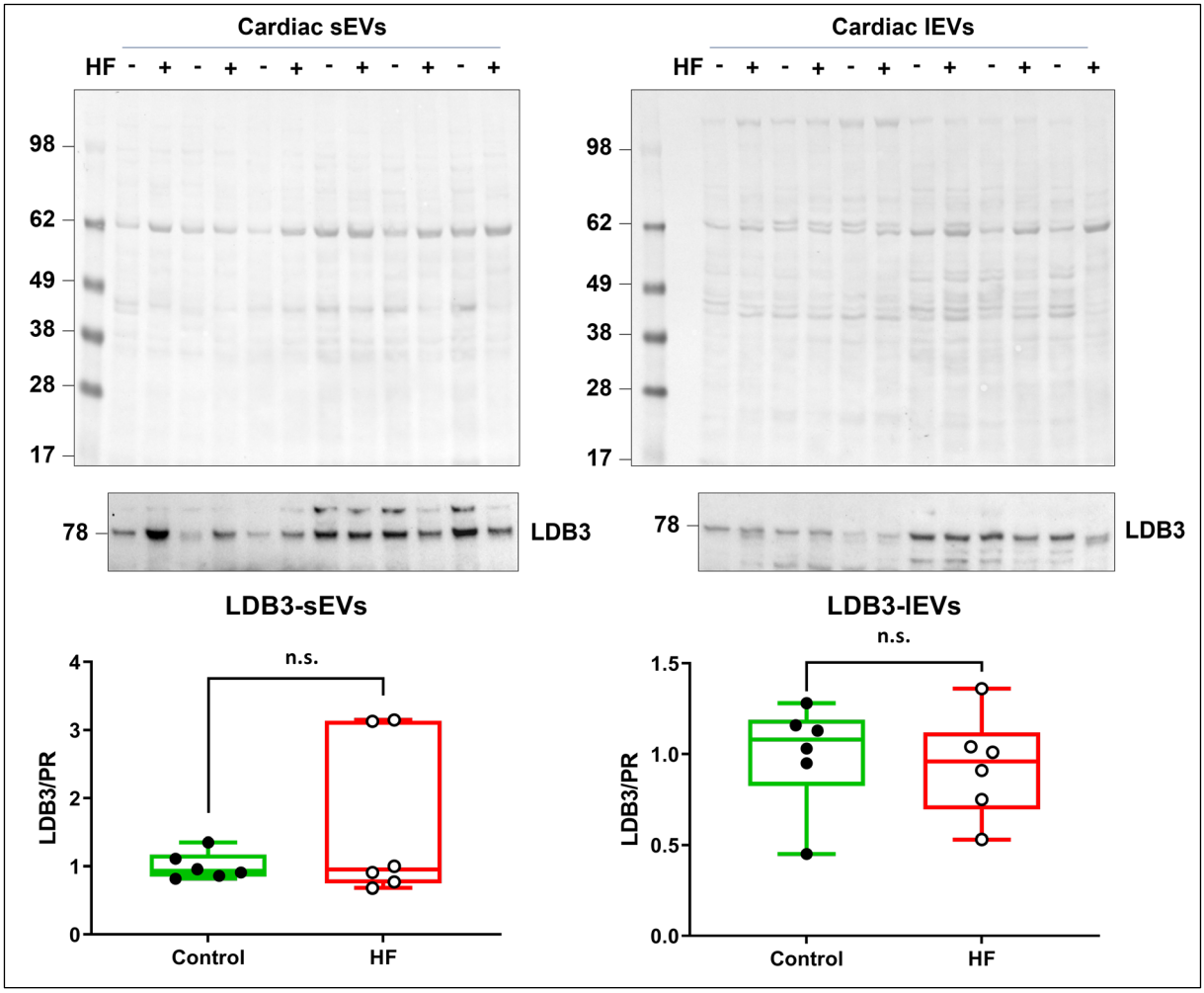


Figure 47. Ponceau Red and western blot to detect LDB3 in human cardiac sEVs (left panel) and lEVs (right panel) obtained from controls and patients with HF. LDB3 was quantified by normalizing to Ponceau Red. 5µg of protein of each sample was loaded.

4.2. Proteomic comparison of cardiac EVs in TG-treated and untreated ADHF

In order to investigate the role of EVs in more aggravated forms of HF, a rat model of acute decompensated heart failure (ADHF) developed by Pr. Paul Mulder (INSERM U1096, Rouen) was analysed. Following induction of myocardial infarction (MI) in adult male Wistar rats by coronary artery ligation, rats developed HF after three months. Acute decompensation was then induced by giving the rats a gavage of salt water (Peschanski et al., 2021). Some rats received an injection of O-GlcNAcylase (OGA) inhibitor Thiamet G (TG) 12 hours following salt treatment. Preliminary results have shown that TG treatment resulted in improved cardiac function and survival outcome in rats with ADHF receiving TG compared those not receiving

it. We were therefore interested in studying the possible role of cardiac EVs in this cardiac improvement.

EVtrap was performed to isolate cardiac EVs from left ventricle tissue of ADHF rats treated or not with TG. Mass spectrometry analysis of EVs from 4 samples of TG-treated ADHF rats and 4 untreated ADHF rats was performed. We identified 1865 proteins detected in at least 3 out of 4 samples in each group. When EV protein abundance was compared between the two groups, there were no significant changes detected (Table S7).

To go further in analysing the proteomic data, we found that all samples displayed LDB3, which was among the 20% to 30% most abundant proteins in these samples. Exosomal proteins, such as tetraspanins (CD63, CD81, CD9) were all detected in varying abundances, while syntenin-1 was detected in 5 out of the 8 samples tested. Conventional EV markers including HSP70, MVP, and HSC70 were also detected in these EVs. Non-EV markers were also detected using this technique. This difference in exosomal marker abundance compared to previous results, where tetraspanins were not detected in sEVs, may be due to the differences in EV populations obtained using the previous techniques and EVtrap. Notably, EVtrap uses the 3,000*g* supernatant followed by ultrafiltration with a 100 kDa filter, and therefore does not exclude lEVs from the sample and studies the totality of EVs. Figure 48 summarizes the mean abundance of previously studied proteins in each group.

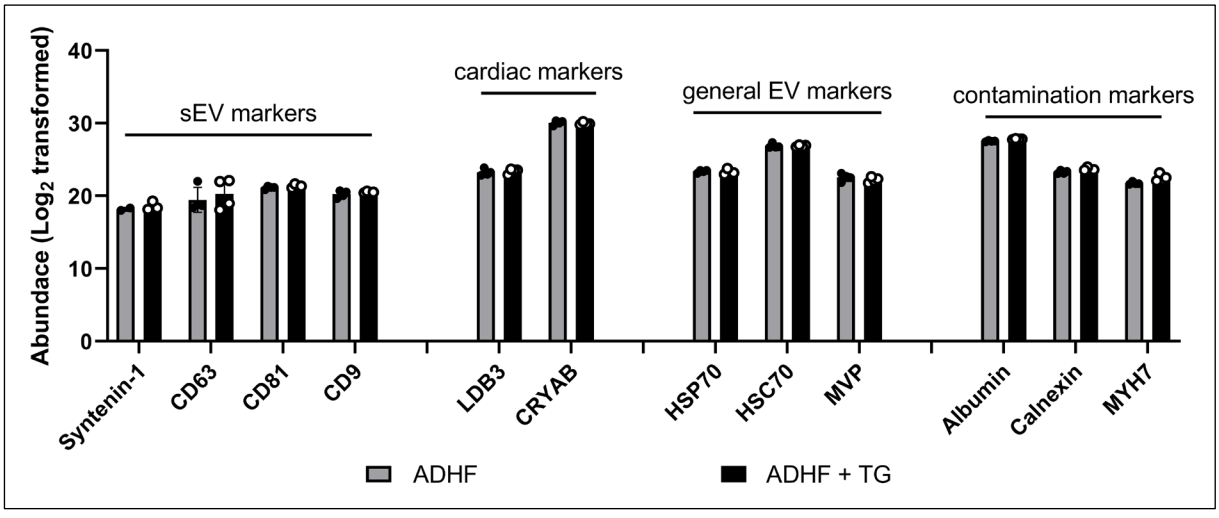


Figure 48. Abundances of the different proteins of interest which were observed in EVs from ADHF rats treated (black bars) or not (grey bars) with Thiamet G (TG). Values are expressed as means of log2-transformed abundance ± SEM.

Although no significant changes in EV protein abundances were observed following TG treatment in ADHF rats, we hypothesized that protein post-translational modifications may still be taking place in TG-treated rats.

4.3. LDB3 O-GlcNAcylation in Thiamet G-treated ADHF rats

4.3.1. Total LDB3 expression in left-ventricular tissue

Before studying LDB3 O-GlcNAcylation, we investigated whether its total level changes in rats with HF, ADHF, or TG-treated ADHF rats. Intracellular levels of LDB3 in left ventricles did not change between the three groups (Figure 49).

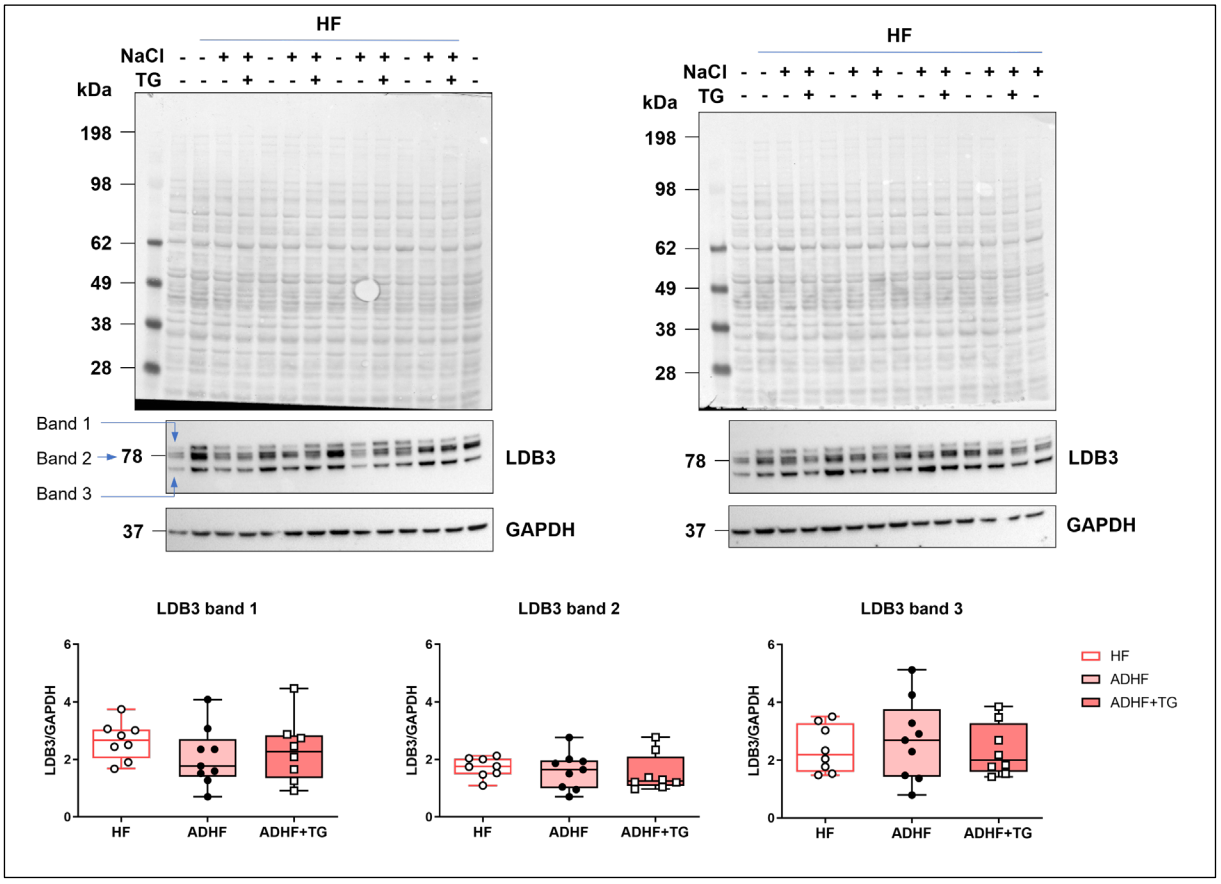


Figure 49. Ponceau Red staining (upper panels) and western blot (lower panels) of LDB3 expression in left-ventricular tissue of adult rats with HF, untreated ADHF (HF+NaCl), and ADHF treated with TG (HF+NaCl+TG). LDB3 was quantified by normalizing to GAPDH expression. 10µg of protein of each sample was loaded.

4.3.2. LDB3 immunoprecipitation and level of O-GlcNAcylation

In order to assess change in LDB3 O-GlcNAcylation between TG-treated and untreated

ADHF rats, an immunoprecipitation (IP) experiment was performed by incubating equal amount of protein extract from left ventricles of ADHF rats treated or not with TG with anti-LDB3 antibody. Using magnetic beads, the antibodies were recuperated and the immunoprecipitated proteins were separated from the supernatant (Figure 50A). Initial samples (input), immunoprecipitated proteins (IP LDB3), and supernatant proteins were then compared for their O-GlcNAcylation level in TG-treated and untreated ADHF rats by western blot (Figure 50B). IP LDB3 revealed a higher level of O-GlcNAcylation in a band corresponding to the MW (~78 kDa) of LDB3. This was confirmed following membrane incubation with LDB3 antibody, which revealed equal amounts of LDB3 being recuperated in IP LDB3 samples.

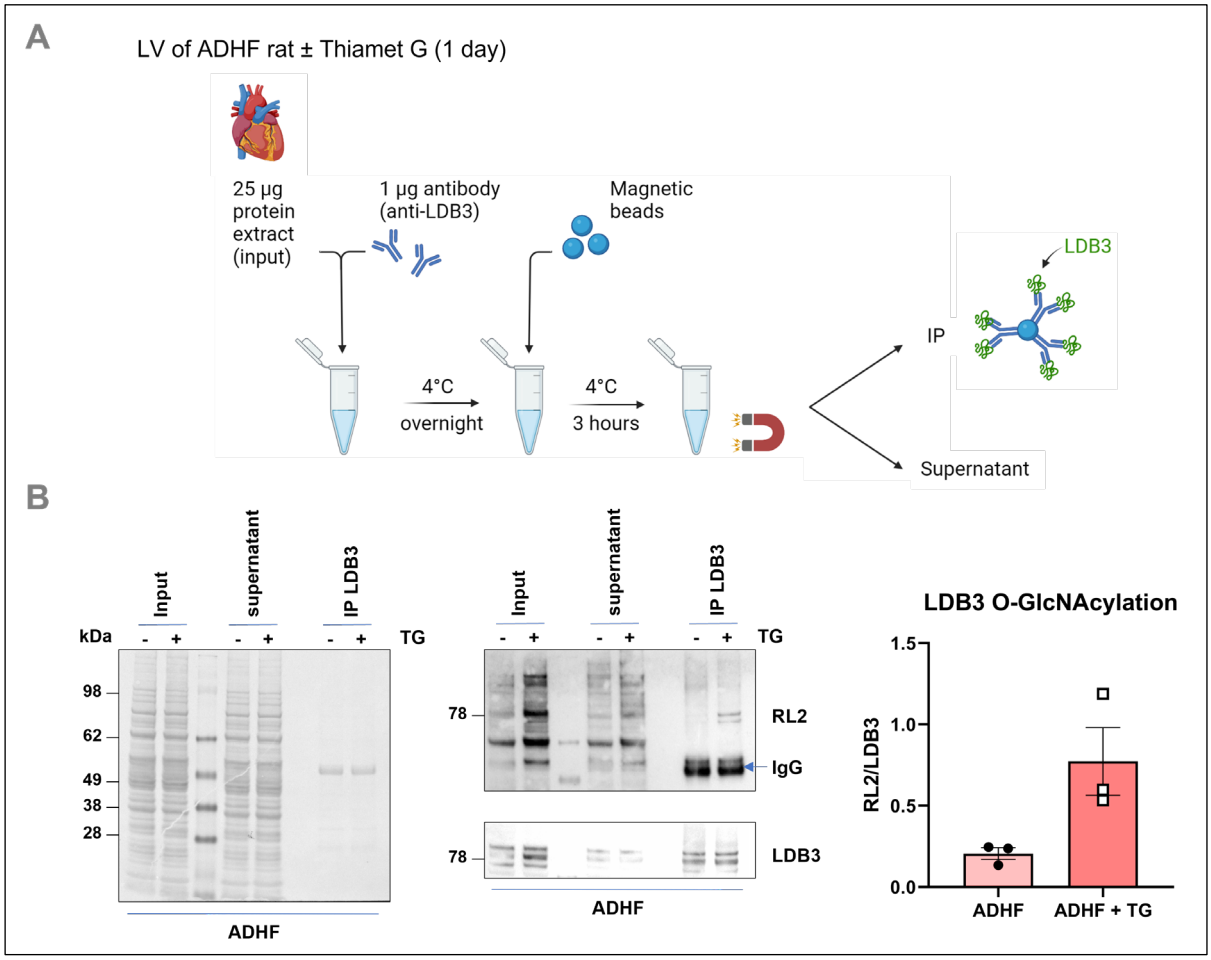


Figure 50. (A) Experimental procedure of LDB3 immunoprecipitation (IP) and separation using magnetic beads. Created using BioRender.com. (B) Ponceau Red staining (left panel) and western blot (right panel) of input, supernatant, and LDB3 immunoprecipitate from left ventricle of a TG-treated and an untreated ADHF rat. Values were represented as mean±SEM (n=3).

4.3.3. Cardiac EVs of ADHF rats

In order to investigate cardiac EVs from TG-treated and untreated ADHF rats, dUC was used to obtain sEVs. We detected a higher level of syntenin-1 in sEVs compared to LV lysate, indicating a successful isolation of exosome-enriched sEVs (Figure 51). LDB3 was also detected in these sEVs. Similarly to results obtained in neonate dUC-sEVs (Figure 43, left panel), a higher MW form of LDB3 was detected in sEVs, while other forms were detected in lysates, implying that cells secrete isoforms of LDB3 different from those present in cells. Interestingly, we detected CRYAB in higher levels in sEVs compared to lysates. In previous results of adult-derived sEVs (Figure 39B, Figure 40, Figure 41) CRYAB was either not detected, or detected in similar amounts to lysates. We hypothesize that this difference may be due to either the sex of the rats (males here vs. females in previous experiments), or the disease state (ADHF here vs healthy in previous experiments). HSC70 was detected in low amounts in sEVs compared to lysates, while calnexin was detected in similar amount in both, consistent with previous results (Figure 39B, Figure 40, Figure 41).

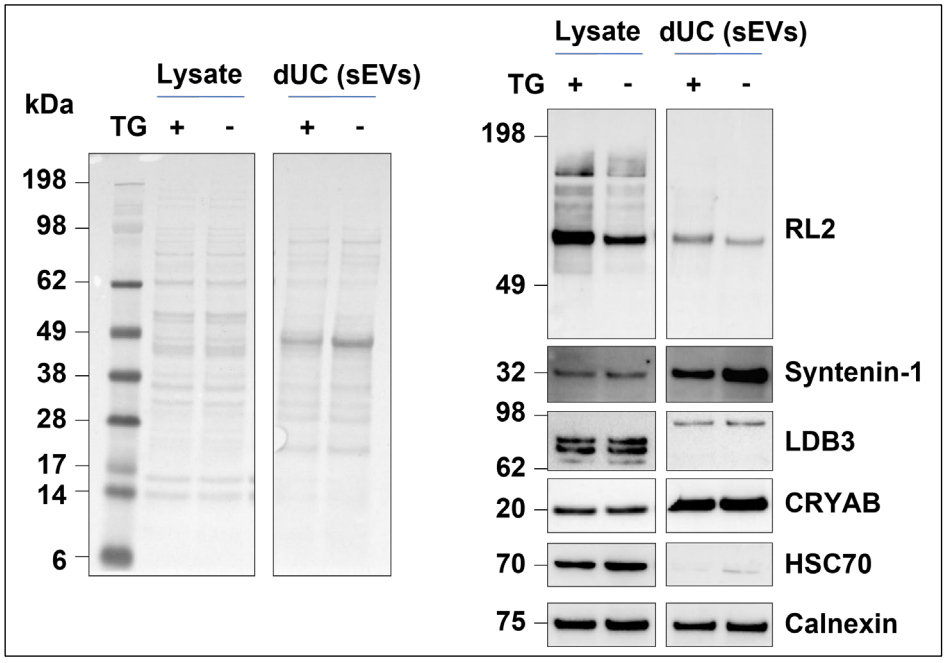


Figure 51. Ponceau Red staining (left panel) and western blot (right panel) of ADHF rat left-ventricular tissue lysate and sEVs isolated by dUC. 5μg of protein of each sample was loaded. Samples were produced by pooling 3 LV samples from each group.

4.3.4. Conclusion

In these experiments, we showed that LDB3 levels remain stable during chronic HF, then during acute decompensation without (ADHF) and with TG treatment (ADHF+TG). These results imply that changes in total LDB3 expression do not take places during worsening of HF, but PTM changes such as O-GlcNAcylation may still take place and can be induced by treatments such as OGA inhibition. Future work may investigate whether the change in LDB3 PTM are carried into EVs, and whether cells secrete O-GlcNAcylated cargo during cardiac distress.

Discussion & Perspectives

Characterization of cardiac EVs

The early detection of worsening heart failure may be an essential tool in the diagnosis and management of this condition. In our team, we have identified three microRNAs (miRNAs) which were elevated in the plasma during heart failure, and hypothesized that these molecules may be transported from the heart into the circulation inside extracellular vesicles (EVs) released from cardiac cells.

Evidence of EVs carrying regulatory molecules, including miRNAs, has been reported in the literature (Chen et al., 2017; Das and Halushka, 2015; Fernández-Messina et al., 2015; Qiu et al., 2018). The importance of EV cargo, be it proteins, lipids, or nucleic acids, as diagnostic and therapeutic tools has also been highlighted in recent publications (del Campo et al., 2022; Glover et al., 2019; Hoshino et al., 2020; Melo et al., 2015; Wang et al., 2020; Xie et al., 2022).

We found that sEVs obtained from the culture media of stressed cardiac cells contain these miRNAs, but do not display conventional protein markers commonly used to identify these sEVs (Figure 26, Figure 35). Previous studies have shown that these markers may not be expressed equally on all EV subtypes, and their presence depends on cellular origin (Crescitelli et al., 2013). Additionally, sEVs may display some tetraspanin markers but not others (Barranco et al., 2019). In our study, we deduced that cardiac EVs may have a unique protein profile.

In order to find specific markers of cardiac EVs, we isolated cardiac EVs from cultured cells and performed a proteomic analysis of the most abundant proteins observed. Little amounts of EVs were recovered from the culture media. This may have been due to the fact that these cells do not produce a high amount of EVs compared to cancer cells or cell lines, which are more frequently studied in EV literature. Indeed, serum-starvation was necessary to induce EV production in the three cell types studied (NRVM, NRVF, H9c2). Cellular stress through this starvation or through chemical treatment have been attested to increase EV production in several cell types (Hahm et al., 2021). Proteomic analysis of abundant proteins in cultured cardiac cells revealed the presence of proteins previously detected in sEVs isolated from cardiac myocyte cultures, such as heat shock proteins, LDHA, actin, and GAPDH (Malik et al., 2013)

(Figure 27B).

It was necessary to obtain a more complete picture of the cardiac EV proteome. EVtrap was therefore used as it combines higher sensitivity (low volume of starting material), and a robust proteomic analysis through LC-MS (Iliuk et al., 2020; Wu et al., 2018). In order to reach physiologically representative results, an *in vivo* sample source was used for this approach and was composed of neonate rat heart tissue and plasma. The use of these sample sources presents some challenges, such as the production of intracellular damage markers during the tissue mincing process necessary to release EVs from the ECM.

An enrichment in membrane proteins, endosomal proteins, and focal adhesion proteins was detected in cardiac EVs. This was consistent with a proteomic study investigating cardiac-derived EVs from adult mouse-derived cardiac EVs (Claridge et al., 2021). Plasma EVs were enriched in proteins typically found in the circulation, such as serum albumin, globulins, globins, and lipoproteins, which was consistent with similar proteomic studies of plasma EVs (Muraoka et al., 2022). By comparing the two groups of EVs, we identified 1033 proteins specifically enriched in cardiac EVs compared to plasma EVs. Out of these proteins, we identified LDB3 and CRYAB to be highly expressed in cardiac EVs, with a respective fold-change difference of 7.3 and 5.4 compared to plasma EVs (Figure 31). We were interested by the two proteins as potential markers of cardiac EVs.

CRYAB is a small heat shock protein that acts as a chaperone and is highly expressed in cardiac tissue (Dimauro et al., 2018). In the heart, it is present in the area surrounding the sarcomere, and was shown to bind with desmin, actin and titin, and prevents abnormal aggregation of sarcomeric structural proteins (Bennardini et al., 1992; Wang et al., 2003). Post-translational modifications of CRYAB were shown to regulate its function (Lambert et al., 2020). Interestingly, the presence of CRYAB in neuronal EVs has been observed in previous studies (Guo et al., 2019), and post-translational modifications such as phosphorylation and O-GlcNAcylation regulated its loading into glioma EVs (Kore and Abraham, 2016). CRYAB was therefore used in addition to LDB3 to verify the presence of cardiac EVs.

We were interested in further investigating LDB3 as an exclusive cardiac EV marker. As described before (section I.1.2 Histology), LDB3 is a sarcomeric protein localized to the Z-discs (Lin et al., 2014). It is also called "Z-band alternatively spliced PDZ-motif" (ZASP) or Cypher. It is present in both cardiac and skeletal muscle cells, although it is alternatively spliced in these tissues (Huang et al., 2003; Martinelli et al., 2014). This may explain the variability of LDB3 molecular weight observed in both tissue and EV samples (Figure 43, Figure 49). Its main role is thought to be in the assembly of the muscular contractile structure, although it may be involved in integrin activation and in sarcomeric signalling via interactions with protein kinase A (PKA) (Bouaouina et al., 2012; Lin et al., 2013). LDB3 mutations were shown to induce cardiomyopathies (Vatta et al., 2003).

We used different techniques that were commonly used for EV isolation on samples obtained from neonate and adult rat cardiac tissue. It was essential that positive EV markers be used to validate EV isolation by the different techniques. As tetraspanin markers were not detected in our samples (Figure 26, Figure 35), other markers were used such as ADAM10 and syntenin-1. These markers have been validated in the literature to be selectively enriched in exosomes, and therefore were useful markers of exosome-enriched sEVs (Kowal et al., 2016; Kugeratski et al., 2021). These markers were detected in sEVs obtained by the different techniques applied to both neonate and adult rat samples. Eventually, syntenin-1 was used as it was most reliably detected.

We selected four EV isolation techniques to apply on neonate and adult rat heart samples in order to validate LDB3 as a cardiac EV marker. These techniques were selected as they are commonly used in EV literature (Gardiner et al., 2016) (Figure 52).

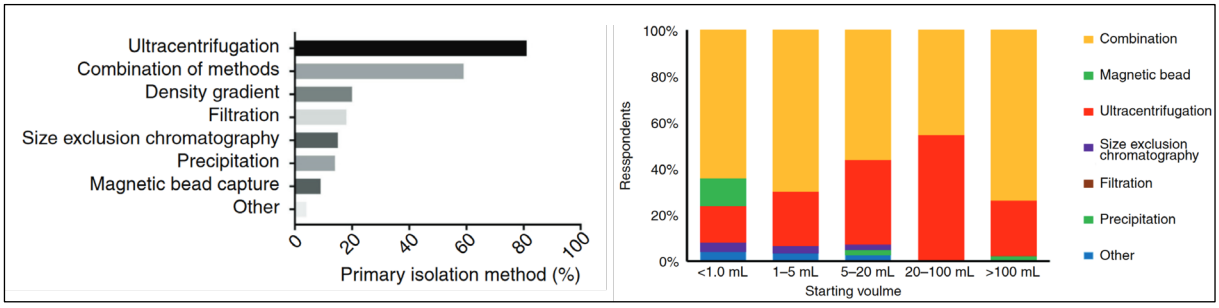


Figure 52. Ranking (left panel) and proportion (right panel) of EV isolation techniques based on an international

survey of members in the International Society of Extracellular Vesicles (ISEV) (Gardiner et al., 2016, fig. 3).

The first technique used was differential ultracentrifugation (dUC), which relies on the capacity of certain particles suspended in solution to pellet at a certain centrifugal force. This technique is the most widely used in EV literature. However, as due to the nature of the sample source we used, dUC risked co-pelleting contaminating intracellular proteins which may be generated during the tissue mincing process. dUC is most efficient when used on cell culture media, where less contamination is produced due to cellular damage. In 2021, a paper suggested that addition of a sucrose cushion to the ultracentrifugation process may reduce contamination generated by EV isolation from tissues (Matejovič et al., 2021). Although this technique was successful in recovering exosome-enriched sEVs, it was not capable of separating calnexin-containing intracellular vesicles, as they likely share the same density characteristics as EVs (Figure 34, Figure 40). cUC produced a lower yield of EVs starting from the same sample volume compared to dUC based on protein quantification. DGUC was used based on other protocols that were suggested for purifying EVs involving the use of an iodixanol density gradient (Crescitelli et al., 2021; Van Deun et al., 2014). Using this technique produced a high purity of EVs as evidenced by their separation from soluble proteins (Figure 36). However, this technique is time-consuming (18 hours centrifugation, in addition to gradient construction and sample collection), and necessitates the removal of the iodixanol since it may disturb downstream analysis due to its viscosity. A dilution of DGUC fractions and another ultracentrifugation were done to remove iodixanol. A relatively low yield is finally obtained, and would only be sufficient for one western blot experiment. For a high EV yield, several variations of EV precipitation have been proposed. The majority of these rely on polyethylene glycol (PEG), which is both easy to use (powder that can be resuspended in solvent and added to EV-containing samples), and requires no ultracentrifugation (a regular table-top centrifuge is sufficient) (García-Romero et al., 2019). A large amount of material was precipitated using this technique on neonate rat heart and plasma samples. Although syntenin-1 was regularly detected using this technique, it was comparatively less enriched in PEG-sEVs compared to dUC-sEVs (Figure 35). This may be due to the co-precipitation of non-vesicular material, as

PEG is not necessarily selective to EV membranes and may precipitate other membranous compartments or protein complexes (Merchant et al., 2017; Monguió-Tortajada et al., 2019). A common way to eliminate some of the co-precipitated non-vesicular components from precipitates involves the use of ultracentrifugation (Ludwig et al., 2018). PEG+UC provided a higher yield of syntenin-1-containing EVs compared to dUC and PEG alone when equal amounts of proteins were loaded (Figure 43). This confirmed exosomal enrichment and elimination of some non-vesicular proteins by the ultracentrifugation step. Interestingly, we found that PEG was not as efficient when applied in adult rat EV isolation. Less precipitate was generated when PEG was applied to these samples compared to neonate samples. This may be due to the differences in composition of the two sample types. It is possible that the use of enzymes on adult tissue samples may modify their properties and the capacity of PEG to precipitate.

We have shown for the first time the association of LDB3 with cardiac EVs. We detected LDB3 in cardiac EVs isolated from both neonate and adult rats, in addition to human cardiac EVs. We then confirmed that it is present inside EVs and is not co-precipitated with soluble proteins (Figure 44).

EVs in the context of ADHF

The acute worsening of chronic heart failure, known as acute decompensate heart failure (ADHF), is a leading reason for worldwide hospitalization and mortality. The conditions of its occurrence and its optimal treatment remain poorly understood (Njoroge and Teerlink, 2021). A model of ADHF was created in rats in the lab of Professor Paul Mulder in the INSERM unit 1096 (Peschanski et al., 2021). The goal was to find novel treatment approaches in the context of ADHF. Early results revealed that changes in the phosphorylation/O-GlcNAcylation balance in the heart induced by the injection of Thiamet G (TG; an OGA inhibitor) (Dubois-Deruy et al., 2015) led to a global increase in protein O-GlcNAcylation and rapid improvement in the cardiac function of ADHF hearts. This suggests that changes in cardiac protein post-translational modifications (PTM) may be a novel approach to treat ADHF. The role of O-GlcNAcylation on contractile proteins has been extensively described in skeletal muscles

(Lambert et al., 2020). Notably, increased O-GlcNAcylation seemed to play a role in modulating calcium activation and protein-protein interactions in the sarcomeres, leading to functional changes in contractile activity (Cieniewski-Bernard et al., 2012; Lambert et al., 2016). In addition to structural proteins, increased O-GlcNAcylation has been linked to re-enforcing mitochondrial function and reducing mitochondrial reactive oxygen species release (Dontaine et al., 2022). Conversely, while increased O-GlcNAcylation has been shown to produce beneficial cardiac effects in other contexts, such as sepsis (Denis et al., 2021; Ferron et al., 2019), it was also shown that a chronic rise in protein O-GlcNAcylation can be detrimental to the capacity of the heart to counter hypertrophic stimuli (Gélinas et al., 2018). Chronic stimulation of O-GlcNAcylation may therefore not be optimal.

In the ADHF model, acute increase in O-GlcNAcylation induced by a single dose of TG 12 hours before sacrifice was sufficient to produce an improvement in cardiac functional parameters. We were interested in studying how TG treatment produced this beneficial effect, and hypothesized that extracellular vesicles may be involved in transmitting functional molecules (proteins, nucleic acids) within cardiac tissue during this treatment. We observed that TG treatment increased left-ventricular O-GlcNAcylation levels (Figure 51), and that cardiac sEVs containing LDB3 from TG-treated ADHF rats show higher O-GlcNAcylation levels compared to non-treated rats (Figure 51). Immunoprecipitation with anti-LDB3 of left-ventricular protein lysates revealed increased LDB3 O-GlcNAcylation in TG-treated ADHF rats compared non-treated rats, confirming that this protein can be O-GlcNAcylated, as suggested in the literature (Leung et al., 2013). These results imply that a transfer of O-GlcNAcylated proteins may be taking place within cardiac tissue upon TG treatment of ADHF rats.

The concept of cardioprotection via EVs has previously been illustrated (Bueno-Betí et al., 2019; Liu et al., 2018; Loyer et al., 2018; Yadid et al., 2020). Animals with HF experienced a better recovery and improved cardiac function when treated with MSC-derived EVs (Timmers et al., 2011). In the context of ADHF rats, it is unclear which cell type is producing the majority of the analysed EVs. LDB3-containing EVs are most likely of cardiomyocyte origin (Figure 32). It is therefore possible that in addition to intracellular elevation of O-GlcNAcylation, an uptake

of O-GlcNAcylated proteins via EVs produced from other cardiac cells is also taking place. These proteins may associate into the sarcomeric structures of the recipient cells and participate in modulating their contractile function.

Further work can validate the capacity of EVs loaded with O-GlcNAcylated proteins to produce a cardioprotective effect on stressed cardiac cells both *in vitro* (cardiac cells treated with stress-inducing agents, such as H_2O_2 or Isoprotenerol) and *in vivo* (HF models).

Clinical potential

Clinical applications of EVs seem to be a promising avenue to be discovered. To date, EV research has focused on the use of biological specimens to determine disease markers, ranging for multiple types of cancer, neurological diseases, and cardiovascular pathologies. Some of these efforts has already translated into clinical use (Cheng and Hill, 2022).

Cardiac EVs should be further investigated as a possible source of information based on their proteomic profiles. Despite the detection of LDB3 as a stable marker for cardiac EVs, it remains challenging to separate these EVs from others originating from different tissues as LDB3 is a cytosolic protein and most likely localizes inside the cardiac EVs. Most EV enrichment approaches detecting specific EV subpopulations rely on surface markers to purify target EVs. Therefore, a combination of both membrane and cytosolic cardiac markers might be necessary to separate cardiac EVs from the circulation. Such membrane markers may include cardiac-specific proteins such as caveolin-3 (Chand et al., 2020). Isolating cardiac EVs from the circulation, followed by transcriptomic/proteomic/PTM analyses of their cargo can provide a complete picture of the changes undergone by cardiac cells in patients with cardiovascular diseases.

On the therapeutic aspect, a possible approach could involve the treatment of infarcted hearts with EVs loaded by O-GlcNAcylated sarcomeric proteins. As EV production in cell lines and stem cells exceeds that of primary cells, a cell line expressing sarcomeric proteins, such as H9c2 cells, could be used to produce these EVs. Acute treatment of H9c2 cells with O-GlcNAc enhancers might result in the loading of highly O-GlcNAcylated sarcomeric proteins into EVs

released into the culture medium. It remains to be seen if H9c2 cells can produce EVs sufficiently and with a similar profile as cardiac EVs obtained from cardiac tissue.

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Annexes

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Lim Domain Binding 3 (Ldb3) Identified as a Potential Marker of Cardiac Extracellular Vesicles

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Abstract: Extracellular vesicles (EVs) are considered as transporters of biomarkers for the diagnosis of cardiac diseases, playing an important role in cell-to-cell communication during physiological and pathological processes. However, specific markers for the isolation and analysis of cardiac EVs are missing, imposing limitation on understanding their function in heart tissue. For this, we performed multiple proteomic approaches to compare EVs isolated from neonate rat cardiomyocytes and cardiac fibroblasts by ultracentrifugation, as well as EVs isolated from minced cardiac tissue and plasma by EVtrap. We identified Ldb3, a cytoskeletal protein which is essential in maintaining Z-disc structural integrity, as enriched in cardiac EVs. This result was validated using different EV isolation techniques showing Ldb3 in both large and small EVs. In parallel, we showed that Ldb3 is almost exclusively detected in the neonate rat heart when compared to other tissues, and specifically in cardiomyocytes compared to cardiac fibroblasts. Furthermore, Ldb3 levels, specifically higher molecular weight isoforms, were decreased in the left ventricle of ischemic heart failure patients compared to control groups, but not in the corresponding EVs. Our results suggest that Ldb3 could be a potential cardiomyocytes derived-EV marker and could be useful to identify cardiac EVs in physiological and pathological conditions.

Keywords: Extracellular vesicles; proteomic analysis; LIM Domain Binding 3; cardiac EV marker; ischemic heart failure; EVtrap

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1. Introduction

Extracellular vesicles (EVs) are lipid bilayer-bound particles secreted by almost all cell types into the extracellular space [1]. Based on their biogenesis, size, and composition, different subtypes of EVs exist, such as exosomes, microvesicles, and apoptotic bodies [2]. EVs carry molecular cargo such as proteins, lipids, and RNA, playing a role in cell-to-cell communication during physiological and pathological processes [3,4]. The content of EVs varies depending on the type and functional state of cells that produce them [5,6]. Furthermore, the double-layered membrane protects the transported molecules from degradation in biological fluids, increasing their stability. For these reasons, EVs are considered as a source of biomarkers and could be used to diagnose pathologies, including cardiac diseases [7–11].

In the heart, different types of cells, including cardiomyocytes, fibroblasts, and endothelial cells, communicate via EVs to maintain cardiac homeostasis [12]. It was shown that cardiac cells can secrete EVs whose number, size, and/or content differ with different pathological status [13–16]. Borosch et al. showed that preconditioning with hypoxia and

isoflurane alters the protein levels of cardiomyocyte- and fibroblast-derived EVs differently [17]. However, the same stimuli did not have the same effect on EV composition depending on their producing cells. Furthermore, EVs secreted by different cardiac cells have been shown to regulate cardiac remodeling (hypertrophy, fibrosis, inflammation) in an autocrine or paracrine fashion [4,16,18–20]. All these data showed the interest in deeply characterizing the cardiac vesicles to better understand their role in heart disease.

EV characterization is a complex process due to their high heterogeneity and to the currently used protocols that cannot guarantee EV purity. Most studies were performed by using cell lines or body fluids. Studies on tissue-derived EVs were increased, but their number is still limited. Proteomic analysis has been used to characterize EVs from cardiac tissue [6,21]. However, variability in protein identification is observed depending on how samples are collected and which method is used to isolate EVs. Consequently, no cardiac-specific markers are fully characterized. Furthermore, previous in vitro proteomic analyses were performed on EVs derived from the same cardiac cell type under different stress conditions [13,14,17]. To our knowledge, no studies have been performed comparing EVs derived from different cardiac cell types with the goal of identifying cell-specific markers.

The aim of this study was to identify specific protein markers that both distinguish cardiac EVs from non-cardiac EVs in the circulation, as well as distinguish the different cardiac cell-derived EVs from each other in order to better understand their role. We identified and validated Ldb3, a cytoskeletal protein which is essential in maintaining Z-disc structural integrity, as a potential cardiomyocyte EV-specific marker via different EV isolation techniques.

2. Results

2.1. Comparative Proteomic Profiling of Cardiac Cell-Derived EVs Isolated by Differential Ultracentrifugation

In order to identify specific markers of cardiac cell-derived EVs, we isolated, by differential ultracentrifugation, large (lEVs) and small EVs (sEVs) from conditioned culture media of neonate cardiac myocytes (NCM) and fibroblasts (NCF) as well as cardiomyoblasts H9c2 (Figure 1A). Nanoparticle tracking analysis (NTA) (Figure 1B and S1) showed that NCFs produced the highest amount of EVs (sEVs: 8.9E6 particles/cell; lEVs: 8.5E5 particles/cell), compared to H9c2 cells (sEVs: 1.2E5 particles/cell; lEVs: 6E4 particles/cell) and NCM (sEVs: 4.4E4 particles/cell; lEVs: 6E3 particles/cell); sEV production was also consistently higher than lEVs in all cell types. Concerning size distribution, NCF EVs displayed a wide difference in size between sEVs and lEVs (sEVs: 120.4 nm/lEVs: 164.3 nm), which was less pronounced in NCM EVs (sEVs: 97.3 nm/lEVs: 107.9 nm) and H9c2 EVs (sEVs: 130 $\pm$ 12 nm/lEVs: 145 $\pm$ 13 nm).

Due to the low abundance of NCM derived EVs, only NCF- and H9c2-derived sEVs were further analyzed for proteomic characterization. Western blot analysis shows increased protein levels of classical exosomal marker CD63 [22] in H9c2- and NCF-derived sEVs (Figure 1C), validating the presence of exosomes in sEVs. The absence of CD9 in these sEVs suggests a specific protein profile of cardiac EVs.

We then performed gel separation and mass spectrometry of proteins revealed by Coomassie blue staining to determine the protein composition of NCF- and H9c2-derived sEVs (Figure 1D). We identified 63 proteins from NCF and 8 proteins from H9c2, including 5 common proteins (such as Col1a2, Fn1, Mfge8, Actb, and Actg1) (Figure 1E, Table S1). Gene ontology (GO) analysis (Figure 1F) for cellular component revealed 24 cytoskeletal proteins (such as actin and tubulin), 12 ribonucleoproteins (such as Rps2/4x/8/9 and Rpl7a/11/15), 6 extracellular matrix proteins (such as Col1a1/2 and Fn1), and 6 DNA-binding proteins (such as histones H4m/2a1e/3-3b/2aj and Morf4l2). Seventeen proteins were associated with positive regulation of protein expression (such as Hspa8, Wnt5a, and Eef1), and 15 with regulation of the apoptotic process (such as Hsp90aa1/a5, Grk2, Rack1, and Tcp1).

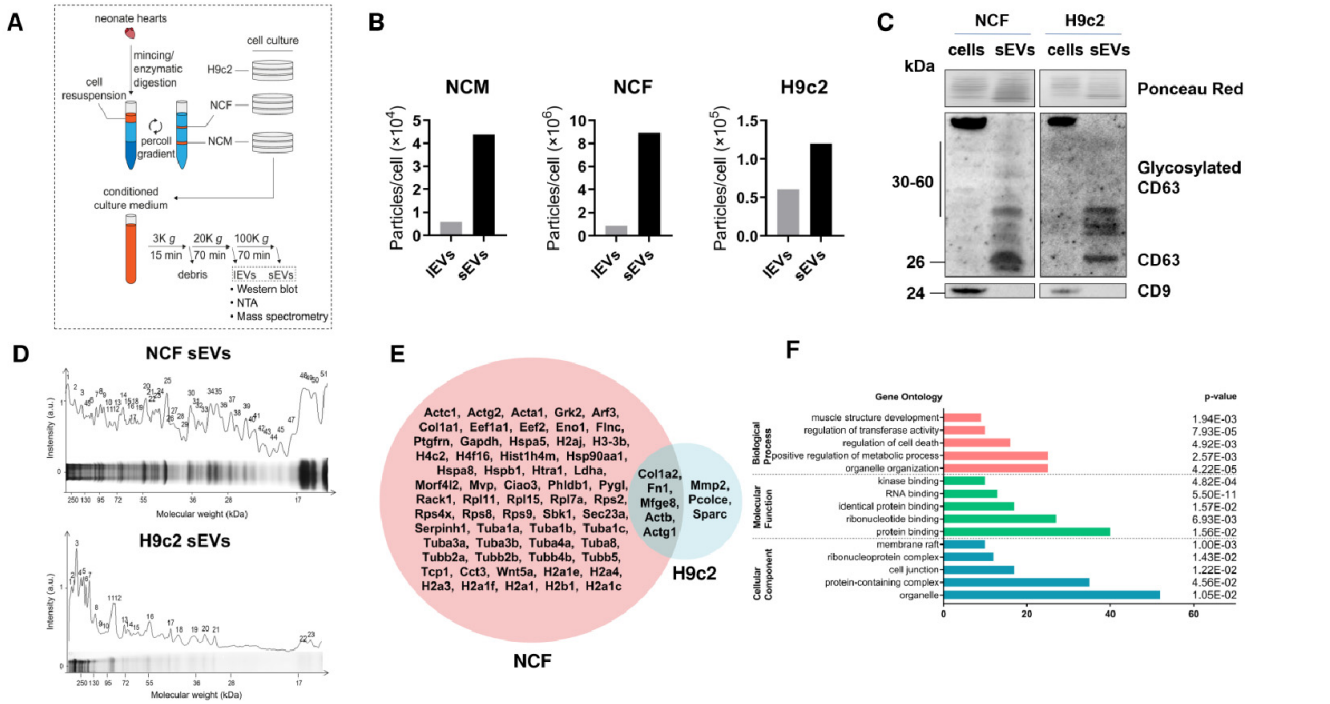


Figure 1. Proteomic analysis of cardiac cells-derived small EVs. (**A**) Isolation procedure of rat cardiac cells and their corresponding EVs. Neonate cardiac myocytes (NCM) and fibroblasts (NCF) isolated from ventricles of 1–3 day old Wistar rats, and cardiomyoblasts H9c2 were cultured in serum-free media for 96 h. Differential ultracentrifugation was used to isolate large (lEVs) and small EVs (sEVs) from conditioned culture medium. K: ×1000. (**B**) Nanoparticle tracking analysis (NTA) measurement of particle concentration in lEV and sEV pellets normalized to the number of producing cells in NCM, NCF, and H9c2 cells. Details are shown in Figure S1. (**C**) Ponceau Red and Western blot of cells and corresponding sEVs to detect exosomal markers CD63 and CD9. (**D**) Coomassie blue staining of gel separated NCF (75 µg) and H9c2 (25 µg) sEV proteins. Highly stained bands (labeled with a number) were used for MALDI-TOF/TOF mass spectrometry (MS). (**E**) Venn diagram representation of sEV proteins detected by MS in NCF (pink) and H9c2 (blue) sEVs. Protein abbreviations are detailed in Table S1 (**F**) GO (Gene Ontology) analysis of enriched GO terms for biological process, molecular function, and cellular component. *p* values were FDR-adjusted.

2.2. Comparative Proteomic Profiling of Cardiac and Plasma-Derived EVs Isolated by EVtrap

To go deeper in understanding the cardiac EV proteome, a more sensitive approach was designed. EV total recovery and purification (EVtrap) was used to purify EVs from the extracellular environment surrounding cardiac cells (Figure 2A).

A total of 3187 EV proteins were detected (Table S2), of which 2629 cardiac proteins and 1905 plasma proteins were analyzed (detected in at least 3 out of 4 samples in each group), with 1775 proteins in common (Figure S2, Table S3). Among identified proteins, we detected most of the proteins (41 out of 66) previously detected in sEVs derived from cardiac cells.

Cardiac EV proteins were compared with the 100 most frequently identified EV proteins according to EV databases ExoCarta and Vesiclepedia. Respectively, 91 and 86 of these proteins were detected in cardiac EVs (Figure 2B, Table S4).

GO analysis (Figure 2C, Tables S5–S8) revealed the presence of typical exosome markers (such as Sdcbp/syntenin–1, Pdcd6ip/alix, tetraspanins CD81/9, Hspa4/8, Lamp2, and Tsg101). Cardiac vesicles were also enriched in membrane proteins (such as annexins, cadherins, cavins, caveolins, clusters of differentiation, and integrins), endosomal proteins (such as Chmp, Rab, EH-domain containing, vacuolar protein sorting-associated, and sorting nexin proteins), focal adhesion proteins (such as LIM domain-containing proteins), and sarcomeric proteins.

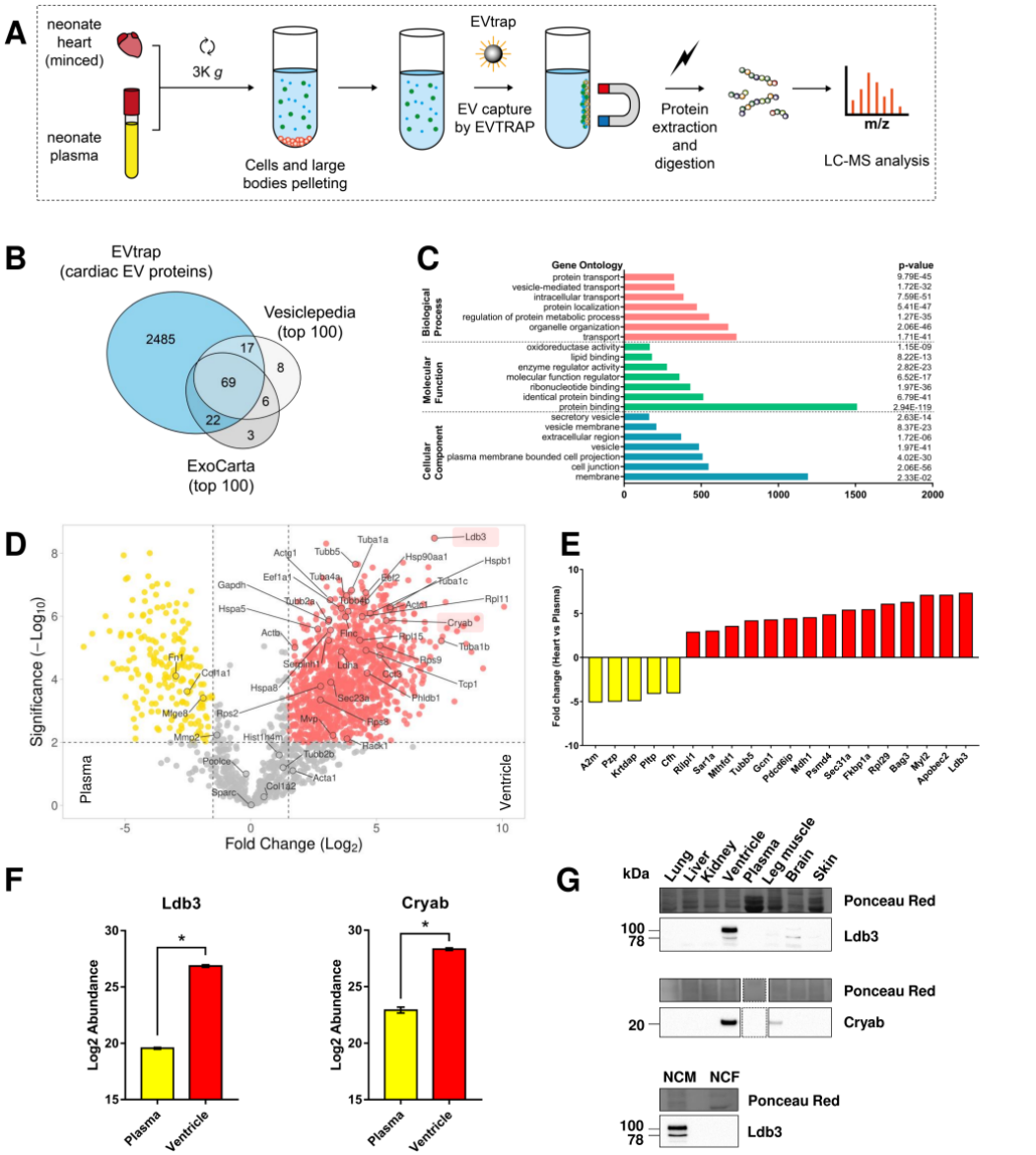


Figure 2. Proteomic analysis of neonatal rat heart and plasma EVs isolated by lipidic affinity. (**A**) Isolation of cardiac and plasma EVs (n = 4) using EV Total Recovery And Purification (EVtrap). Ventricles of 1–3 day old Wistar rats were minced using fine scissors before being resuspended in ice-cold ADS buffer. EVs were purified from ADS (cardiac) and plasma by binding to magnetic beads with lipidic affinity to membrane-bound particles, then lysed for analysis by liquid chromatography-mass spectrometry (LC-MS). K: ×1000. (**B**) Venn diagram of cardiac EV proteins (blue) compared to top 100 EV proteins identified in the public databases Vesiclepedia and ExoCarta. (**C**) GO analysis on the cardiac EV proteins to identify enriched GO terms. (**D**) Volcano plot comparing cardiac (red dots) and plasma (yellow dots) EV protein abundances. Proteins with p value < 0.01 and fold change > 1.5 were considered significant for the analysis. Only proteins detected by previous MALDI-TOF analysis, in addition to Ldb3 (LIM domain binding 3) and Cryab (Alpha-crystallin B chain), were labeled. (**E**) Bar plot representing the most significantly different (lowest p-value) proteins in plasma (yellow bars) and cardiac (red bars) EVs. (**F**) Bar plot of Ldb3 and Cryab abundances (log2 transformed) in plasma and heart. Error bars = SEM, * $p < 0.05$. (**G**) Quantification by Western blot of Ldb3 and Cryab expression in different tissues obtained from neonatal rat (upper panel) and in neonate cardiac myocytes (NCM) and fibroblasts (NCF) (lower panel). Equal amount of proteins were loaded for each blot as shown by Ponceau Red staining.

Abundance of cardiac and plasma EV proteins were then compared showing 1033 cardiac EV-enriched proteins, while 180 proteins were plasma EV-enriched (Figure 2D, Table S3). Compared to plasma EVs, we showed that Ldb3 is the most significantly abundant protein (×160, $p = 0.03$) in cardiac EVs (Figure 2D–F) while the previously reported cardiac marker Cryab was less enriched (×40, $p = 0.03$) (Figure 2D,F).

2.3. Ldb3 as a Potential Cardiac EV Marker

To validate that Ldb3 is a cardiac-specific marker, its expression was evaluated in various neonate rat tissues (lung, liver, kidney, heart, plasma, leg muscle, brain, and skin). Ldb3 protein level was higher in heart tissue, confirming its relative cardiac specificity, while low amounts were detected in the brain (Figure 2G). Cryab was also found to be cardiac-enriched, with low amounts in leg muscle tissue. Additionally, within cardiac tissue Ldb3 expression was cardiomyocyte-specific compared to cardiac fibroblasts, suggesting that Ldb3 could be a marker of cardiomyocytes-derived EVs (Figure 2G).

In order to further confirm Ldb3 as a cardiac EV marker, isolation of neonate rat cardiac EVs was performed using different approaches: ultracentrifugation (UC), polyethylene glycol precipitation (PEG), or a mixed technique combining the two (PEG + UC) (Figure 3A).

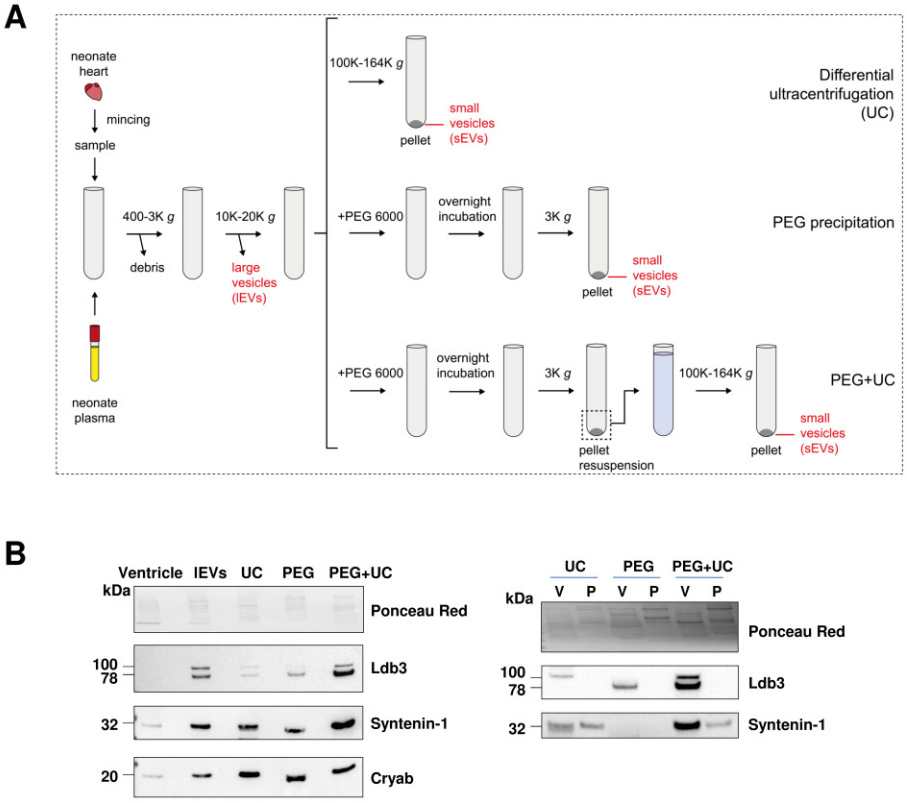


Figure 3. Ldb3 is enriched in cardiac EVs compared to heart tissue and plasma EVs. (**A**) Scheme of the three EV isolation techniques from neonate rat heart: ultracentrifugation (UC), polyethylene glycol precipitation without (PEG) or with UC (PEG + UC). K: ×1000. (**B**) Detection of Ldb3, syntenin–1, and Cryab by Western blot of EV populations obtained using the three isolation techniques. Equal amount of proteins were loaded for each blot as shown by Ponceau Red staining. V: ventricle; P: plasma.

The different EV populations were analyzed by Western blotting. We found that Ldb3, Syntenin–1, an exosomal marker, and Cryab, were abundant in EV samples (Figure 3B, left) compared to ventricular tissue. Syntenin–1 was most enriched in EVs obtained by PEG + UC, implying higher exosomal retention using this approach. Cryab was detected similarly in the 10K pellet, UC, PEG, and PEG + UC, indicating that it may be loaded into both lEVs and sEVs, with a higher concentration being loaded into sEVs. Ldb3 also appeared to be

enriched in both lEVs and sEVs compared to heart tissue. Ldb3 was most abundant in sEVs that were isolated using PEG + UC compared to UC and PEG alone.

These techniques were applied to obtain EVs from ventricles and plasma in order to confirm that Ldb3 is cardiac EV-specific (Figure 3B, right). Both Ldb3 and syntenin–1 enrichment were detected in PEG + UC compared to the other techniques, and Ldb3 was only observed in cardiac EV samples, validating the EVtrap result. It should be noted that the expression profile of Ldb3 differed between samples, as two isoforms appeared in different EV samples. The higher MW isoform was enriched in UC-EVs, while the lower isoform appeared with PEG. Both were present in PEG + UC, indicating a possible influence of Ldb3 isoform on which EV subpopulation it will be loaded into.

2.4. Size Exclusion Chromatography Validated Ldb3 Loading into EVs

Size exclusion chromatography (SEC) was used to separate cardiac EVs from non-vesicular components (NV) (Figure 4A).

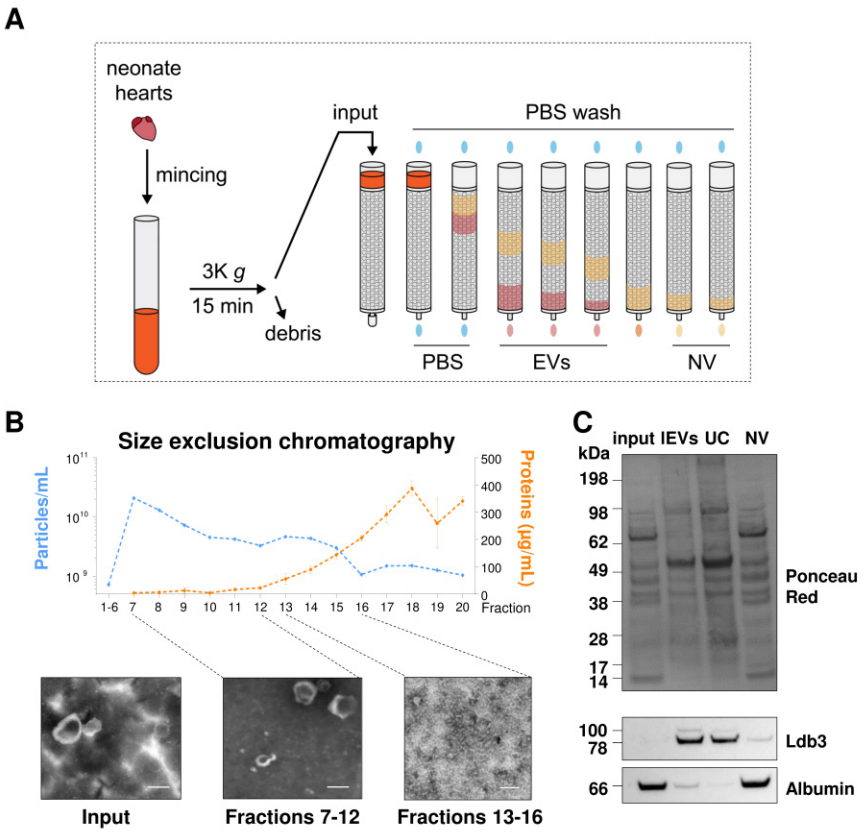


Figure 4. Ldb3 is a specific marker of cardiac EVs. (**A**) Protocol of size exclusion chromatography (SEC) to separate EVs from non-vesicular factors (NV). K: ×1000. (**B**) Graph representation of NTA particle count (blue) and protein concentrations (orange) for each SEC fraction. Representative transmission electron microscopy images of unpurified EVs (solution obtained after centrifugation at 3000× *g*) and different pools of SEC fractions (7–12 and 13–16) are presented below. Scale bars = 150 nm. (**C**) Quantification of Ldb3 and albumin by Western blot of EVs obtained by differential ultracentrifugation (UC) and in SEC fraction 20 (NV).

The non-purified sample (input) was loaded into a SEC column and 30 fractions were analyzed. NTA and protein concentration measurement for each fraction shows that particle concentration was the highest on fraction 7, progressively reducing until the final fractions, while protein concentration increased (Figure 4B). These results, in addition to TEM imaging of pooled fractions, confirm that EVs were mainly eluted in the fractions 7–12, with NV eluting mostly after fraction 12. SEC fraction 20 was taken as NV for Western blot comparison with EV fractions obtained by UC and the original input sample (Figure 4C).

Ldb3 was enriched in EV fractions compared to the NV fraction. Conversely, albumin appeared to be enriched in the NV fraction, indicating successful separation of EVs from NV. This confirms that Ldb3 is loaded into EVs and is not co-pelleting with non-vesicular components during EV isolation.

2.5. Ldb3 Levels Are Increased in Left Ventricle of Heart Failure Rats and Patients with Ischemic Cardiomyopathy but Not in Cardiac EVs

We previously observed an alteration of sarcomere structure in the left ventricle (LV) of rats with coronary ligated heart failure (HF) [23]. We were therefore interested in studying cardiac Ldb3 expression during HF following myocardial infarction. We found that due to alternative splicing, many Ldb3 isoforms were observed in rat heart, and the profile of this protein differs in neonatal and adult rats (Figure S3). Moreover, levels of Ldb3 (high isoforms) decreased in HF rats compared to control, while low Ldb3 isoform (~32 kDa) remained unchanged. This result was validated in LV of patients with ischemic cardiomyopathy who underwent a cardiac transplantation (Figure 5A).

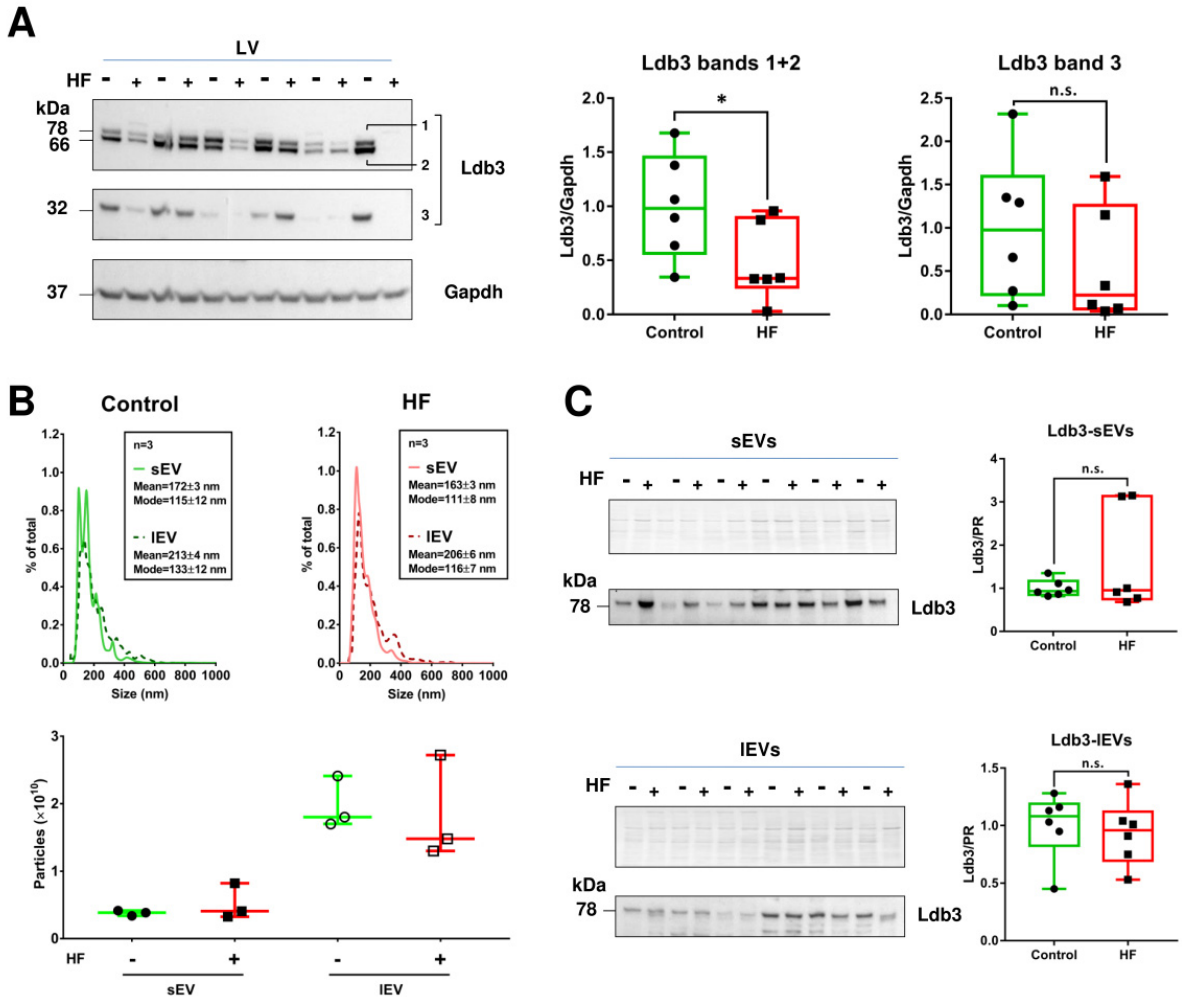


Figure 5. Ldb3 levels decrease in heart tissue, but not in cardiac EVs, during HF. (**A**) Western blots detecting Ldb3 expression in its 3 isoforms in left-ventricular tissue from control and HF patients. (**B**) NTA measuring particle size distribution (top panel) and concentration (bottom panel) of cardiac EVs isolated from the same patient tissues by UC. (**C**) Ldb3 detection in small (sEVs, top panel) and large EVs (lEVs, bottom panel). Data are expressed as median with interquartile range. * $p < 0.05$.

Next, we verified if Ldb3 levels change in cardiac EVs during HF. Cardiac tissue from 6 control and 6 ischemic HF patients were minced and digested with collagenase II, then

UC was used to isolate EVs. As observed by NTA analysis (Figure 5B), we isolated more lEVs than sEVs, and the amount and the size distribution profile of these EVs was similar between control and HF patients. Contrary to what was observed in LV, only one Ldb3 isoform was detected (high, ~78 kDa), and its level was not changed between EVs of control and HF samples (Figure 5C).

3. Discussion

In this study, our aim was to identify specific EV markers of cardiac EVs allowing us to distinguish them from non-cardiac EVs in the circulation. Here, we identified Ldb3 as a potential cardiomyocyte-derived EV marker.

EVs are considered as transporters of biomarkers for the diagnosis of cardiac diseases, playing an important role in cell-to-cell communication during physiological and pathological processes, hence the interest in deeply characterizing these vesicles to better understand their role in heart disease.

EV characterization is a complex process due to their high heterogeneity and the lack of methods to fully separate different EV subpopulations [24,25]. Furthermore, currently used protocols cannot guarantee EV purity [26,27]. Previous studies were performed to isolate and characterize EVs from cardiac tissue from minced or perfused cardiac tissue with or without enzymatic digestion [6,18,21,28]. Proteomic studies widely used UC with or without sucrose gradient to isolate EVs. Differences in protein identification were observed depending on how samples were collected and which method was used to isolate them. The protein profile for EVs isolated from different rat tissues by UC followed by sucrose gradient was compared and identified Caveolin-3 (Cav3) as a marker of cardiac EVs, but this microvesicle marker [29] could be expressed by other tissues. In order to find specific cardiac EV markers, we performed a comparative proteomic analysis on EVs isolated by EVtrap from neonate rat plasma and cardiac tissue. EVtrap is a novel, fast, reproducible, and high-recovery EV isolation method with relatively low contamination levels [30]. It was used to isolate EVs from plasma and urine for phosphoproteomic analysis [30,31]. This technique was used for the first time to isolate EVs from cardiac tissue. Compared to previous studies using UC, little amount of tissue is required. Both lEVs and sEVs were collected. In addition to the 2 cardiac EVs markers previously characterized, Cav3 and Cryab, we identified Ldb3 as most significantly enriched in cardiac EV compared to plasma EVs. Ldb3 was detected in both cardiac lEVs and sEVs isolated by other techniques which are cheaper and more available than EVtrap. We confirmed that Ldb3 is more enriched in cardiac sEVs compared to plasma EVs. Comparing the expression of Ldb3 and albumin in unfiltered EVs, lEVs and sEVs obtained by UC, and SEC non-vesicular fraction confirmed that Ldb3 is loaded into EVs and is not a protein contaminant. We then validated the presence of Ldb3 in human cardiac EVs isolated by UC. All this data suggests Ldb3 as a potential cardiac- EVs marker.

Furthermore, we have demonstrated that Ldb3 is almost exclusively expressed in the heart compared to other neonate rat tissue, and specifically in cardiomyocytes compared to cardiac fibroblasts, suggesting Ldb3 as a novel cardiomyocyte-derived EV marker. Similarly to Cav3 and Cryab, Ldb3 is expressed in skeletal muscle. Ldb3, also known as Cypher (in murines) or ZASP (in humans), is a PDZ and LIM domain-containing protein that localizes to the Z-disc in striated skeletal and cardiac muscle cells [32]. Due to alternative splicing, several forms of Ldb3 exist which may be exclusively skeletal or cardiac, or common isoforms for both tissues. It has been shown that the Ldb3 isoform possessing exon 4 are predominantly expressed in cardiac tissue, whereas the isoforms possessing exon 6 are more prominent in skeletal muscle [33]. In our study, we observed that several Ldb3 isoforms exist in heart tissue, while only one isoform was secreted in EVs. A possible way to identify whether the EV-secreted isoform is cardiac-specific is by using antibodies that bind specifically to the cardiac exon (exon 4). Notably, we observed that cardiac Ldb3 isoforms differ between neonate and adult rats, implying age-dependent changes in its splicing and function.

Ldb3 is part of the protein complex that maintains the structural integrity of sarcomeres during muscle contraction by binding to alpha-actinin and myotilin via its PDZ domain and plays a role in signaling through its interactions with PKC via its LIM domain [34,35]. It was shown that deletion of Ldb3 in a mouse model resulted in neonatal lethality associated with Z-disc disorganization and fragmentation in both skeletal and cardiac muscle cells [36,37]. Furthermore, Ldb3 variants have been observed to be associated with myopathy in human patients [38,39]. In this study, we showed that the expression of high MW Ldb3 isoforms decreased in LV of HF patients with ischemic cardiomyopathy, as well as in LV of HF rats in which we have previously observed LV structural alterations, desmin aggregate accumulation, and sarcomere disruption [23,40]. However, no difference on Ldb3 levels were observed in lEVs and sEVs isolated from HF patients compared to control. These results showed that intraventricular and not EV-Ldb3 levels are associated with HF.

In summary, we showed the presence of Ldb3 in cardiac EVs by using different sample preparation methods, fresh or frozen tissue, minced with or without enzymatic digestion, and different isolation techniques. We suggest that Ldb3 can act as a potential marker of cardiac EVs specifically derived from cardiomyocytes. It should be noted that despite using several EV isolation techniques, it is currently not possible to completely eliminate contamination of EV samples with soluble proteins, lipoprotein aggregates, intracellular vesicles, or organelle vesicles produced by cell damage. Complementary experiments can be performed to confirm Ldb3 loading into EVs and its presence in released EVs. Ldb3 localization in EVs is also unclear. Future experiments may validate Ldb3 presence inside or at the surface of EVs. It is likely loaded inside EVs along other EV cargo proteins, but may also associate with integrin proteins on EV membranes, allowing for its potential use as an EV immunocapture target.

To conclude, this is the first study showing the presence of Ldb3 in cardiac EVs and suggests that Ldb3 could be used to identify these EVs in physiological and pathological conditions.

4. Materials and Methods

4.1. Cellular Models

4.1.1. Primary Cultures of Neonate Rat Cardiomyocytes (NCM) and Cardiac Fibroblasts (NCF)

NCM and NCF were isolated from heart ventricles of one- to three-day old Wistar rats (Janvier Labs, Le Genest-Saint-Isle, France) as previously described [41]. Briefly, minced ventricular tissue was digested with type II collagenase (LS004174, Worthington, Lakewood, NJ, USA) and pancreatin (P3292, Sigma-Aldrich, St. Louis, MO, USA), and dissociated cells were pelleted by centrifugation at 800× *g*. NCMs were separated from NCFs via discontinuous Percoll gradient (bottom 58.5%, top 40.5% [*v*/*v*], P4937, Sigma-Aldrich, St. Louis, MO, USA) for 30 min at 1600× *g*. NCMs were seeded at 2.5 × 10^6 cells per 100 mm collagen-coated culture dish and were cultured in a 4:1 mixture of DMEM (D1152, Sigma Aldrich, St. Louis, MO, USA) and Medium 199 (M4530 Sigma-Aldrich, St. Louis, MO, USA), supplemented with 10% horse serum (HS) (16050122, Thermo Fisher Scientific, Waltham, MA, USA), 5% fetal calf serum (FCS) (30-2020, ATCC, Manassas, VA, USA), and 1% penicillin-streptomycin (PS) (15140-122, Gibco, Waltham, MA, USA) for 5 days at 37 °C under 5% CO_2 atmosphere. NCFs were seeded at 2 × 10^6 cells per 100 mm culture dish and were cultured in DMEM (31966-02, Gibco, Waltham, MA, USA), 10% FCS, and 1% PS for 48 h at 37 °C under 5% CO_2 atmosphere. NCF at passage 1 were used for experiments.

4.1.2. Rat Cardiac Myoblasts

H9c2 cells (CRL-1446, ATCC, Manassas, VA, USA) were cultured in similar conditions as NCFs and used at passages 8 to 15 for experiments.

4.2. Animal Model

All animal experiments were performed according to the Guide for the Care and Use of Laboratory Animals published by the US National Institutes of Health (NIH publication

NO1-OD-4-2-139, revised in 2011). MI was induced in 10-week-old male Wistar rats (Janvier, Le Genest St isle, France) by ligation of the left anterior descending coronary artery and animals were sacrificed 2 months post-MI as previously described [42]. All tissues were stored at −80 °C before use.

4.3. Human Cardiac Biopsies

Human heart tissue was obtained from the cardiovascular biobank of Bichat Hospital in Paris (BB-0033-00029, coordinator Dr JB Michel) with approval by the Inserm Institutional Review Board. Explanted heart tissues were obtained from patients undergoing heart transplantation for end-stage ischemic heart failure and from patients who died of non-cardiac causes. Samples were quick-frozen and stored at −80 °C. All materials from patients were recovered as surgical waste with informed consent of the donors and with approval of the local ethical boards ("Centre Hospitalier et Universitaire de Lille", Lille, according to the Declaration of Helsinki).

4.4. EV Isolation

4.4.1. Sample Preparation

One- to three-day old rats were sacrificed using decapitation. Mixed venous and arterial blood from decapitated rats was collected into EDTA tubes (16.444.100, Sarstedt, Nümbrecht, Germany) and was centrifuged at 2000× *g* for 5 min without brake to obtain plasma (100 µL/rat). Hearts were quickly excised and placed in ice-cold conservation buffer ADS (6.8 g/L NaCl, 1 g/L glucose, 0.12 g/L NaH_2PO_4, 0.4 g/L KCl, 0.1 g/L $MgSO_4$, 4.76 g/L HEPES, pH 7.4) [18]. Atria and surrounding tissue were removed. Ventricles were washed then minced in ice-cold conservation buffer (100 µL/ventricle). Adult tissue samples were prepared similarly, with the addition of a digestion step after mincing. Minced tissue (~200 mg) was incubated in 6-mL of 1 mg/mL type II collagenase (LS004174, Worthington, Lakewood, NJ, USA) at 37 °C for 30 min with agitation. To isolate EVs secreted by cells, NCM, NCF and H9c2 were incubated in a 50% reduced volume of serum-free culture medium for 96 h. EV-containing conservation buffer, plasma, and conditioned culture media were centrifuged at low speed (400 to 3000× *g*) to remove debris and dead cells. The supernatant containing unpurified EVs was used for further analyses. Unless stated otherwise, all manipulations were performed at 4 °C.

4.4.2. Differential Ultracentrifugation (UC)

Unpurified EV solution was further ultracentrifuged at 4 °C at medium speed (10,000 to 20,000× *g*) for 70 min to pellet large EVs, then at high speed (100,000 to 164,000× *g*) for 70 min to pellet small EVs. Rotors used were either Beckman 50.2Ti or SW-32.1 (337901/369651 Beckman Coulter France, Villepinte, France).

4.4.3. Polyethylene Glycol (PEG) Precipitation

After medium speed ultracentrifugation, supernatants were incubated with 10% PEG 6000 (P0903, TCI Chemicals, Tokyo, Japan) overnight at 4 °C. The white precipitate containing EVs formed was pelleted by a low-speed centrifugation (3000× *g*) for 15 min at 4 °C. For PEG precipitation followed by UC (PEG + UC), PEG pellet was resuspended in filtered phosphate buffered saline (PBS) and ultracentrifuged at high speed (100,000 to 164,000× *g*) for 70 min at 4 °C.

4.4.4. Size Exclusion Chromatography (SEC)

Unpurified EV solution from ventricles (500 µL) were analyzed through qEV original size exclusion columns containing resins of 70 nm pore size (Izon Science, Christchurch, New Zealand), pre-washed at room temperature with filtered and degasified PBS. Fractions of 500 µL were collected with a constant flow of PBS, then stored at −80 °C until use.

4.4.5. EV Total Recovery and Purification (EVtrap)

Unpurified EVs from plasma and minced ventricles were captured and processed using magnetic EVtrap beads as previously described [30]. Briefly, unpurified EV solution from ventricles (3000× g supernatant) was filtered using a 100,000 Da filter (Amicon® Ultra-15 Centrifugal Filter Unit, UFC9100, Millipore, Burlington, MA, USA) allowing the removal of free molecules with small molecular mass. Samples were then washed and diluted 1:10 with PBS (1X). In order to isolate EVs, magnetic EVtrap beads were added to the filtered solution at 1:10 v/v ratio, followed by shaking for 1 hr. The beads were then captured using a magnetic separator rack, and the supernatant was removed. Beads were washed using PBS.

4.5. Nanoparticle Tracking Analysis (NTA)

Samples were analyzed using a NanoSight NS300 instrument (Malvern Panalytical, Malvern, UK) according to the manufacturer's software manual (NanoSight NS300 User Manual, MAN0541-01-EN-00, 2017). Samples were diluted in filtered PBS (1X), and videos of 1 min were performed with the camera level setting at 14 and detection threshold at 4. Videos were analyzed with Nanosight NTA software version 3.2 build 3.1.46 (Malvern Panalytical, Malvern, UK). To compare the concentration of particles detected from different samples, values were normalized to cell number.

4.6. Transmission Electron Microscopy (TEM)

Five µL from each sample were deposited on a 400-mesh copper grid covered with a Formvar-carbon film for 5 min at RT. The grid was dried, and 10 µL of phosphotungstic acid (19500, EMS, Hatfield, PA, USA) was added on the grid for 5 min at RT to negatively stain the biological structures. The grid was dried and observed at 80 kV with an electron microscope (H7500, Hitachi, Tokyo, Japan) equipped with a digital camera (AMT, Woburn, MA, USA).

4.7. Western Blot

Proteins were extracted from organ tissue, cells, and EV pellets in RIPA buffer containing 50 mM Tris base, 150 mM NaCl, 100 mM sodium orthovanadate, 1% NP40, 1% SDS, 0.1% sodium desoxycholate, 1% Complete™ Protease Inhibitor Cocktail (11697498001, Roche Diagnostics, Basel, Switzerland), and 1% antiphosphatase, phosphatase inhibitor cocktail 2 and 3 (P5726 and P0044, Sigma Aldrich, St. Louis, MO, USA) as has been previously conducted [41]. Protein concentration was measured using Pierce™ BCA Protein Assay Kit (23225, Thermo Fisher Scientific, Waltham, MA, USA) or Bradford assay (#5000006, Bio-Rad Laboratories, Hercules, CA, USA) according to manufacturer instructions. Equal amounts of protein were diluted in reducing sample buffer and boiled for 10 min at 70–95 °C. Samples were loaded into Bio-Rad or NuPAGE gels (Invitrogen, Waltham, MA, USA) then migrated. Transfer was performed using Trans-Blot Turbo™ transfer system (Bio-Rad Laboratories) for 10 min at 1.3 A and 25 mV onto a 0.2 µm nitrocellulose membrane (170-4158, Bio-Rad Laboratories, Hercules, CA, USA). Membranes were blocked using 5% milk in TBS-tween solution (0.1 M Tris HCl pH 7.4, 0.1% [v/v] tween, 150 mM NaCl), then incubated with primary antibodies overnight at 4 °C (Table S9). Incubation with HRP-conjugated secondary antibodies at a dilution of 1:5000–1:10,000 was performed the following day for 1 h at RT. Proteins were detected by incubating membranes in Clarity™ Western ECL Substrate (Bio-Rad Laboratories, Hercules, CA, USA) for 5 min. Images were acquired using ChemiDoc Imaging System (Bio-Rad Laboratories, Hercules, CA, USA).

4.8. Proteomics

EV proteins isolated from NCF and H9c2 separated using sodium dodecyl sulfate–polyacrylamide gel electrophoresis were fixed with 50% ethanol and 2% orthophosphoric acid for 1 h at RT. Gels were washed, then incubated in a pre-soak solution (15% ammonium sulfate, 17% ethanol, 2% orthophosphoric acid) for 20 min at RT. Gel fragments were excised

and proteins were digested using trypsin (V5280, Promega, Madison, WI, USA) followed by MALDI-TOF/TOF analysis as described previously [41].

EVs captured using EVtrap were lysed for protein extraction using a phase-transfer surfactant (PTS)-aided procedure. Proteins were reduced and alkylated with 10 mM TCEP and 40 mM CAA at 95 °C for 10 min. Samples were diluted five-fold with 50 mM triethylammonium bicarbonate and digested with Lys-C (Wako, Osaka, Japan) at 1:100 [wt/wt] for 3 h at 37 °C, before overnight trypsin digestion (1:50 wt/wt) at 37 °C. LC-MS/MS analysis was performed as described previously [30].

4.9. Data Analysis

Bar and column graphs were generated using GraphPad Prism (v7.0.0). EVtrap protein abundance was analyzed using Perseus v1.6.5 software (https://maxquant.net/perseus/, accessed on 1 October 2019). Proteins not detected in at least 3/4 of the samples (EVtrap analysis) in each group were excluded. Protein abundances were transformed to Log2. Missing values were substituted by values from the normal distribution. Groups were compared by a two-tailed Student's *t* test ($p < 0.05$) using the Benjamini–Hochberg correction. Differences in abundance (Log2 transformed) and *p* values were visualized on a Volcano plot by entering Perseus data into VolcaNoseR web app [43].

Gene Ontology (GO) analysis was performed on proteins identified by MALDI-TOF/TOF and LC-MS/MS using PANTHER GO [44–46]. Protein names were compared to the available Rattus norvegicus reference proteome (21,585 proteins; released 2020-11-01).

EVtrap proteins selected after MS identification were compared to Vesiclepedia [47] and Exocarta [48] databases using FunRich (v3.1.3) [49]. Overlap values between the 3 groups were visualized using the Eulerr R package [50].

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/ijms23137374/s1.

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Data Availability Statement: The data presented in this study are available in "Full unedited gel for figures" Supplemental Files.

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Table S1. Protein abundances in plasma (P) and heart (H) EVs isolated by Evtrap. Values were log2 transformed.

#	Description	Gene name	Accession	P3	P5	P7	P9	H3-H4	H5-H6	H7-H8	H9-H10
1	[F-actin]-monooxygenase MICAL1 OS=Rattus norvegicus OX=10116 GN=Mical1 PE=1 SV=1	Mical1	D3ZBP4	21.577	23.1448	21.3218	22.4698	21.4478	21.7627	21.2148	21.0646
2	[Protein ADP-ribosylarginine] hydrolase OS=Rattus norvegicus OX=10116 GN=Adprh PE=1 SV=2	Adprh	Q02589	NaN	13.8832	NaN	NaN	17.3865	16.0974	NaN	NaN
3	[Protein ADP-ribosylarginine] hydrolase-like protein 1 OS=Rattus norvegicus OX=10116 GN=Adprhl1 PE=2 SV=1	Adprhl1	Q5XIB3	17.8803	17.5435	17.2002	NaN	22.8116	22.8729	23.499	23.1449
4	10 kDa heat shock protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hspe1 PE=1 SV=3	Hspe1	P26772	18.0013	18.8925	17.356	16.3787	18.1018	21.5543	20.9278	21.2031
5	14-3-3 protein beta/alpha OS=Rattus norvegicus OX=10116 GN=Ywhab PE=1 SV=3	Ywhab	P35213	17.8842	17.988	18.1101	16.9028	21.5685	21.5334	21.3389	21.6546
6	14-3-3 protein epsilon OS=Rattus norvegicus OX=10116 GN=Ywhae PE=1 SV=1	Ywhae	P62260	22.136	22.5497	22.4638	22.354	25.3768	24.9575	25.2069	25.3782
7	14-3-3 protein eta OS=Rattus norvegicus OX=10116 GN=Ywhah PE=1 SV=2	Ywhah	P68511	18.3934	20.3949	18.326	18.0075	23.6171	23.2965	23.3551	23.4702
8	14-3-3 protein gamma OS=Rattus norvegicus OX=10116 GN=Ywhag PE=1 SV=2	Ywhag	P61983	19.9415	19.2559	20.1161	18.3497	23.5692	23.5153	23.4735	23.5569
9	14-3-3 protein theta OS=Rattus norvegicus OX=10116 GN=Ywhaq PE=1 SV=1	Ywhaq	P68255	20.4312	20.8216	20.9613	20.2768	23.9693	24.0115	24.0344	24.0001
10	14-3-3 protein zeta/delta OS=Rattus norvegicus OX=10116 GN=Ywhaz PE=1 SV=1	Ywhaz	A0A0G2JV65	21.4317	21.4574	21.4794	21.7198	23.8875	23.5161	23.7483	24.0221
11	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma OS=Rattus norvegicus OX=10116 GN=Plcg1 PE=1 SV=1	Plcg1	G3V845	NaN	NaN	NaN	NaN	18.1249	18.1104	18.1235	17.9335
12	2,4-dienoyl CoA reductase 1, mitochondrial, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Decr1 PE=1 SV=1	Decr1	G3V734	NaN	NaN	NaN	NaN	NaN	18.3089	16.0297	16.8558
13	26S proteasome non-ATPase regulatory subunit 1 OS=Rattus norvegicus OX=10116 GN=Psmd1 PE=1 SV=1	Psmd1	G3V8B6	21.5596	20.3509	21.2405	21.024	24.3745	23.6441	24.2489	24.2919
14	26S proteasome non-ATPase regulatory subunit 10 OS=Rattus norvegicus OX=10116 GN=Psmd10 PE=2 SV=1	Psmd10	Q9Z2X3	NaN	NaN	NaN	NaN	16.6533	16.8451	NaN	16.7069
15	26S proteasome non-ATPase regulatory subunit 11 OS=Rattus norvegicus OX=10116 GN=Psmd11 PE=1 SV=2	Psmd11	F1LMZ8	22.5354	20.4158	20.2731	19.9597	23.4367	22.5856	23.1721	23.1242
16	26S proteasome non-ATPase regulatory subunit 13 OS=Rattus norvegicus OX=10116 GN=Psmd13 PE=1 SV=1	Psmd13	B0BN93	21.7536	20.6128	20.5688	20.3441	23.9266	22.8465	23.449	23.5578
17	26S proteasome non-ATPase regulatory subunit 2 OS=Rattus norvegicus OX=10116 GN=Psmd2 PE=1 SV=1	Psmd2	Q4FZT9	19.4835	19.4415	20.2629	19.752	24.4674	23.5272	24.2571	24.057
18	26S proteasome non-ATPase regulatory subunit 9 OS=Rattus norvegicus OX=10116 GN=Psmd9 PE=1 SV=1	Psmd9	G3V9P0	16.5006	15.6256	16.1362	21.314	21.7042	21.0609	21.7914	21.83
19	26S proteasome regulatory subunit 4 OS=Rattus norvegicus OX=10116 GN=Psmc1 PE=1 SV=1	Psmc1	P62193	18.6063	18.2353	18.1664	19.5827	23.5747	22.9311	23.5596	23.4338
20	26S proteasome regulatory subunit 6A OS=Rattus norvegicus OX=10116 GN=Psmc3 PE=1 SV=1	Psmc3	Q6P6U2	19.037	19.0903	19.2941	19.1639	23.8109	22.9557	23.6552	23.6113
21	26S proteasome regulatory subunit 6B OS=Rattus norvegicus OX=10116 GN=Psmc4 PE=1 SV=1	Psmc4	Q63570	17.4584	16.6329	17.6373	17.81	22.8857	22.9384	23.2085	23.0553
22	26S proteasome regulatory subunit 7 OS=Rattus norvegicus OX=10116 GN=Psmc2 PE=1 SV=1	Psmc2	G3V7L6	20.4998	20.6202	20.2401	20.1006	24.4982	23.7689	24.2412	24.1402
23	26S proteasome regulatory subunit 8 OS=Rattus norvegicus OX=10116 GN=Psmc5 PE=1 SV=1	Psmc5	P62198	20.6506	20.0085	19.8684	21.628	24.3257	24.0002	24.175	24.0899
24	28 kDa heat- and acid-stable phosphoprotein OS=Rattus norvegicus OX=10116 GN=Pdap1 PE=1 SV=1	Pdap1	Q62785	NaN	NaN	NaN	NaN	17.9504	17.6051	NaN	17.0494
25	28S ribosomal protein S31, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrps31 PE=2 SV=1	Mrps31	B0BN56	NaN	NaN	14.5554	16.7957	NaN	15.4413	NaN	NaN
26	2-oxoglutarate dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ogdh PE=1 SV=1	Ogdh	Q5XI78	21.5647	20.6256	20.4189	20.5155	20.4346	21.7392	21.3721	21.5895
27	3'(2'),5'-bisphosphate nucleotidase 1 OS=Rattus norvegicus OX=10116 GN=Bpnt1 PE=1 SV=1	Bpnt1	A0A0G2K0V3	15.5126	NaN	14.5002	15.4964	20.3571	19.176	19.6817	19.717
28	30 kDa adipocyte complement-related protein OS=Rattus norvegicus OX=10116 GN=Adipoq PE=1 SV=1	Adipoq	Q8K3R4	NaN	18.0943	17.884	17.1735	NaN	NaN	NaN	NaN
29	39S ribosomal protein L11, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrpl11 PE=2 SV=1	mrpl11	Q5XIE3	NaN	16.8269	NaN	NaN	NaN	NaN	NaN	NaN
30	3-alpha-hydroxysteroid dehydrogenase OS=Rattus norvegicus OX=10116 GN=Akr1c9 PE=1 SV=1	Akr1c14	P23457	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
31	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Rattus norvegicus OX=10116 GN=Hsd17b10 PE=1 SV=1	Hsd17b10	B0BMW2	NaN	15.7691	14.7504	15.832	NaN	19.5376	18.9848	19.5253
32	3-ketoacyl-CoA thiolase A, peroxisomal OS=Rattus norvegicus OX=10116 GN=Acaa1a PE=1 SV=2	Acaa1a	P21775	15.5377	NaN	15.1962	NaN	17.9249	18.4332	18.3098	17.6853
33	3-ketoacyl-CoA thiolase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acaa2 PE=1 SV=3	Acaa2	G3V9U2	19.7138	18.9962	18.3694	17.1577	19.5139	21.9019	20.832	20.7461
34	3-mercaptopyruvate sulfurtransferase OS=Rattus norvegicus OX=10116 GN=Mpst PE=1 SV=3	Mpst	P97532	17.8855	19.4692	19.4669	18.31	21.323	20.2827	20.8182	20.5398
35	3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Rattus norvegicus OX=10116 GN=Papss1 PE=1 SV=1	Papss1	A0A0G2K0L0	19.2341	18.7365	19.1047	20.3372	18.7157	18.6687	17.7464	18.4703
36	3-phosphoinositide-dependent protein kinase 1 OS=Rattus norvegicus OX=10116 GN=Pdpk1 PE=1 SV=2	Pdpk1	O55173	NaN	NaN	NaN	NaN	17.1896	16.9207	17.3272	16.8992
37	40S ribosomal protein S10 OS=Rattus norvegicus OX=10116 GN=Rps10 PE=2 SV=1	Rps10	P63326	18.5036	18.7372	18.6846	19.1976	23.5772	24.4833	24.3641	24.1345
38	40S ribosomal protein S11 OS=Rattus norvegicus OX=10116 GN=Rps11 PE=1 SV=3	Rps11	P62282	17.3726	16.8912	17.8735	17.1158	23.6916	24.6649	24.2899	24.0499
39	40S ribosomal protein S12 OS=Rattus norvegicus OX=10116 GN=Rps12 PE=1 SV=1	Rps12	Q6PDW1	20.5545	20.7114	19.9386	20.1295	23.7345	22.5869	23.0445	22.9681
40	40S ribosomal protein S13 OS=Rattus norvegicus OX=10116 GN=Rps13 PE=1 SV=2	Rps13	P62278	20.6032	20.3256	20.4125	20.8478	22.6817	23.7179	23.4662	23.3455
41	40S ribosomal protein S14 OS=Rattus norvegicus OX=10116 GN=Rps14 PE=2 SV=3	Rps14	P13471	19.046	18.3513	18.7353	18.4341	24.2063	24.3707	24.2693	23.8836
42	40S ribosomal protein S15 OS=Rattus norvegicus OX=10116 GN=Rps15 PE=1 SV=2	Rps15	P62845	NaN	NaN	NaN	NaN	17.8101	21.3465	20.4473	20.3674
43	40S ribosomal protein S15a OS=Rattus norvegicus OX=10116 GN=Rps15a PE=1 SV=2	Rps15a	P62246	19.6241	19.2059	18.6305	17.1626	23.1724	23.91	23.7176	23.5161
44	40S ribosomal protein S16 OS=Rattus norvegicus OX=10116 GN=Rps16 PE=1 SV=2	Rps16	P62250	22.8413	22.5536	22.2536	20.8269	23.6125	24.2837	24.3456	24.2583
45	40S ribosomal protein S17-like OS=Rattus norvegicus OX=10116 GN=LOC100362366 PE=3 SV=1	LOC100362366	D3ZFA8	23.2879	23.6831	23.5029	22.5434	23.3684	23.718	23.3963	23.3917
46	40S ribosomal protein S2 OS=Rattus norvegicus OX=10116 GN=Rps2 PE=1 SV=1	Rps2	P27952	22.1752	21.4203	21.7113	21.6468	23.6882	25.0789	24.6998	24.5946
47	40S ribosomal protein S21 OS=Rattus norvegicus OX=10116 GN=Rps21 PE=1 SV=1	Rps21	P05765	NaN	NaN	16.2494	13.2925	20.0665	19.6202	19.6078	19.3819
48	40S ribosomal protein S23 OS=Rattus norvegicus OX=10116 GN=Rps23 PE=1 SV=3	Rps23	P62268	17.1798	16.9664	16.0387	15.3215	22.3867	23.2917	22.8913	22.7757
49	40S ribosomal protein S24 OS=Rattus norvegicus OX=10116 GN=LOC100363469 PE=3 SV=1	LOC100363469	D4ACJ1	15.8421	NaN	16.3647	14.3297	21.1037	22.3133	21.948	21.5748
50	40S ribosomal protein S25 OS=Rattus norvegicus OX=10116 GN=Rps25 PE=2 SV=1	Rps25	P62853	19.4534	18.751	19.0026	19.4667	22.7526	24.3402	23.8691	23.6676
51	40S ribosomal protein S26 OS=Rattus norvegicus OX=10116 GN=Rps26 PE=3 SV=3	Rps26	P62856	18.2331	17.5269	17.0661	17.7637	22.1456	23.4461	22.8908	22.5809

52	40S ribosomal protein S27-like OS=Rattus norvegicus OX=10116 GN=Rps27l PE=1 SV=3	Rps27l	P24051	NaN	17.3075	16.7399	16.2955	23.6686	23.1227	22.9147	22.809
53	40S ribosomal protein S28 OS=Rattus norvegicus OX=10116 GN=Rps28 PE=1 SV=1	Rps28	P62859	18.0211	15.9826	17.452	16.4707	21.5546	20.7861	20.7722	20.8805
54	40S ribosomal protein S29 OS=Rattus norvegicus OX=10116 GN=Rps29 PE=1 SV=2	Rps29	P62275	17.6027	17.3419	17.9549	18.066	21.0594	19.3887	19.1361	18.9045
55	40S ribosomal protein S3 OS=Rattus norvegicus OX=10116 GN=Rps3 PE=1 SV=1	Rps3	P62909	19.7694	19.4875	19.2378	20.1239	24.6543	24.8691	24.7844	24.6901
56	40S ribosomal protein S30 OS=Rattus norvegicus OX=10116 GN=LOC100360647 PE=1 SV=1	Fau	Q5BJN7	18.0543	18.92	19.4732	19.6319	20.7544	20.9875	20.662	20.8326
57	40S ribosomal protein S3a OS=Rattus norvegicus OX=10116 GN=LOC100365839 PE=3 SV=1	LOC100365839	M0R6L4	20.625	19.6504	20.1198	20.0665	23.3065	25.0063	24.6768	24.58
58	40S ribosomal protein S4 OS=Rattus norvegicus OX=10116 GN=Rps4x PE=3 SV=1	Rps4x-ps9	A0A0H2UHX3	22.1607	21.3412	21.8946	22.1006	24.5881	25.0854	25.1008	24.8512
59	40S ribosomal protein S5 OS=Rattus norvegicus OX=10116 GN=Rps5 PE=1 SV=1	Rps5	B0BN81	18.8413	18.5911	18.6008	19.8603	23.088	24.4085	23.9152	23.9522
60	40S ribosomal protein S6 OS=Rattus norvegicus OX=10116 GN=Rps6 PE=1 SV=1	Rps6	P62755	19.243	18.8957	18.5832	19.9071	23.3563	24.5012	24.2024	23.885
61	40S ribosomal protein S7 OS=Rattus norvegicus OX=10116 GN=Rps7 PE=1 SV=1	Rps7	P62083	18.5362	17.9788	17.4242	17.3557	21.8278	22.3186	21.8586	22.2272
62	40S ribosomal protein S8 OS=Rattus norvegicus OX=10116 GN=Rps8 PE=1 SV=2	Rps8	P62243	21.6736	21.0522	20.9839	20.1415	23.1269	24.3296	23.781	23.6846
63	40S ribosomal protein S9 OS=Rattus norvegicus OX=10116 GN=Rps9 PE=1 SV=4	Rps9	P29314	19.5874	18.9907	18.8434	18.2578	23.3501	24.4918	24.2881	24.1016
64	40S ribosomal protein SA OS=Rattus norvegicus OX=10116 GN=Rpsa PE=1 SV=3	Rpsa	P38983	19.8537	18.663	19.4231	18.4923	22.5598	22.3883	22.4553	22.3278
65	4F2 cell-surface antigen heavy chain OS=Rattus norvegicus OX=10116 GN=Slc3a2 PE=1 SV=1	Slc3a2	A0A0H2UHQ0	20.2137	19.6762	19.0975	20.3293	20.149	20.2945	20.0859	19.9492
66	4-trimethylaminobutyraldehyde dehydrogenase OS=Rattus norvegicus OX=10116 GN=Aldh9a1 PE=1 SV=1	Aldh9a1	A0A0G2JSI1	19.8296	19.281	19.5442	19.5362	21.5358	23.0075	23.5355	23.6099
67	5'-3' exoribonuclease OS=Rattus norvegicus OX=10116 GN=Xrn2 PE=1 SV=3	Xrn2	D4A914	NaN	NaN	NaN	NaN	17.8484	NaN	NaN	16.575
68	5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Rattus norvegicus OX=10116 GN=Prkaa1 PE=1 SV=2	Prkaa1	P54645	17.3891	17.4151	17.1832	16.8551	20.4615	19.9503	20.0275	19.8996
69	5'-AMP-activated protein kinase subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Prkab1 PE=1 SV=4	Prkab1	P80386	14.9937	17.1217	NaN	17.8972	21.1532	21.11	21.3647	20.7956
70	5'-AMP-activated protein kinase subunit beta-2 OS=Rattus norvegicus OX=10116 GN=Prkab2 PE=1 SV=1	Prkab2	A0A0G2JVK3	NaN	NaN	NaN	16.2858	19.2768	17.9252	18.5649	18.4571
71	5'-AMP-activated protein kinase subunit gamma-1 OS=Rattus norvegicus OX=10116 GN=Prkag1 PE=1 SV=3	Prkag1	P80385	19.0321	19.793	19.6227	19.4859	22.3195	21.0236	21.501	21.8986
72	5'-nucleotidase OS=Rattus norvegicus OX=10116 GN=Nt5e PE=1 SV=1	Nt5e	P21588	15.4982	17.1178	15.8524	15.883	19.7549	19.725	19.1321	19.23
73	5'-nucleotidase, cytosolic IA OS=Rattus norvegicus OX=10116 GN=Nt5c1a PE=1 SV=1	Nt5c1a	D3ZVD3	NaN	NaN	NaN	NaN	16.8297	16.6248	17.4309	16.8353
74	5'-nucleotidase, cytosolic II OS=Rattus norvegicus OX=10116 GN=Nt5c2 PE=1 SV=3	Nt5c2	D3ZMY7	NaN	NaN	14.9033	15.9384	22.8403	22.9559	23.0194	22.7077
75	5-oxoprolinase OS=Rattus norvegicus OX=10116 GN=Oplah PE=1 SV=2	Oplah	P97608	14.7094	15.2543	16.0216	NaN	18.6018	19.5075	19.8038	18.7703
76	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hspd1 PE=1 SV=1	Hspd1	P63039	22.4427	21.9312	21.4405	22.514	22.9162	23.8701	23.7031	23.9484
77	60S acidic ribosomal protein P0 OS=Rattus norvegicus OX=10116 GN=Rplp0 PE=1 SV=2	Rplp0	P19945	20.9476	20.6664	20.9898	21.0686	23.5859	24.6529	24.1575	24.2425
78	60S acidic ribosomal protein P1 OS=Rattus norvegicus OX=10116 GN=Rplp1 PE=3 SV=1	Rplp1	P19944	18.0158	18.3784	18.6782	20.134	20.7568	21.8721	21.502	21.7976
79	60S acidic ribosomal protein P2 OS=Rattus norvegicus OX=10116 GN=Rplp2 PE=1 SV=2	Rplp2	P02401	20.661	20.4489	20.0626	21.6685	23.8611	24.8854	24.5544	24.4953
80	60S ribosomal export protein NMD3 OS=Rattus norvegicus OX=10116 GN=Nmd3 PE=1 SV=2	Nmd3	F6PUQ7	NaN	NaN	NaN	NaN	17.1786	NaN	17.1298	17.0884
81	60S ribosomal protein L10 OS=Rattus norvegicus OX=10116 GN=Rpl10 PE=1 SV=3	Rpl10	Q6PDV7	17.6493	17.5291	16.41	17.8647	22.432	24.0013	23.5267	23.4187
82	60S ribosomal protein L10a OS=Rattus norvegicus OX=10116 GN=Rpl10a PE=1 SV=2	Rpl10a	P62907	17.4413	19.6817	18.4217	18.6544	22.8309	24.2857	23.9076	23.8479
83	60S ribosomal protein L11 OS=Rattus norvegicus OX=10116 GN=Rpl11 PE=1 SV=2	Rpl11	P62914	19.3606	18.4076	19.2623	18.994	23.3585	23.5974	23.4391	23.3408
84	60S ribosomal protein L12 OS=Rattus norvegicus OX=10116 GN=Rpl12 PE=2 SV=1	Rpl12	P23358	21.0335	20.4813	20.2363	20.7703	24.0275	24.629	24.4834	24.4751
85	60S ribosomal protein L13 OS=Rattus norvegicus OX=10116 GN=LOC100360491 PE=3 SV=1	LOC100360491	D3ZRM9	20.9968	20.3918	20.8559	20.6344	24.6549	25.206	24.9463	24.9867
86	60S ribosomal protein L13a OS=Rattus norvegicus OX=10116 GN=Rpl13a PE=1 SV=1	Rpl13a	Q5RK10	17.8098	17.1713	17.3381	17.2249	22.2465	23.6121	23.2838	23.188
87	60S ribosomal protein L14 OS=Rattus norvegicus OX=10116 GN=Rpl14 PE=1 SV=1	Rpl14	B5DEM5	18.9927	18.6632	18.8996	18.4426	22.0263	23.739	23.0123	22.9474
88	60S ribosomal protein L15 OS=Rattus norvegicus OX=10116 GN=Rpl15 PE=1 SV=2	Rpl15	P61314	19.4249	18.9351	18.6196	18.9169	22.6394	23.7561	23.4878	23.3608
89	60S ribosomal protein L17 OS=Rattus norvegicus OX=10116 GN=Rpl17 PE=1 SV=1	Rpl17	A0A0H2UHQ1	18.8436	18.2375	18.0565	17.0483	22.0972	23.7078	23.0481	23.3687
90	60S ribosomal protein L18 OS=Rattus norvegicus OX=10116 GN=Rpl18 PE=1 SV=1	Rpl18	A0A0H2UHS7	20.0316	19.6388	19.7368	18.6902	22.6898	23.3313	23.1707	23.0762
91	60S ribosomal protein L18a OS=Rattus norvegicus OX=10116 GN=Rpl18a PE=2 SV=1	Rpl18a	P62718	18.154	18.392	18.2696	18.4436	22.1391	23.4757	23.0928	23.0073
92	60S ribosomal protein L19 OS=Rattus norvegicus OX=10116 GN=Rpl19 PE=1 SV=1	Rpl19	P84100	18.145	16.9723	17.7086	16.4401	21.8464	23.2869	22.7186	22.6188
93	60S ribosomal protein L22 OS=Rattus norvegicus OX=10116 GN=LOC100360057 PE=1 SV=1	LOC100360057	Q6PDV8	NaN	NaN	NaN	16.6101	22.4137	22.6614	22.4876	22.3167
94	60S ribosomal protein L23 OS=Rattus norvegicus OX=10116 GN=Rpl23 PE=2 SV=1	Rpl23	P62832	18.5614	19.4448	19.0388	17.7091	24.7752	23.9361	23.7031	23.5703
95	60S ribosomal protein L24 OS=Rattus norvegicus OX=10116 GN=Rpl24 PE=2 SV=1	Rpl24	P83732	19.8939	19.4833	19.5672	19.8592	22.5941	23.5025	23.3795	23.2263
96	60S ribosomal protein L26 OS=Rattus norvegicus OX=10116 GN=Rpl26 PE=1 SV=1	Rpl26	G3V6I9	16.8634	19.0885	20.5042	20.106	21.6568	22.8692	22.8181	22.6502
97	60S ribosomal protein L27 OS=Rattus norvegicus OX=10116 GN=Rpl27 PE=2 SV=2	Rpl27	P61354	17.9593	NaN	17.7186	18.0523	21.254	22.0901	21.8761	21.6367
98	60S ribosomal protein L29 OS=Rattus norvegicus OX=10116 GN=Rpl29 PE=1 SV=3	Rpl29	P25886	14.3557	14.2463	14.3497	NaN	20.2104	20.6636	20.6607	20.0801
99	60S ribosomal protein L29 OS=Rattus norvegicus OX=10116 PE=3 SV=1	M0RCI7_RAT	M0RCI7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
100	60S ribosomal protein L3 OS=Rattus norvegicus OX=10116 GN=Rpl3 PE=1 SV=3	Rpl3	P21531	19.3503	17.3889	19.2139	17.9182	23.1325	24.3579	23.9749	23.8824
101	60S ribosomal protein L30 OS=Rattus norvegicus OX=10116 GN=Rpl30 PE=3 SV=2	Rpl30	P62890	17.7884	NaN	NaN	NaN	20.3669	21.7154	21.5417	21.2295
102	60S ribosomal protein L31 OS=Rattus norvegicus OX=10116 GN=Rpl31 PE=2 SV=1	Rpl31	P62902	17.5239	17.5369	16.4286	16.019	22.1606	23.3625	23.0518	22.9463
103	60S ribosomal protein L32 OS=Rattus norvegicus OX=10116 GN=Rpl32 PE=1 SV=2	Rpl32	P62912	18.3468	18.5239	18.0237	19.1346	22.1244	22.6187	22.8604	22.6536
104	60S ribosomal protein L34 OS=Rattus norvegicus OX=10116 GN=Rpl34 PE=1 SV=1	Rpl34	B2RZD4	17.0581	16.0318	17.3853	16.0886	21.5482	22.6554	22.1873	22.3198

105	60S ribosomal protein L35 OS=Rattus norvegicus OX=10116 GN=Rpl35 PE=1 SV=3	Rpl35	P17078	NaN	NaN	NaN	NaN	19.7336	20.2912	19.6569	20.342
106	60S ribosomal protein L35a OS=Rattus norvegicus OX=10116 GN=Rpl35a PE=3 SV=1	Rpl35al1	P04646	17.1119	18.3554	18.896	17.5708	21.1938	22.2211	21.7827	21.618
107	60S ribosomal protein L36 OS=Rattus norvegicus OX=10116 PE=3 SV=1	LOC100361060	D3ZZ95	17.3796	15.637	15.7667	15.1929	19.3503	21.143	20.8191	20.5976
108	60S ribosomal protein L36a OS=Rattus norvegicus OX=10116 GN=Rpl36a PE=1 SV=2	Rpl36a	P83883	NaN	NaN	NaN	14.7513	18.9151	20.3468	20.6433	19.9957
109	60S ribosomal protein L37a OS=Rattus norvegicus OX=10116 GN=Rpl37a PE=3 SV=1	Rpl37a	A0A0H2UHU1	17.367	16.2433	NaN	16.5871	20.6058	21.4199	21.0952	21.082
110	60S ribosomal protein L4 OS=Rattus norvegicus OX=10116 GN=Rpl4 PE=1 SV=1	Rpl4	Q6P3V9	20.1076	19.8638	20.2875	20.1171	23.3692	24.9361	24.3889	24.3914
111	60S ribosomal protein L5 OS=Rattus norvegicus OX=10116 GN=Rpl5 PE=1 SV=3	Rpl5	P09895	19.4905	16.3204	19.1028	18.7257	20.9739	21.2954	20.0356	20.2079
112	60S ribosomal protein L6 OS=Rattus norvegicus OX=10116 PE=3 SV=1	Rpl6-ps1	F1LQS3	20.2902	18.9811	20.4885	19.9034	23.1299	24.9036	24.0754	24.0548
113	60S ribosomal protein L7 OS=Rattus norvegicus OX=10116 GN=Rpl7 PE=1 SV=1	Rpl7	B0K031	18.8411	19.1015	18.7443	18.4406	22.8717	24.5842	24.069	23.9909
114	60S ribosomal protein L7a-like OS=Rattus norvegicus OX=10116 GN=LOC108349606 PE=4 SV=1	LOC108349606	D3ZU22	18.8358	18.9594	19.6351	18.9665	22.8421	23.9026	23.6561	23.4525
115	60S ribosomal protein L9 OS=Rattus norvegicus OX=10116 GN=Rpl9 PE=1 SV=1	Rpl9	P17077	17.2453	19.0366	17.4381	18.5936	22.4767	23.5146	23.4047	23.1411
116	6-phosphogluconate dehydrogenase, decarboxylating OS=Rattus norvegicus OX=10116 GN=Kif1b PE=1 SV=1	Kif1b	A0A0G2K7Q8	16.9229	18.391	18.6753	18.2822	17.4788	18.2636	17.6421	17.7977
117	6-phosphogluconolactonase OS=Rattus norvegicus OX=10116 GN=Pgls PE=1 SV=1	Pgls	G3V8D5	15.6835	16.759	17.3502	17.4347	19.8466	20.3032	20.5238	20.4737
118	72 kDa type IV collagenase OS=Rattus norvegicus OX=10116 GN=Mmp2 PE=1 SV=3	Mmp2	E9PSM5	18.5241	18.9788	19.363	18.965	16.8429	18.1197	17.8147	17.673
119	A kinase (PRKA) anchor protein 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Akap1 PE=1 SV=2	Akap1	D4A9M6	19.8814	19.2852	20.0689	20.0565	20.4047	20.7339	20.3172	20.0453
120	Ab1-205 OS=Rattus norvegicus OX=10116 GN=Surf4 PE=1 SV=1	Surf4	Q7TP91	17.6559	19.408	16.2065	17.9126	19.579	19.6744	19.2298	19.239
121	Ab2-292 OS=Rattus norvegicus OX=10116 GN=Sec62 PE=1 SV=1	Sec62	Q7TP42	NaN	NaN	NaN	NaN	18.0981	18.3891	17.2851	18.0664
122	Abhydrolase domain containing 4 (Predicted) OS=Rattus norvegicus OX=10116 GN=Abhd4 PE=1 SV=1	Abhd4	D3ZAW4	14.189	15.1313	NaN	NaN	19.1158	18.198	17.6017	18.0578
123	Abi1 protein OS=Rattus norvegicus OX=10116 GN=Abi1 PE=1 SV=1	Abi1	A2VD09	NaN	NaN	NaN	13.4573	17.5873	18.5082	18.5696	18.1639
124	ABR, RhoGEF and GTPase-activating protein OS=Rattus norvegicus OX=10116 GN=Abr PE=1 SV=1	Abr	A0A0G2JTR4	17.1712	17.5288	NaN	17.3591	19.3703	18.3496	19.4477	19.1971
125	ABRA C-terminal-like OS=Rattus norvegicus OX=10116 GN=Abracl PE=1 SV=1	Abracl	D3ZSL2	NaN	NaN	NaN	NaN	18.5359	17.831	19.0899	19.2228
126	Abraxas 2, BRISC complex subunit OS=Rattus norvegicus OX=10116 GN=Abraxas2 PE=1 SV=3	Abraxas2	D4A415	16.4186	16.5895	15.5801	16.0384	18.2179	19.0664	19.5127	18.9651
127	Ac1002 OS=Rattus norvegicus OX=10116 GN=Adh4 PE=1 SV=1	Adh4	Q7TQ90	19.6106	18.3773	19.5056	19.7835	19.7748	19.8859	19.7475	19.3483
128	Ac1164 OS=Rattus norvegicus OX=10116 GN=Pdhx PE=1 SV=1	Pdhx	Q7TQ85	NaN	NaN	NaN	NaN	NaN	16.7388	15.8513	16.0908
129	Ac1288 OS=Rattus norvegicus OX=10116 PE=1 SV=1	Hook3	Q7TQ77	15.3924	NaN	15.3865	NaN	20.2047	19.2403	19.6589	19.2656
130	Ac1873 OS=Rattus norvegicus OX=10116 GN=Fga PE=1 SV=1	Fga	Q7TQ70	29.5045	29.1484	29.26	29.5205	27.9967	27.829	27.2763	28.183
131	Ac2-190 OS=Rattus norvegicus OX=10116 GN=Impad1 PE=1 SV=1	Bpnt2	Q7TPJ5	NaN	19.411	NaN	19.2479	NaN	NaN	NaN	NaN
132	Ac2-246 OS=Rattus norvegicus OX=10116 GN=Phf5a PE=1 SV=1	Phf5a	Q7TPJ6	NaN	NaN	15.1388	15.3139	16.2386	18.1659	17.1529	17.0833
133	Ac2-269 OS=Rattus norvegicus OX=10116 GN=LOC100911453 PE=1 SV=1	Wdr77	Q7TPI7	16.4696	NaN	15.5395	NaN	16.0444	15.7851	16.6534	16.6617
134	Acad9 protein OS=Rattus norvegicus OX=10116 GN=Acad9 PE=1 SV=1	Acad9	B1WC61	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
135	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acat1 PE=1 SV=1	Acat1	P17764	19.0069	18.6776	18.2143	15.9192	19.5608	21.6978	20.9573	21.4046
136	Acetyl-CoA carboxylase 1 OS=Rattus norvegicus OX=10116 GN=Acaca PE=1 SV=1	Acaca	P11497	19.7562	19.1755	19.7245	18.5386	19.8912	19.8548	20.5218	20.4034
137	Acetyl-CoA carboxylase beta OS=Rattus norvegicus OX=10116 GN=Acacb PE=1 SV=1	Acacb	A0A0G2K1F2	20.6422	20.3177	20.8144	20.9863	22.8809	24.0242	24.0462	23.6189
138	Acetyl-Coenzyme A dehydrogenase, medium chain OS=Rattus norvegicus OX=10116 GN=Acadm PE=1 SV=1	Acadm	G3V796	19.1056	19.8783	18.1863	19.866	17.9092	18.1317	NaN	18.3954
139	Acid ceramidase OS=Rattus norvegicus OX=10116 GN=Asah1 PE=1 SV=1	Asah1	A0A0G2K8T0	NaN	16.968	NaN	NaN	16.9834	17.0433	NaN	16.6759
140	Acid sphingomyelinase-like phosphodiesterase OS=Rattus norvegicus OX=10116 GN=Smpdl3b PE=2 SV=1	Smpdl3b	Q4V7D9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
141	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Rattus norvegicus OX=10116 GN=Anp32a PE=1 SV=2	Anp32a	F7EL36	16.5832	14.5425	15.6077	NaN	20.174	19.9959	20.2821	20.3065
142	Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Rattus norvegicus OX=10116 GN=Anp32e PE=2 SV=1	Anp32e	Q5XIE0	NaN	NaN	NaN	NaN	18.3955	18.8387	17.7531	18.5909
143	Aconitate hydratase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Aco2 PE=1 SV=2	Aco2	Q9ER34	19.6919	20.692	20.3624	16.5099	21.541	24.1961	23.4459	23.6629
144	Actin, alpha cardiac muscle 1 OS=Rattus norvegicus OX=10116 GN=Actc1 PE=2 SV=1	Actc1	P68035	22.6518	21.6768	21.9586	22.5053	28.0246	27.5073	27.7064	27.755
145	Actin, alpha skeletal muscle OS=Rattus norvegicus OX=10116 GN=Acta1 PE=1 SV=1	Acta1	P68136	20.1544	20.8752	21.5136	23.64	23.6436	22.5497	23.4697	23.1894
146	Actin, beta-like 2 OS=Rattus norvegicus OX=10116 GN=Actbl2 PE=1 SV=1	Actbl2	D3ZRN3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
147	Actin, cytoplasmic 1 OS=Rattus norvegicus OX=10116 GN=Actb PE=1 SV=1	Actb	P60711	20.1318	20.0746	20.0533	20.5537	21.9362	21.8979	21.87	22.1001
148	Actin, cytoplasmic 2 OS=Rattus norvegicus OX=10116 GN=Actg1 PE=1 SV=1	Actg1	P63259	25.9183	26.3255	26.0478	26.0909	29.5021	29.0325	29.2095	29.2591
149	Actinin alpha 2 OS=Rattus norvegicus OX=10116 GN=Actn2 PE=1 SV=1	Actn2	D3ZCV0	NaN	NaN	NaN	NaN	18.6383	18.6989	18.5277	18.2462
150	Actin-related protein 2 OS=Rattus norvegicus OX=10116 GN=Actr2 PE=2 SV=1	Actr2	Q5M7U6	19.0403	18.1868	18.5962	18.5933	21.2119	20.83	21.3146	21.1742
151	Actin-related protein 2/3 complex inhibitor OS=Rattus norvegicus OX=10116 GN=Arpin PE=1 SV=1	Arpin	D4A1B2	NaN	NaN	NaN	NaN	18.5505	16.3621	17.8163	17.9605
152	Actin-related protein 2/3 complex subunit 1A OS=Rattus norvegicus OX=10116 GN=Arpc1a PE=2 SV=1	Arpc1a	Q99PD4	NaN	NaN	NaN	NaN	16.8796	19.7814	19.9533	19.844
153	Actin-related protein 2/3 complex subunit 1B OS=Rattus norvegicus OX=10116 GN=Arpc1b PE=1 SV=3	Arpc1b	O88656	NaN	NaN	NaN	NaN	NaN	NaN	NaN	16.9885
154	Actin-related protein 2/3 complex subunit 3 OS=Rattus norvegicus OX=10116 GN=Arpc3 PE=1 SV=1	Arpc3	B2GV73	17.6064	18.663	18.2516	18.8223	21.2365	21.0234	21.1429	21.2991
155	Actin-related protein 2/3 complex subunit 4 OS=Rattus norvegicus OX=10116 GN=Arpc4 PE=1 SV=1	Arpc4	B2RZ72	17.3649	18.1628	16.943	19.2266	20.1585	20.0996	20.4336	20.5544
156	Actin-related protein 2/3 complex subunit 5 OS=Rattus norvegicus OX=10116 GN=Arpc5 PE=1 SV=3	Arpc5	Q4KLF8	NaN	16.683	NaN	NaN	20.7181	19.8955	20.9565	20.8793
157	Actin-related protein 2/3 complex subunit 5-like protein OS=Rattus norvegicus OX=10116 GN=Arpc5l PE=1 SV=2	Arpc5l-ps1	A1L108	15.0294	NaN	15.4489	NaN	19.1367	19.8258	19.8594	20.2025

158	Actin-related protein 3 OS=Rattus norvegicus OX=10116 GN=Actr3 PE=1 SV=1	Actr3	A0A0G2K1C0	18.4049	17.8568	19.3168	18.5639	20.4455	20.8374	21.1734	21.0403
159	Activator of Hsp90 ATPase activity 1 OS=Rattus norvegicus OX=10116 GN=Ahsa1 PE=1 SV=1	Ahsa1	B0BN63	17.8925	15.0277	16.8042	19.0874	23.1594	22.7796	23.1133	23.0246
160	Activator of HSP90 ATPase homolog 2 OS=Rattus norvegicus OX=10116 GN=Ahsa2 PE=1 SV=1	Ahsa2	A0A0G2K7W5	NaN	NaN	NaN	NaN	NaN	18.8146	19.3537	18.6115
161	Acyl carrier protein OS=Rattus norvegicus OX=10116 GN=Ndufab1 PE=1 SV=1	Ndufab1	D3ZF13	NaN	14.9791	14.5831	NaN	18.0007	19.4939	19.0662	19.4267
162	Acylamino-acid-releasing enzyme OS=Rattus norvegicus OX=10116 GN=Apeh PE=1 SV=1	Apeh	G3V9E4	NaN	16.513	15.6812	NaN	NaN	NaN	NaN	NaN
163	Acyl-CoA synthetase short-chain family member 2 OS=Rattus norvegicus OX=10116 GN=Acss2 PE=1 SV=1	Acss2	G3V9U0	NaN	16.1221	15.5552	NaN	18.9025	19.2006	19.0948	18.8723
164	Acyl-CoA thioesterase 11 OS=Rattus norvegicus OX=10116 GN=Acot11 PE=4 SV=3	Acot11	F1LX28	18.3423	16.1683	16.9713	19.4391	23.229	22.7515	22.4471	22.0121
165	Acyl-CoA-binding domain-containing protein 6 OS=Rattus norvegicus OX=10116 GN=Acbd6 PE=1 SV=1	Acbd6	Q5RJK8	NaN	NaN	NaN	NaN	17.456	16.5878	16.4185	16.6867
166	Acyl-CoA-binding protein OS=Rattus norvegicus OX=10116 GN=Dbi PE=1 SV=1	Dbi	Q6TXF3	21.1772	23.2302	20.1888	20.8541	20.2436	20.8094	20.3059	20.1435
167	Acyl-coenzyme A thioesterase 1 OS=Rattus norvegicus OX=10116 GN=Acot1 PE=1 SV=1	Acot1	O88267	NaN	NaN	NaN	NaN	16.961	16.6283	16.0603	NaN
168	Acyl-coenzyme A thioesterase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acot2 PE=1 SV=1	Acot2	O55171	16.3346	15.6836	14.8185	NaN	18.2292	17.4743	17.8002	17.753
169	Acyl-protein thioesterase 1 OS=Rattus norvegicus OX=10116 GN=Lypla1 PE=1 SV=1	Lypla1	P70470	15.6897	NaN	16.3288	NaN	20.8519	20.326	20.7824	20.7794
170	Acyl-protein thioesterase 2 OS=Rattus norvegicus OX=10116 GN=Lypla2 PE=1 SV=1	Lypla2	Q9QYL8	NaN	NaN	NaN	NaN	20.5083	19.2199	19.9661	20.2288
171	ADAM metallopeptidase domain 19 OS=Rattus norvegicus OX=10116 GN=Adam19 PE=4 SV=1	Adam19	D3ZPM7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
172	Adapter molecule crk OS=Rattus norvegicus OX=10116 GN=Crk PE=1 SV=1	Crk	Q63768	NaN	NaN	14.2369	NaN	19.0241	17.8535	18.6793	18.0823
173	Adaptin ear-binding coat-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Necap2 PE=1 SV=2	Necap2	Q6P756	NaN	NaN	NaN	NaN	16.1959	14.4051	15.5253	15.1353
174	Adaptor protein, phosphotyrosine-interacting with PH domain and leucine zipper 1 OS=Rattus norvegicus OX=10116 GN=A	Appl1	D3ZWA8	NaN	NaN	NaN	NaN	18.1898	NaN	17.1688	17.7426
175	Adaptor-related protein complex 3 subunit delta 1 OS=Rattus norvegicus OX=10116 GN=Ap3d1 PE=1 SV=1	Ap3d1	B5DFK6	15.7806	15.3367	18.0449	17.3816	20.1024	20.2314	20.1021	20.2347
176	Adducin 1 (Alpha), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Add1 PE=1 SV=1	Add1	A0A0G2JSM7	16.5993	17.1595	14.6504	16.7643	20.9281	20.4027	20.2781	20.0879
177	Adducin 3 (Gamma), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Add3 PE=1 SV=1	Add3	G3V9D7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
178	Adenine phosphoribosyltransferase OS=Rattus norvegicus OX=10116 GN=Aprt PE=1 SV=1	Aprt	P36972	16.9976	17.7029	18.0748	17.3249	21.502	21.0029	21.2749	21.3313
179	Adenosine kinase OS=Rattus norvegicus OX=10116 GN=Adk PE=1 SV=1	Adk	A0A0G2K6X9	NaN	16.0037	NaN	NaN	17.661	17.5104	17.6641	17.5467
180	Adenosylhomocysteinase OS=Rattus norvegicus OX=10116 GN=Ahcy PE=1 SV=3	Ahcy	P10760	16.3714	16.6136	15.951	17.2253	20.8099	22.2067	22.644	22.1634
181	Adenylate kinase isoenzyme 1 OS=Rattus norvegicus OX=10116 GN=Ak1 PE=1 SV=3	Ak1	P39069	19.8535	19.6574	19.0467	19.6209	24.7479	24.1198	24.5109	24.3742
182	Adenylosuccinate lyase OS=Rattus norvegicus OX=10116 GN=Adsl PE=1 SV=1	Adsl	D3ZW08	18.4072	17.6289	17.6796	17.2636	22.4312	22.8475	22.9068	22.9569
183	Adenylosuccinate synthetase isozyme 1 OS=Rattus norvegicus OX=10116 GN=Adssl1 PE=1 SV=1	Adss1	M0R629	14.8116	NaN	NaN	16.5213	18.5957	18.5197	18.6881	18.5289
184	Adenylosuccinate synthetase isozyme 2 OS=Rattus norvegicus OX=10116 GN=Adss PE=1 SV=1	Adss	D4AEP0	16.7056	16.4954	16.0302	17.0663	18.1913	18.5641	19.8786	19.0617
185	Adenylyl cyclase-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Cap1 PE=1 SV=3	Cap1	Q08163	19.7215	19.7139	20.3118	18.5851	22.7958	21.9302	22.7841	22.3605
186	Adenylyl cyclase-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Cap2 PE=1 SV=1	Cap2	P52481	18.9966	19.5509	17.9406	18.0872	23.8329	22.4218	23.3084	23.0399
187	Adenylyltransferase and sulfurtransferase MOCS3 OS=Rattus norvegicus OX=10116 GN=Mocs3 PE=1 SV=1	Mocs3	D4A8L5	17.3691	16.9906	17.0173	17.3127	15.9256	NaN	16.4058	15.4446
188	Adhesion G protein-coupled receptor E5 OS=Rattus norvegicus OX=10116 GN=Adgre5 PE=1 SV=1	Adgre5	A0A0G2JSI4	18.1661	21.5566	17.3124	20.1741	17.2057	17.6879	16.7856	16.6626
189	Adhesion G protein-coupled receptor F5 OS=Rattus norvegicus OX=10116 GN=Adgrf5 PE=1 SV=1	Adgrf5	A0A0G2JZZ0	19.9792	18.4759	19.0574	18.7897	17.3864	17.6084	16.5665	17.7808
190	Adipocyte plasma membrane-associated protein OS=Rattus norvegicus OX=10116 GN=Apmap PE=1 SV=1	Apmap	A0A0G2K6G2	18.4084	15.6845	16.8731	18.235	17.4589	14.3794	17.0229	16.9633
191	Adiponectin a OS=Rattus norvegicus OX=10116 GN=C1qb PE=1 SV=1	C1qb	G3V7N9	21.9715	21.6979	21.8535	20.7417	19.0865	20.922	20.3376	20.6228
192	ADP/ATP translocase 1 OS=Rattus norvegicus OX=10116 GN=Slc25a4 PE=1 SV=3	Slc25a4	Q05962	24.0906	25.8177	23.8946	24.9933	25.1611	25.9177	25.5468	25.5771
193	ADP/ATP translocase 2 OS=Rattus norvegicus OX=10116 GN=Slc25a5 PE=1 SV=3	Slc25a5	Q09073	21.4162	21.0789	20.646	21.2575	21.4445	22.0165	22.0298	21.8417
194	ADP-dependent glucokinase OS=Rattus norvegicus OX=10116 GN=Adpgk PE=1 SV=1	Adpgk	G3V784	NaN	NaN	NaN	NaN	16.3407	NaN	16.9223	17.2421
195	ADP-ribosylation factor 1 OS=Rattus norvegicus OX=10116 GN=Arf1 PE=1 SV=2	Arf1	P84079	21.4866	20.9229	22.0753	22.1787	25.439	24.7921	25.1947	25.1081
196	ADP-ribosylation factor 2 OS=Rattus norvegicus OX=10116 GN=Arf2 PE=2 SV=1	Arf2	P84082	NaN	NaN	15.1594	NaN	19.8875	18.7087	19.1041	19.2252
197	ADP-ribosylation factor 4 OS=Rattus norvegicus OX=10116 GN=Arf4 PE=2 SV=2	Arf4	P61751	19.9378	18.8944	18.7105	19.2188	23.9384	23.3259	23.5012	23.4401
198	ADP-ribosylation factor 5 OS=Rattus norvegicus OX=10116 GN=Arf5 PE=1 SV=2	Arf5	P84083	20.4304	18.1339	19.9624	17.167	23.4746	22.7826	23.0143	22.902
199	ADP-ribosylation factor 6 OS=Rattus norvegicus OX=10116 GN=Arf6 PE=1 SV=2	Arf6	P62332	16.3328	15.3028	16.1214	NaN	20.0882	18.863	19.3093	19.5551
200	ADP-ribosylation factor GTPase-activating protein 1 OS=Rattus norvegicus OX=10116 GN=Arfgap1 PE=1 SV=1	Arfgap1	Q62848	19.2447	18.9077	19.1918	19.3531	22.6356	23.0732	22.6889	22.8017
201	ADP-ribosylation factor GTPase-activating protein 2 OS=Rattus norvegicus OX=10116 GN=Arfgap2 PE=1 SV=1	Arfgap2	Q3MID3	14.4304	NaN	17.0037	14.7072	20.5233	20.509	20.4711	20.239
202	ADP-ribosylation factor GTPase-activating protein 3 OS=Rattus norvegicus OX=10116 GN=Arfgap3 PE=1 SV=1	Arfgap3	A0A0G2K4J0	17.6914	14.2577	NaN	NaN	17.6236	NaN	17.8407	15.2712
203	ADP-ribosylation factor-binding protein GGA3 OS=Rattus norvegicus OX=10116 GN=Gga3 PE=1 SV=1	Gga3	A0A0G2JV04	NaN	NaN	16.907	15.9124	20.5624	20.4577	20.8666	20.1132
204	ADP-ribosylation factor-like 6 interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Arl6ip1 PE=1 SV=1	Arl6ip1	Q7TMZ5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
205	ADP-ribosylation factor-like protein 1 OS=Rattus norvegicus OX=10116 GN=Arl1 PE=1 SV=1	Arl1	P61212	NaN	NaN	NaN	NaN	17.6939	NaN	17.8756	18.0268
206	ADP-ribosylation factor-like protein 2 OS=Rattus norvegicus OX=10116 GN=Arl2 PE=1 SV=2	Arl2	G3V8V0	NaN	NaN	NaN	NaN	16.6444	NaN	17.3082	NaN
207	ADP-ribosylation factor-like protein 3 OS=Rattus norvegicus OX=10116 GN=Arl3 PE=1 SV=2	Arl3	F8WG91	NaN	NaN	NaN	17.3824	18.5993	17.7459	18.63	18.2971
208	ADP-ribosylation factor-like protein 8B OS=Rattus norvegicus OX=10116 GN=Arl8b PE=2 SV=1	Arl8b	Q66HA6	16.1448	NaN	NaN	14.9357	19.856	20.5997	19.8388	20.0006
209	ADP-sugar pyrophosphatase OS=Rattus norvegicus OX=10116 GN=Nudt5 PE=1 SV=1	Nudt5	A0A140TAD1	NaN	14.6426	NaN	NaN	19.2245	18.4075	18.9797	18.8499
210	Afamin OS=Rattus norvegicus OX=10116 GN=Afm PE=1 SV=1	Afm	G3V9R9	22.4489	22.4242	22.9074	21.8165	18.1134	18.7883	19.0242	18.5987

211	Aflatoxin B1 aldehyde reductase member 2 OS=Rattus norvegicus OX=10116 GN=Akr7a2 PE=1 SV=2	Akr7a2	Q8CG45	NaN	NaN	15.1311	15.8339	19.5606	19.7668	20.1609	19.2889
212	AH receptor-interacting protein OS=Rattus norvegicus OX=10116 GN=Aip PE=1 SV=1	Aip	Q5FWY5	NaN	13.3701	NaN	NaN	22.1045	21.3857	21.9123	21.858
213	AHNAK nucleoprotein OS=Rattus norvegicus OX=10116 GN=Ahnak PE=1 SV=1	Ahnak	A0A0G2JUA5	23.4998	23.4211	23.381	24.164	27.7126	27.7434	28.0411	27.6183
214	A-kinase anchor protein 12 OS=Rattus norvegicus OX=10116 GN=Akap12 PE=1 SV=1	Akap12	Q5QD51	21.4741	22.2922	22.3732	21.6342	24.205	24.3213	24.0345	23.9232
215	A-kinase anchor protein 13 OS=Rattus norvegicus OX=10116 GN=Akap13 PE=1 SV=2	Akap13	F1M3G7	19.2724	19.2871	19.6642	19.3311	22.2354	22.9225	22.4269	22.0519
216	A-kinase anchor protein 2 OS=Rattus norvegicus OX=10116 GN=Akap2 PE=1 SV=2	Akap2	F1LPQ9	24.1628	25.6843	24.154	26.1715	24.3071	24.7333	24.2137	24.2499
217	A-kinase anchor protein 8 OS=Rattus norvegicus OX=10116 GN=Akap8 PE=1 SV=1	Akap8	Q63014	NaN	NaN	NaN	NaN	17.1904	NaN	NaN	17.053
218	A-kinase anchor protein SPHKAP OS=Rattus norvegicus OX=10116 GN=Sphkap PE=1 SV=1	Sphkap	A0A0G2K3J4	18.1694	19.5567	18.5687	17.5418	22.0479	22.0202	22.0265	21.9263
219	A-kinase-anchoring protein 10 OS=Rattus norvegicus OX=10116 GN=Akap10 PE=1 SV=1	Akap10	F1LNB3	NaN	NaN	NaN	19.0732	16.2483	NaN	16.007	NaN
220	AKT1 substrate 1 OS=Rattus norvegicus OX=10116 GN=Akt1s1 PE=1 SV=1	Akt1s1	D3ZH75	23.8168	22.4217	22.3943	23.8624	22.3734	21.9524	21.8369	21.7108
221	Alanine--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Aars PE=1 SV=3	Aars1	P50475	19.5077	18.8872	20.1046	19.4109	21.6743	21.7088	23.3449	21.9706
222	Alanyl-tRNA editing protein Aarsd1 OS=Rattus norvegicus OX=10116 GN=Aarsd1 PE=1 SV=1	Aarsd1	Q5XI97	NaN	NaN	NaN	NaN	19.0076	21.5883	22.3148	20.6149
223	Alcohol dehydrogenase [NADP(+)] OS=Rattus norvegicus OX=10116 GN=Akr1a1 PE=1 SV=2	Akr1a1	P51635	18.5683	17.8698	18.3483	18.3113	18.7108	19.1128	18.4896	18.2571
224	Alcohol dehydrogenase 1 OS=Rattus norvegicus OX=10116 GN=Adh1 PE=1 SV=3	Adh1	P06757	18.6174	18.1246	18.8228	19.0949	20.5703	20.1408	20.1622	20.3022
225	Aldehyde dehydrogenase family 16 member A1 OS=Rattus norvegicus OX=10116 GN=Aldh16a1 PE=2 SV=1	Aldh16a1	Q3T1L0	17.303	18.3231	18.645	18.6016	20.0402	20.7795	21.8647	21.832
226	Aldehyde dehydrogenase family 5, subfamily A1 OS=Rattus norvegicus OX=10116 GN=Aldh5a1 PE=1 SV=1	Aldh5a1	G3V945	NaN	NaN	NaN	NaN	NaN	NaN	15.9352	NaN
227	Aldehyde dehydrogenase family 6, subfamily A1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Aldh6a1 PE=1 SV=1	Aldh6a1	G3V7J0	NaN	NaN	14.767	NaN	15.8393	18.0217	17.4718	18.0152
228	Aldehyde dehydrogenase OS=Rattus norvegicus OX=10116 GN=Aldh3b1 PE=3 SV=1	Aldh3b1	A0A0G2K7W2	18.0503	17.7024	17.885	17.9629	NaN	NaN	NaN	NaN
229	Aldehyde dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Aldh2 PE=1 SV=2	Aldh2	F1LN88	18.1634	17.2504	17.9097	18.2062	21.4767	22.2507	21.4708	21.7446
230	Aldose reductase OS=Rattus norvegicus OX=10116 GN=Akr1b1 PE=1 SV=3	Akr1b1	P07943	18.6484	18.1004	18.6992	18.6983	23.1018	23.028	23.0516	22.8064
231	Alkaline phosphatase, tissue-nonspecific isozyme OS=Rattus norvegicus OX=10116 GN=Alpl PE=1 SV=2	Alpl	P08289	16.2663	16.7399	16.9286	15.6585	NaN	14.6041	NaN	NaN
232	Alkylglycerone-phosphate synthase OS=Rattus norvegicus OX=10116 GN=Agps PE=1 SV=3	Agps	F1M9Q8	NaN	NaN	NaN	NaN	18.9325	18.7886	17.1417	18.1357
233	Allograft inflammatory factor 1-like OS=Rattus norvegicus OX=10116 GN=Aif1l PE=4 SV=1	Aif1l	D3ZRD9	NaN	NaN	NaN	NaN	19.476	18.7206	19.0136	19.013
234	All-trans-13,14-dihydroretinol saturase, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Retsat PE=1 SV=1	Retsat	G3V7V6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
235	Alpha- and gamma-adaptin-binding protein p34 OS=Rattus norvegicus OX=10116 GN=Aagab PE=1 SV=1	Aagab	Q9R0Z7	NaN	NaN	NaN	NaN	17.312	NaN	15.8058	16.1608
236	Alpha globin OS=Rattus norvegicus OX=10116 GN=Hba-a3 PE=1 SV=2	Hba-a3	Q63910	21.648	20.7815	21.2721	20.0636	17.8487	17.0803	15.5179	16.1943
237	Alpha glucosidase 2 alpha neutral subunit (Predicted) OS=Rattus norvegicus OX=10116 GN=Ganab PE=1 SV=1	Ganab	D3ZAN3	18.5041	17.3244	16.9135	17.7282	21.3305	21.5225	21.1582	21.6684
238	Alpha hemoglobin-stabilizing protein OS=Rattus norvegicus OX=10116 GN=Ahsp PE=1 SV=1	Ahsp	A9UMW3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
239	alpha-1,2-Mannosidase OS=Rattus norvegicus OX=10116 GN=Man1a1 PE=1 SV=1	Man1a1	A0A0G2JW29	14.7528	14.4484	16.0143	16.3859	NaN	NaN	NaN	NaN
240	Alpha-1,4 glucan phosphorylase OS=Rattus norvegicus OX=10116 GN=Pygb PE=1 SV=2	Pygb	G3V6Y6	19.5889	18.1711	18.7777	19.2163	24.2441	25.4092	25.4538	25.1628
241	Alpha-1,4 glucan phosphorylase OS=Rattus norvegicus OX=10116 GN=Pygm PE=1 SV=1	Pygm	G3V8V3	22.6622	21.964	21.7983	21.705	26.6586	27.3777	27.5683	27.2429
242	Alpha-1-acid glycoprotein OS=Rattus norvegicus OX=10116 GN=Orm1 PE=1 SV=1	Orm1	A0A0H2UHF8	18.0818	19.9362	20.199	17.5132	17.8648	17.7204	17.3468	18.1043
243	Alpha-1-antiproteinase OS=Rattus norvegicus OX=10116 GN=Serpina1 PE=1 SV=1	Serpina1	A0A0G2JZ73	28.0029	28.0758	28.3712	29.2919	23.6134	23.149	22.9384	23.3722
244	Alpha-1-inhibitor 3 OS=Rattus norvegicus OX=10116 GN=A1i3 PE=1 SV=1	LOC297568	P14046	23.0722	23.2462	23.6874	23.6745	19.399	18.45	17.9103	19.7068
245	Alpha-1-macroglobulin OS=Rattus norvegicus OX=10116 GN=A1m PE=1 SV=1	Pzp	Q63041	27.7727	28.1986	28.291	28.1326	23.4544	22.9736	23.0452	23.0628
246	Alpha-2 antiplasmin OS=Rattus norvegicus OX=10116 GN=Serpinf1 PE=1 SV=1	Serpinf1	Q80ZA3	20.5705	19.7686	20.88	20.1609	18.3401	19.0376	19.1565	18.0782
247	Alpha-2B adrenergic receptor OS=Rattus norvegicus OX=10116 GN=Adra2b PE=2 SV=2	Adra2b	P19328	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
248	Alpha-2-glycoprotein 1, zinc OS=Rattus norvegicus OX=10116 GN=Azgp1 PE=1 SV=1	Azgp1	Q3B8R6	19.4239	19.4041	19.8595	20.6695	18.1465	NaN	17.7168	14.5793
249	Alpha-2-HS-glycoprotein OS=Rattus norvegicus OX=10116 GN=Ahsg PE=1 SV=2	Ahsg	P24090	28.4023	28.1415	28.2216	27.8859	26.7115	26.0649	25.8771	26.5026
250	Alpha-2-macroglobulin OS=Rattus norvegicus OX=10116 GN=A2m PE=2 SV=2	A2m	P06238	29.6014	29.706	29.9158	29.926	24.9138	24.7663	24.4899	24.7711
251	Alpha-actinin-1 OS=Rattus norvegicus OX=10116 GN=Actn1 PE=1 SV=1	Actn1	Q6T487	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
252	Alpha-actinin-4 OS=Rattus norvegicus OX=10116 GN=Actn4 PE=1 SV=1	Actn4	A0A0G2K5U9	17.4021	18.0361	16.5061	17.7813	20.4395	19.3797	20.2744	20.5911
253	Alpha-aminoadipic semialdehyde dehydrogenase OS=Rattus norvegicus OX=10116 GN=Aldh7a1 PE=1 SV=2	Aldh7a1	Q64057	NaN	14.6846	14.4674	15.4783	19.2907	19.9258	20.2265	20.3761
254	Alpha-centractin OS=Rattus norvegicus OX=10116 GN=Actr1a PE=1 SV=1	Actr1a	P85515	18.0792	17.6692	18.4743	18.4086	23.2622	23.4083	23.6725	23.3846
255	Alpha-crystallin B chain OS=Rattus norvegicus OX=10116 GN=Cryab PE=1 SV=1	Cryab	P23928	23.6745	22.7175	22.8418	22.4836	28.0346	28.2887	28.5871	28.3772
256	Alpha-fetoprotein OS=Rattus norvegicus OX=10116 GN=Afp PE=2 SV=1	Afp	P02773	30.0508	29.6959	30.2383	30.0179	26.1854	25.4956	25.3696	25.7806
257	Alpha-fetoprotein OS=Rattus norvegicus OX=10116 GN=Afp PE=4 SV=1	Afp	G3V6D0	25.1521	25.1563	25.1957	25.5825	20.9119	20.3875	20.221	20.7706
258	Alpha-kinase 2 OS=Rattus norvegicus OX=10116 GN=Alpk2 PE=4 SV=3	Alpk2	F1LTG2	17.8497	17.1432	16.2031	18.7193	20.3398	20.9675	19.2853	18.9582
259	Alpha-kinase 3 OS=Rattus norvegicus OX=10116 GN=Alpk3 PE=1 SV=2	Alpk3	D3ZH28	15.7401	15.3815	16.0691	16.6917	15.923	17.5139	16.4163	NaN
260	Alpha-parvin OS=Rattus norvegicus OX=10116 GN=Parva PE=1 SV=1	Parva	G3V818	15.355	17.1655	17.7819	15.5465	20.4835	20.7587	21.2273	20.8756
261	Alpha-soluble NSF attachment protein OS=Rattus norvegicus OX=10116 GN=Napa PE=1 SV=2	Napa	P54921	20.7623	20.5814	20.9099	20.642	22.7719	22.8476	22.5447	22.6017
262	Alpha-synuclein OS=Rattus norvegicus OX=10116 GN=Snca PE=1 SV=1	Snca	P37377	20.2383	18.8465	20.1319	19.6381	17.554	18.0951	16.9964	16.8823
263	Alpha-tubulin N-acetyltransferase 1 OS=Rattus norvegicus OX=10116 GN=Atat1 PE=1 SV=1	Atat1	Q6MG11	NaN	NaN	NaN	NaN	17.2408	NaN	17.3294	16.9793

264	Aly/REF export factor OS=Rattus norvegicus OX=10116 GN=Alyref PE=1 SV=1	Alyref	D3ZXH7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
265	Ameloblastin OS=Rattus norvegicus OX=10116 GN=Ambn PE=2 SV=1	Ambn	Q62840	17.8232	18.4389	18.0279	19.5319	NaN	NaN	19.1264	18.9707
266	Amino acid transporter OS=Rattus norvegicus OX=10116 GN=Slc1a5 PE=1 SV=3	Slc1a5	D3ZJ25	17.0707	16.3316	16.6072	17.6843	NaN	NaN	NaN	NaN
267	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Rattus norvegicus OX=10116 GN=Aimp2 PE=2	Aimp2	Q32PX2	19.0984	18.168	18.5531	18.5326	22.4754	22.1938	22.6571	22.6138
268	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 OS=Rattus norvegicus OX=10116 GN=Aimp1 PE=	Aimp1	Q4G079	18.5395	18.3147	18.1685	17.7102	23.6724	23.4253	23.6339	23.5914
269	Aminoacylase-1A OS=Rattus norvegicus OX=10116 GN=Acy1a PE=1 SV=1	Acy1	Q6AYS7	NaN	NaN	NaN	14.4202	17.1647	17.0323	17.3751	16.4957
270	Aminopeptidase B OS=Rattus norvegicus OX=10116 GN=Rnpep PE=1 SV=1	Rnpep	G3V6V1	14.8074	15.7228	16.1924	14.9907	18.2564	21.5984	21.9155	21.5718
271	Aminopeptidase N OS=Rattus norvegicus OX=10116 GN=Anpep PE=1 SV=2	Anpep	P15684	18.4926	18.3778	18.6953	19.1037	19.2301	19.0958	18.1754	18.2352
272	Aminopeptidase OS=Rattus norvegicus OX=10116 GN=Npepps PE=1 SV=1	Npepps	F1M9V7	17.6474	18.4641	17.7501	18.8788	17.9643	21.8545	22.2612	22.1172
273	Aminopeptidase-like 1 OS=Rattus norvegicus OX=10116 GN=Npepl1 PE=1 SV=2	Npepl1	D4A3E2	16.0516	16.5058	16.6718	16.0463	17.798	NaN	18.8752	18.1378
274	AMP deaminase 1 OS=Rattus norvegicus OX=10116 GN=Ampd1 PE=1 SV=1	Ampd1	P10759	19.5986	19.2738	18.7387	18.8063	NaN	17.2562	16.6921	17.8008
275	AMP deaminase 2 OS=Rattus norvegicus OX=10116 GN=Ampd2 PE=1 SV=2	Ampd2	Q02356	NaN	NaN	NaN	NaN	NaN	17.966	18.5208	NaN
276	Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (Glycogen debranching enzyme, glycogen storage disease type III) (Predic	Agl	D4AEH9	16.6182	15.9136	15.1524	18.1402	21.2882	21.6775	21.6104	21.313
277	Amyloid-beta A4 precursor protein-binding family A member 3 OS=Rattus norvegicus OX=10116 GN=Apba3 PE=1 SV=2	Apba3	O70248	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
278	Anamorsin OS=Rattus norvegicus OX=10116 GN=Ciapin1 PE=1 SV=1	Ciapin1	Q5XID1	19.4475	18.3239	18.5971	18.2426	22.2998	21.6029	21.7988	21.6011
279	Anaphase promoting complex subunit 1 (Predicted) OS=Rattus norvegicus OX=10116 GN=Anapc1 PE=1 SV=2	Anapc1	F1M801	19.1669	19.3329	18.5496	18.1241	18.9528	18.6618	18.7653	18.7278
280	Anaphase promoting complex subunit 7 (Predicted) OS=Rattus norvegicus OX=10116 GN=Anapc7 PE=1 SV=1	Anapc7	D3ZIT4	NaN	NaN	NaN	NaN	NaN	16.2616	16.1468	16.0562
281	Androgen-binding protein (Fragment) OS=Rattus norvegicus OX=10116 GN=Apbh PE=2 SV=1	Apbh	D2XZ41	19.5688	19.9082	20.3438	19.8752	16.3372	NaN	15.3516	NaN
282	Angio-associated migratory protein (Predicted) OS=Rattus norvegicus OX=10116 GN=Aamp PE=1 SV=1	Aamp	G3V7V2	NaN	NaN	NaN	NaN	16.239	17.5189	18.1574	16.8973
283	Angiopoietin-like 3 OS=Rattus norvegicus OX=10116 GN=Angptl3 PE=1 SV=1	Angptl3	F7FHP0	17.1297	16.9693	17.4207	NaN	NaN	NaN	NaN	NaN
284	Angiopoietin-like 6 OS=Rattus norvegicus OX=10116 GN=Angptl6 PE=1 SV=1	Angptl6	B2RYM1	17.8445	17.0394	16.9799	16.1265	16.6132	NaN	16.3289	16.7648
285	Angiotensinogen OS=Rattus norvegicus OX=10116 GN=Agt PE=1 SV=1	Agt	P01015	23.7919	24.2447	24.4333	23.343	20.707	20.1575	19.8028	19.7358
286	Anillin, actin-binding protein OS=Rattus norvegicus OX=10116 GN=Anln PE=1 SV=3	Anln	D4A0V6	16.6107	17.1146	16.6793	16.9045	NaN	NaN	NaN	NaN
287	Anion exchange protein OS=Rattus norvegicus OX=10116 GN=Slc4a1 PE=1 SV=1	Slc4a1	F8WFT7	25.2599	25.3069	24.6385	25.351	20.3907	19.2689	19.1231	19.3187
288	Anionic trypsin-1 OS=Rattus norvegicus OX=10116 GN=Prss1 PE=1 SV=1	Prss1	P00762	20.4838	19.7051	20.1707	20.8092	NaN	NaN	NaN	NaN
289	Ankycorbin OS=Rattus norvegicus OX=10116 GN=Rai14 PE=1 SV=2	Rai14	Q5U312	16.8377	16.7048	17.2081	16.5465	20.5071	20.2982	20.2975	20.198
290	Ankyrin 1 OS=Rattus norvegicus OX=10116 GN=Ank1 PE=1 SV=1	Ank1	D3Z9Z0	22.1838	22.2368	21.0639	22.3526	19.2171	19.5383	19.8251	19.3355
291	Ankyrin repeat and FYVE domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Ankfy1 PE=1 SV=3	Ankfy1	D4A1J6	13.6366	NaN	NaN	NaN	NaN	16.4724	18.2126	15.8307
292	Ankyrin repeat and LEM domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Ankle1 PE=4 SV=2	Ankle1	D4A332	19.7897	19.3549	19.2561	17.4827	19.6133	18.6432	19.2744	19.333
293	Ankyrin repeat and MYND domain-containing 2 OS=Rattus norvegicus OX=10116 GN=Ankmy2 PE=1 SV=1	Ankmy2	A0A0G2K8N6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
294	Ankyrin repeat and SAM domain containing 1 (Predicted) OS=Rattus norvegicus OX=10116 GN=Anks1a PE=1 SV=1	Anks1a	D4AC12	15.7149	NaN	NaN	18.2338	19.3833	19.7994	19.6582	19.5231
295	Ankyrin repeat domain 17 OS=Rattus norvegicus OX=10116 GN=Ankrd17 PE=1 SV=1	Ankrd17	A0A0G2JVW3	NaN	NaN	NaN	NaN	20.2796	20.3915	20.0662	19.8494
296	Ankyrin-3 OS=Rattus norvegicus OX=10116 GN=Ank3 PE=1 SV=3	Ank3	O70511	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
297	Annexin A1 OS=Rattus norvegicus OX=10116 GN=Anxa1 PE=1 SV=2	Anxa1	P07150	22.3052	22.3983	22.2301	22.5598	22.0697	22.5349	22.0238	22.0577
298	Annexin A2 OS=Rattus norvegicus OX=10116 GN=Anxa2 PE=1 SV=2	Anxa2	Q07936	22.3561	23.5438	22.6002	22.1788	25.15	24.8499	24.8635	24.9121
299	Annexin A3 OS=Rattus norvegicus OX=10116 GN=Anxa3 PE=1 SV=4	Anxa3	P14669	NaN	16.8836	16.4676	15.7377	17.2279	18.2469	17.5074	17.7918
300	Annexin A5 OS=Rattus norvegicus OX=10116 GN=Anxa5 PE=1 SV=3	Anxa5	P14668	19.6751	21.1855	21.0106	21.1377	22.9453	22.8927	22.5957	22.4776
301	Annexin OS=Rattus norvegicus OX=10116 GN=Anxa11 PE=1 SV=1	Anxa11	Q5XI77	17.461	18.1067	17.949	16.4499	23.2877	22.6399	23.3108	23.2191
302	Annexin OS=Rattus norvegicus OX=10116 GN=Anxa4 PE=1 SV=1	Anxa4	Q5U362	NaN	NaN	NaN	NaN	17.8723	NaN	18.5697	18.145
303	Annexin OS=Rattus norvegicus OX=10116 GN=Anxa6 PE=1 SV=1	Anxa6	Q6IMZ3	21.1047	21.9493	21.795	20.4945	25.3037	25.2215	25.2229	25.3797
304	Annexin OS=Rattus norvegicus OX=10116 GN=Anxa7 PE=1 SV=1	Anxa7	Q6IRJ7	18.9755	19.5281	19.6437	18.366	22.4018	21.2006	21.9465	22.141
305	Antisecretory factor OS=Rattus norvegicus OX=10116 GN=Psmd4 PE=1 SV=1	Psmd4	O88321	18.6568	18.6496	18.8171	18.7633	23.6486	23.2152	23.591	23.8145
306	AP complex subunit beta OS=Rattus norvegicus OX=10116 GN=Ap1b1 PE=1 SV=3	Ap1b1	G3V9N8	16.2483	17.3606	16.3194	16.8423	21.6803	20.8303	20.8535	21.0787
307	AP complex subunit sigma OS=Rattus norvegicus OX=10116 GN=Ap1s1 PE=1 SV=1	Ap1s1	B5DFI3	NaN	NaN	NaN	NaN	14.539	NaN	18.2199	18.0973
308	AP complex subunit sigma OS=Rattus norvegicus OX=10116 GN=Ap3s1 PE=1 SV=1	Ap3s1	G3V9Y9	14.6297	NaN	NaN	NaN	15.7032	17.7677	17.8855	17.9869
309	AP complex subunit sigma OS=Rattus norvegicus OX=10116 GN=Ap3s2 PE=1 SV=1	Ap3s2	A0A0G2K302	NaN	NaN	NaN	NaN	18.1313	18.2481	17.768	17.6688
310	AP-1 complex subunit mu-1 OS=Rattus norvegicus OX=10116 GN=Ap1m1 PE=1 SV=3	Ap1m1	Q32Q06	18.9126	NaN	NaN	NaN	19.5576	17.8338	18.362	19.1124
311	AP-2 complex subunit alpha OS=Rattus norvegicus OX=10116 GN=Ap2a1 PE=1 SV=1	Ap2a1	D3ZUY8	18.964	19.4251	18.8429	20.5095	22.1118	21.7548	21.5454	21.5688
312	AP-2 complex subunit alpha OS=Rattus norvegicus OX=10116 GN=Ap2a2 PE=1 SV=1	Ap2a2	Q66HM2	23.181	23.1166	22.8078	21.1562	23.3249	23.0095	22.7455	22.9124
313	AP-2 complex subunit beta OS=Rattus norvegicus OX=10116 GN=Ap2b1 PE=1 SV=1	Ap2b1	P62944	19.8583	19.9123	19.303	19.1927	24.3071	24.0721	23.769	23.7033
314	AP-2 complex subunit mu OS=Rattus norvegicus OX=10116 GN=Ap2m1 PE=1 SV=1	Ap2m1	P84092	19.588	19.1846	18.5021	15.2774	22.8761	22.7121	22.5036	22.5492
315	AP2-associated protein kinase 1 OS=Rattus norvegicus OX=10116 GN=Aak1 PE=1 SV=2	Aak1	F1LRI7	23.7463	23.793	22.0585	23.0579	23.812	23.999	23.6695	23.8134
316	AP-3 complex subunit beta OS=Rattus norvegicus OX=10116 GN=Ap3b1 PE=1 SV=1	Ap3b1	A0A0G2JWD6	19.7462	19.4132	19.1638	19.8627	22.0174	21.5236	21.5848	21.4811

317	AP-3 complex subunit mu-1 OS=Rattus norvegicus OX=10116 GN=Ap3m1 PE=1 SV=1	Ap3m1	P53676	16.0586	17.7003	15.6614	15.8135	19.9509	19.6406	19.7275	19.7685
318	AP-4 complex subunit mu-1 OS=Rattus norvegicus OX=10116 GN=Ap4m1 PE=1 SV=1	Ap4m1	Q2PWT8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
319	Api5 protein OS=Rattus norvegicus OX=10116 GN=Api5 PE=1 SV=1	Api5	B1WC49	NaN	NaN	NaN	NaN	20.9007	19.4436	20.1282	19.7553
320	Apolipoprotein A-I OS=Rattus norvegicus OX=10116 GN=Apoa1 PE=1 SV=2	Apoa1	P04639	29.2852	29.106	29.243	28.7279	26.9187	26.0347	26.235	26.5566
321	Apolipoprotein A-II OS=Rattus norvegicus OX=10116 GN=Apoa2 PE=2 SV=1	Apoa2	P04638	27.0079	25.3791	27.0053	26.9811	23.9021	23.638	24.0336	24.6817
322	Apolipoprotein A-IV OS=Rattus norvegicus OX=10116 GN=Apoa4 PE=1 SV=2	Apoa4	P02651	30.3191	30.406	30.1093	30.0767	27.1654	26.3806	26.0428	26.2225
323	Apolipoprotein A-V OS=Rattus norvegicus OX=10116 GN=Apoa5 PE=1 SV=1	Apoa5	A0A0H2UHP7	18.6784	17.2434	18.5017	17.7889	21.6731	20.6366	21.2502	21.1153
324	Apolipoprotein B editing complex 2 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Apobec2 PE=1 SV=1	Apobec2	B4F789	15.3558	15.6009	15.9891	15.1932	22.8257	22.1724	22.6751	22.7507
325	Apolipoprotein B-100 OS=Rattus norvegicus OX=10116 GN=Apob PE=1 SV=1	Apob	F1M6Z1	29.2603	28.5976	28.7578	28.8451	25.4774	24.7092	24.4454	24.5916
326	Apolipoprotein C-I OS=Rattus norvegicus OX=10116 GN=Apoc1 PE=3 SV=1	Apoc1	P19939	27.7958	27.4485	27.3402	27.6868	23.9835	24.2858	23.7908	24.2314
327	Apolipoprotein C-II (Predicted) OS=Rattus norvegicus OX=10116 GN=Apoc2 PE=1 SV=1	Apoc2	G3V8D4	27.7453	27.6529	27.495	27.4644	25.7765	25.1592	25.1541	25.5142
328	Apolipoprotein C-III OS=Rattus norvegicus OX=10116 GN=Apoc3 PE=1 SV=1	Apoc3	A0A0G2K8Q1	25.5645	25.5686	25.6731	26.2592	22.929	22.6484	22.5364	22.8629
329	Apolipoprotein C-IV OS=Rattus norvegicus OX=10116 GN=Apoc4 PE=2 SV=2	Apoc4	P55797	25.768	25.8971	26.0417	26.4632	22.4725	21.4909	21.5824	21.6756
330	Apolipoprotein D OS=Rattus norvegicus OX=10116 GN=Apod PE=3 SV=1	Apod	M0R4S2	20.2209	20.6094	20.1471	19.6448	15.5426	17.2387	15.5579	14.9804
331	Apolipoprotein E OS=Rattus norvegicus OX=10116 GN=Apoe PE=1 SV=1	Apoe	A0A0G2K151	28.4553	28.0658	28.0939	27.9884	25.8756	25.7251	25.46	25.6407
332	Apolipoprotein F OS=Rattus norvegicus OX=10116 GN=Apof PE=2 SV=1	Apof	Q5M889	18.7409	19.6791	19.7952	17.8587	17.6377	18.5542	18.5476	17.7529
333	Apolipoprotein H OS=Rattus norvegicus OX=10116 GN=Apoh PE=1 SV=1	Apoh	Q5I0M1	26.3871	25.9977	26.566	26.5672	23.6991	23.7524	23.028	23.8298
334	Apolipoprotein M OS=Rattus norvegicus OX=10116 GN=Apom PE=1 SV=2	Apom	P14630	24.9349	24.5554	25.1204	25.2071	22.5233	22.2888	22.6168	22.9385
335	Apolipoprotein N OS=Rattus norvegicus OX=10116 GN=Apon PE=1 SV=1	Apon	Q5M890	23.199	22.0803	22.7655	22.8055	19.4245	15.305	18.7484	19.0541
336	Apoptosis and caspase activation inhibitor OS=Rattus norvegicus OX=10116 GN=Aven PE=1 SV=1	Aven	D3Z853	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
337	Apoptosis regulator BAX OS=Rattus norvegicus OX=10116 GN=Bax PE=1 SV=1	Bax	G3V8T9	14.8345	NaN	15.1065	14.6572	21.2272	20.3135	20.7476	20.7708
338	Apoptosis-inducing factor 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Aifm1 PE=1 SV=1	Aifm1	Q9JM53	18.8768	18.375	17.9304	NaN	NaN	17.025	16.8076	16.0441
339	Aquaporin-1 OS=Rattus norvegicus OX=10116 GN=Aqp1 PE=1 SV=4	Aqp1	P29975	18.7636	19.165	19.0344	18.8438	21.4689	21.0582	20.8935	21.1891
340	ARF GTPase-activating protein GIT1 OS=Rattus norvegicus OX=10116 GN=Git1 PE=1 SV=1	Git1	Q9Z272	22.4538	23.3049	21.9655	22.8073	22.7916	23.4846	23.3734	22.9585
341	Arfaptin-1 OS=Rattus norvegicus OX=10116 GN=Arfip1 PE=1 SV=1	Arfip1	Q9JHU5	16.7395	17.431	NaN	NaN	20.2365	20.5715	20.2738	20.8869
342	Arf-GAP domain and FG repeat-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Agfg1 PE=1 SV=1	Agfg1	Q4KLH5	NaN	NaN	NaN	NaN	21.2407	20.0492	20.7599	20.7976
343	ArfGAP with FG repeats 2 OS=Rattus norvegicus OX=10116 GN=Agfg2 PE=1 SV=1	Agfg2	A0A0G2K7G2	NaN	NaN	NaN	NaN	19.7022	18.8915	19.6476	19.4487
344	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3 OS=Rattus norvegicus OX=10116 GN=Agap3 PE=4 SV=1	Agap3	A0A0G2JZ83	NaN	NaN	14.7206	NaN	NaN	15.9655	NaN	NaN
345	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 OS=Rattus norvegicus OX=10116 GN=Arap1 PE=1 SV=1	Arap1	F1LM60	15.3398	NaN	NaN	NaN	NaN	15.7371	NaN	NaN
346	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2 OS=Rattus norvegicus OX=10116 GN=Arap2 PE=1 SV=1	Arap2	A0A0G2K7I9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
347	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2 OS=Rattus norvegicus OX=10116 GN=Asap2 PE=1 SV=1	Asap2	A0A0G2K808	25.1304	26.4434	24.9988	23.841	24.5021	24.7686	24.451	24.4411
348	Arginase-1 OS=Rattus norvegicus OX=10116 GN=Arg1 PE=1 SV=2	Arg1	P07824	18.6522	20.9401	18.3927	19.3435	17.5027	17.7393	17.7623	18.3828
349	Arginine--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Rars PE=1 SV=2	Rars1	P40329	17.5194	16.8578	19.0052	18.8833	23.8004	23.4714	23.8155	23.7038
350	Argininosuccinate lyase OS=Rattus norvegicus OX=10116 GN=Asl PE=2 SV=1	Asl	P20673	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
351	Arginyl-tRNA--protein transferase 1 OS=Rattus norvegicus OX=10116 GN=Ate1 PE=1 SV=1	Ate1	D4A2N1	NaN	NaN	NaN	NaN	17.6481	18.6163	18.3138	17.7596
352	Armadillo repeat containing 6 OS=Rattus norvegicus OX=10116 GN=Armc6 PE=1 SV=1	Armc6	B2RYL4	16.8004	16.7348	16.4369	17.6449	19.2222	19.6303	20.3553	20.8064
353	Armadillo repeat-containing 8 OS=Rattus norvegicus OX=10116 GN=Armc8 PE=1 SV=2	Armc8	F1M943	NaN	NaN	NaN	NaN	18.8811	16.9187	18.6391	18.372
354	Armadillo repeat-containing X-linked protein 3 OS=Rattus norvegicus OX=10116 GN=Armcx3 PE=1 SV=1	Armcx3	A0A0G2KAU2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
355	ARP1 actin-related protein 1 homolog B OS=Rattus norvegicus OX=10116 GN=Actr1b PE=1 SV=1	Actr1b	B2RYJ7	NaN	NaN	NaN	NaN	19.4456	20.1137	19.9588	19.1647
356	ARP10 actin-related protein 10 homolog (S. cerevisiae) OS=Rattus norvegicus OX=10116 GN=Actr10 PE=1 SV=1	Actr10	Q5M9F7	NaN	NaN	NaN	16.9929	20.0296	20.3996	20.8476	20.4469
357	Arp2/3 complex 34 kDa subunit OS=Rattus norvegicus OX=10116 GN=Arpc2 PE=1 SV=1	Arpc2	A0A0G2K9A2	16.2191	16.4099	15.2477	14.4669	19.2758	18.802	19.7004	19.6877
358	Arsenite methyltransferase OS=Rattus norvegicus OX=10116 GN=As3mt PE=1 SV=1	As3mt	Q8VHT6	18.4163	NaN	NaN	17.5741	20.4289	20.05	20.3949	20.5991
359	Aryl hydrocarbon receptor nuclear translocator OS=Rattus norvegicus OX=10116 GN=Arnt PE=1 SV=1	Arnt	F1LMF9	20.985	19.685	19.9425	21.3742	16.5181	NaN	15.2977	NaN
360	Asparagine synthetase domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Asnsd1 PE=4 SV=1	Asnsd1	D3ZWR3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
361	Asparaginyl-tRNA synthetase OS=Rattus norvegicus OX=10116 GN=Nars PE=1 SV=2	Nars1	F1LPV0	20.1837	19.9877	19.9933	18.6461	21.8237	22.2712	22.6249	22.5886
362	Aspartate aminotransferase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Got1 PE=1 SV=3	Got1	P13221	16.5599	16.5253	18.0416	16.4311	21.2344	21.5653	21.5283	21.1185
363	Aspartate aminotransferase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Got2 PE=1 SV=2	Got2	P00507	17.7415	19.1569	17.0038	15.8685	19.8394	22.1912	21.3619	21.5622
364	Aspartate-beta-hydroxylase OS=Rattus norvegicus OX=10116 GN=Asph PE=1 SV=1	Asph	A0A096MKE0	14.3461	15.1109	13.7416	NaN	16.974	17.458	16.7695	17.2921
365	Aspartate--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Dars PE=1 SV=1	Dars1	P15178	19.0435	18.4487	18.2097	19.89	24.1184	23.8312	24.2951	24.3976
366	Aspartyl aminopeptidase OS=Rattus norvegicus OX=10116 GN=Dnpep PE=1 SV=1	Dnpep	Q4V8H5	19.0881	19.0434	19.016	20.3406	21.5233	22.5679	22.6325	22.1644
367	Asporin OS=Rattus norvegicus OX=10116 GN=Aspn PE=1 SV=1	Aspn	Q5XIH1	18.1963	17.5913	18.2715	19.3743	17.1638	17.8346	18.1603	17.8487
368	ASPSCR1, UBX domain-containing tether for SLC2A4 OS=Rattus norvegicus OX=10116 GN=Aspscr1 PE=1 SV=2	Aspscr1	F1LR71	NaN	14.2831	NaN	NaN	16.8896	16.4822	17.0189	NaN
369	Astrocytic phosphoprotein PEA-15 OS=Rattus norvegicus OX=10116 GN=Pea15 PE=1 SV=1	Pea15	Q5U318	NaN	NaN	NaN	15.3773	20.4077	18.8138	19.3458	19.5458

370	Ataxin 2 OS=Rattus norvegicus OX=10116 GN=Atxn2 PE=1 SV=3	Atxn2	F1M049	16.8427	16.8061	16.4648	17.2206	20.935	21.408	21.0349	20.5858
371	Ataxin 2-like OS=Rattus norvegicus OX=10116 GN=Atxn2l PE=1 SV=1	Atxn2l	B3DMA1	18.5174	17.1616	19.1491	18.8786	21.9268	22.764	22.208	22.0165
372	Ataxin 7-like 3B OS=Rattus norvegicus OX=10116 GN=Atxn7l3b PE=1 SV=1	Atxn7l3b	D3ZFQ1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
373	Ataxin-10 OS=Rattus norvegicus OX=10116 GN=Atxn10 PE=1 SV=1	Atxn10	Q9ER24	19.2928	18.737	18.5872	20.5618	23.2242	22.5601	23.5936	23.2071
374	Atlastin GTPase 2 OS=Rattus norvegicus OX=10116 GN=Atl2 PE=1 SV=1	Atl2	F1LQ09	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
375	ATP synthase F(0) complex subunit B1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5pb PE=1 SV=1	Atp5pb	P19511	17.8627	18.7089	18.0097	16.1001	20.5773	22.1378	21.5226	21.8149
376	ATP synthase mitochondrial F1 complex assembly factor 1 OS=Rattus norvegicus OX=10116 GN=Atpaf1 PE=1 SV=1	Atpaf1	D3ZY50	NaN	NaN	NaN	NaN	16.7979	15.805	15.9072	16.2253
377	ATP synthase protein 8 OS=Rattus norvegicus OX=10116 GN=Mt-atp8 PE=1 SV=2	mt-Atp8	P11608	19.4559	21.9188	19.086	19.8101	19.3024	21.6501	21.2803	21.1076
378	ATP synthase subunit alpha OS=Rattus norvegicus OX=10116 GN=Atp5f1a PE=1 SV=1	Atp5f1a	F1LP05	22.8563	22.7345	22.2467	22.0451	24.3178	25.8434	25.5566	25.6133
379	ATP synthase subunit beta OS=Rattus norvegicus OX=10116 GN=Atp5f1b PE=1 SV=1	Atp5f1b	G3V6D3	22.6098	22.7217	21.6596	21.835	24.1855	25.6798	25.5335	25.747
380	ATP synthase subunit d, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5pd PE=1 SV=3	Atp5pd	P31399	20.0747	20.3934	19.0766	19.4433	22.0086	23.3872	22.8391	23.3583
381	ATP synthase subunit delta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5f1d PE=1 SV=1	Atp5f1d	G3V7Y3	18.3756	18.7515	18.1558	16.8491	21.9089	22.855	22.2934	22.4739
382	ATP synthase subunit e, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5me PE=1 SV=3	Atp5me	P29419	17.996	18.8844	17.7007	18.025	20.2925	21.607	21.3523	21.5565
383	ATP synthase subunit epsilon, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5f1e PE=1 SV=2	Atp5f1e	P29418	16.1813	16.9991	15.9304	NaN	19.1674	20.8592	20.5272	20.4997
384	ATP synthase subunit f, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5mf PE=1 SV=1	Atp5mf	D3ZAF6	16.6538	17.1587	15.9678	20.2087	18.0264	19.8534	19.439	19.6385
385	ATP synthase subunit g, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5mg PE=1 SV=2	Atp5mg	Q6PDU7	17.5666	17.5919	16.2589	NaN	19.7511	21.9543	21.681	21.9918
386	ATP synthase subunit O, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5po PE=1 SV=1	Atp5po	Q06647	19.1758	20.225	19.2875	18.7309	22.1935	23.5571	23.1559	23.4751
387	ATP synthase-coupling factor 6, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5pf PE=1 SV=1	Atp5pf	P21571	17.8408	17.4465	16.1976	17.707	20.0678	21.4019	21.0304	21.1838
388	ATPase Asna1 OS=Rattus norvegicus OX=10116 GN=Asna1 PE=1 SV=1	Get3	G3V9T7	NaN	NaN	NaN	17.2848	22.0292	21.1715	21.4083	21.4678
389	ATPase H+-transporting V1 subunit A OS=Rattus norvegicus OX=10116 GN=Atp6v1a PE=1 SV=1	Atp6v1a	D4A133	16.7599	16.7791	16.5041	19.3947	19.7859	20.5724	21.0129	21.1767
390	ATPase H+-transporting V1 subunit D OS=Rattus norvegicus OX=10116 GN=Atp6v1d PE=1 SV=1	Atp6v1d	Q6P503	NaN	16.0087	16.3117	16.9389	16.982	19.3236	18.6271	19.0472
391	ATPase, H+ transporting, V1 subunit E isoform 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Atp6v1e1 PE=1 SV=	Atp6v1e1	G3V7L8	17.3722	17.6335	17.5131	17.4417	20.2466	20.4362	21.4734	21.0186
392	ATP-binding cassette sub-family D member 3 OS=Rattus norvegicus OX=10116 GN=Abcd3 PE=1 SV=3	Abcd3	P16970	15.3047	14.8614	14.461	15.1102	15.506	18.5296	NaN	18.7661
393	ATP-binding cassette subfamily E member 1 OS=Rattus norvegicus OX=10116 GN=Abce1 PE=1 SV=1	Abce1	D3ZD23	17.3269	17.7916	17.6462	17.4683	20.1281	19.0399	20.06	19.7734
394	ATP-binding cassette sub-family F member 1 OS=Rattus norvegicus OX=10116 GN=Abcf1 PE=1 SV=1	Abcf1	Q6MG08	13.2406	14.3144	14.2037	16.4287	21.2508	21.7047	21.9032	21.7983
395	ATP-binding cassette subfamily F member 2 OS=Rattus norvegicus OX=10116 GN=Abcf2 PE=1 SV=1	Abcf2	A2VD14	NaN	20.5772	20.3127	17.9276	19.15	19.5073	19.104	18.9728
396	ATP-binding cassette sub-family F member 3 OS=Rattus norvegicus OX=10116 GN=Abcf3 PE=2 SV=1	Abcf3	Q66H39	15.3703	17.6071	15.8546	16.008	21.5425	21.1993	20.8512	20.9663
397	ATP-citrate synthase OS=Rattus norvegicus OX=10116 GN=Acly PE=1 SV=1	Acly	G3V9G4	15.5135	16.6185	15.2476	15.9469	18.9287	18.6308	19.4209	19.0551
398	ATP-dependent 6-phosphofructokinase OS=Rattus norvegicus OX=10116 GN=Pfkm PE=1 SV=1	Pfkm	A0A0G2KBC7	21.7061	21.7307	21.2378	21.2355	26.2804	25.6737	26.1845	25.9097
399	ATP-dependent 6-phosphofructokinase, liver type OS=Rattus norvegicus OX=10116 GN=Pfkl PE=1 SV=3	Pfkl	P30835	16.9092	16.0062	15.5016	15.4145	21.2806	21.9413	23.1928	22.4197
400	ATP-dependent 6-phosphofructokinase, platelet type OS=Rattus norvegicus OX=10116 GN=Pfkp PE=1 SV=2	Pfkp	P47860	19.6434	19.8246	19.7175	17.8011	25.6941	25.218	25.8786	25.7149
401	ATP-dependent RNA helicase DDX1 OS=Rattus norvegicus OX=10116 GN=Ddx1 PE=1 SV=1	Ddx1	Q641Y8	18.2634	18.1603	14.0032	18.4915	21.9833	21.1059	21.0251	21.0071
402	Atrial natriuretic peptide receptor 3 OS=Rattus norvegicus OX=10116 GN=Npr3 PE=2 SV=1	Npr3	P41740	NaN	NaN	NaN	NaN	17.1304	17.187	16.6317	17.3277
403	Attractin OS=Rattus norvegicus OX=10116 GN=Atrn PE=2 SV=1	Atrn	Q99J86	17.9052	18.1418	18.1814	17.4106	18.7871	17.7189	17.7391	17.5998
404	Autophagy protein 5 OS=Rattus norvegicus OX=10116 GN=Atg5 PE=2 SV=1	Atg5	Q3MQ06	NaN	NaN	NaN	NaN	16.3925	16.2833	16.2712	16.57
405	Autophagy-related 16-like 1 OS=Rattus norvegicus OX=10116 GN=Atg16l1 PE=1 SV=1	Atg16l1	A0A0G2K9U6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
406	Baculoviral IAP repeat-containing 6 OS=Rattus norvegicus OX=10116 GN=Birc6 PE=1 SV=1	Birc6	A0A0G2JZ53	17.5578	15.1758	16.6575	18.2026	19.9031	20.5606	20.4923	19.9708
407	BAG family molecular chaperone regulator 5 OS=Rattus norvegicus OX=10116 GN=Bag5 PE=1 SV=1	Bag5	Q5QJC9	14.8693	NaN	13.7151	NaN	19.3876	18.6093	18.9493	18.681
408	Band 3 anion transport protein OS=Rattus norvegicus OX=10116 GN=Slc4a1 PE=1 SV=3	Slc4a1	P23562	19.1495	19.1315	18.6583	19.4469	NaN	NaN	NaN	NaN
409	Band 4.1-like protein 1-like OS=Rattus norvegicus OX=10116 GN=Epb41l1 PE=1 SV=1	Epb41l1	A0A0G2K0F3	16.9783	15.3045	16.5973	17.8058	16.8855	16.0538	15.6177	16.2829
410	Barrier-to-autointegration factor OS=Rattus norvegicus OX=10116 GN=Banf1 PE=1 SV=1	Banf1	Q9R1T1	22.3011	21.6737	21.3001	21.2716	21.8598	23.6548	22.8943	22.2817
411	Basal cell adhesion molecule OS=Rattus norvegicus OX=10116 GN=Bcam PE=2 SV=1	Bcam	Q9ESS6	20.0684	19.8239	19.5285	19.4089	21.6103	21.603	21.4139	21.3632
412	Basic leucine zipper and W2 domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Bzw1 PE=1 SV=1	Bzw1	Q6P7P5	NaN	16.3813	17.3609	18.0785	21.1342	21.2625	21.544	20.8865
413	Basic leucine zipper and W2 domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Bzw2 PE=1 SV=1	Bzw2	Q9WTT7	17.001	17.4721	16.5665	18.2427	22.555	21.7424	22.4837	21.8645
414	Basigin OS=Rattus norvegicus OX=10116 GN=Bsg PE=1 SV=2	Bsg	P26453	18.5676	19.2113	18.7905	18.6932	22.9109	22.9735	22.639	22.6816
415	B-cell receptor-associated protein 29 OS=Rattus norvegicus OX=10116 GN=Bcap29 PE=1 SV=1	Bcap29	Q5XIU4	NaN	NaN	NaN	NaN	18.4814	18.6411	18.3755	18.0675
416	B-cell receptor-associated protein 31 OS=Rattus norvegicus OX=10116 GN=Bcap31 PE=1 SV=1	Bcap31	Q6AY58	19.5316	17.9274	16.0331	20.6255	20.5812	21.0971	20.6803	20.863
417	Bcl2-associated athanogene 2 OS=Rattus norvegicus OX=10116 GN=Bag2 PE=4 SV=2	Bag2	F1LQH9	NaN	NaN	NaN	NaN	16.6146	18.7513	18.7286	18.9744
418	Bcl2-associated athanogene 3 OS=Rattus norvegicus OX=10116 GN=Bag3 PE=1 SV=1	Bag3	Q5U2U8	18.3848	18.4181	17.8711	17.8124	24.5346	24.5997	24.3317	24.0726
419	Beta-1,4-galactosyltransferase 1 OS=Rattus norvegicus OX=10116 GN=B4galt1 PE=1 SV=1	B4galt1	G3V722	18.6945	15.7855	16.977	17.4012	16.1838	16.1281	16.2302	NaN
420	Beta-2-microglobulin OS=Rattus norvegicus OX=10116 GN=B2m PE=1 SV=1	B2m	P07151	21.1033	20.995	21.0867	19.5725	19.3753	19.4241	18.9446	19.6936
421	Beta-adducin OS=Rattus norvegicus OX=10116 GN=Add2 PE=1 SV=1	Add2	F8WFS9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
422	Beta-casein OS=Rattus norvegicus OX=10116 GN=Csn2 PE=3 SV=1	Csn2	G3V9R5	21.2826	19.9666	20.7965	15.6997	17.8756	17.7944	17.885	17.5395

423	Beta-defensin 4 OS=Rattus norvegicus OX=10116 GN=Defb4 PE=2 SV=1	Defb4	O88514	17.7699	NaN	17.1754	18.7029	NaN	NaN	NaN	NaN
424	Beta-enolase OS=Rattus norvegicus OX=10116 GN=Eno3 PE=1 SV=3	Eno3	P15429	25.3012	25.6704	25.8987	25.9767	25.0499	24.9653	25.2301	25.2713
425	BICD family-like cargo adaptor 1 OS=Rattus norvegicus OX=10116 GN=Bicdl1 PE=4 SV=1	Bicdl1	A0A0G2JY46	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
426	Bifunctional epoxide hydrolase 2 OS=Rattus norvegicus OX=10116 GN=Ephx2 PE=1 SV=1	Ephx2	P80299	15.2321	NaN	NaN	NaN	19.1586	19.104	19.2006	18.8024
427	Bifunctional purine biosynthesis protein PURH OS=Rattus norvegicus OX=10116 GN=Atic PE=1 SV=2	Atic	O35567	18.534	17.7125	17.6256	18.2769	20.4595	20.5858	21.3889	21.1839
428	Biliverdin reductase A OS=Rattus norvegicus OX=10116 GN=Blvra PE=1 SV=1	Blvra	P46844	16.4238	16.6313	16.036	14.5546	20.5107	19.8036	20.1055	19.3202
429	Biliverdin reductase A OS=Rattus norvegicus OX=10116 GN=Blvra PE=1 SV=1	Blvra	Q6AZ33	NaN	NaN	NaN	15.9333	17.7475	16.6108	17.7106	18.2664
430	Biliverdin reductase B OS=Rattus norvegicus OX=10116 GN=Blvrb PE=1 SV=1	Blvrb	B5DF65	17.5679	18.1959	18.3275	17.8926	19.3848	19.1286	19.8392	19.4112
431	Biogenesis of lysosome-related organelles complex-1 subunit 2 OS=Rattus norvegicus OX=10116 GN=Bloc1s2 PE=2 SV=1	Bloc1s2	Q32WR5	NaN	NaN	NaN	NaN	17.0974	16.6654	16.8536	16.5781
432	Biotinidase OS=Rattus norvegicus OX=10116 GN=Btd PE=1 SV=1	Btd	A0A140TAI2	17.2378	17.5575	17.428	16.7911	15.9885	16.0158	15.5225	NaN
433	Bleomycin hydrolase OS=Rattus norvegicus OX=10116 GN=Blmh PE=1 SV=1	Blmh	A1A5L1	20.0369	21.2414	19.8629	23.5313	19.3742	19.9796	19.5603	19.5553
434	Blood group Rh(D) polypeptide OS=Rattus norvegicus OX=10116 GN=Rhd PE=2 SV=1	Rhd	O88298	16.461	16.5276	NaN	16.7936	NaN	NaN	NaN	NaN
435	Blood vessel epicardial substance OS=Rattus norvegicus OX=10116 GN=Bves PE=1 SV=2	Bves	Q3BCU4	18.0632	17.9602	18.7135	18.5599	21.204	21.2878	20.8021	20.5502
436	Bone marrow stromal cell-derived ubiquitin-like protein OS=Rattus norvegicus OX=10116 GN=Ubl7 PE=1 SV=1	Ubl7	Q6AY24	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
437	BPI fold-containing family A member 1 OS=Rattus norvegicus OX=10116 GN=Bpifa1 PE=2 SV=1	Bpifa1	Q8K4I4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
438	BPI fold-containing family A member 2 OS=Rattus norvegicus OX=10116 GN=Bpifa2 PE=1 SV=1	Bpifa2	Q63471	17.8572	NaN	17.2355	21.4806	NaN	NaN	NaN	14.3492
439	BPI fold-containing family A, member 2F OS=Rattus norvegicus OX=10116 GN=Bpifa2f PE=2 SV=1	Bpifa2f	Q63550	19.9587	18.4742	20.6278	23.9529	16.1024	NaN	15.9057	16.1912
440	BPI fold-containing family B member 1 OS=Rattus norvegicus OX=10116 GN=Bpifb1 PE=4 SV=1	Bpifb1	A0A140TAH2	21.6797	21.4232	21.0443	21.8856	18.3985	17.0931	17.8444	16.6425
441	Brain acid soluble protein 1 OS=Rattus norvegicus OX=10116 GN=Basp1 PE=1 SV=1	Basp1	A0A0G2K1L8	19.792	20.3325	20.7977	19.8233	22.4077	22.1533	21.7204	22.2801
442	Brain acid soluble protein 1 OS=Rattus norvegicus OX=10116 GN=Basp1 PE=1 SV=2	Basp1	Q05175	NaN	NaN	NaN	NaN	19.8486	19.7782	19.2517	19.3839
443	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 OS=Rattus norvegicus OX=10116 GN=Baiap2l1 PE=	Baiap2l1	Q3KR97	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
444	Breast cancer anti-estrogen resistance protein 1 OS=Rattus norvegicus OX=10116 GN=Bcar1 PE=1 SV=2	Bcar1	D3ZE30	NaN	14.8428	14.9108	NaN	19.6566	19.1268	19.4287	19.3361
445	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Rattus norvegicus OX=10116 GN=Arfgef1 PE=1 SV=1	Arfgef1	D4A631	19.3675	18.9617	18.1736	19.3806	19.3433	17.3338	18.9303	18.9762
446	BRICK1, SCAR/WAVE actin-nucleating complex subunit OS=Rattus norvegicus OX=10116 GN=Brk1 PE=1 SV=1	Brk1	D3ZUP5	NaN	NaN	NaN	NaN	17.761	18.8307	18.4285	18.4374
447	Bridging integrator 2 OS=Rattus norvegicus OX=10116 GN=Bin2 PE=1 SV=1	Bin2	Q68FR2	14.3434	15.5379	15.3951	NaN	15.1944	15.0534	NaN	NaN
448	Bridging integrator 3 OS=Rattus norvegicus OX=10116 GN=Bin3 PE=1 SV=3	Bin3	F1LN96	NaN	NaN	16.8547	NaN	18.5553	NaN	NaN	NaN
449	BRISC and BRCA1-A complex member 1 OS=Rattus norvegicus OX=10116 GN=Babam1 PE=1 SV=1	Babam1	Q5XIJ6	14.3107	14.1441	14.517	NaN	20.4869	20.9328	20.694	20.501
450	BRISC and BRCA1-A complex member 2 OS=Rattus norvegicus OX=10116 GN=Babam2 PE=1 SV=1	Babam2	Q6P7Q1	NaN	NaN	NaN	16.0165	17.2302	19.2054	19.2251	18.9036
451	BRO1 domain-containing protein BROX OS=Rattus norvegicus OX=10116 GN=Brox PE=2 SV=1	Brox	Q4V8K5	NaN	NaN	NaN	NaN	18.3031	16.8373	18.8437	16.3727
452	BSD domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Bsdc1 PE=1 SV=3	Bsdc1	D4A3M7	15.1384	NaN	NaN	NaN	16.2698	16.7089	17.4339	17.5556
453	BTB (POZ) domain containing 1 OS=Rattus norvegicus OX=10116 GN=Btbd1 PE=2 SV=1	Btbd1	Q5RKI2	19.4012	19.1799	18.2624	19.1966	15.8355	18.2	17.2877	17.7974
454	BUB3 mitotic checkpoint protein OS=Rattus norvegicus OX=10116 GN=Bub3 PE=1 SV=1	Bub3	Q4FZS2	16.4272	16.3985	16.8791	NaN	17.7306	19.0595	17.2697	17.5377
455	BWK-1 OS=Rattus norvegicus OX=10116 GN=Gid8 PE=1 SV=1	Gid8	Q6YDN8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
456	BWK4 OS=Rattus norvegicus OX=10116 GN=Erp44 PE=1 SV=1	Erp44	Q5VLR5	19.9306	18.0976	18.8519	19.111	21.0666	21.7735	20.8375	21.1886
457	C1q and TNF-related 3 OS=Rattus norvegicus OX=10116 GN=C1qtnf3 PE=2 SV=1	C1qtnf3	B1WC91	18.2199	19.1033	19.2916	15.834	NaN	15.5251	NaN	NaN
458	C1r protein OS=Rattus norvegicus OX=10116 GN=C1r PE=1 SV=1	C1r	B5DEH7	23.306	23.2209	23.0207	22.9396	20.0044	19.8174	19.763	19.662
459	C-1-tetrahydrofolate synthase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Mthfd1 PE=1 SV=1	Mthfd1	G3V6S5	21.7326	21.61	21.9158	21.5362	25.1313	25.0996	25.4405	25.2291
460	C4b-binding protein alpha chain OS=Rattus norvegicus OX=10116 GN=C4bpa PE=1 SV=1	C4bpa	Q5M891	20.8562	21.5627	21.3722	20.7671	18.6665	18.8625	18.3188	18.862
461	C4b-binding protein beta chain OS=Rattus norvegicus OX=10116 GN=C4bpb PE=1 SV=1	C4bpb	A0A5C5	17.0164	17.3458	18.2669	17.6344	15.1001	NaN	NaN	NaN
462	Cadherin 11 OS=Rattus norvegicus OX=10116 GN=Cdh11 PE=1 SV=1	Cdh11	F1MAH6	19.4118	17.2082	18.9017	18.9902	17.6931	17.9077	18.7234	18.429
463	Cadherin 13 OS=Rattus norvegicus OX=10116 GN=Cdh13 PE=1 SV=1	Cdh13	Q8R490	NaN	14.9538	NaN	NaN	18.2838	18.9582	19.034	19.1009
464	Cadherin 15 OS=Rattus norvegicus OX=10116 GN=Cdh15 PE=2 SV=1	Cdh15	Q75NI5	19.8697	18.942	19.6826	20.2185	17.5164	17.5792	NaN	15.6128
465	Cadherin 5 OS=Rattus norvegicus OX=10116 GN=Cdh5 PE=1 SV=2	Cdh5	F1M7E5	24.2731	23.6646	23.7812	23.8733	21.5069	20.8255	20.4562	21.2457
466	Cadherin-1 OS=Rattus norvegicus OX=10116 GN=Cdh1 PE=1 SV=1	Cdh1	Q9R0T4	17.7176	17.2864	15.5589	16.5189	NaN	15.3897	16.4837	19.109
467	Cadherin-2 OS=Rattus norvegicus OX=10116 GN=Cdh2 PE=1 SV=1	Cdh2	G3V803	NaN	NaN	14.4234	NaN	19.3238	18.8924	18.7662	19.6603
468	Cadherin-6 OS=Rattus norvegicus OX=10116 GN=Cdh6 PE=1 SV=3	Cdh6	F1LQP8	16.8268	15.9783	17.0102	16.7864	17.3532	NaN	NaN	17.1218
469	Calcipressin-1 OS=Rattus norvegicus OX=10116 GN=Rcan1 PE=2 SV=1	Rcan1	Q6IN33	NaN	NaN	NaN	17.0999	17.2774	NaN	16.3728	15.7925
470	Calcium and integrin-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Cib1 PE=1 SV=3	Cib1	Q9R010	16.0626	15.4999	15.9706	NaN	16.1356	NaN	15.9712	NaN
471	Calcium/calmodulin-dependent protein kinase kinase 2 OS=Rattus norvegicus OX=10116 GN=Camkk2 PE=1 SV=3	Camkk2	F1LPT4	18.5001	20.0172	16.694	15.7769	15.5767	19.4399	17.1322	16.6794
472	Calcium/calmodulin-dependent protein kinase type 1 OS=Rattus norvegicus OX=10116 GN=Camk1 PE=1 SV=2	Camk1	Q63450	16.7708	NaN	16.2191	NaN	19.8745	19.2497	20.0408	19.8282
473	Calcium/calmodulin-dependent protein kinase type II subunit beta OS=Rattus norvegicus OX=10116 GN=Camk2b PE=1 SV=	Camk2b	F1LNI8	NaN	NaN	NaN	NaN	19.0138	19.36	19.1419	18.6426
474	Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Rattus norvegicus OX=10116 GN=Camk2d PE=1 SV	Camk2d	P15791	16.6002	17.8406	18.8765	NaN	22.5947	23.3849	23.1759	23.0821
475	Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Rattus norvegicus OX=10116 GN=Camk2g PE=1 S	Camk2g	P11730	NaN	NaN	NaN	NaN	20.2753	20.4569	20.3747	20.3017

476	Calcium-binding and coiled-coil domain-containing protein 1-like OS=Rattus norvegicus OX=10116 GN=Calcoco1 PE=1 SV=	Calcoco1	A0A0G2K0S1	NaN	NaN	NaN	NaN	15.5615	15.9332	15.6552	15.0728
477	Calcium-binding protein 39 OS=Rattus norvegicus OX=10116 GN=Cab39 PE=1 SV=1	Cab39	A0A0G2JZH0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
478	Calcium-binding protein 39-like OS=Rattus norvegicus OX=10116 GN=Cab39l PE=1 SV=1	Cab39l	Q5XIJ7	NaN	NaN	NaN	NaN	NaN	NaN	17.1974	NaN
479	Calcium-regulated heat stable protein 1 OS=Rattus norvegicus OX=10116 GN=Carhsp1 PE=1 SV=1	Carhsp1	Q9WU49	16.2777	NaN	NaN	NaN	20.776	21.5171	21.6909	21.6962
480	Calcyclin-binding protein OS=Rattus norvegicus OX=10116 GN=Cacybp PE=1 SV=1	Cacybp	Q6AYK6	14.7231	17.0918	16.5726	15.7029	21.1903	18.8891	19.9557	20.2042
481	Caldesmon 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Cald1 PE=1 SV=1	Cald1	G3V9E3	18.1668	NaN	16.4082	18.8728	22.2047	20.5182	20.3548	20.1519
482	Calmodulin-3 OS=Rattus norvegicus OX=10116 GN=Calm3 PE=1 SV=1	Calm3	P0DP31	21.1407	21.6211	21.5144	22.0055	24.2731	24.1078	23.9929	24.0456
483	Calmodulin-regulated spectrin-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Camsap1 PE=1 SV=2	Camsap1	D3Z8E6	NaN	NaN	NaN	NaN	14.1522	16.1383	15.5877	15.3281
484	Calnexin OS=Rattus norvegicus OX=10116 GN=Canx PE=1 SV=1	Canx	P35565	21.6804	22.57	21.4284	21.2081	24.3326	24.669	24.0465	24.3472
485	Calpain small subunit 1 OS=Rattus norvegicus OX=10116 GN=Capns1 PE=1 SV=3	Capns1	Q64537	19.9087	20.6022	20.8343	19.9127	23.5219	24.1134	24.382	24.3065
486	Calpain-1 catalytic subunit OS=Rattus norvegicus OX=10116 GN=Capn1 PE=1 SV=1	Capn1	F1LS29	17.0649	19.2571	17.7513	18.476	19.9483	19.916	19.8701	19.3355
487	Calpain-2 catalytic subunit OS=Rattus norvegicus OX=10116 GN=Capn2 PE=1 SV=3	Capn2	Q07009	20.3846	20.5989	20.799	20.2533	24.1225	24.5388	24.8317	24.744
488	Calpastatin OS=Rattus norvegicus OX=10116 GN=Cast PE=1 SV=1	Cast	F1LPH1	15.8006	18.2527	14.7255	16.4174	21.7308	21.6485	21.6281	21.8904
489	Calponin (Fragment) OS=Rattus norvegicus OX=10116 GN=Cnn2 PE=1 SV=3	Cnn2	D3ZRX9	14.8734	15.7197	15.4072	NaN	21.4814	21.1043	21.1564	20.9675
490	Calponin-1 OS=Rattus norvegicus OX=10116 GN=Cnn1 PE=1 SV=1	Cnn1	Q08290	18.2752	17.7561	17.7443	16.1894	22.3297	21.4607	21.8512	21.6664
491	Calponin-3 OS=Rattus norvegicus OX=10116 GN=Cnn3 PE=1 SV=1	Cnn3	P37397	18.6581	18.9359	17.7672	17.1539	22.6011	22.4513	22.4082	22.2258
492	Calreticulin OS=Rattus norvegicus OX=10116 GN=Calr PE=1 SV=1	Calr	P18418	21.081	21.2392	20.7985	20.4118	23.3543	24.0917	23.5932	23.937
493	Calsequestrin OS=Rattus norvegicus OX=10116 GN=Casq2 PE=1 SV=2	Casq2	F1M944	20.3839	20.1107	20.7394	19.4907	23.3945	24.1898	23.3448	23.5185
494	Calsequestrin-1 OS=Rattus norvegicus OX=10116 GN=Casq1 PE=1 SV=2	Casq1	P19633	16.9045	17.1491	17.164	15.6729	17.6622	16.9865	17.2951	17.2206
495	Calumenin OS=Rattus norvegicus OX=10116 GN=Calu PE=1 SV=1	Calu	G3V6S3	18.8967	18.4049	18.8919	19.7538	21.9533	22.7665	21.834	22.1485
496	cAMP-dependent protein kinase catalytic subunit beta OS=Rattus norvegicus OX=10116 GN=Prkacb PE=1 SV=2	Prkacb	P68182	14.9018	15.8895	16.477	NaN	20.4752	20.5316	21.4452	20.8583
497	cAMP-dependent protein kinase inhibitor alpha OS=Rattus norvegicus OX=10116 GN=Pkia PE=1 SV=2	Pkia	P63249	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
498	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Rattus norvegicus OX=10116 GN=Prkar1a PE=1 SV=2	Prkar1a	P09456	19.1293	18.344	19.0406	18.8412	24.3774	23.773	24.0728	24.0342
499	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Rattus norvegicus OX=10116 GN=Prkar2a PE=1 SV=1	Prkar2a	A0A0G2K405	NaN	NaN	NaN	NaN	19.4635	19.756	19.0638	18.3706
500	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus OX=10116 GN=Prkar2b PE=1 SV=3	Prkar2b	P12369	16.7157	16.4296	16.6226	14.2797	20.6708	20.3139	20.6322	20.5665
501	cAMP-specific 3',5'-cyclic phosphodiesterase 4B OS=Rattus norvegicus OX=10116 GN=Pde4b PE=1 SV=4	Pde4b	P14646	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
502	cAMP-specific 3',5'-cyclic phosphodiesterase 4D OS=Rattus norvegicus OX=10116 GN=Pde4d PE=1 SV=4	Pde4d	P14270	15.6698	16.2541	17.8445	18.7411	21.8521	21.0686	21.4988	21.4553
503	Canopy 2 homolog (Zebrafish) OS=Rattus norvegicus OX=10116 GN=Cnpy2 PE=1 SV=1	Cnpy2	A0JN30	NaN	NaN	NaN	NaN	NaN	18.9472	19.8696	NaN
504	Cap-binding complex-dependent translation initiation factor OS=Rattus norvegicus OX=10116 GN=Ctif PE=1 SV=1	Ctif	A0A0G2JZZ3	NaN	NaN	NaN	NaN	17.5616	16.7235	17.5547	NaN
505	Capping protein regulator and myosin 1 linker 1 OS=Rattus norvegicus OX=10116 GN=Carmil1 PE=1 SV=1	Carmil1	A0A0G2JXG7	NaN	NaN	NaN	NaN	18.0513	17.5538	18.3096	17.8963
506	Caprin-1 OS=Rattus norvegicus OX=10116 GN=Caprin1 PE=1 SV=1	Caprin1	A0A0G2K8H0	17.1917	18.1311	17.2035	16.3785	22.6005	23.2892	22.2454	22.3672
507	Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase OS=Rattus norvegicus OX=10116 GN=C	Cad	D4A8A0	20.2177	19.1497	19.6849	20.0701	23.4847	24.5866	24.5102	24.2737
508	Carbonic anhydrase 1 OS=Rattus norvegicus OX=10116 GN=Ca1 PE=1 SV=1	Car1	B0BNN3	20.8011	20.8943	20.8589	20.0972	20.4153	20.0567	19.964	19.9044
509	Carbonic anhydrase 2 OS=Rattus norvegicus OX=10116 GN=Ca2 PE=1 SV=2	Car2	P27139	19.584	18.904	20.0679	19.862	14.476	18.1639	18.4545	18.5856
510	Carbonic anhydrase 3 OS=Rattus norvegicus OX=10116 GN=Ca3 PE=1 SV=3	Ca3	P14141	17.7175	19.9044	20.2726	19.7943	16.3734	17.0347	NaN	NaN
511	Carbonyl reductase [NADPH] 1-like OS=Rattus norvegicus OX=10116 GN=Cbr1 PE=1 SV=1	LOC100360601	A0A0G2JSV2	16.7901	NaN	16.0044	NaN	18.0409	19.2828	18.3766	17.0192
512	Carbonyl reductase [NADPH] 1-like OS=Rattus norvegicus OX=10116 GN=LOC102556347 PE=1 SV=1	LOC102556347	M0R3X6	17.0264	19.2273	18.0701	16.6706	24.0532	24.8699	24.8116	23.8379
513	Carboxypeptidase A4 OS=Rattus norvegicus OX=10116 GN=Cpa4 PE=4 SV=1	Cpa4	D3ZHS5	18.2953	17.6839	17.9621	18.4831	18.1514	17.8341	17.4819	18.0445
514	Carboxypeptidase B2 OS=Rattus norvegicus OX=10116 GN=Cpb2 PE=2 SV=1	Cpb2	Q9EQV9	21.1245	20.86	20.9118	20.6835	17.3485	16.8986	16.753	16.4136
515	Carboxypeptidase D OS=Rattus norvegicus OX=10116 GN=Cpd PE=1 SV=2	Cpd	F1LPC6	NaN	NaN	13.9261	NaN	19.0724	18.4776	18.0704	18.0014
516	Carboxypeptidase N catalytic chain OS=Rattus norvegicus OX=10116 GN=Cpn1 PE=2 SV=1	Cpn1	Q9EQV8	21.01	20.6167	20.5831	20.5723	19.2648	19.4716	19.0033	19.3271
517	Carboxypeptidase N subunit 2 OS=Rattus norvegicus OX=10116 GN=Cpn2 PE=1 SV=1	Cpn2	F1LQT4	20.4244	21.4835	20.6922	20.4938	15.473	16.2899	NaN	15.8778
518	Carboxypeptidase OS=Rattus norvegicus OX=10116 GN=Ctsa PE=1 SV=1	Ctsa	Q6AYS3	18.3556	18.8041	17.1701	17.241	15.2681	18.5084	16.8043	16.8741
519	Carboxypeptidase Q OS=Rattus norvegicus OX=10116 GN=Cpq PE=1 SV=1	Cpq	Q6IRK9	18.7598	16.5357	18.2371	18.0373	16.4682	15.1929	14.7837	NaN
520	Cardiac phospholamban OS=Rattus norvegicus OX=10116 GN=Pln PE=1 SV=1	Pln	P61016	NaN	14.9161	15.3155	13.5049	24.3755	25.0345	24.3146	24.3296
521	Cardiac troponin C OS=Rattus norvegicus OX=10116 GN=Tnnc1 PE=2 SV=1	Tnnc1	Q4PP99	NaN	13.7763	20.689	20.1039	24.4754	23.0678	23.3511	23.6727
522	CArG-binding factor A OS=Rattus norvegicus OX=10116 GN=Hnrnpab PE=1 SV=1	Hnrnpab	Q9QX80	14.0974	15.6513	15.8631	15.8962	21.489	21.581	21.1986	21.0464
523	Carnitine O-palmitoyltransferase 1, liver isoform OS=Rattus norvegicus OX=10116 GN=Cpt1a PE=1 SV=2	Cpt1a	P32198	21.2015	21.1508	20.2876	19.2782	20.1259	19.4575	20.1194	20.0607
524	Carnitine O-palmitoyltransferase 1, muscle isoform OS=Rattus norvegicus OX=10116 GN=Cpt1b PE=1 SV=1	Cpt1b	Q63704	NaN	16.4776	15.3263	15.964	20.9136	22.2118	20.8243	21.1475
525	Cartilage oligomeric matrix protein OS=Rattus norvegicus OX=10116 GN=Comp PE=1 SV=1	Comp	P35444	17.1863	16.8595	18.8384	18.1467	15.4241	15.8242	NaN	NaN
526	Casein kinase II subunit alpha OS=Rattus norvegicus OX=10116 GN=Csnk2a1 PE=1 SV=2	Csnk2a1	P19139	NaN	NaN	NaN	NaN	16.8968	16.8326	16.811	16.325
527	Casein kinase II subunit beta OS=Rattus norvegicus OX=10116 GN=Csnk2b PE=1 SV=1	Csnk2b	P67874	NaN	NaN	17.235	18.3194	18.1612	NaN	NaN	NaN
528	Cask-interacting protein 2 OS=Rattus norvegicus OX=10116 GN=Caskin2 PE=1 SV=1	Caskin2	D4A9T0	18.762	18.5179	17.7341	17.9103	19.2159	20.4738	19.8305	19.1603

529	Caspase 14 OS=Rattus norvegicus OX=10116 GN=Casp14 PE=3 SV=1	Casp14	D3ZZ65	17.3346	20.5518	17.5981	20.1773	13.8412	18.6673	18.6892	18.8182
530	Caspase-3 OS=Rattus norvegicus OX=10116 GN=Casp3 PE=2 SV=2	Casp3	P55213	15.3854	NaN	15.4146	15.0961	18.4369	18.1042	19.1681	19.1589
531	Castration induced prostatic apoptosis-related protein 1 OS=Rattus norvegicus OX=10116 GN=Parm1 PE=1 SV=3	Parm1	F1LQ50	NaN	NaN	14.8244	NaN	18.3477	18.4125	18.3037	18.3519
532	Catalase OS=Rattus norvegicus OX=10116 GN=Cat PE=1 SV=3	Cat	P04762	19.8895	21.0883	19.7902	19.1338	22.9565	23.6162	22.9557	22.8551
533	Catechol O-methyltransferase OS=Rattus norvegicus OX=10116 GN=Comt PE=1 SV=2	Comt	P22734	15.4262	NaN	NaN	15.9083	19.0025	19.002	18.5678	18.7579
534	Catechol-O-methyltransferase domain containing 1 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Comt	Comtd1	D3ZM21	16.1584	NaN	NaN	15.5305	16.8802	18.0309	16.2058	17.467
535	Catenin (Cadherin associated protein), alpha 1 OS=Rattus norvegicus OX=10116 GN=Ctnna1 PE=1 SV=1	Ctnna1	Q5U302	18.5368	19.1999	17.567	18.2597	23.4045	23.148	23.017	23.047
536	Catenin (Cadherin associated protein), beta 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ctnnb1 PE=1 SV=1	Ctnnb1	A0A0G2JT93	17.3216	16.3951	18.0526	17.3938	21.2125	20.6684	20.7514	20.6743
537	Catenin (Cadherin associated protein), delta 1 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ctnnd1 PE	Ctnnd1	D3ZZZ9	NaN	16.0678	NaN	16.0492	21.1628	21.1373	20.4415	20.6967
538	Cathelicidin antimicrobial peptide OS=Rattus norvegicus OX=10116 GN=Camp PE=1 SV=1	Camp	G3V8S9	22.0981	22.053	21.9724	22.6558	17.1282	16.0361	16.2135	NaN
539	Cathepsin B OS=Rattus norvegicus OX=10116 GN=Ctsb PE=1 SV=1	Ctsb	Q6IN22	19.1468	18.2996	19.3715	18.9039	18.5963	17.9358	17.117	18.5229
540	Cathepsin D OS=Rattus norvegicus OX=10116 GN=Ctsd PE=1 SV=1	Ctsd	P24268	19.5964	21.0721	19.92	19.8717	19.2751	20.8019	20.0974	19.499
541	Cathepsin S OS=Rattus norvegicus OX=10116 GN=Ctss PE=2 SV=1	Ctss	Q02765	NaN	NaN	15.8208	16.5878	NaN	NaN	NaN	NaN
542	Cation-dependent mannose-6-phosphate receptor OS=Rattus norvegicus OX=10116 GN=M6pr PE=1 SV=1	M6pr	Q6AY20	19.0089	19.608	19.1195	17.5357	22.3758	22.5954	22.0773	22.1473
543	Caveolae-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Cavin1 PE=1 SV=1	Cavin1	G3V8L9	19.4373	19.5119	19.9675	19.5558	23.8314	23.9576	24.2335	24.2025
544	Caveolae-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Cavin2 PE=1 SV=3	Cavin2	Q66H98	18.756	17.6796	18.3113	17.8964	22.6546	22.1694	22.5721	22.4495
545	Caveolae-associated protein 3 OS=Rattus norvegicus OX=10116 GN=Cavin3 PE=1 SV=1	Cavin3	Q9Z1H9	NaN	NaN	NaN	NaN	15.8785	16.4489	15.8138	16.1904
546	Caveolae-associated protein 4 OS=Rattus norvegicus OX=10116 GN=Cavin4 PE=1 SV=1	Cavin4	B1PRL5	16.0511	15.2444	15.9813	15.9942	19.982	20.4062	20.1915	20.2083
547	Caveolin-1 OS=Rattus norvegicus OX=10116 GN=Cav1 PE=1 SV=3	Cav1	P41350	18.0002	15.8413	16.9226	16.1336	21.1618	21.4371	21.0088	21.18
548	Caveolin-3 OS=Rattus norvegicus OX=10116 GN=Cav3 PE=1 SV=1	Cav3	P51638	NaN	NaN	NaN	NaN	19.3381	18.9452	17.6572	18.7714
549	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1 OS=Rattus norvegicus OX=10116 GN=Cit	Cited1	Q4V8P1	NaN	NaN	NaN	NaN	17.4336	NaN	NaN	17.0189
550	CCN family member 3 OS=Rattus norvegicus OX=10116 GN=Ccn3 PE=1 SV=1	Ccn3	Q9QZQ5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
551	CCR4-NOT transcription complex subunit 10 OS=Rattus norvegicus OX=10116 GN=Cnot10 PE=2 SV=1	Cnot10	Q5XIA4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
552	CCR4-NOT transcription complex subunit 9 OS=Rattus norvegicus OX=10116 GN=Cnot9 PE=1 SV=1	Cnot9	Q5PQL2	NaN	17.9601	NaN	18.6799	20.2413	19.9648	18.9365	17.6776
553	CCR4-NOT transcription complex, subunit 1 OS=Rattus norvegicus OX=10116 GN=Cnot1 PE=1 SV=1	Cnot1	G3V7M0	NaN	NaN	15.718	17.5226	20.591	20.5467	20.2407	19.989
554	CCR4-NOT transcription complex, subunit 2 OS=Rattus norvegicus OX=10116 GN=Cnot2 PE=1 SV=1	Cnot2	A0A0G2K717	NaN	NaN	NaN	NaN	17.0764	17.6809	17.1417	16.718
555	CCR4-NOT transcription complex, subunit 3 OS=Rattus norvegicus OX=10116 GN=Cnot3 PE=1 SV=2	Cnot3	D3ZUV9	19.8983	19.6274	19.6758	18.2742	19.9756	19.0699	19.0678	19.557
556	CD163 antigen (Predicted) OS=Rattus norvegicus OX=10116 GN=Cd163 PE=1 SV=1	Cd163	D3Z9U2	19.5809	19.7898	19.0741	18.9411	18.5696	18.8988	18.1479	18.9822
557	CD248 antigen, endosialin (Predicted) OS=Rattus norvegicus OX=10116 GN=Cd248 PE=4 SV=1	Cd248	D3ZN06	16.8611	17.271	16.7164	15.7799	16.7164	NaN	17.0959	16.8815
558	CD2-associated protein OS=Rattus norvegicus OX=10116 GN=Cd2ap PE=1 SV=2	Cd2ap	F1LRS8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
559	CD34 antigen (Predicted) OS=Rattus norvegicus OX=10116 GN=Cd34 PE=1 SV=1	Cd34	B1PLB1	18.1254	17.646	17.2298	15.0643	20.4808	20.4008	20.1444	20.2082
560	CD44 antigen OS=Rattus norvegicus OX=10116 GN=Cd44 PE=1 SV=3	Cd44	D3ZGF1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
561	CD48 antigen OS=Rattus norvegicus OX=10116 GN=Cd48 PE=1 SV=1	Cd48	P10252	17.4776	17.2664	17.4068	16.9539	18.4524	20.0918	19.7724	19.3871
562	CD55 molecule OS=Rattus norvegicus OX=10116 GN=Cd55 PE=1 SV=1	Cd55	A0A0G2QC50	15.2198	15.771	17.0279	17.5286	NaN	15.4832	NaN	NaN
563	CD59 glycoprotein OS=Rattus norvegicus OX=10116 GN=Cd59 PE=1 SV=2	Cd59	P27274	20.4379	20.6672	21.226	19.7472	20.775	20.4699	20.0124	20.1635
564	CD9 antigen OS=Rattus norvegicus OX=10116 GN=Cd9 PE=1 SV=2	Cd9	P40241	20.1848	19.8484	19.762	19.0788	20.1327	20.1733	19.7294	20.1427
565	CD99 molecule (Xg blood group) OS=Rattus norvegicus OX=10116 GN=Cd99 PE=1 SV=1	Cd99	B4F7A5	NaN	NaN	NaN	NaN	20.495	20.3868	20.3251	20.6656
566	CDC42 effector protein (Rho GTPase binding) 3 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Cdc42ep	Cdc42ep3	Q0VGK8	NaN	NaN	NaN	NaN	17.5565	17.462	17.0629	17.5351
567	CDC42 effector protein (Rho GTPase binding) 4 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Cdc42ep	Cdc42ep4	B1WC33	NaN	NaN	NaN	NaN	21.37	20.1982	20.2054	19.8759
568	Cdc42 effector protein 1 OS=Rattus norvegicus OX=10116 GN=Cdc42ep1 PE=1 SV=1	Cdc42ep1	A1A5P0	NaN	15.6604	15.4106	NaN	18.1069	17.9194	17.3759	17.3643
569	Cdc42 effector protein 2 OS=Rattus norvegicus OX=10116 GN=Cdc42ep2 PE=1 SV=1	Cdc42ep2	Q5PQP4	16.5451	NaN	16.94	17.3768	17.3197	16.8668	16.4681	16.4685
570	CDGSH iron sulfur domain 2 OS=Rattus norvegicus OX=10116 GN=Cisd2 PE=1 SV=1	Cisd2	D4AAE9	19.5097	19.5379	20.0827	19.6943	18.2352	19.2612	18.0481	18.2055
571	CDGSH iron-sulfur domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Cisd1 PE=3 SV=1	Cisd1	B0K020	16.814	15.8441	15.7965	14.345	20.4228	21.3904	20.984	20.8633
572	CDP-diacylglycerol--inositol 3-phosphatidyltransferase OS=Rattus norvegicus OX=10116 GN=Cdipt PE=1 SV=1	Cdipt	P70500	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
573	CDW92 antigen, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Slc44a1 PE=1 SV=1	Slc44a1	A0A0G2K0P8	19.1665	19.1343	18.6802	18.1146	19.4267	19.1505	18.7033	18.8005
574	Cell cycle and apoptosis regulator 2 OS=Rattus norvegicus OX=10116 GN=Ccar2 PE=1 SV=1	Ccar2	F1LM55	18.3349	17.1539	18.7622	NaN	18.7151	19.0609	19.2511	18.7201
575	Cell cycle control protein OS=Rattus norvegicus OX=10116 GN=Tmem30a PE=1 SV=1	Tmem30a	A0A0G2JXG3	NaN	NaN	NaN	16.1269	17.4136	17.2878	17.1739	16.8307
576	Cell division control protein 42 homolog OS=Rattus norvegicus OX=10116 GN=Cdc42 PE=1 SV=1	Cdc42	A0A0G2JSM8	NaN	NaN	19.7996	NaN	19.144	18.8016	18.8093	19.0254
577	Cell division control protein 42 homolog OS=Rattus norvegicus OX=10116 GN=Cdc42 PE=1 SV=2	Cdc42	Q8CFN2	20.184	20.5082	20.6461	19.4683	22.7722	22.1129	22.2101	22.6812
578	Cell growth regulator with EF hand domain 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Cgref1 PE=1 SV=1	Cgref1	A0A0A0MXV3	18.5317	18.8213	18.8754	19.0665	16.1523	17.1389	17.5251	17.3198
579	Cell surface glycoprotein MUC18 OS=Rattus norvegicus OX=10116 GN=Mcam PE=1 SV=2	Mcam	Q9EPF2	13.9534	14.6399	15.8045	17.0854	21.0935	20.7188	20.6657	20.4868
580	Cellular nucleic acid-binding protein OS=Rattus norvegicus OX=10116 GN=Cnbp PE=2 SV=1	Cnbp	P62634	NaN	16.2581	NaN	15.5746	22.0077	20.9794	20.6063	21.0281
581	Centromere/kinetochore protein zw10 homolog OS=Rattus norvegicus OX=10116 GN=Zw10 PE=2 SV=3	Zw10	Q4V8C2	17.247	16.769	17.502	16.8777	18.8629	19.6414	18.8798	19.4208

582	Centrosomal protein 170B OS=Rattus norvegicus OX=10116 GN=Cep170b PE=1 SV=1	Cep170b	D4A1G8	NaN	NaN	15.8862	NaN	NaN	15.6276	NaN	NaN
583	Centrosomal protein 350 OS=Rattus norvegicus OX=10116 GN=Cep350 PE=1 SV=3	Cep350	F1LPD3	19.0111	18.7235	19.4701	18.8291	17.8467	NaN	17.0539	18.194
584	Centrosomal protein 97 OS=Rattus norvegicus OX=10116 GN=Cep97 PE=1 SV=1	Cep97	D4AC95	NaN	NaN	NaN	NaN	NaN	16.4532	NaN	NaN
585	Cerebellar degeneration-related protein 2-like OS=Rattus norvegicus OX=10116 GN=Cdr2l PE=4 SV=2	Cdr2l	D4ABP3	NaN	NaN	NaN	NaN	15.5487	16.2429	15.946	15.6608
586	Ceruloplasmin OS=Rattus norvegicus OX=10116 GN=Cp PE=1 SV=1	Cp	A0A0G2K9I6	25.1179	25.5833	25.6644	25.1247	21.6507	21.4949	21.1672	21.1816
587	cGMP-inhibited 3',5'-cyclic phosphodiesterase A OS=Rattus norvegicus OX=10116 GN=Pde3a PE=1 SV=1	Pde3a	Q62865	22.176	21.5414	21.8174	22.2248	21.8452	21.2624	21.6302	21.7681
588	Chaperonin containing Tcp1, subunit 6A (Zeta 1) OS=Rattus norvegicus OX=10116 GN=Cct6a PE=1 SV=1	Cct6a	Q3MHS9	20.4235	21.1793	20.0189	20.5602	23.8821	23.4814	24.7451	25.2927
589	Chaperonin subunit 8 (Theta) (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Cct8 PE=1 SV=1	Cct8	D4ACB8	20.5826	19.9447	20.3595	21.0546	24.6812	24.4709	25.2907	25.653
590	Charged multivesicular body protein 2A OS=Rattus norvegicus OX=10116 GN=Chmp2a PE=1 SV=1	Chmp2a	B2RZB5	16.4817	18.76	17.5315	16.457	20.9279	20.4734	20.5088	20.5058
591	Charged multivesicular body protein 2B OS=Rattus norvegicus OX=10116 GN=Chmp2b PE=1 SV=2	Chmp2b	F1M8B7	NaN	NaN	NaN	NaN	NaN	NaN	18.1734	NaN
592	Charged multivesicular body protein 3 OS=Rattus norvegicus OX=10116 GN=Chmp3 PE=1 SV=3	Chmp3	Q8CGS4	NaN	14.6458	NaN	NaN	18.5346	17.3556	17.7286	18.0511
593	Charged multivesicular body protein 6 OS=Rattus norvegicus OX=10116 GN=Chmp6 PE=1 SV=1	Chmp6	D3ZDR2	18.8762	18.6075	18.6753	18.7302	19.5903	19.0564	18.559	19.0154
594	Chloride intracellular channel protein 1 OS=Rattus norvegicus OX=10116 GN=Clic1 PE=1 SV=1	Clic1	Q6MG61	21.1434	21.473	21.5706	21.352	21.4702	23.7654	24.5065	23.2595
595	Chloride intracellular channel protein OS=Rattus norvegicus OX=10116 GN=Clic3 PE=3 SV=1	Clic3	D3ZY91	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
596	Chloride intracellular channel protein OS=Rattus norvegicus OX=10116 GN=Clic4 PE=1 SV=1	Clic4	G3V8C4	19.0355	19.4335	19.7769	19.9968	22.6833	23.1912	23.9106	22.8935
597	CHMP family, member 7 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Chmp7 PE=1 SV=1	Chmp7	D4A7H9	20.2102	19.2491	19.5209	19.3177	21.4528	20.9262	21.0859	21.1056
598	Choline/ethanolamine kinase OS=Rattus norvegicus OX=10116 GN=Chkb PE=1 SV=3	Chkb	O54783	NaN	NaN	NaN	NaN	NaN	17.3112	17.0456	16.8914
599	Choline-phosphate cytidylyltransferase A OS=Rattus norvegicus OX=10116 GN=Pcyt1a PE=1 SV=2	Pcyt1a	P19836	17.5054	18.7389	16.753	18.9253	22.4992	21.9067	22.5818	22.4042
600	Chondroitin sulfate proteoglycan 4 OS=Rattus norvegicus OX=10116 GN=Cspg4 PE=1 SV=2	Cspg4	Q00657	NaN	NaN	15.0234	NaN	17.2568	17.6518	17.0646	17.3699
601	Chromatin-modifying protein 4B-like 1 OS=Rattus norvegicus OX=10116 GN=Chmp4bl1 PE=1 SV=1	Chmp4bl1	D4A9Z8	NaN	NaN	NaN	NaN	16.9972	16.9431	16.6624	16.9788
602	Chromobox 3 OS=Rattus norvegicus OX=10116 GN=Cbx3 PE=1 SV=1	Cbx3	Q5RJK5	15.688	NaN	NaN	NaN	18.7451	19.1917	19.0738	19.4193
603	Chromodomain helicase DNA-binding protein 4 OS=Rattus norvegicus OX=10116 GN=Chd4 PE=1 SV=3	Chd4	E9PU01	15.5911	NaN	13.5439	10.7351	NaN	NaN	10.0294	9.58723
604	Chromosome segregation 1-like OS=Rattus norvegicus OX=10116 GN=Cse1l PE=1 SV=1	Cse1l	D3ZPR0	17.961	17.8657	18.6203	17.9181	22.5265	22.7444	23.2473	23.0967
605	Chymotrypsinogen B OS=Rattus norvegicus OX=10116 GN=Ctrb1 PE=1 SV=1	Ctrb1	F1MA56	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
606	Cilia- and flagella-associated protein 20 OS=Rattus norvegicus OX=10116 GN=Cfap20 PE=4 SV=1	Cfap20	A0A0H2UI05	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
607	Ciliary rootlet coiled-coil, rootletin OS=Rattus norvegicus OX=10116 GN=Crocc PE=1 SV=2	Crocc	F1M6Q2	19.9379	21.191	19.4493	21.2429	18.8462	20.2743	18.6166	18.5995
608	Citrate synthase OS=Rattus norvegicus OX=10116 GN=Cs PE=1 SV=1	Cs	G3V936	17.0167	18.2757	16.2923	21.7722	18.453	21.7195	20.5965	20.676
609	C-Jun-amino-terminal kinase-interacting protein 3 OS=Rattus norvegicus OX=10116 GN=Mapk8ip3 PE=1 SV=2	Mapk8ip3	E9PSK7	NaN	NaN	NaN	NaN	NaN	16.7079	16.6758	NaN
610	Clathrin coat assembly protein AP180 OS=Rattus norvegicus OX=10116 GN=Snap91 PE=1 SV=3	Snap91	F1LRK0	17.4956	17.9827	17.5501	15.9355	21.2098	19.7314	19.9295	20.0818
611	Clathrin heavy chain OS=Rattus norvegicus OX=10116 GN=Cltc PE=1 SV=1	Cltc	F1M779	22.7374	22.9049	22.4376	22.5055	25.8925	24.9136	24.598	24.6427
612	Clathrin interactor 1 OS=Rattus norvegicus OX=10116 GN=Clint1 PE=1 SV=1	Clint1	A0A0G2JW94	17.0254	NaN	17.6763	NaN	18.4309	16.8195	17.4391	16.9709
613	Clathrin interactor 1 OS=Rattus norvegicus OX=10116 GN=Clint1 PE=1 SV=1	Clint1	Q6DGF2	19.1012	18.5373	19.0229	18.9419	22.896	22.0429	21.9889	22.0772
614	Clathrin light chain A OS=Rattus norvegicus OX=10116 GN=Clta PE=1 SV=1	Clta	P08081	19.9563	19.6474	18.7089	18.48	22.1645	20.5052	20.7024	20.4313
615	Clathrin light chain B OS=Rattus norvegicus OX=10116 GN=Cltb PE=1 SV=1	Cltb	P08082	19.5075	15.9275	16.12	17.6293	22.9358	21.7108	20.8079	20.6178
616	Cleavage and polyadenylation specific factor 6, 68kDa (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Cps	Cpsf6	D3ZPL1	20.1733	20.0233	19.8869	20.0719	20.4296	19.4479	18.8954	17.7063
617	Cleavage and polyadenylation-specific factor 1 OS=Rattus norvegicus OX=10116 GN=Cpsf1 PE=1 SV=1	Cpsf1	B5DEL2	20.5146	19.8504	20.1891	18.9052	20.5413	19.3793	20.229	18.7972
618	Cleavage stimulation factor subunit 2, tau variant OS=Rattus norvegicus OX=10116 GN=Cstf2t PE=1 SV=1	Cstf2t	M0R6B9	NaN	NaN	NaN	NaN	17.4985	16.9163	16.8951	16.658
619	CLIP-associating protein 2 OS=Rattus norvegicus OX=10116 GN=Clasp2 PE=1 SV=1	Clasp2	A0A0G2JZM8	NaN	16.4982	17.0227	17.4422	18.6822	19.6419	19.4478	18.3018
620	CLPTM1, transmembrane protein OS=Rattus norvegicus OX=10116 GN=Clptm1 PE=1 SV=1	Clptm1	B2RYF6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
621	Clustered mitochondria protein homolog OS=Rattus norvegicus OX=10116 GN=Cluh PE=1 SV=1	Cluh	A0A0U1RRV5	20.7447	20.1949	19.9616	20.6831	22.5939	23.0376	22.9257	22.7161
622	Clusterin OS=Rattus norvegicus OX=10116 GN=Clu PE=1 SV=1	Clu	G3V836	25.529	25.335	25.1048	25.2868	22.5161	22.1476	21.2456	21.8512
623	Coactosin-like protein OS=Rattus norvegicus OX=10116 GN=Cotl1 PE=1 SV=1	Cotl1	B0BNA5	16.4216	17.543	18.3085	15.1843	18.686	18.236	18.3954	19.304
624	Coagulation factor IX OS=Rattus norvegicus OX=10116 GN=F9 PE=2 SV=2	F9	P16296	18.8907	18.1678	18.2566	17.4809	18.2337	NaN	16.4475	17.9546
625	Coagulation factor V OS=Rattus norvegicus OX=10116 GN=F5 PE=1 SV=1	F5	A0A0G2JXI1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
626	Coagulation factor V OS=Rattus norvegicus OX=10116 GN=F5 PE=1 SV=1	F5	A0A0G2K3W2	24.3581	24.3469	24.6565	24.2178	21.5805	21.3954	21.2499	21.6042
627	Coagulation factor X OS=Rattus norvegicus OX=10116 GN=F10 PE=1 SV=1	F10	A0A0H2UHR6	21.3197	21.3511	21.4079	20.4972	17.6374	18.1618	18.3401	17.075
628	Coagulation factor XI OS=Rattus norvegicus OX=10116 GN=F11 PE=1 SV=1	F11	A0A0G2K4I9	19.3227	18.9142	19.6949	18.5924	15.7706	NaN	16.2632	16.371
629	Coagulation factor XII OS=Rattus norvegicus OX=10116 GN=F12 PE=1 SV=1	F12	A0A0H2UI19	21.069	21.4402	21.9952	21.0627	18.9066	17.3444	17.803	18.3526
630	Coagulation factor XIII A chain OS=Rattus norvegicus OX=10116 GN=F13a1 PE=1 SV=1	F13a1	G3V811	19.7308	19.6809	19.8654	19.081	19.1892	16.7831	18.3793	18.1663
631	Coagulation factor XIII B chain OS=Rattus norvegicus OX=10116 GN=F13b PE=1 SV=1	F13b	B1H260	20.3296	19.6861	20.1485	19.5299	17.8438	19.4843	18.5977	18.7989
632	Coatomer protein complex, subunit zeta 1 OS=Rattus norvegicus OX=10116 GN=Copz1 PE=1 SV=1	Copz1	D4A8T3	16.8611	17.6201	15.6458	15.7804	20.4391	19.4569	19.8433	19.7043
633	Coatomer protein complex, subunit zeta 2 OS=Rattus norvegicus OX=10116 GN=Copz2 PE=1 SV=2	Copz2	D4ADP9	NaN	14.0705	14.6024	19.6417	19.1417	18.661	18.741	19.1783
634	Coatomer subunit alpha OS=Rattus norvegicus OX=10116 GN=Copa PE=1 SV=1	Copa	G3V6T1	19.3312	18.4851	18.5891	19.7103	23.3728	23.7694	23.5852	24.0833

635	Coatomer subunit beta OS=Rattus norvegicus OX=10116 GN=Copb1 PE=1 SV=1	Copb1	P23514	17.7188	17.2381	17.4791	15.9051	22.1783	22.8414	22.5168	22.9776
636	Coatomer subunit beta' OS=Rattus norvegicus OX=10116 GN=Copb2 PE=1 SV=3	Copb2	O35142	26.6522	26.6973	26.5352	26.6736	24.3303	24.025	23.8147	24.043
637	Coatomer subunit delta OS=Rattus norvegicus OX=10116 GN=Arcn1 PE=2 SV=1	Arcn1	Q66H80	18.8845	20.3829	19.4048	19.1416	21.5502	21.9278	21.6772	22.1429
638	Coatomer subunit epsilon OS=Rattus norvegicus OX=10116 GN=Cope PE=1 SV=3	Cope	G3V8Q1	15.9051	15.6292	17.1111	16.8071	21.3899	21.8079	21.3778	22.0589
639	Coatomer subunit gamma OS=Rattus norvegicus OX=10116 GN=Copg1 PE=1 SV=1	Hmces	A0A0G2K1F3	18.9944	17.9099	17.8917	18.8732	21.9844	21.7653	21.9193	22.4426
640	Coatomer subunit gamma OS=Rattus norvegicus OX=10116 GN=Copg2 PE=1 SV=1	Copg2	A0A0H2UHV9	15.7593	12.9841	15.6857	NaN	19.4658	19.5216	19.2876	19.5745
641	COBW domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Cbwd1 PE=2 SV=2	Cbwd1	Q99MB4	NaN	15.7662	NaN	18.9155	19.299	19.184	18.4477	18.1342
642	Codanin 1 OS=Rattus norvegicus OX=10116 GN=Cdan1 PE=4 SV=2	Cdan1	D4A1U4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
643	Coenzyme A synthase OS=Rattus norvegicus OX=10116 GN=Coasy PE=1 SV=1	Coasy	Q5XIA5	NaN	NaN	NaN	14.6792	17.5277	16.5062	17.2609	17.2964
644	Cofilin 2 OS=Rattus norvegicus OX=10116 GN=Cfl2 PE=1 SV=1	Cfl2	M0RC65	17.4597	17.7017	18.0975	17.722	22.6144	21.5905	22.0915	22.5153
645	Cofilin-1 OS=Rattus norvegicus OX=10116 GN=Cfl1 PE=1 SV=3	Cfl1	P45592	21.796	21.9526	22.2761	21.8381	24.8584	24.1431	24.7969	25.5915
646	Coiled coil domain-containing 88A OS=Rattus norvegicus OX=10116 GN=Ccdc88a PE=1 SV=3	Ccdc88a	D3ZYD7	18.937	19.1572	18.9761	17.5897	17.6459	17.8155	18.2938	17.9256
647	Coiled-coil domain-containing 141 OS=Rattus norvegicus OX=10116 GN=Ccdc141 PE=1 SV=2	Ccdc141	D3ZEY0	19.9005	19.7096	19.7759	19.5519	20.9124	22.3069	21.674	21.4002
648	Coiled-coil domain-containing 6 OS=Rattus norvegicus OX=10116 GN=Ccdc6 PE=1 SV=3	Ccdc6	D4AEK9	16.1286	15.974	13.5274	15.2333	19.4778	19.323	18.5727	19.4113
649	Coiled-coil domain-containing protein 43 OS=Rattus norvegicus OX=10116 GN=Ccdc43 PE=1 SV=2	Ccdc43	Q5BK07	NaN	NaN	NaN	16.1112	17.9452	19.0182	18.2224	18.3482
650	Coiled-coil domain-containing protein 47 OS=Rattus norvegicus OX=10116 GN=Ccdc47 PE=2 SV=1	Ccdc47	Q5U2X6	NaN	NaN	13.7748	14.7087	17.5095	18.2977	15.8529	17.1685
651	Coiled-coil domain-containing protein 8 OS=Rattus norvegicus OX=10116 GN=Ccdc8 PE=1 SV=1	Ccdc8	P62521	NaN	NaN	NaN	NaN	20.1307	21.4754	20.8568	20.6457
652	Coiled-coil domain-containing protein 91 OS=Rattus norvegicus OX=10116 GN=Ccdc91 PE=1 SV=1	Ccdc91	Q6AY97	14.7179	NaN	16.3045	15.8984	18.2984	17.5855	18.0781	18.3185
653	Coiled-coil domain-containing protein 93 OS=Rattus norvegicus OX=10116 GN=Ccdc93 PE=1 SV=1	Ccdc93	Q5BJT7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
654	Coiled-coil glutamate-rich protein 2 OS=Rattus norvegicus OX=10116 GN=Ccer2 PE=4 SV=1	Ccer2	M0R3Q4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
655	Cold shock domain-containing protein E1 OS=Rattus norvegicus OX=10116 GN=Csde1 PE=2 SV=1	Csde1	P18395	18.1019	17.1258	15.3265	18.4895	21.2459	21.4245	21.9136	21.5135
656	Cold-inducible RNA-binding protein OS=Rattus norvegicus OX=10116 GN=Cirbp PE=2 SV=1	Cirbp	P60825	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
657	Colipase OS=Rattus norvegicus OX=10116 GN=Clps PE=4 SV=1	Clps	F1LNA9	20.1834	18.2215	21.0439	21.2353	NaN	15.2144	NaN	15.964
658	Collagen alpha-1(I) chain OS=Rattus norvegicus OX=10116 GN=Col1a1 PE=1 SV=5	Col1a1	P02454	21.403	21.662	22.0259	21.2534	18.3699	19.5977	18.8542	19.4103
659	Collagen alpha-1(III) chain OS=Rattus norvegicus OX=10116 GN=Col3a1 PE=2 SV=3	Col3a1	P13941	16.9237	16.9025	17.2788	16.7997	18.2696	NaN	NaN	18.0928
660	Collagen alpha-1(XI) chain OS=Rattus norvegicus OX=10116 GN=Col11a1 PE=1 SV=2	Col11a1	P20909	19.172	18.5301	18.9003	18.81	20.4227	20.08	20.2339	20.2957
661	Collagen alpha-1(XII) chain OS=Rattus norvegicus OX=10116 GN=Col12a1 PE=1 SV=1	Col12a1	A0A0G2KAJ7	19.086	19.6876	19.8542	19.0448	19.7089	20.2846	19.6111	19.6544
662	Collagen alpha-2(I) chain OS=Rattus norvegicus OX=10116 GN=Col1a2 PE=1 SV=3	Col1a2	P02466	17.2038	17.5479	17.8875	16.8484	NaN	18.9635	18.9005	18.0256
663	Collagen beta(1-O)galactosyltransferase 1 OS=Rattus norvegicus OX=10116 GN=Colgalt1 PE=1 SV=1	Colgalt1	B1H282	NaN	NaN	NaN	NaN	16.1697	16.2756	16.2473	16.1454
664	Collagen type IV alpha 1 chain OS=Rattus norvegicus OX=10116 GN=Col4a1 PE=1 SV=1	Col4a1	F1MA59	16.0207	16.0836	15.9231	NaN	NaN	NaN	NaN	NaN
665	Collagen type IV alpha 2 chain OS=Rattus norvegicus OX=10116 GN=Col4a2 PE=1 SV=3	Col4a2	F1M6Q3	16.4841	16.0825	16.6706	15.9335	18.6401	17.3987	16.9131	17.7141
666	Collagen type IV alpha 3-binding protein OS=Rattus norvegicus OX=10116 GN=Col4a3bp PE=1 SV=2	Cert1	D4ACN6	NaN	NaN	NaN	NaN	NaN	16.4334	NaN	NaN
667	Collagen type VI alpha 1 chain OS=Rattus norvegicus OX=10116 GN=Col6a1 PE=1 SV=1	Col6a1	D3ZUL3	19.2094	18.7362	19.444	19.6138	19.0425	18.56	18.7192	19.2104
668	Collagen type X alpha 1 chain OS=Rattus norvegicus OX=10116 GN=Col10a1 PE=4 SV=1	Col10a1	A0A0G2K7A5	15.7154	15.2107	15.9015	16.3815	NaN	NaN	NaN	NaN
669	Collagen type XIV alpha 1 chain OS=Rattus norvegicus OX=10116 GN=Col14a1 PE=1 SV=3	Col14a1	D3ZZT9	NaN	NaN	16.6159	NaN	18.9822	19.4508	19.3306	18.4077
670	Collagen type XV alpha 1 chain OS=Rattus norvegicus OX=10116 GN=Col15a1 PE=1 SV=1	Col15a1	A0A0G2JV12	17.058	14.8687	16.7472	NaN	NaN	17.6871	16.5186	NaN
671	Collagen type XVIII alpha 1 chain OS=Rattus norvegicus OX=10116 GN=Col18a1 PE=1 SV=2	Col18a1	F1LR02	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
672	Collectin sub-family member 10 (C-type lectin) (Predicted) OS=Rattus norvegicus OX=10116 GN=Colec10 PE=1 SV=1	Colec10	D4A7F6	20.1723	19.1244	18.9798	19.8345	14.9174	NaN	15.3527	NaN
673	Collectin sub-family member 11 OS=Rattus norvegicus OX=10116 GN=Colec11 PE=1 SV=2	Colec11	F1LSS7	20.9283	19.9491	20.3046	19.1073	16.3428	17.0237	16.0694	16.2975
674	Collectin-12 OS=Rattus norvegicus OX=10116 GN=Colec12 PE=2 SV=1	Colec12	Q4V885	17.2215	NaN	17.4205	NaN	NaN	17.3984	16.8267	17.1285
675	COMM domain containing 10, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Commd10 PE=1 SV=1	Commd10	Q68FS9	NaN	NaN	NaN	NaN	18.9559	19.0725	18.7873	18.8471
676	COMM domain containing 7, isoform CRA_d OS=Rattus norvegicus OX=10116 GN=Commd7 PE=1 SV=1	Commd7	Q499V0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
677	COMM domain containing 9, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Commd9 PE=1 SV=1	Commd9	Q3MIE7	NaN	NaN	NaN	NaN	19.0685	17.7693	18.3666	17.4991
678	COMM domain-containing 6 OS=Rattus norvegicus OX=10116 GN=Commd6 PE=1 SV=1	Commd6	D4A8E7	NaN	NaN	NaN	NaN	17.3223	17.4498	17.7182	17.4426
679	COMM domain-containing protein 3 OS=Rattus norvegicus OX=10116 GN=Commd3 PE=1 SV=1	Commd3	Q6P9U3	16.5184	15.3562	15.9962	16.7495	16.4798	17.8341	17.2044	18.0621
680	Common salivary protein 1 OS=Rattus norvegicus OX=10116 GN=Csap1 PE=4 SV=1	Csap1	M0R7K9	NaN	16.6483	16.8593	18.6699	NaN	19.1612	19.4367	19.4018
681	Complement C1q subcomponent subunit A OS=Rattus norvegicus OX=10116 GN=C1qa PE=1 SV=2	C1qa	P31720	20.7882	21.0223	20.8108	21.0427	19.6296	20.1333	19.2755	19.7221
682	Complement C1q subcomponent subunit C OS=Rattus norvegicus OX=10116 GN=C1qc PE=1 SV=1	C1qc	A0A0H2UHK1	20.9422	21.1122	21.4292	19.9086	19.311	20.0188	19.2917	19.802
683	Complement C1s subcomponent OS=Rattus norvegicus OX=10116 GN=C1s PE=1 SV=1	C1s	G3V7L3	22.2741	22.2429	25.3216	22.527	19.1224	18.6918	18.2419	18.9641
684	Complement C2 OS=Rattus norvegicus OX=10116 GN=C2 PE=1 SV=1	C2	Q6MG73	18.2778	19.4678	19.375	18.0714	18.671	18.8173	18.7934	18.3113
685	Complement C3 OS=Rattus norvegicus OX=10116 GN=C3 PE=1 SV=1	C3	M0RBF1	28.4524	28.521	28.7191	28.993	25.2862	25.2691	25.0708	25.5885
686	Complement C4 OS=Rattus norvegicus OX=10116 GN=C4 PE=1 SV=3	C4a	P08649	24.818	25.2104	25.1985	24.8521	21.3002	21.3722	21.3988	21.1125
687	Complement C4B (Chido blood group) OS=Rattus norvegicus OX=10116 GN=C4b PE=1 SV=1	C4b	Q6MG90	NaN	NaN	18.5564	19.0298	NaN	17.9747	NaN	NaN

688	Complement C5 OS=Rattus norvegicus OX=10116 GN=C5 PE=1 SV=2	C5	A0A096P6L9	23.1611	22.8195	23.108	22.7357	20.6972	19.4526	19.8549	19.558
689	Complement C7 OS=Rattus norvegicus OX=10116 GN=C7 PE=1 SV=1	C7	A0A0G2K7X7	21.0742	20.7626	21.0048	21.4567	20.3153	20.4267	21.6036	20.1687
690	Complement C8 alpha chain OS=Rattus norvegicus OX=10116 GN=C8a PE=1 SV=1	C8a	D3ZWD6	21.374	21.5724	21.7868	21.4607	19.3909	19.8604	18.9915	19.302
691	Complement C8 gamma chain OS=Rattus norvegicus OX=10116 GN=C8g PE=1 SV=1	C8g	D3ZPI8	18.7386	17.9434	18.9449	15.882	16.2279	NaN	16.8745	16.0298
692	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=C1qbp P	C1qbp	O35796	NaN	17.0074	NaN	NaN	17.7722	19.4769	19.2312	19.5299
693	Complement component C1q receptor OS=Rattus norvegicus OX=10116 GN=Cd93 PE=1 SV=1	Cd93	Q9ET61	16.1072	15.9283	16.5832	16.9687	17.6828	19.1013	17.4398	17.4919
694	Complement component C6 OS=Rattus norvegicus OX=10116 GN=C6 PE=2 SV=1	C6	Q811M5	19.4669	19.8373	19.8425	18.6404	18.1506	17.6761	17.9179	18.5523
695	Complement component C8 beta chain OS=Rattus norvegicus OX=10116 GN=C8b PE=2 SV=2	C8b	P55314	21.3772	21.2889	21.9005	21.4833	18.9478	19.6017	18.8885	19.2731
696	Complement component C9 OS=Rattus norvegicus OX=10116 GN=C9 PE=1 SV=1	C9	F7F389	22.12	22.9087	22.0344	21.5369	19.823	18.9176	18.1947	19.1655
697	Complement component receptor 1-like protein OS=Rattus norvegicus OX=10116 GN=Cr1l PE=1 SV=1	Cd46	A0A0G2K7Y0	19.4787	19.3384	19.4121	19.8167	20.9212	20.9898	20.5452	20.764
698	Complement factor B OS=Rattus norvegicus OX=10116 GN=Cfb PE=1 SV=1	Cfb	G3V615	21.0478	21.2004	20.6871	20.9356	17.74	NaN	NaN	16.038
699	Complement factor B OS=Rattus norvegicus OX=10116 GN=Cfb PE=1 SV=1	Cfb	Q7TP05	24.2379	24.3751	24.4514	24.2139	21.0564	20.4727	20.3394	20.5499
700	Complement factor D OS=Rattus norvegicus OX=10116 GN=Cfd PE=1 SV=1	Cfd	G3V7H3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
701	Complement factor H OS=Rattus norvegicus OX=10116 GN=Cfh PE=1 SV=1	Cfh	G3V9R2	24.4832	24.4523	24.7386	24.4454	20.6615	20.4686	20.3777	20.5493
702	Complement factor H-related protein B OS=Rattus norvegicus OX=10116 GN=LOC100361907 PE=1 SV=1	LOC100361907	A0A0G2JYC4	19.1923	17.7294	18.9094	19.1266	17.2541	18.6859	18.0957	17.0229
703	Complement factor I OS=Rattus norvegicus OX=10116 GN=Cfi PE=1 SV=1	Cfi	A0A0G2K135	23.1764	23.451	23.6442	22.9398	18.7416	18.9277	18.325	19.3845
704	Complement factor properdin OS=Rattus norvegicus OX=10116 GN=Cfp PE=1 SV=1	Cfp	B0BNN4	20.261	20.7877	20.8624	20.3403	18.1479	19.2024	18.9486	18.3128
705	Component of oligomeric golgi complex 4 OS=Rattus norvegicus OX=10116 GN=Cog4 PE=1 SV=1	Cog4	D3ZZM3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
706	Condensin complex subunit 2 OS=Rattus norvegicus OX=10116 GN=Ncaph PE=1 SV=3	Ncaph	D4A8M7	19.0014	18.0452	18.7301	17.4471	21.9709	21.3811	21.9284	21.8863
707	Connective tissue growth factor OS=Rattus norvegicus OX=10116 GN=Ctgf PE=2 SV=1	Ccn2	Q9R1E9	15.0122	NaN	15.7677	NaN	NaN	NaN	NaN	NaN
708	Conserved oligomeric Golgi complex subunit 7 OS=Rattus norvegicus OX=10116 GN=Cog7 PE=2 SV=1	Cog7	Q3T1G7	NaN	NaN	NaN	NaN	NaN	16.186	16.663	15.7558
709	COP9 (Constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana) (Predicted), isoform CRA_a OS=Rattus n	Cops6	D3ZI16	16.4389	16.1567	15.8563	15.8596	20.764	20.4084	20.2922	20.6891
710	COP9 (Constitutive photomorphogenic) homolog, subunit 7b (Arabidopsis thaliana) (Predicted), isoform CRA_b OS=Rattus	Cops7b	D3ZU52	NaN	15.6569	NaN	NaN	19.0281	18.3633	19.0777	18.7067
711	COP9 signalosome complex subunit 1 OS=Rattus norvegicus OX=10116 GN=Gps1 PE=1 SV=1	Gps1	A0A0G2JT06	24.2774	25.6268	24.0134	25.2142	23.936	24.2797	23.6019	23.4582
712	COP9 signalosome complex subunit 2 OS=Rattus norvegicus OX=10116 GN=Cops2 PE=1 SV=1	Cops2	P61203	17.4302	17.3246	17.1423	NaN	21.4063	21.0807	21.3058	21.3883
713	COP9 signalosome complex subunit 3 OS=Rattus norvegicus OX=10116 GN=Cops3 PE=1 SV=1	Cops3	Q68FW9	18.3359	18.4748	17.8793	17.7289	21.9897	21.3991	21.688	21.4911
714	COP9 signalosome complex subunit 4 OS=Rattus norvegicus OX=10116 GN=Cops4 PE=1 SV=1	Cops4	Q68FS2	19.7852	21.3007	20.3553	18.2774	22.6599	21.9894	22.2916	22.3246
715	COP9 signalosome complex subunit 8 OS=Rattus norvegicus OX=10116 GN=Cops8 PE=2 SV=1	Cops8	Q6P4Z9	15.9493	15.1006	15.6345	NaN	21.3684	20.6098	20.4677	20.2266
716	COP9 signalosome subunit 5 OS=Rattus norvegicus OX=10116 GN=Cops5 PE=1 SV=1	Cops5	F7EUU4	15.398	18.4424	14.633	16.7187	20.3958	19.0494	19.4415	19.1478
717	COP9 signalosome subunit 7A OS=Rattus norvegicus OX=10116 GN=Cops7a PE=1 SV=1	Cops7a	F1MAA2	18.2917	18.1177	17.9023	18.7888	20.7867	19.5323	19.6317	19.8831
718	Copine 3 OS=Rattus norvegicus OX=10116 GN=Cpne3 PE=1 SV=1	Cpne3	D3ZLA3	16.9301	16.4045	16.1754	NaN	NaN	17.4662	17.0422	NaN
719	Copine-7 OS=Rattus norvegicus OX=10116 GN=Cpne7 PE=1 SV=1	Cpne7	H1UBN0	17.2519	16.6862	17.7089	17.6184	NaN	NaN	NaN	15.0233
720	Copper chaperone for superoxide dismutase OS=Rattus norvegicus OX=10116 GN=Ccs PE=1 SV=1	Ccs	A0A0G2JSZ9	18.7052	16.9765	18.3318	18.5426	21.0114	20.4949	20.7413	20.9126
721	Copper transport protein ATOX1 OS=Rattus norvegicus OX=10116 GN=Atox1 PE=1 SV=1	Atox1	Q9WUC4	15.3374	16.5293	17.0602	NaN	18.1223	18.8092	18.9397	20.5885
722	Cordon-bleu WH2 repeat protein-like 1 OS=Rattus norvegicus OX=10116 GN=Cobll1 PE=1 SV=2	Cobll1	F1M124	NaN	NaN	NaN	NaN	18.6608	19.2685	19.0358	18.4606
723	Cornichon family AMPA receptor auxiliary protein 4 OS=Rattus norvegicus OX=10116 GN=Cnih4 PE=1 SV=1	Cnih4	D3ZTY0	NaN	NaN	NaN	NaN	17.4433	18.1192	17.1186	17.668
724	Cornifin-A OS=Rattus norvegicus OX=10116 GN=Sprr1a PE=4 SV=1	Sprr1a	G3V755	NaN	17.9991	NaN	17.0674	20.0487	19.8242	NaN	19.1329
725	Coronin OS=Rattus norvegicus OX=10116 GN=Coro7 PE=1 SV=1	Coro7	A0A0G2K9F9	NaN	NaN	19.349	18.2392	18.8669	18.4958	19.1918	18.8664
726	Coronin-1A OS=Rattus norvegicus OX=10116 GN=Coro1a PE=1 SV=3	Coro1a	Q91ZN1	15.7838	17.5915	16.4648	NaN	NaN	NaN	NaN	NaN
727	Cortactin, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Cttn PE=1 SV=3	Cttn	D3ZGE6	18.9487	17.0353	18.2915	17.0762	22.0244	22.1155	22.166	22.1156
728	Corticosteroid-binding globulin OS=Rattus norvegicus OX=10116 GN=Serpina6 PE=1 SV=2	Serpina6	P31211	22.8137	21.9448	22.7188	22.7547	18.4597	17.1902	18.2423	17.0096
729	Coxsackievirus and adenovirus receptor homolog OS=Rattus norvegicus OX=10116 GN=Cxadr PE=1 SV=2	Cxadr	Q9R066	NaN	15.2455	NaN	NaN	20.9054	20.2153	20.4107	20.4698
730	C-reactive protein OS=Rattus norvegicus OX=10116 GN=Crp PE=1 SV=1	Crp	P48199	20.3117	21.033	21.216	20.7873	16.5045	19.3741	19.0731	18.7724
731	Creatine kinase B-type OS=Rattus norvegicus OX=10116 GN=Ckb PE=1 SV=2	Ckb	P07335	19.4565	19.8214	20.0603	19.6792	22.9302	22.7381	23.6837	23.3611
732	Creatine kinase M-type OS=Rattus norvegicus OX=10116 GN=Ckm PE=1 SV=1	Ckm	A0A0G2JSP8	24.5226	24.5938	24.8458	23.922	25.0061	27.9216	28.4719	28.2076
733	Creatine kinase S-type, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ckmt2 PE=1 SV=1	Ckmt2	A0A0G2JVQ1	NaN	17.0359	NaN	17.1836	NaN	NaN	NaN	NaN
734	Creatine kinase S-type, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ckmt2 PE=1 SV=2	Ckmt2	P09605	NaN	16.5894	15.9126	16.2913	15.4424	NaN	NaN	NaN
735	CREB-binding protein OS=Rattus norvegicus OX=10116 GN=Crebbp PE=1 SV=1	Crebbp	F1M9G7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
736	CREB-regulated transcription coactivator 2 OS=Rattus norvegicus OX=10116 GN=Crtc2 PE=1 SV=1	Crtc2	Q3LRZ1	19.271	18.5675	19.0418	19.038	19.045	17.8583	17.9487	18.781
737	CREB-regulated transcription coactivator 3 OS=Rattus norvegicus OX=10116 GN=Crtc3 PE=1 SV=2	Crtc3	F1LVL6	19.1949	19.1081	19.376	20.1384	19.7156	18.7446	18.9903	19.3344
738	Crk-like protein OS=Rattus norvegicus OX=10116 GN=Crkl PE=1 SV=1	Crkl	Q5U2U2	NaN	NaN	NaN	NaN	19.2305	18.8542	17.6185	17.9173
739	Crystallin beta-gamma domain-containing 3 OS=Rattus norvegicus OX=10116 GN=Crybg3 PE=1 SV=2	Crybg3	F1M8T4	15.488	16.7597	17.2381	NaN	17.9564	19.0488	18.9353	19.4191
740	C-terminal-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ctbp1 PE=1 SV=3	Ctbp1	Q9Z2F5	18.7031	16.8488	18.0925	17.2256	21.6165	21.044	21.4037	21.342

741	C-terminal-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Ctbp2 PE=1 SV=2	Ctbp2	Q9EQH5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
742	CTP synthase OS=Rattus norvegicus OX=10116 GN=Ctps1 PE=1 SV=1	Ctps1	B1WC02	19.7054	18.9396	18.2197	15.5282	22.397	21.9254	22.7707	22.9616
743	C-type lectin domain family 10 member A OS=Rattus norvegicus OX=10116 GN=Clec10a PE=1 SV=1	Clec10a	P49301	16.739	16.0168	16.2162	16.3325	NaN	16.6729	NaN	16.6708
744	C-type lectin domain family 11 member A OS=Rattus norvegicus OX=10116 GN=Clec11a PE=2 SV=1	Clec11a	O88201	21.4256	21.0323	21.6807	21.471	18.6958	16.4783	15.4597	16.6025
745	C-type lectin domain family 3, member B OS=Rattus norvegicus OX=10116 GN=Clec3b PE=1 SV=1	Clec3b	D3ZUU6	18.3515	19.8146	19.1704	19.4827	16.5183	17.3718	16.9576	17.6792
746	C-type mannose receptor 2 OS=Rattus norvegicus OX=10116 GN=Mrc2 PE=1 SV=2	Mrc2	F1LMA7	17.9165	18.2211	18.2216	16.4642	17.9209	18.575	17.5443	17.8109
747	CUGBP Elav-like family member 1 OS=Rattus norvegicus OX=10116 GN=Celf1 PE=2 SV=1	Celf1	Q4QQT3	NaN	14.8731	NaN	NaN	21.1667	19.9706	20.1203	20.2314
748	CUGBP Elav-like family member 2 OS=Rattus norvegicus OX=10116 GN=Celf2 PE=1 SV=2	Celf2	Z4YNP1	14.9275	NaN	15.2582	NaN	17.5721	18.4066	16.964	17.5575
749	Cullin 2 OS=Rattus norvegicus OX=10116 GN=Cul2 PE=1 SV=1	Cul2	A0A0G2K761	16.9046	16.0075	13.3649	14.0285	19.831	19.4768	19.5229	19.7279
750	Cullin 4A OS=Rattus norvegicus OX=10116 GN=Cul4a PE=1 SV=1	Cul4a	B2RYJ3	20.2781	19.8384	20.192	20.2626	19.6183	19.3834	19.6555	19.6497
751	Cullin 4B OS=Rattus norvegicus OX=10116 GN=Cul4b PE=1 SV=1	Cul4b	D3ZK73	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
752	Cullin-3 OS=Rattus norvegicus OX=10116 GN=Cul3 PE=1 SV=2	Cul3	B5DF89	NaN	16.3695	14.1554	NaN	20.3889	21.0022	21.1546	20.962
753	Cullin-5 OS=Rattus norvegicus OX=10116 GN=Cul5 PE=1 SV=1	Cul5	A0A0H2UHG3	21.1169	19.8634	18.6867	NaN	21.3956	20.1228	21.0331	20.4691
754	Cullin-7 OS=Rattus norvegicus OX=10116 GN=Cul7 PE=1 SV=1	Cul7	A0A0H2UHP4	NaN	NaN	NaN	NaN	16.2679	15.6367	16.3764	18.6907
755	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus OX=10116 GN=Cand1 PE=1 SV=1	Cand1	P97536	18.5442	19.4789	19.3775	19.3551	23.5006	23.3571	23.888	23.414
756	Cullin-associated NEDD8-dissociated protein 2 OS=Rattus norvegicus OX=10116 GN=Cand2 PE=4 SV=1	Cand2	A0A0G2K139	18.5355	18.38	17.8003	17.5369	22.4033	24.1607	24.4887	23.9098
757	Cyclin-dependent kinase 1 OS=Rattus norvegicus OX=10116 GN=Cdk1 PE=1 SV=1	Cdk1	P39951	19.2548	21.3768	18.2891	20.8891	22.8408	22.3638	22.79	22.8116
758	Cyclin-dependent kinase 16 OS=Rattus norvegicus OX=10116 GN=Cdk16 PE=1 SV=1	Cdk16	Q68G39	NaN	NaN	NaN	NaN	18.6825	18.7308	18.6271	18.3062
759	Cyclin-dependent kinase 2 OS=Rattus norvegicus OX=10116 GN=Cdk2 PE=1 SV=1	Cdk2	Q6P751	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
760	Cyclin-dependent kinase 4 OS=Rattus norvegicus OX=10116 GN=Cdk4 PE=1 SV=1	Cdk4	P35426	NaN	NaN	NaN	NaN	19.5901	19.0351	19.2278	18.5248
761	Cyclin-dependent-like kinase 5 OS=Rattus norvegicus OX=10116 GN=Cdk5 PE=1 SV=1	Cdk5	Q03114	15.8922	16.6611	15.6799	NaN	17.8036	17.3548	17.7721	17.3789
762	Cyclin-G-associated kinase OS=Rattus norvegicus OX=10116 GN=Gak PE=1 SV=1	Gak	F1LMD9	NaN	NaN	NaN	NaN	20.4504	17.5326	16.6399	17.788
763	Cystatin-B OS=Rattus norvegicus OX=10116 GN=Cstb PE=1 SV=1	Cstb	P01041	NaN	NaN	NaN	15.6641	21.2387	21.0246	21.0959	21.0532
764	Cystatin-C OS=Rattus norvegicus OX=10116 GN=Cst3 PE=1 SV=2	Cst3	P14841	21.1807	20.3104	21.0851	19.9347	18.7677	20.6496	20.3404	20.3912
765	Cysteine and glycine-rich protein 1 OS=Rattus norvegicus OX=10116 GN=Csrp1 PE=1 SV=2	Csrp1	P47875	17.285	16.2494	17.4068	16.9682	20.6403	20.8747	20.8098	20.3703
766	Cysteine and glycine-rich protein 3 OS=Rattus norvegicus OX=10116 GN=Csrp3 PE=1 SV=1	Csrp3	G3V7U0	20.5041	19.8495	20.2804	20.1255	25.1552	25.3489	25.2616	24.5316
767	Cysteine and histidine-rich domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Chordc1 PE=3 SV=1	Chordc1	D4A4T9	16.4548	17.9657	16.6467	18.3871	20.4156	19.2652	20.383	20.2737
768	Cysteine-rich protein 1 OS=Rattus norvegicus OX=10116 GN=Crip1 PE=1 SV=2	Crip1	P63255	19.2806	19.6775	19.1545	15.583	19.3882	21.2658	20.8967	20.6297
769	Cysteine-rich protein 2 OS=Rattus norvegicus OX=10116 GN=Crip2 PE=2 SV=1	Crip2	P36201	22.2938	22.6306	21.9515	22.0787	26.0718	25.4865	25.9302	25.5513
770	Cysteine-rich with EGF-like domain protein 1 OS=Rattus norvegicus OX=10116 GN=Creld1 PE=2 SV=1	Creld1	Q4V7F2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
771	Cytochrome b5 OS=Rattus norvegicus OX=10116 GN=Cyb5a PE=1 SV=2	Cyb5a	P00173	15.7583	NaN	NaN	NaN	NaN	17.7517	17.5605	17.9922
772	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Uqcrc1 PE=1 SV=1	Uqcrc1	Q68FY0	18.9554	19.8207	18.3328	18.6724	21.4951	23.1496	22.7965	23.0128
773	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Uqcrc2 PE=1 SV=2	Uqcrc2	P32551	21.3821	21.9246	22.4447	21.6014	22.3228	23.676	23.4553	23.4611
774	Cytochrome b-c1 complex subunit 6, mitochondrial OS=Rattus norvegicus OX=10116 GN=Uqcrh PE=3 SV=1	Uqcrh	Q5M9I5	16.6143	NaN	NaN	NaN	NaN	20.1164	19.9539	20.4449
775	Cytochrome b-c1 complex subunit 7 OS=Rattus norvegicus OX=10116 GN=Uqcrb PE=1 SV=1	Uqcrb	B2RYS2	19.2765	19.2856	17.7605	16.7821	21.0168	22.5011	22.1996	22.2633
776	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Rattus norvegicus OX=10116 GN=Uqcrfs1 PE=1 SV=2	Uqcrfs1	P20788	18.6956	19.4115	18.3437	17.8562	20.4329	21.923	21.5111	21.9115
777	Cytochrome c heme lyase OS=Rattus norvegicus OX=10116 GN=Hccs PE=1 SV=1	Hccs	D3ZL85	NaN	NaN	NaN	NaN	17.5553	18.4742	17.1725	18.2113
778	Cytochrome c oxidase assembly factor COX20 OS=Rattus norvegicus OX=10116 GN=Cox20 PE=1 SV=1	Cox20	D3ZYU4	17.0667	15.5731	NaN	NaN	NaN	17.2011	16.6305	17.1212
779	Cytochrome c oxidase subunit 2 OS=Rattus norvegicus OX=10116 GN=Mtco2 PE=1 SV=3	mt-Co2	P00406	19.4747	19.9141	17.9984	18.6312	21.6606	22.9116	22.5908	22.9972
780	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox4i1 PE=1 SV=1	Cox4i1	P10888	19.9735	20.4596	18.9382	18.5412	22.3051	23.7474	23.3211	23.5098
781	Cytochrome c oxidase subunit 5A, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox5a PE=1 SV=1	Cox5a	P11240	18.9914	18.7973	16.8299	17.4571	21.5118	22.9953	22.5524	22.7532
782	Cytochrome c oxidase subunit 5B, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox5b PE=1 SV=2	Cox5b	P12075	15.8844	15.1022	NaN	NaN	19.1494	21.334	21.0013	21.5061
783	Cytochrome c oxidase subunit 6C-2 OS=Rattus norvegicus OX=10116 GN=Cox6c2 PE=1 SV=3	Cox6c	P11951	16.6146	18.2527	NaN	15.2147	20.6967	22.2734	21.7867	22.1377
784	Cytochrome c oxidase subunit 7A2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox7a2 PE=1 SV=1	Cox7a2	P35171	16.207	16.2131	15.9259	NaN	19.6617	21.7486	21.2299	21.2096
785	Cytochrome c oxidase subunit 7A2-like OS=Rattus norvegicus OX=10116 GN=Cox7a2l PE=1 SV=1	Cox7a2l	D3ZYX8	16.7072	16.7663	NaN	NaN	15.2889	17.1485	16.82	16.9241
786	Cytochrome c oxidase subunit 7B, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox7b PE=1 SV=3	Cox7b	P80431	15.7271	16.1786	NaN	NaN	17.7174	19.7123	19.1623	19.3541
787	Cytochrome c oxidase subunit 7C, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox7c PE=1 SV=2	Cox7c	P80432	17.557	18.3843	16.5354	16.955	19.7868	21.3638	20.7632	21.1858
788	Cytochrome c oxidase subunit OS=Rattus norvegicus OX=10116 GN=Cox6b1 PE=1 SV=1	Cox6b1	D3ZD09	NaN	17.1086	NaN	NaN	21.1281	21.5312	21.5184	21.5628
789	Cytochrome c-1 OS=Rattus norvegicus OX=10116 GN=Cyc1 PE=1 SV=3	Cyc1	D3ZFQ8	17.6592	17.7038	NaN	17.4771	19.7111	21.0156	21.0276	20.9973
790	Cytoglobin OS=Rattus norvegicus OX=10116 GN=Cygb PE=1 SV=1	Cygb	Q921A4	NaN	14.7051	NaN	NaN	18.7095	18.4713	18.5594	18.7447
791	Cytohesin-2 OS=Rattus norvegicus OX=10116 GN=Cyth2 PE=4 SV=1	Cyth2	F1LSU6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
792	Cytoplasmic aconitate hydratase OS=Rattus norvegicus OX=10116 GN=Aco1 PE=1 SV=1	Aco1	G3V6S2	17.9131	16.7224	17.0029	17.8211	20.2694	20.8567	21.429	21.4389
793	Cytoplasmic dynein 1 heavy chain 1 OS=Rattus norvegicus OX=10116 GN=Dync1h1 PE=1 SV=2	Dync1h1	M0R9X8	24.8613	24.5272	24.3266	23.8789	27.4083	27.4937	27.7022	27.4741

794	Cytoplasmic dynein 1 intermediate chain 2 OS=Rattus norvegicus OX=10116 GN=Dync1i2 PE=1 SV=1	Dync1i2	Q6AZ35	22.2414	21.9181	23.5369	22.4566	23.2499	23.1872	23.8325	24.1532
795	Cytoplasmic dynein 1 light intermediate chain 1 OS=Rattus norvegicus OX=10116 GN=Dync1li1 PE=1 SV=1	Dync1li1	G3V7G0	17.8029	18.1454	18.4285	19.924	22.7198	23.1948	23.3696	23.0924
796	Cytoplasmic dynein 1 light intermediate chain 2 OS=Rattus norvegicus OX=10116 GN=Dync1li2 PE=1 SV=1	Dync1li2	Q5D023	14.8901	NaN	14.2099	15.6517	22.7055	22.6918	23.0273	22.6349
797	Cytoplasmic FMR1-interacting protein OS=Rattus norvegicus OX=10116 GN=Cyfip1 PE=1 SV=1	Cyfip1	D4A8H8	16.9078	17.1766	16.0084	18.0655	21.4508	20.9898	21.2153	21.2048
798	Cytoplasmic linker-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Clasp1 PE=1 SV=3	Clasp1	F1LNR0	19.9604	20.1538	20.2619	19.3263	21.7118	22.2215	21.7646	21.2934
799	Cytoplasmic polyadenylation element binding protein 4 (Predicted) OS=Rattus norvegicus OX=10116 GN=Cpeb4 PE=1 SV=1	Cpeb4	D3ZKL3	NaN	NaN	NaN	NaN	16.9325	NaN	16.4922	NaN
800	Cytoplasmic tRNA 2-thiolation protein 2 OS=Rattus norvegicus OX=10116 GN=Ctu2 PE=1 SV=1	Ctu2	A0A0G2JUT8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
801	Cytoskeleton-associated protein 4 OS=Rattus norvegicus OX=10116 GN=Ckap4 PE=1 SV=2	Ckap4	D3ZH41	19.6547	20.1934	19.9489	19.5971	23.3862	23.6396	23.2461	23.6764
802	Cytoskeleton-associated protein 5 OS=Rattus norvegicus OX=10116 GN=Ckap5 PE=1 SV=3	Ckap5	F1M949	19.4319	21.6503	18.7707	20.6852	23.1502	23.8688	23.1804	23.0286
803	Cytosol aminopeptidase OS=Rattus norvegicus OX=10116 GN=Lap3 PE=1 SV=1	Lap3	Q68FS4	16.4497	18.0515	16.3905	16.1771	19.6324	19.9824	20.2667	19.5755
804	Cytosolic acyl coenzyme A thioester hydrolase OS=Rattus norvegicus OX=10116 GN=Acot7 PE=1 SV=4	Acot7	Q64559	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
805	Cytosolic Fe-S cluster assembly factor NUBP1 OS=Rattus norvegicus OX=10116 GN=Nubp1 PE=1 SV=1	Nubp1	Q5I0L4	NaN	NaN	NaN	15.8774	21.5833	20.8998	21.1427	21.1924
806	Cytosolic Fe-S cluster assembly factor NUBP2 OS=Rattus norvegicus OX=10116 GN=Nubp2 PE=1 SV=1	Nubp2	Q68FS1	20.6775	21.1451	20.6925	19.6726	22.0063	21.265	21.2224	21.108
807	Cytosolic iron-sulfur assembly component 2B OS=Rattus norvegicus OX=10116 GN=Ciao2b PE=1 SV=1	Ciao2b	D3Z8Q7	15.8958	15.9844	15.3859	16.2533	NaN	18.5456	19.3918	19.4861
808	Cytosolic iron-sulfur assembly component 3 OS=Rattus norvegicus OX=10116 GN=Ciao3 PE=2 SV=1	Ciao3	Q5BK18	NaN	14.1343	NaN	14.5996	18.7591	18.4198	18.7265	18.5106
809	Cytosolic non-specific dipeptidase OS=Rattus norvegicus OX=10116 GN=Cndp2 PE=1 SV=1	Cndp2	Q6Q0N1	18.6489	20.7581	19.7403	19.5403	18.6929	20.9029	21.1968	20.8982
810	D-3-phosphoglycerate dehydrogenase OS=Rattus norvegicus OX=10116 GN=Phgdh PE=1 SV=3	Phgdh	O08651	21.3332	21.3485	21.5405	21.6519	23.0269	22.9806	23.3592	23.4618
811	DAZ associated protein 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Dazap1 PE=1 SV=1	Dazap1	Q4KLZ3	NaN	NaN	NaN	NaN	18.6712	17.6845	17.3973	17.4453
812	DCN1-like protein OS=Rattus norvegicus OX=10116 GN=Dcun1d1 PE=1 SV=1	Dcun1d1	A0A0G2K8D6	NaN	NaN	NaN	NaN	16.7582	NaN	15.5555	NaN
813	DDB1- and CUL4-associated factor 11 OS=Rattus norvegicus OX=10116 GN=Dcaf11 PE=1 SV=1	Dcaf11	Q5M9G8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
814	DDB1 and CUL4-associated factor 7 OS=Rattus norvegicus OX=10116 GN=Dcaf7 PE=1 SV=1	Dcaf7	B2RZ68	14.935	NaN	NaN	NaN	18.6311	19.2645	18.3482	18.4244
815	DDB1- and CUL4-associated factor 8 OS=Rattus norvegicus OX=10116 GN=Dcaf8 PE=1 SV=1	Dcaf8	Q5U2M6	NaN	15.7357	NaN	19.5836	19.1444	17.5862	19.2105	19.0489
816	D-dopachrome decarboxylase OS=Rattus norvegicus OX=10116 GN=Ddt PE=1 SV=3	Ddt	P80254	16.8815	16.6625	15.705	16.4186	18.8468	17.8275	18.3738	19.0341
817	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ddx17 PE=1 SV=1	Ddx17	A0A096MIX2	17.6299	17.052	NaN	18.3638	19.3961	17.7852	16.8385	17.6686
818	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a OS=Rattus norvegicus OX=10116 GN=Ddx19a PE=1 SV=1	Ddx19a	Q68FX3	19.0152	18.8174	19.2543	18.5441	23.7136	23.0157	23.6312	23.6304
819	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 OS=Rattus norvegicus OX=10116 GN=Ddx5 PE=1 SV=1	Ddx5	Q6AYI1	18.5765	17.9702	18.519	NaN	22.8295	22.2074	22.2845	22.0265
820	Dead end homolog 1 (Zebrafish) OS=Rattus norvegicus OX=10116 GN=Hars PE=1 SV=1	Hars1	Q4QQV4	17.4772	17.6348	17.5631	17.4394	20.0224	19.0868	19.2692	19.584
821	DEAD-box helicase 19A OS=Rattus norvegicus OX=10116 GN=Ddx19a PE=1 SV=1	Ddx19a	A0A0G2JUH2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
822	DEAD-box helicase 3, X-linked OS=Rattus norvegicus OX=10116 GN=Ddx3x PE=1 SV=1	Ddx3x	A0A0G2K719	20.5746	20.0252	20.2767	20.7584	24.0707	23.7277	23.6751	23.6452
823	DEAD-box helicase 6 OS=Rattus norvegicus OX=10116 GN=Ddx6 PE=1 SV=1	Ddx6	D3ZD73	14.8622	NaN	NaN	NaN	20.8185	20.6823	20.6841	20.3985
824	DEAH (Asp-Glu-Ala-His) box polypeptide 15 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Dhx15 PE=	Dhx15	D3ZD97	NaN	NaN	NaN	NaN	18.1444	18.7438	17.4901	NaN
825	Death domain-containing membrane protein NRADD OS=Rattus norvegicus OX=10116 GN=Nradd PE=1 SV=2	Nradd	Q8K5A9	NaN	NaN	15.2402	NaN	19.3693	18.7677	19.4457	19.2406
826	Decapping mRNA 1A OS=Rattus norvegicus OX=10116 GN=Dcp1a PE=1 SV=1	Dcp1a	D4AE80	NaN	17.3918	15.0013	15.8241	18.4154	18.9425	18.0905	18.1276
827	Dedicator of cytokinesis 6 OS=Rattus norvegicus OX=10116 GN=Dock6 PE=1 SV=1	Dock6	A0A0G2KAH4	NaN	16.3183	15.9679	NaN	17.0738	NaN	NaN	17.1898
828	Dedicator of cytokinesis 7 OS=Rattus norvegicus OX=10116 GN=Dock7 PE=1 SV=1	Dock7	A0A0G2K3H2	17.4477	17.56	17.2965	18.3846	20.0109	21.2353	20.8798	20.8046
829	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ech1 PE=1 SV=2	Ech1	Q62651	17.0201	16.4223	17.6024	17.2993	16.2209	19.9404	18.0672	17.767
830	Delta-aminolevulinic acid dehydratase OS=Rattus norvegicus OX=10116 GN=Alad PE=1 SV=1	Alad	P06214	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
831	Deltex E3 ubiquitin ligase 3 OS=Rattus norvegicus OX=10116 GN=Dtx3 PE=4 SV=2	Dtx3	F1LY78	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
832	Deltex E3 ubiquitin ligase 4 OS=Rattus norvegicus OX=10116 GN=Dtx4 PE=4 SV=1	Dtx4	A0A0G2K048	NaN	15.9822	NaN	NaN	NaN	17.8464	18.3224	18.5349
833	DENN domain-containing 4C OS=Rattus norvegicus OX=10116 GN=Dennd4c PE=1 SV=1	Dennd4c	A0A0G2K089	17.7895	NaN	14.8028	NaN	19.9312	19.0321	18.9087	18.33
834	DENN domain-containing protein 5A OS=Rattus norvegicus OX=10116 GN=Dennd5a PE=2 SV=1	Dennd5a	G3V7Q0	NaN	15.9173	NaN	NaN	17.2471	17.1914	17.2929	16.9468
835	Deoxyhypusine hydroxylase OS=Rattus norvegicus OX=10116 GN=Dohh PE=2 SV=1	Dohh	Q5PPJ4	NaN	NaN	NaN	NaN	17.5021	NaN	17.8572	18.0695
836	Deoxyribose-phosphate aldolase OS=Rattus norvegicus OX=10116 GN=Dera PE=1 SV=3	Dera	F1M1H0	NaN	NaN	14.9781	NaN	18.8449	19.2608	20.1766	20.1884
837	Deoxythymidylate kinase OS=Rattus norvegicus OX=10116 GN=Dtymk PE=1 SV=1	Dtymk	D3ZUJ5	17.2695	17.6052	17.1818	17.5394	19.0466	18.4425	18.6418	17.5515
838	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Rattus norvegicus OX=10116 GN=Dut PE=2 SV=3	Dut	P70583	NaN	NaN	NaN	NaN	16.57	16.9335	16.4742	16.1835
839	Dermokine OS=Rattus norvegicus OX=10116 GN=Dmkn PE=4 SV=1	Dmkn	A0A0G2K3X0	15.3128	NaN	NaN	15.839	NaN	17.4872	16.5847	NaN
840	Desmin OS=Rattus norvegicus OX=10116 GN=Des PE=1 SV=1	Des	Q6P725	17.3611	17.8031	18.0728	16.6891	21.4388	21.6567	21.484	21.8834
841	Desmocollin 1 OS=Rattus norvegicus OX=10116 GN=Dsc1 PE=4 SV=1	Dsc1	A0A0G2KA90	18.516	20.8328	18.1689	18.1837	17.9248	18.5202	17.704	16.5551
842	Desmoglein 1 OS=Rattus norvegicus OX=10116 GN=Dsg1 PE=4 SV=1	Dsg1	D3ZM39	20.2493	21.6618	19.3181	20.9705	19.6164	20.1468	18.7414	18.1282
843	Desmoplakin OS=Rattus norvegicus OX=10116 GN=Dsp PE=1 SV=1	Dsp	F1LMV6	22.8625	24.1065	22.5237	24.1577	23.0896	23.7771	22.7915	22.681
844	Destrin OS=Rattus norvegicus OX=10116 GN=Dstn PE=1 SV=3	Dstn	Q7M0E3	19.6938	20.118	20.3103	19.2627	23.8176	23.0834	23.6761	23.5205
845	Deubiquitinating protein VCIP135 OS=Rattus norvegicus OX=10116 GN=Vcpip1 PE=1 SV=2	Vcpip1	Q8CF97	16.7383	17.2881	17.2478	16.4401	20.589	20.0752	19.7227	16.7846
846	Developmentally-regulated GTP-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Drg1 PE=1 SV=1	Drg1	Q5I0F0	15.9211	NaN	16.5768	14.7342	20.6673	20.1931	20.4746	20.4233

847	Developmentally-regulated GTP-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Drg2 PE=1 SV=1	Drg2	A0A0G2KAI8	21.6934	21.1117	18.5824	18.7718	21.7051	20.366	21.312	20.8023
848	Diacylglycerol kinase zeta OS=Rattus norvegicus OX=10116 GN=Dgkz PE=1 SV=1	Dgkz	O08560	18.1642	16.1431	NaN	14.4736	20.106	20.0086	20.721	20.704
849	Dickkopf WNT-signaling pathway inhibitor 3 OS=Rattus norvegicus OX=10116 GN=Dkk3 PE=2 SV=1	Dkk3	B1H219	15.946	NaN	16.2565	16.6656	18.2519	NaN	17.5818	17.4546
850	Dihydrofolate reductase OS=Rattus norvegicus OX=10116 GN=Dhfr PE=1 SV=3	Dhfr	Q920D2	18.7703	17.1609	19.0607	18.8645	19.652	17.7544	18.7705	19.4035
851	Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex), isoform CRA_a OS=Rattus norvegicus	Dlst	G3V6P2	14.8533	14.3833	NaN	NaN	18.8786	21.1394	20.5962	21.0544
852	Dihydrolipoyl dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Dld PE=1 SV=1	Dld	Q6P6R2	17.8053	NaN	18.5816	18.4089	16.7543	20.6062	19.6282	20.2951
853	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Rattus norv	Dlat	P08461	17.6077	19.0059	17.2439	17.6696	19.9486	21.5558	21.3244	21.4952
854	Dihydropteridine reductase OS=Rattus norvegicus OX=10116 GN=Qdpr PE=1 SV=1	Qdpr	P11348	NaN	14.8108	NaN	NaN	17.8825	17.3591	17.4759	17.2104
855	Dihydropyrimidinase-related protein 2 OS=Rattus norvegicus OX=10116 GN=Dpysl2 PE=1 SV=1	Dpysl2	P47942	18.3356	19.1969	18.9757	18.8223	24.3047	24.4314	24.151	23.9772
856	Dihydropyrimidinase-related protein 3 OS=Rattus norvegicus OX=10116 GN=Dpysl3 PE=1 SV=2	Dpysl3	Q62952	18.6833	19.363	18.9455	18.4365	24.3245	24.0968	24.0614	23.9913
857	Dipeptidyl peptidase 2 OS=Rattus norvegicus OX=10116 GN=Dpp7 PE=1 SV=1	Dpp7	Q9EPB1	NaN	NaN	NaN	NaN	16.1998	17.3512	NaN	NaN
858	Dipeptidyl peptidase 3 OS=Rattus norvegicus OX=10116 GN=Dpp3 PE=1 SV=2	Dpp3	O55096	NaN	NaN	15.952	NaN	NaN	18.0272	18.5953	16.9183
859	Dipeptidyl peptidase 4 OS=Rattus norvegicus OX=10116 GN=Dpp4 PE=1 SV=1	Dpp4	A0A0G2K238	15.2194	17.0148	16.4091	16.3666	19.4421	19.0747	18.076	18.7695
860	Diphosphoinositol polyphosphate phosphohydrolase 1 OS=Rattus norvegicus OX=10116 GN=Nudt3 PE=1 SV=1	Nudt3	Q566C7	NaN	NaN	NaN	NaN	19.1015	19.1979	19.7229	19.1659
861	Diphosphoinositol polyphosphate phosphohydrolase 2 OS=Rattus norvegicus OX=10116 GN=Nudt4 PE=2 SV=1	Nudt4	Q99MY2	16.6863	NaN	16.5514	17.1437	19.8986	19.3148	19.467	19.5743
862	Diphthine--ammonia ligase OS=Rattus norvegicus OX=10116 GN=Dph6 PE=1 SV=3	Dph6	F1LP07	NaN	NaN	NaN	NaN	16.9312	16.6801	17.3499	16.8373
863	Disabled homolog 2 OS=Rattus norvegicus OX=10116 GN=Dab2 PE=1 SV=1	Dab2	O88797	16.6279	17.3667	16.583	16.3112	20.0828	18.6059	18.9672	19.0884
864	Disabled homolog 2-interacting protein OS=Rattus norvegicus OX=10116 GN=Dab2ip PE=1 SV=1	Dab2ip	A0A0G2JTF2	NaN	NaN	NaN	NaN	15.5336	17.6713	16.2474	NaN
865	Disco-interacting protein 2 homolog B OS=Rattus norvegicus OX=10116 GN=Dip2b PE=1 SV=1	Dip2b	A0A0G2JY22	NaN	NaN	NaN	NaN	19.2377	18.0936	17.7715	NaN
866	Discs, large homolog-associated protein 4 (Drosophila) OS=Rattus norvegicus OX=10116 GN=Dlgap4 PE=1 SV=1	Dlgap4	G3V927	NaN	NaN	NaN	NaN	NaN	NaN	15.735	NaN
867	Dishevelled segment polarity protein 2 OS=Rattus norvegicus OX=10116 GN=Dvl2 PE=1 SV=2	Dvl2	D3ZB71	NaN	17.532	NaN	NaN	19.0497	18.3126	18.579	18.8949
868	Dishevelled segment polarity protein 3 OS=Rattus norvegicus OX=10116 GN=Dvl3 PE=1 SV=2	Dvl3	D4ADV8	16.7609	NaN	NaN	NaN	18.7385	17.6958	18.7792	18.5496
869	Dishevelled-binding antagonist of beta-catenin 3 OS=Rattus norvegicus OX=10116 GN=Dact3 PE=1 SV=1	Dact3	M0R4J7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
870	Disks large homolog 1 OS=Rattus norvegicus OX=10116 GN=Dlg1 PE=1 SV=1	Dlg1	A0A0G2K1M2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
871	Divalent cation tolerant protein CUTA, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Cuta PE=1 SV=1	Cuta	G3V616	NaN	NaN	NaN	NaN	17.4445	16.7975	NaN	NaN
872	DLG-associated protein 5 OS=Rattus norvegicus OX=10116 GN=Dlgap5 PE=2 SV=1	Dlgap5	B1WC75	NaN	NaN	16.8453	NaN	18.2452	19.0779	18.7842	19.0428
873	DNA damage-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ddb1 PE=1 SV=1	Ddb1	G3V8T4	19.931	19.5215	19.2572	19.2599	22.7692	21.833	22.374	22.4399
874	DNA damage-inducible 1 homolog 2 OS=Rattus norvegicus OX=10116 GN=Ddi2 PE=1 SV=1	Ddi2	A0A096MJP9	16.4724	14.5376	15.8032	16.3945	18.8289	18.4911	18.4605	18.1573
875	DNA fragmentation factor subunit alpha OS=Rattus norvegicus OX=10116 GN=Dffa PE=1 SV=1	Dffa	A0A0G2JY18	18.5219	18.3065	NaN	NaN	20.6842	19.7054	19.6028	19.786
876	DNA helicase OS=Rattus norvegicus OX=10116 GN=Mcm2 PE=1 SV=2	Mcm2	D3ZP96	21.6599	21.6761	22.4836	22.2178	21.0079	21.1346	21.8316	21.7415
877	DNA helicase OS=Rattus norvegicus OX=10116 GN=Mcm3 PE=1 SV=3	Mcm3	D3ZFP4	19.4194	18.6585	18.6576	20.0128	22.1729	21.1901	21.727	21.3228
878	DNA helicase OS=Rattus norvegicus OX=10116 GN=Mcm4 PE=1 SV=1	Mcm4	G3V681	16.8679	17.3751	17.1788	16.5752	22.0445	22.3527	22.7701	22.1873
879	DNA helicase OS=Rattus norvegicus OX=10116 GN=Mcm5 PE=1 SV=1	Mcm5	A0A0G2JY07	15.6218	16.7219	16.1753	15.3052	21.6726	21.0594	21.6607	21.4198
880	DNA helicase OS=Rattus norvegicus OX=10116 GN=Mcm6 PE=1 SV=1	Mcm6	A9CMB8	15.0768	16.9592	14.7692	17.7309	21.7304	21.8214	22.6001	22.4193
881	DNA ligase OS=Rattus norvegicus OX=10116 GN=Lig1 PE=1 SV=1	Lig1	Q566D8	NaN	NaN	NaN	NaN	18.0364	16.5942	NaN	NaN
882	DNA mismatch repair protein Mlh1 OS=Rattus norvegicus OX=10116 GN=Mlh1 PE=2 SV=1	Mlh1	P97679	NaN	NaN	NaN	NaN	16.8502	NaN	16.938	16.8045
883	DNA mismatch repair protein OS=Rattus norvegicus OX=10116 GN=Msh2 PE=1 SV=1	Msh2	B1WBQ7	14.5889	NaN	15.7179	NaN	18.259	17.1344	15.9223	17.1651
884	DNA polymerase epsilon subunit 3 OS=Rattus norvegicus OX=10116 GN=Pole3 PE=1 SV=1	Pole3	Q642A5	NaN	NaN	NaN	NaN	17.8187	16.6661	17.1853	16.9944
885	DNA primase large subunit OS=Rattus norvegicus OX=10116 GN=Prim2 PE=2 SV=1	Prim2	O89044	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
886	DNA replication licensing factor MCM7 OS=Rattus norvegicus OX=10116 GN=Mcm7 PE=1 SV=1	Mcm7	Q6AYN8	15.844	15.538	16.1485	15.7106	20.8728	21.204	21.8734	21.9702
887	DNA-directed RNA polymerase II subunit GRINL1A OS=Rattus norvegicus OX=10116 GN=Polr2m PE=2 SV=1	Myzap	H8Y6S5	NaN	15.8966	15.6614	16.0649	20.3944	20.1774	20.2282	19.9304
888	DNA-directed RNA polymerase subunit beta OS=Rattus norvegicus OX=10116 GN=Polr2b PE=1 SV=1	Polr2b	G3V8Y5	NaN	NaN	13.2968	NaN	19.8356	20.1808	19.9535	19.9242
889	DNA-directed RNA polymerase subunit beta OS=Rattus norvegicus OX=10116 GN=Polr3b PE=3 SV=1	Polr3b	D3ZV30	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
890	DnaJ (Hsp40) homolog, subfamily A, member 2 OS=Rattus norvegicus OX=10116 GN=Dnaja2 PE=1 SV=1	Dnaja2	Q5M9H7	19.2542	18.1977	18.9262	18.6646	23.2393	22.6407	23.0097	22.8995
891	DnaJ (Hsp40) homolog, subfamily A, member 4 OS=Rattus norvegicus OX=10116 GN=Dnaja4 PE=1 SV=1	Dnaja4	Q4QR73	15.9072	NaN	16.2604	NaN	21.0595	20.2472	20.472	20.3152
892	DnaJ (Hsp40) homolog, subfamily B, member 1 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Dnajb1 P	Dnajb1	B0K030	16.1104	16.3913	15.6021	17.3961	20.0845	19.1222	19.3289	19.9291
893	DnaJ (Hsp40) homolog, subfamily B, member 4 OS=Rattus norvegicus OX=10116 GN=Dnajb4 PE=1 SV=1	Dnajb4	Q5XIP0	15.4893	NaN	15.7688	14.6212	21.4943	21.5066	21.2312	21.49
894	DnaJ (Hsp40) homolog, subfamily C, member 9 (Predicted) OS=Rattus norvegicus OX=10116 GN=Dnajc9 PE=1 SV=1	Dnajc9	A8QIC3	16.0608	14.2055	NaN	NaN	21.0835	21.2605	21.1872	20.7328
895	DnaJ heat shock protein family (Hsp40) member B2 OS=Rattus norvegicus OX=10116 GN=Dnajb2 PE=1 SV=1	Dnajb2	B2RYA8	NaN	NaN	NaN	NaN	NaN	NaN	16.9803	17.6451
896	DnaJ heat shock protein family (Hsp40) member B5 OS=Rattus norvegicus OX=10116 GN=Dnajb5 PE=4 SV=1	Dnajb5	A0A0G2K9H9	NaN	14.9004	NaN	NaN	19.5536	20.097	19.6604	19.683
897	DnaJ heat shock protein family (Hsp40) member C13 OS=Rattus norvegicus OX=10116 GN=Dnajc13 PE=1 SV=2	Dnajc13	D3ZN27	18.3511	19.0024	18.4877	18.6392	21.5036	21.6943	21.348	21.434
898	DnaJ heat shock protein family (Hsp40) member C7 OS=Rattus norvegicus OX=10116 GN=Dnajc7 PE=1 SV=1	Dnajc7	A0A0G2K435	17.0853	17.499	17.2765	18.3686	21.6155	21.0267	21.7082	21.7506
899	DnaJ homolog subfamily A member 1 OS=Rattus norvegicus OX=10116 GN=Dnaja1 PE=1 SV=1	Dnaja1	P63036	NaN	15.6815	NaN	NaN	20.0996	19.5477	19.1267	18.1559

900	DnaJ homolog subfamily B member 11 OS=Rattus norvegicus OX=10116 GN=Dnajb11 PE=2 SV=1	Dnajb11	Q6TUG0	16.0273	16.4939	16.1348	15.3695	18.9773	18.733	18.9179	18.8622
901	DnaJ homolog subfamily B member 6 OS=Rattus norvegicus OX=10116 GN=Dnajb6 PE=1 SV=1	Dnajb6	Q6AYU3	14.5609	NaN	NaN	NaN	17.177	18.6234	17.6602	16.5897
902	DnaJ homolog subfamily C member 5 OS=Rattus norvegicus OX=10116 GN=Dnajc5 PE=1 SV=1	Dnajc5	P60905	16.0742	16.9339	15.6612	15.6923	18.7671	18.7893	18.6426	19.0258
903	DnaJ homolog subfamily C member 8 OS=Rattus norvegicus OX=10116 GN=Dnajc8 PE=1 SV=1	Dnajc8	A0A0G2K751	16.1856	NaN	16.2376	NaN	17.5805	16.7062	17.738	17.3402
904	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Rattus norvegicus OX=10116 GN=Ddost	Ddost	Q641Y0	16.471	15.6983	16.8446	16.6923	20.1068	18.4364	18.3886	19.8921
905	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Rattus norvegicus OX=10116 GN=Rpn1 PE=1	Rpn1	Q6P7A7	20.1153	19.8913	20.1145	19.8041	22.4702	22.8697	22.3873	22.9437
906	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Rattus norvegicus OX=10116 GN=Rpn2 PE=2	Rpn2	P25235	19.1422	19.1396	19.3584	19.7393	20.6558	21.3529	20.6959	21.2421
907	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Rattus norvegicus OX=10116 GN=Dad1 I	Dad1	P61805	18.9947	19.1532	19.9747	18.8842	19.731	19.7793	19.5009	19.5368
908	Dolichyl-phosphate mannosyltransferase subunit 1, catalytic OS=Rattus norvegicus OX=10116 GN=Dpm1 PE=1 SV=1	Dpm1	D4A8N1	NaN	15.3546	NaN	NaN	17.5768	17.5201	17.0535	17.1153
909	Down syndrome critical region homolog 2 (Human) (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Psms	Psmg1	D4AAH6	NaN	NaN	NaN	NaN	18.3575	17.2013	18.6684	18.1469
910	Drebrin OS=Rattus norvegicus OX=10116 GN=Dbn1 PE=1 SV=3	Dbn1	Q07266	16.869	16.1395	16.1581	16.6003	18.7811	19.1644	19.8571	19.6449
911	Drebrin-like protein OS=Rattus norvegicus OX=10116 GN=Dbnl PE=1 SV=1	Dbnl	Q9JHL4	17.6369	14.9989	17.1199	15.2582	22.8493	23.1358	23.2484	22.7903
912	Dual specificity mitogen-activated protein kinase kinase 1 OS=Rattus norvegicus OX=10116 GN=Map2k1 PE=1 SV=2	Map2k1	Q01986	14.9086	NaN	15.4428	12.6835	22.829	22.5665	22.936	22.8706
913	Dual specificity mitogen-activated protein kinase kinase 2 OS=Rattus norvegicus OX=10116 GN=Map2k2 PE=1 SV=1	Map2k2	P36506	NaN	NaN	15.6792	NaN	20.5341	19.8407	20.1188	18.4528
914	Dual specificity tyrosine-phosphorylation-regulated kinase 1A OS=Rattus norvegicus OX=10116 GN=Dyrk1a PE=1 SV=2	Dyrk1a	Q63470	NaN	NaN	15.8254	NaN	18.5498	18.1292	18.4686	18.0827
915	Dual-specificity phosphatase 27, atypical OS=Rattus norvegicus OX=10116 GN=Dusp27 PE=1 SV=1	Styxl2	D3ZRM0	NaN	NaN	NaN	NaN	17.9909	18.8365	18.776	18.6889
916	Dual-specificity phosphatase 3 OS=Rattus norvegicus OX=10116 GN=Dusp3 PE=1 SV=1	Dusp3	A0A0G2K3I9	NaN	NaN	NaN	15.6102	21.3696	20.4142	20.6707	20.0964
917	Dymeclin OS=Rattus norvegicus OX=10116 GN=Dym PE=2 SV=1	Dym	B4F766	NaN	NaN	NaN	NaN	17.7817	16.8324	17.9795	16.7294
918	Dynactin subunit 1 OS=Rattus norvegicus OX=10116 GN=Dctn1 PE=1 SV=1	LOC500227	A0A0G2K428	19.9877	18.8335	20.0919	19.1694	23.6389	24.424	24.4666	23.9229
919	Dynactin subunit 2 OS=Rattus norvegicus OX=10116 GN=Dctn2 PE=1 SV=1	Dctn2	A0A0G2JUC7	16.3072	17.3041	14.7338	15.2164	23.0976	22.7586	23.3487	22.8849
920	Dynactin subunit 3 OS=Rattus norvegicus OX=10116 GN=Dctn3 PE=1 SV=1	Dctn3	D4A1B8	19.9478	NaN	15.1676	15.4932	21.0823	21.2871	21.3841	21.1655
921	Dynactin subunit 4 OS=Rattus norvegicus OX=10116 GN=Dctn4 PE=1 SV=1	Dctn4	Q9QUR2	14.8768	15.3604	14.8933	14.1493	19.0501	20.0116	20.0273	19.6076
922	Dynactin subunit 5 OS=Rattus norvegicus OX=10116 GN=Dctn5 PE=1 SV=1	Dctn5	G3V8C0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
923	Dynamin-1-like protein OS=Rattus norvegicus OX=10116 GN=Dnm1l PE=1 SV=1	Dnm1l	O35303	20.2183	19.6189	20.1363	19.8196	24.8044	24.2706	24.6566	24.5105
924	Dynamin-2 OS=Rattus norvegicus OX=10116 GN=Dnm2 PE=1 SV=1	Dnm2	P39052	20.3851	19.7607	20.4967	21.385	22.3897	21.488	22.0571	21.6916
925	Dynamin-3 OS=Rattus norvegicus OX=10116 GN=Dnm3 PE=1 SV=2	Dnm3	Q08877	NaN	NaN	NaN	NaN	16.9232	15.6338	16.8763	NaN
926	Dynein assembly factor 4, axonemal OS=Rattus norvegicus OX=10116 GN=Dnaaf4 PE=1 SV=1	Dnaaf4	Q5VJS5	21.7619	22.5456	21.6563	22.5044	20.4835	21.5445	21.0137	21.1835
927	Dynein light chain 1, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Dynll1 PE=1 SV=1	Dynll1	P63170	19.5181	19.3673	19.3145	18.9863	23.0482	23.7001	23.3842	23.214
928	Dynein light chain 2, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Dynll2 PE=1 SV=1	Dynll2	Q78P75	NaN	16.3748	NaN	16.2425	18.6512	18.8982	18.6952	18.5061
929	Dynein light chain roadblock-type 1 OS=Rattus norvegicus OX=10116 GN=Dynlrb1 PE=1 SV=3	Dynlrb1	P62628	14.6553	NaN	NaN	NaN	20.8407	21.0094	21.0577	20.8298
930	Dynein light chain Tctex-type 1 OS=Rattus norvegicus OX=10116 GN=Dynlt1 PE=1 SV=1	Dynlt1	Q9Z336	NaN	NaN	NaN	NaN	19.842	19.7344	20.1814	19.7604
931	Dystonin OS=Rattus norvegicus OX=10116 GN=Dst PE=1 SV=3	Dst	D3ZC56	19.3886	19.4155	19.8452	19.273	23.2184	24.0034	24.0967	24.0517
932	Dystrobrevin OS=Rattus norvegicus OX=10116 GN=Dtna PE=1 SV=3	Dtna	D4A772	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
933	E3 ubiquitin-protein ligase HUWE1 (Fragment) OS=Rattus norvegicus OX=10116 GN=Huwe1 PE=1 SV=2	Huwe1	P51593	NaN	NaN	NaN	NaN	18.0532	NaN	16.9653	NaN
934	E3 ubiquitin-protein ligase HUWE1 OS=Rattus norvegicus OX=10116 GN=Huwe1 PE=1 SV=1	Huwe1	A0A0G2JVW5	15.9389	18.4973	18.3352	18.3269	21.5887	20.6577	20.4019	21.0477
935	E3 ubiquitin-protein ligase OS=Rattus norvegicus OX=10116 GN=Nedd4 PE=1 SV=1	Nedd4	A0A0G2K8P3	21.3513	21.8178	22.4068	22.052	23.6969	24.4673	24.5479	24.1615
936	E3 ubiquitin-protein ligase PPP1R11 OS=Rattus norvegicus OX=10116 GN=Ppp1r11 PE=2 SV=2	Ppp1r11	Q6MFY6	NaN	13.9479	13.8424	NaN	15.3471	NaN	16.7465	16.4482
937	E3 ubiquitin-protein ligase RNF114 OS=Rattus norvegicus OX=10116 GN=Rnf114 PE=2 SV=1	Rnf114	Q6J2U6	16.8913	16.0908	16.0548	13.9806	21.6342	20.1677	20.7069	20.6541
938	E3 ubiquitin-protein ligase TRIP12 OS=Rattus norvegicus OX=10116 GN=Trip12 PE=1 SV=1	Trip12	A0A1W2Q676	14.8863	NaN	15.2604	15.7085	18.1431	18.2089	17.8906	17.1704
939	E3 ubiquitin-protein ligase UBR4 OS=Rattus norvegicus OX=10116 GN=Ubr4 PE=1 SV=1	Ubr4	F1LQI5	14.9962	17.909	16.4557	16.5448	22.0433	21.6763	21.7894	21.7087
940	Early endosome antigen 1 OS=Rattus norvegicus OX=10116 GN=Eea1 PE=1 SV=1	Eea1	A0A0G2K051	15.728	15.3826	14.7958	NaN	18.3142	17.6131	17.134	16.6943
941	Echinoderm microtubule-associated protein-like 2 OS=Rattus norvegicus OX=10116 GN=Eml2 PE=1 SV=1	Eml2	Q6P6T4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
942	Echinoderm microtubule-associated protein-like 4 OS=Rattus norvegicus OX=10116 GN=Eml4 PE=1 SV=1	Eml4	A0A0G2K2Z0	NaN	NaN	NaN	NaN	18.2208	18.7233	19.2218	19.1083
943	Ecm29 proteasome adaptor and scaffold OS=Rattus norvegicus OX=10116 GN=Ecpas PE=1 SV=3	Ecpas	F1M446	NaN	NaN	NaN	NaN	18.2851	17.4232	18.7255	18.8925
944	Ectonucleoside triphosphate diphosphohydrolase 1 OS=Rattus norvegicus OX=10116 GN=Entpd1 PE=3 SV=3	Entpd1	F1M0G3	NaN	NaN	NaN	NaN	21.0445	21.2996	20.9227	20.6818
945	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1 OS=Rattus norvegicus OX=10116 GN=Enpp1 PE=1 SV=	Enpp1	Q924C3	NaN	NaN	NaN	NaN	16.5775	16.6221	NaN	NaN
946	Eefsec protein OS=Rattus norvegicus OX=10116 GN=Eefsec PE=1 SV=1	Eefsec	B5DEJ5	17.3823	17.5959	14.2193	19.0082	18.5133	17.4883	16.0593	17.5718
947	EF-hand domain-containing protein D2 OS=Rattus norvegicus OX=10116 GN=Efhd2 PE=1 SV=1	Efhd2	Q4FZY0	NaN	15.1897	NaN	NaN	19.6068	18.6653	18.6379	19.2351
948	EGF-containing fibulin-like extracellular matrix protein 1 OS=Rattus norvegicus OX=10116 GN=Efemp1 PE=1 SV=1	Efemp1	O35568	NaN	NaN	18.5693	14.8225	NaN	NaN	NaN	NaN
949	EH domain-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ehbp1 PE=1 SV=3	Ehbp1	F1LVX2	15.3762	NaN	NaN	NaN	17.7975	15.2228	15.5252	15.74
950	EH domain-binding protein 1-like 1 OS=Rattus norvegicus OX=10116 GN=Ehbp1l1 PE=1 SV=1	Ehbp1l1	A0A0G2K6R8	18.903	18.824	17.4591	17.1647	22.3223	22.2496	22.2581	21.7629
951	EH domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Ehd1 PE=1 SV=1	Ehd1	Q641Z6	20.9006	20.5396	20.6241	20.7614	23.5788	23.048	23.307	23.2661
952	EH domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Ehd2 PE=1 SV=1	Ehd2	Q4V8H8	17.504	17.2356	18.1731	17.4646	20.9055	20.5718	20.742	20.4798

953	EH domain-containing protein 3 OS=Rattus norvegicus OX=10116 GN=Ehd3 PE=1 SV=2	Ehd3	Q8R491	15.9575	15.2309	16.2063	17.5724	NaN	15.6951	15.7123	15.2436
954	EH-domain-containing 4 OS=Rattus norvegicus OX=10116 GN=Ehd4 PE=1 SV=1	Ehd4	Q8R3Z7	22.3995	22.343	22.8552	22.3373	24.2208	23.8165	23.9982	23.763
955	Elastin microfibril interfacer 1 OS=Rattus norvegicus OX=10116 GN=Emilin1 PE=1 SV=1	Emilin1	D3Z9E1	17.6459	16.8999	18.4472	17.8843	18.5068	17.1674	16.1289	16.06
956	Elastin OS=Rattus norvegicus OX=10116 GN=Eln PE=1 SV=2	Eln	D4A9U4	19.4962	19.884	19.5388	19.0635	20.3434	19.4787	19.2135	20.6675
957	ELAV-like protein 1 OS=Rattus norvegicus OX=10116 GN=Elavl1 PE=1 SV=1	Elavl1	B5DF91	16.4719	14.4683	15.5551	NaN	20.5272	20.2282	20.0242	19.4504
958	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Rattus norvegicus OX=10116 GN=Etfa PE=1 SV=4	Etfa	P13803	19.8924	19.9439	19.9362	19.9471	22.1684	22.1775	21.7924	21.7739
959	Electron transfer flavoprotein subunit beta OS=Rattus norvegicus OX=10116 GN=Etfb PE=1 SV=3	Etfb	Q68FU3	19.0093	19.6378	17.7663	17.2936	21.1363	21.8907	21.1932	21.5195
960	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Etfdh PE=1 S	Etfdh	Q66HF3	16.7016	15.8585	NaN	NaN	19.6991	19.774	19.8566	20.0137
961	ELKS/Rab6-interacting/CAST family member 1 OS=Rattus norvegicus OX=10116 GN=Erc1 PE=1 SV=1	Erc1	A0A0G2JYT1	17.4128	16.2935	17.4346	NaN	18.681	20.5204	19.6993	18.7962
962	Elongation factor 1-alpha 1 OS=Rattus norvegicus OX=10116 GN=Eef1a1 PE=2 SV=1	Eef1a1	P62630	25.9294	25.3474	25.7994	25.7606	29.5629	29.0673	29.3743	29.2591
963	Elongation factor 1-alpha 2 OS=Rattus norvegicus OX=10116 GN=Eef1a2 PE=1 SV=1	Eef1a2	P62632	17.0921	18.3352	18.0392	17.3076	24.2622	23.8534	24.2791	24.3526
964	Elongation factor 1-delta OS=Rattus norvegicus OX=10116 GN=Eef1d PE=1 SV=2	Eef1d	Q68FR9	20.0348	18.7471	19.4052	19.9398	24.7441	23.5812	24.2233	24.2328
965	Elongation factor 1-gamma OS=Rattus norvegicus OX=10116 GN=Eef1g PE=2 SV=3	Eef1g	Q68FR6	20.1988	20.1323	20.2354	19.6855	24.0622	22.6211	23.0572	23.0673
966	Elongation factor 2 OS=Rattus norvegicus OX=10116 GN=Eef2 PE=1 SV=4	Eef2	P05197	22.5169	22.5738	22.8199	22.8905	27.6274	26.9198	27.2894	27.2607
967	Elongation factor Tu, mitochondrial OS=Rattus norvegicus OX=10116 GN=Tufm PE=1 SV=1	Tufm	P85834	17.3153	18.0256	15.7228	17.0054	19.6279	20.2144	20.7391	20.8814
968	Elongation factor-like GTPase 1 OS=Rattus norvegicus OX=10116 GN=Efl1 PE=1 SV=2	Efl1	D3ZXJ5	NaN	NaN	NaN	14.0398	17.3724	17.2222	17.2717	17.5527
969	Elongator complex protein 1 OS=Rattus norvegicus OX=10116 GN=Elp1 PE=1 SV=2	Elp1	F1LP76	20.6505	20.9392	21.2174	20.7491	22.8434	23.1576	23.572	23.3714
970	Elongator complex protein 2 OS=Rattus norvegicus OX=10116 GN=Elp2 PE=2 SV=1	Elp2	Q496Z0	17.2021	17.551	16.6718	16.6233	19.7526	20.4917	20.4951	20.2497
971	Elongator complex protein 3 OS=Rattus norvegicus OX=10116 GN=Elp3 PE=1 SV=2	Elp3	D4ACM1	17.2202	17.035	16.9129	17.6218	20.774	20.6996	21.1765	20.4728
972	Elongator complex protein 5 OS=Rattus norvegicus OX=10116 GN=Elp5 PE=1 SV=1	Elp5	B0BMU7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
973	Elongin-B OS=Rattus norvegicus OX=10116 GN=Elob PE=1 SV=1	Elob	P62870	16.4424	14.9704	17.4391	16.86	22.5077	22.0386	22.3295	22.3056
974	Elongin-C OS=Rattus norvegicus OX=10116 GN=Eloc PE=1 SV=1	Eloc	P83941	NaN	15.2133	15.347	15.8713	22.5259	21.8604	21.9459	21.8885
975	Embigin OS=Rattus norvegicus OX=10116 GN=Emb PE=1 SV=1	Emb	O88775	19.85	20.1287	19.1956	20.172	16.6674	18.397	17.6489	18.3876
976	Ena/VASP-like protein OS=Rattus norvegicus OX=10116 GN=Evl PE=1 SV=1	Evl	F1M8I7	NaN	NaN	NaN	NaN	17.7454	17.8793	18.5787	17.6061
977	ENAH, actin regulator OS=Rattus norvegicus OX=10116 GN=Enah PE=1 SV=1	Enah	A0A0G2K6I4	20.4185	20.4093	20.3503	19.9754	22.7873	23.1733	23.3447	22.7937
978	ENAH, actin regulator OS=Rattus norvegicus OX=10116 GN=Enah PE=1 SV=1	Enah	Q5XHX3	15.3737	15.3125	NaN	NaN	18.2936	18.3399	18.246	17.6127
979	Endoglin OS=Rattus norvegicus OX=10116 GN=Eng PE=1 SV=2	Eng	M0RBA8	15.0461	NaN	15.0903	NaN	20.7634	20.9734	20.4864	21.0081
980	Endomucin OS=Rattus norvegicus OX=10116 GN=Emcn PE=2 SV=1	Emcn	Q6AY82	14.4713	NaN	15.0047	NaN	19.6737	19.7535	20.1529	20.2692
981	Endophilin-A2 OS=Rattus norvegicus OX=10116 GN=Sh3gl1 PE=1 SV=1	Sh3gl1	O35964	19.9627	19.3922	20.5363	20.8901	21.5067	21.7394	21.6264	21.1513
982	Endophilin-B1 OS=Rattus norvegicus OX=10116 GN=Sh3glb1 PE=2 SV=1	Sh3glb1	Q6AYE2	19.848	19.4237	18.1434	18.7341	23.6679	22.9218	23.6623	23.1456
983	Endophilin-B2 OS=Rattus norvegicus OX=10116 GN=Sh3glb2 PE=1 SV=1	Sh3glb2	A0A0G2K9P4	18.3384	18.0578	16.5608	17.6934	22.4522	21.8108	22.1575	21.7555
984	Endoplasmic reticulum chaperone BiP OS=Rattus norvegicus OX=10116 GN=Hspa5 PE=1 SV=1	Hspa5	P06761	22.8681	23.1521	23.0946	23.3804	25.8481	25.9739	25.4572	25.888
985	Endoplasmic reticulum metallopeptidase 1 OS=Rattus norvegicus OX=10116 GN=Ermp1 PE=1 SV=1	Ermp1	F1M6W2	15.7951	15.3289	16.2375	16.0929	15.7007	17.145	17.0854	17.1818
986	Endoplasmic reticulum protein SC65 OS=Rattus norvegicus OX=10116 GN=P3h4 PE=2 SV=3	P3h4	Q64375	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
987	Endoplasmic reticulum resident protein 29 OS=Rattus norvegicus OX=10116 GN=Erp29 PE=1 SV=2	Erp29	P52555	17.2115	19.9322	18.0128	16.5016	19.9969	21.2518	20.2487	20.7385
988	Endoplasmic reticulum-golgi intermediate compartment 1 OS=Rattus norvegicus OX=10116 GN=Ergic1 PE=1 SV=2	Ergic1	F1LU48	17.9383	17.4469	15.9443	14.9795	21.3975	21.7353	21.4429	21.1309
989	Endoplasmin OS=Rattus norvegicus OX=10116 GN=Hsp90b1 PE=1 SV=1	Hsp90b1	A0A0A0MY09	21.3421	22.0727	21.4522	21.3057	24.6407	24.9025	24.4706	25.0086
990	Endothelin-converting enzyme 1 OS=Rattus norvegicus OX=10116 GN=Ece1 PE=1 SV=2	Ece1	P42893	NaN	NaN	NaN	NaN	18.4901	18.7283	18.3612	18.5189
991	Engulfment and cell motility 2 OS=Rattus norvegicus OX=10116 GN=Elmo2 PE=1 SV=1	Elmo2	G3V982	NaN	NaN	NaN	NaN	NaN	NaN	16.7491	NaN
992	Enhancer of mRNA-decapping 3 OS=Rattus norvegicus OX=10116 GN=Edc3 PE=1 SV=3	Edc3	F1M7Z1	NaN	NaN	NaN	NaN	17.6301	17.5104	17.5476	NaN
993	Enhancer of mRNA-decapping protein 4 OS=Rattus norvegicus OX=10116 GN=Edc4 PE=1 SV=1	Edc4	Q3ZAV8	19.8706	19.3262	19.2793	18.3969	20.9184	20.441	20.8161	21.0884
994	Enoyl-CoA delta isomerase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Eci2 PE=1 SV=1	Eci2	Q5XIC0	15.8395	17.5451	NaN	17.8046	19.1052	20.4586	18.9735	19.6006
995	Enoyl-CoA delta isomerase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Eci3 PE=1 SV=1	Eci3	A0A0G2K277	NaN	NaN	NaN	NaN	16.0217	17.2278	16.615	16.4979
996	Enoyl-CoA hydratase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Echs1 PE=1 SV=1	Echs1	P14604	NaN	15.9389	NaN	15.5291	16.7678	18.8945	18.3688	18.5812
997	Ephrin B1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Efnb1 PE=2 SV=1	Efnb1	Q6P7B6	NaN	12.5813	13.5992	NaN	13.3181	14.9021	15.4065	15.8885
998	Epidermal growth factor receptor pathway substrate 15 OS=Rattus norvegicus OX=10116 GN=Eps15 PE=1 SV=2	Eps15	E9PSY8	14.6564	12.8331	15.0694	15.5038	18.0193	17.7236	18.0704	16.5718
999	Epidermal growth factor receptor pathway substrate 15-like 1 OS=Rattus norvegicus OX=10116 GN=Eps15l1 PE=1 SV=3	Eps15l1	D3ZJR1	14.844	13.9204	16.1184	16.7072	21.8267	20.836	20.6869	21.1726
1000	Epithelial membrane protein 3 OS=Rattus norvegicus OX=10116 GN=Emp3 PE=2 SV=1	Emp3	Q9QYW5	NaN	NaN	NaN	NaN	NaN	NaN	15.7934	17.2609
1001	EPM2A-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Epm2aip1 PE=1 SV=3	Epm2aip1	F1M471	NaN	NaN	NaN	NaN	18.3837	17.4529	17.0729	16.916
1002	EPS8-like 2 OS=Rattus norvegicus OX=10116 GN=Eps8l2 PE=1 SV=2	Eps8l2	F7DLY1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1003	Epsilon 1 globin OS=Rattus norvegicus OX=10116 GN=Hbe1 PE=1 SV=1	Hbe1	O88752	21.0316	21.2957	21.4445	20.9182	18.3246	17.2092	18.0479	19.3155
1004	Epsilon 3 globin OS=Rattus norvegicus OX=10116 GN=Hbg1 PE=2 SV=1	Hbg1	O88754	21.5072	20.3289	20.8946	21.376	19.8813	19.8468	19.9171	19.6456
1005	Epsin-1 OS=Rattus norvegicus OX=10116 GN=Epn1 PE=1 SV=1	Epn1	A0A140TAC3	NaN	15.9271	NaN	14.9624	18.6673	19.5528	19.2097	19.5355

1006	Epsin-3 OS=Rattus norvegicus OX=10116 GN=Epn3 PE=1 SV=1	Epn3	Q4V882	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1007	Equilibrative nucleoside transporter 1 OS=Rattus norvegicus OX=10116 GN=Slc29a1 PE=1 SV=3	Slc29a1	O54698	16.8798	16.768	16.2079	17.1445	16.516	NaN	NaN	16.2541
1008	ER lumen protein-retaining receptor 2 OS=Rattus norvegicus OX=10116 GN=Kdelr2 PE=2 SV=1	Kdelr2	Q5U305	17.1232	19.3736	18.8435	18.1547	18.9012	20.8088	19.1179	17.9714
1009	ER membrane protein complex subunit 1 OS=Rattus norvegicus OX=10116 GN=Emc1 PE=1 SV=1	Emc1	D4A994	19.7271	19.2313	19.0584	19.8589	18.0564	17.9962	17.5442	17.6054
1010	ER membrane protein complex subunit 2 OS=Rattus norvegicus OX=10116 GN=Emc2 PE=2 SV=1	Emc2	B0BNG0	NaN	NaN	NaN	NaN	18.3625	18.8507	18.2203	18.2147
1011	ER membrane protein complex subunit 8 OS=Rattus norvegicus OX=10116 GN=Emc8 PE=2 SV=1	Emc8	Q5FVL2	NaN	15.0592	NaN	NaN	18.1474	18.306	18.2544	18.2748
1012	ERCC excision repair 6-like, spindle assembly checkpoint helicase OS=Rattus norvegicus OX=10116 GN=Ercc6l PE=1 SV=1	Ercc6l	D4A0G9	20.4239	21.0048	19.5673	14.4399	19.2248	19.7589	19.2707	19.4412
1013	Erlin-2 OS=Rattus norvegicus OX=10116 GN=Erlin2 PE=1 SV=1	Erlin2	B5DEH2	15.5356	15.9177	15.5473	NaN	18.0009	18.8462	18.4584	18.9643
1014	ERO1-like protein alpha OS=Rattus norvegicus OX=10116 GN=Ero1a PE=1 SV=1	Ero1a	Q8R4A1	17.4137	17.2976	17.5259	16.7728	19.688	19.6844	19.2857	19.6572
1015	Erythrocyte membrane protein band 4.1 OS=Rattus norvegicus OX=10116 GN=Epb41 PE=1 SV=1	Epb41	A0A0G2K161	20.6422	20.8109	19.5174	19.4939	17.5773	17.5441	15.8515	16.1574
1016	Erythrocyte membrane protein band 4.1-like 2 OS=Rattus norvegicus OX=10116 GN=Epb41l2 PE=1 SV=3	Epb41l2	D3ZDT1	22.0924	21.9955	22.7306	22.5962	19.9628	20.1676	19.7258	19.7928
1017	Erythrocyte membrane protein band 4.1-like 3 OS=Rattus norvegicus OX=10116 GN=Epb41l3 PE=1 SV=1	Epb41l3	Q9JMB3	15.1165	NaN	14.8153	NaN	20.3917	19.9549	18.4886	19.7755
1018	Erythrocyte membrane protein band 4.2 OS=Rattus norvegicus OX=10116 GN=Epb42 PE=1 SV=1	Epb42	B5DF57	22.3352	22.1294	21.9481	22.4234	19.2352	19.4982	19.6533	19.6238
1019	ES1 protein homolog, mitochondrial OS=Rattus norvegicus OX=10116 PE=1 SV=2	Gatd3a	P56571	15.7177	14.6704	NaN	NaN	NaN	17.4094	16.6699	16.4249
1020	Estradiol 17-beta-dehydrogenase 11 OS=Rattus norvegicus OX=10116 GN=Hsd17b11 PE=2 SV=1	Hsd17b11	Q6AYS8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1021	Ethanolamine-phosphate cytidylyltransferase OS=Rattus norvegicus OX=10116 GN=Pcyt2 PE=1 SV=1	Pcyt2	O88637	16.9471	NaN	17.5	15.6292	19.3417	15.52	18.6245	18.7494
1022	Eukaryotic initiation factor 4A-II OS=Rattus norvegicus OX=10116 GN=Eif4a2 PE=1 SV=1	Eif4a2	Q5RKI1	NaN	NaN	16.6368	NaN	20.8369	19.7168	20.4957	20.5361
1023	Eukaryotic initiation factor 4A-III OS=Rattus norvegicus OX=10116 GN=Eif4a3 PE=1 SV=1	Eif4a3	Q3B8Q2	NaN	14.5609	NaN	NaN	18.2815	17.9693	17.5904	17.5285
1024	Eukaryotic peptide chain release factor GTP-binding subunit ERF3B-like OS=Rattus norvegicus OX=10116 GN=Gspt1 PE=1 S	Gspt1	Q6AYD5	19.6665	13.9494	16.979	16.7296	23.0498	22.6129	23.0969	22.9909
1025	Eukaryotic peptide chain release factor subunit 1 OS=Rattus norvegicus OX=10116 GN=Etf1 PE=2 SV=3	Etf1	Q5U2Q7	17.8577	17.8414	18.3579	18.4765	22.0381	21.4717	21.9065	21.8133
1026	Eukaryotic translation elongation factor 1 beta 2 OS=Rattus norvegicus OX=10116 GN=Eef1b2 PE=1 SV=1	Eef1b2	B5DEN5	17.4474	17.5602	18.1036	18.1204	21.5325	20.2984	20.7477	20.8623
1027	Eukaryotic translation elongation factor 1 epsilon 1 OS=Rattus norvegicus OX=10116 GN=Eef1e1 PE=1 SV=1	Eef1e1	B2RYN3	20.4075	20.7403	20.8858	20.319	21.4652	21.1422	21.4998	21.3275
1028	Eukaryotic translation initiation factor 1 OS=Rattus norvegicus OX=10116 GN=Eif1 PE=1 SV=1	Eif1	B0K008	17.1161	16.8992	17.4102	17.0638	20.459	20.1073	20.4847	20.5661
1029	Eukaryotic translation initiation factor 2 subunit 1 OS=Rattus norvegicus OX=10116 GN=Eif2s1 PE=1 SV=2	Eif2s1	P68101	18.5222	18.2874	17.2367	16.7071	22.8996	22.6689	22.6179	22.5529
1030	Eukaryotic translation initiation factor 2 subunit 3, X-linked OS=Rattus norvegicus OX=10116 GN=Eif2s3 PE=1 SV=2	Eif2s3	P81795	17.0302	18.8872	18.1214	18.9258	22.2305	22.1752	22.2747	21.8964
1031	Eukaryotic translation initiation factor 2 subunit beta OS=Rattus norvegicus OX=10116 GN=Eif2s2 PE=1 SV=1	Eif2s2	Q6P685	18.1449	18.18	17.5213	18.0117	22.1183	21.941	21.9185	21.8053
1032	Eukaryotic translation initiation factor 2D OS=Rattus norvegicus OX=10116 GN=Eif2d PE=1 SV=1	Eif2d	Q5PPG7	NaN	NaN	NaN	NaN	17.3122	17.189	NaN	NaN
1033	Eukaryotic translation initiation factor 3 subunit A OS=Rattus norvegicus OX=10116 GN=Eif3a PE=2 SV=2	Eif3a	Q1JU68	15.2925	17.9854	NaN	NaN	21.6097	21.3761	21.2994	21.3703
1034	Eukaryotic translation initiation factor 3 subunit B OS=Rattus norvegicus OX=10116 GN=Eif3b PE=1 SV=1	Eif3b	Q4G061	19.8576	17.7201	17.612	17.9485	20.7355	19.2486	20.1188	20.2383
1035	Eukaryotic translation initiation factor 3 subunit C OS=Rattus norvegicus OX=10116 GN=Eif3c PE=1 SV=1	Eif3c	B5DFC8	17.8364	17.0691	17.3889	19.5657	20.8815	20.5453	20.839	20.3334
1036	Eukaryotic translation initiation factor 3 subunit D OS=Rattus norvegicus OX=10116 GN=Eif3d PE=1 SV=1	Eif3d	Q6AYK8	NaN	NaN	NaN	NaN	19.2061	18.1173	18.7177	18.4629
1037	Eukaryotic translation initiation factor 3 subunit E OS=Rattus norvegicus OX=10116 GN=LOC100909481 PE=3 SV=1	LOC100365062	A0A0G2K273	NaN	NaN	NaN	NaN	20.3128	20.1832	20.5073	20.0503
1038	Eukaryotic translation initiation factor 3 subunit F OS=Rattus norvegicus OX=10116 GN=Eif3f PE=1 SV=3	Eif3f	D4AC36	14.859	16.5318	15.7502	17.9387	21.5057	20.869	21.2478	21.0544
1039	Eukaryotic translation initiation factor 3 subunit G OS=Rattus norvegicus OX=10116 GN=Eif3g PE=1 SV=1	Eif3g	Q5RK09	17.8331	18.6757	16.05	17.6197	21.3497	20.7341	20.9792	20.7851
1040	Eukaryotic translation initiation factor 3 subunit H OS=Rattus norvegicus OX=10116 GN=Eif3h PE=1 SV=1	Eif3h	Q6P9U8	13.9717	NaN	14.7202	NaN	19.5857	19.5847	19.3158	19.6777
1041	Eukaryotic translation initiation factor 3 subunit I OS=Rattus norvegicus OX=10116 GN=Eif3i PE=2 SV=1	Eif3i	B0BNA7	14.5026	NaN	NaN	NaN	20.3504	20.0346	20.4459	20.1832
1042	Eukaryotic translation initiation factor 3 subunit J OS=Rattus norvegicus OX=10116 GN=Eif3j PE=1 SV=1	Eif3j	A0JPM9	NaN	16.2052	NaN	NaN	20.9932	19.8399	20.0393	20.4532
1043	Eukaryotic translation initiation factor 3 subunit K OS=Rattus norvegicus OX=10116 GN=Eif3k PE=1 SV=1	Eif3k	A0A0G2JU77	NaN	NaN	NaN	NaN	17.2332	15.3225	15.9992	16.3093
1044	Eukaryotic translation initiation factor 3 subunit M OS=Rattus norvegicus OX=10116 GN=Eif3m PE=1 SV=1	Eif3m	D3ZAZ0	17.1138	15.8339	16.9323	17.1733	20.4284	19.4657	20.0502	18.846
1045	Eukaryotic translation initiation factor 3, subunit 6 interacting protein OS=Rattus norvegicus OX=10116 GN=Eif3l PE=1 SV=	Eif3l	G3V7G9	NaN	NaN	NaN	NaN	17.8706	NaN	NaN	17.8468
1046	Eukaryotic translation initiation factor 4 gamma, 1 OS=Rattus norvegicus OX=10116 GN=Eif4g1 PE=1 SV=1	Eif4g1	D3ZU13	19.9141	20.2959	20.0443	19.4905	24.5872	24.4546	24.4384	24.1697
1047	Eukaryotic translation initiation factor 4 gamma, 3 OS=Rattus norvegicus OX=10116 GN=Eif4g3 PE=1 SV=2	Eif4g3	D4A554	15.2929	19.2212	17.1162	17.9895	20.7058	21.7062	21.2409	20.5906
1048	Eukaryotic translation initiation factor 4, gamma 2 OS=Rattus norvegicus OX=10116 GN=Eif4g2 PE=1 SV=2	Eif4g2	F1LN59	17.2535	16.6141	17.7131	15.7751	22.3894	21.6853	21.7083	21.6284
1049	Eukaryotic translation initiation factor 4A1 OS=Rattus norvegicus OX=10116 GN=Eif4a1 PE=1 SV=1	Eif4a1	Q6P3V8	20.538	21.0183	20.791	20.1219	24.7337	23.9245	24.7073	24.4557
1050	Eukaryotic translation initiation factor 4B OS=Rattus norvegicus OX=10116 GN=Eif4b PE=1 SV=1	Eif4b	Q5RKG9	18.3063	18.8935	18.9382	NaN	21.0468	19.9424	19.9552	20.388
1051	Eukaryotic translation initiation factor 4E binding protein 2, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Eif4ebp2	Eif4ebp2	Q497A9	NaN	NaN	NaN	NaN	16.4942	16.4416	17.2843	NaN
1052	Eukaryotic translation initiation factor 4E family member 2 OS=Rattus norvegicus OX=10116 GN=Eif4e2 PE=1 SV=1	Chrng	A0A0G2K933	NaN	14.2995	NaN	14.6834	17.2714	NaN	16.8444	16.7516
1053	Eukaryotic translation initiation factor 4E OS=Rattus norvegicus OX=10116 GN=Eif4e PE=1 SV=1	Eif4e	A0A1W2Q627	17.8575	21.381	18.4306	16.283	20.1387	21.3072	19.5459	19.0161
1054	Eukaryotic translation initiation factor 4E-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Eif4ebp1 PE=1 SV=3	Eif4ebp1	Q62622	NaN	NaN	NaN	NaN	21.617	20.7264	21.5945	21.3611
1055	Eukaryotic translation initiation factor 4E-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Ankhd1 PE=1 SV=1	Ankhd1	A0A0G2K916	15.1441	15.9046	NaN	NaN	18.4758	NaN	17.7701	NaN
1056	Eukaryotic translation initiation factor 4H OS=Rattus norvegicus OX=10116 GN=Eif4h PE=1 SV=1	Eif4h	Q5XI72	18.609	17.2948	15.3248	18.7022	22.9054	20.807	21.1229	21.0204
1057	Eukaryotic translation initiation factor 5A-1 OS=Rattus norvegicus OX=10116 GN=Eif5a PE=1 SV=3	Eif5a	Q3T1J1	17.9877	18.9335	18.9697	18.8245	23.0983	22.7062	22.541	23.0585
1058	Eukaryotic translation initiation factor 5B OS=Rattus norvegicus OX=10116 GN=Eif5b PE=1 SV=1	Eif5b	B2GUV7	NaN	NaN	NaN	NaN	20.3472	20.2254	20.5172	20.4496

1059	Eukaryotic translation initiation factor 6 OS=Rattus norvegicus OX=10116 GN=Eif6 PE=1 SV=1	Eif6	A0A0G2K110	NaN	16.0215	NaN	NaN	17.3023	18.0568	17.9871	18.4594
1060	Exocyst complex component 1 OS=Rattus norvegicus OX=10116 GN=Exoc1 PE=1 SV=1	Exoc1	A0A0G2JYT4	17.7318	18.4812	17.6683	NaN	19.4254	20.513	20.3337	20.0527
1061	Exocyst complex component 4 OS=Rattus norvegicus OX=10116 GN=Exoc4 PE=1 SV=1	Exoc4	Q62824	NaN	17.4869	17.8184	NaN	18.1789	19.1279	19.6401	19.2052
1062	Exocyst complex component 7 OS=Rattus norvegicus OX=10116 GN=Exoc7 PE=1 SV=1	Exoc7	O54922	NaN	NaN	NaN	NaN	17.6059	17.7115	18.2942	18.1878
1063	Exocyst complex component 8 OS=Rattus norvegicus OX=10116 GN=Exoc8 PE=1 SV=1	Exoc8	O54924	NaN	NaN	NaN	NaN	18.3344	18.853	18.2996	18.3594
1064	Exopolyphosphatase PRUNE1 OS=Rattus norvegicus OX=10116 GN=Prune1 PE=1 SV=1	Prune1	Q6AYG3	16.3583	16.2144	17.7819	17.7659	19.9812	19.6579	20.2057	19.9416
1065	Exportin 5 OS=Rattus norvegicus OX=10116 GN=Xpo5 PE=1 SV=1	Xpo5	D3ZQE8	NaN	14.1516	NaN	NaN	16.9473	17.7005	18.0668	17.5224
1066	Exportin 7 OS=Rattus norvegicus OX=10116 GN=Xpo7 PE=1 SV=1	Xpo7	A0A0G2JWA3	19.4516	18.9465	19.4499	19.6488	16.9162	19.6771	19.3758	18.8138
1067	Exportin-1 OS=Rattus norvegicus OX=10116 GN=Xpo1 PE=1 SV=1	Xpo1	Q80U96	18.4315	19.2673	18.9521	17.8578	22.4966	22.4231	22.6878	22.5043
1068	Extended synaptotagmin-1 OS=Rattus norvegicus OX=10116 GN=Esyt1 PE=1 SV=1	Esyt1	Q9Z1X1	NaN	NaN	NaN	NaN	NaN	16.7578	NaN	NaN
1069	Extracellular link domain-containing 1 (Predicted) OS=Rattus norvegicus OX=10116 GN=Lyve1 PE=1 SV=1	Lyve1	D3ZD19	16.8328	16.4727	16.0512	NaN	NaN	NaN	15.7174	15.3496
1070	Extracellular matrix protein 1 OS=Rattus norvegicus OX=10116 GN=Ecm1 PE=1 SV=2	Ecm1	Q62894	15.2622	15.6637	NaN	NaN	NaN	NaN	NaN	14.4551
1071	Extracellular superoxide dismutase [Cu-Zn] OS=Rattus norvegicus OX=10116 GN=Sod3 PE=1 SV=2	Sod3	Q08420	18.5479	18.879	19.9928	19.8449	17.4616	16.6184	16.5411	18.0654
1072	Eyes absent homolog OS=Rattus norvegicus OX=10116 GN=Eya3 PE=1 SV=1	Eya3	A0A0G2JZ01	NaN	NaN	17.2259	NaN	18.1181	16.4864	18.0803	NaN
1073	Ezrin OS=Rattus norvegicus OX=10116 GN=Ezr PE=1 SV=3	Ezr	P31977	20.1879	20.0655	21.0744	19.0997	23.0496	22.6511	22.3722	22.9006
1074	F-actin-capping protein subunit alpha-1 OS=Rattus norvegicus OX=10116 GN=Capza1 PE=1 SV=1	Capza1	B2GUZ5	18.7007	19.1627	19.0303	19.5281	22.91	21.9756	22.0208	22.1942
1075	F-actin-capping protein subunit alpha-2 OS=Rattus norvegicus OX=10116 GN=Capza2 PE=1 SV=1	Capza2	Q3T1K5	14.8509	17.7883	17.4996	18.1312	22.5652	21.5513	21.63	21.6775
1076	F-actin-capping protein subunit beta OS=Rattus norvegicus OX=10116 GN=Capzb PE=1 SV=1	Capzb	Q5XI32	19.3492	19.3193	20.0083	21.5069	23.3394	22.8468	22.9469	22.8845
1077	FAD synthase OS=Rattus norvegicus OX=10116 GN=Flad1 PE=1 SV=2	Flad1	D4A4P4	NaN	16.6581	17.5435	NaN	17.8977	17.1504	17.4448	17.6455
1078	Fam49b protein OS=Rattus norvegicus OX=10116 GN=Fam49b PE=1 SV=1	Cyrib	B2GUZ9	17.4649	18.4102	16.8767	17.9085	20.9282	20.3652	20.8617	20.7687
1079	Family with sequence similarity 114, member A1 OS=Rattus norvegicus OX=10116 GN=Fam114a1 PE=1 SV=2	Fam114a1	D4A777	22.3919	21.8142	21.7805	21.4441	22.5974	21.7936	21.941	21.7784
1080	Family with sequence similarity 120A OS=Rattus norvegicus OX=10116 GN=Fam120a PE=1 SV=2	Fam120a	D4AB03	18.5072	19.361	18.9756	19.3858	21.645	22.4331	21.8423	21.5198
1081	Family with sequence similarity 126, member A OS=Rattus norvegicus OX=10116 GN=Fam126a PE=1 SV=1	Fam126a	D4AE31	NaN	NaN	NaN	NaN	NaN	17.373	NaN	NaN
1082	Family with sequence similarity 168, member A OS=Rattus norvegicus OX=10116 GN=Fam168a PE=1 SV=1	Fam168a	D3ZHW1	NaN	NaN	NaN	NaN	18.0934	16.5743	16.9214	17.3109
1083	Family with sequence similarity 49, member A OS=Rattus norvegicus OX=10116 GN=Fam49a PE=1 SV=1	Cyria	B0BN65	18.6316	18.5056	17.1752	17.5468	21.2345	21.9408	22.5601	22.142
1084	Far upstream element-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Fubp1 PE=1 SV=1	Fubp1	A0A140TAJ3	18.5544	19.0549	18.8361	18.8788	22.3027	21.2491	21.3741	21.2057
1085	Far upstream element-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Khsrp PE=1 SV=1	Khsrp	A0A0G2K2B3	17.375	17.5256	17.4744	15.0223	23.6086	23.1015	23.0998	23.0269
1086	Far upstream element-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Fubp3 PE=1 SV=1	Fubp3	G3V829	NaN	NaN	NaN	NaN	17.9002	17.2694	17.087	17.5312
1087	Farnesyl pyrophosphate synthase OS=Rattus norvegicus OX=10116 GN=Fdps PE=1 SV=1	Rusc1	A0A0G2JXT3	NaN	NaN	15.1027	15.2167	19.5991	19.6378	19.8268	19.8864
1088	FAS-associated death domain protein OS=Rattus norvegicus OX=10116 GN=Fadd PE=1 SV=1	Fadd	Q8R2E7	15.0876	14.7684	15.717	NaN	19.8519	18.1871	19.4253	19.3718
1089	FAS-associated factor 1 OS=Rattus norvegicus OX=10116 GN=Faf1 PE=1 SV=1	Faf1	Q924K2	17.0361	17.5755	17.6291	16.1564	20.0313	19.1671	19.763	19.7176
1090	Fascin OS=Rattus norvegicus OX=10116 GN=Fscn1 PE=1 SV=2	Fscn1	P85845	NaN	16.5217	17.4059	14.6836	18.6588	18.9775	19.2254	19.0269
1091	Fatty acid synthase OS=Rattus norvegicus OX=10116 GN=Fasn PE=1 SV=3	Fasn	P12785	19.75	19.8062	19.9326	19.6205	22.2021	23.2585	23.7587	23.6474
1092	Fatty acid-binding protein 5 OS=Rattus norvegicus OX=10116 GN=Fabp5 PE=1 SV=3	Fabp5	P55053	22.1741	22.4461	23.0942	22.3514	23.2974	22.7276	22.9075	23.1654
1093	Fatty acid-binding protein, adipocyte OS=Rattus norvegicus OX=10116 GN=Fabp4 PE=1 SV=1	Fabp4	A0A0G2K586	19.7859	20.5546	21.7828	20.6278	22.016	21.9381	22.3462	21.4685
1094	Fatty acid-binding protein, heart OS=Rattus norvegicus OX=10116 GN=Fabp3 PE=1 SV=2	Fabp3	P07483	NaN	16.352	16.3532	14.8407	24.2234	24.004	23.9086	23.8459
1095	Fatty aldehyde dehydrogenase OS=Rattus norvegicus OX=10116 GN=Aldh3a2 PE=1 SV=1	Aldh3a2	A0A0G2JY43	NaN	NaN	15.1542	18.5225	17.3689	17.4278	17.2486	17.5759
1096	F-BAR domain only protein 2 OS=Rattus norvegicus OX=10116 GN=Fcho2 PE=1 SV=1	Fcho2	D3ZYR1	15.0264	15.3737	15.4582	15.6615	NaN	16.8983	17.1815	16.2693
1097	F-box only protein 30 OS=Rattus norvegicus OX=10116 GN=Fbxo30 PE=1 SV=1	Fbxo30	Q5XI67	17.2544	16.5706	16.7953	16.0357	19.5774	18.7759	19.3304	19.2867
1098	F-box only protein 9 OS=Rattus norvegicus OX=10116 GN=Fbxo9 PE=1 SV=1	Fbxo9	Q5U2X1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1099	F-box protein 21 OS=Rattus norvegicus OX=10116 GN=Fbxo21 PE=1 SV=3	Fbxo21	F1M5Q6	NaN	NaN	14.8697	NaN	18.7036	18.4602	18.7498	18.4219
1100	F-box protein 40 OS=Rattus norvegicus OX=10116 GN=Fbxo40 PE=4 SV=2	Fbxo40	F1LXQ1	NaN	14.0422	14.9283	NaN	20.0065	19.7035	19.8707	19.5875
1101	Fc fragment of IgG-binding protein OS=Rattus norvegicus OX=10116 GN=Fcgbp PE=1 SV=3	Fcgbp	D3ZJF8	24.1002	25.0036	23.4506	22.9208	23.4402	23.7703	23.2274	23.3945
1102	Fermitin family member 2 OS=Rattus norvegicus OX=10116 GN=Fermt2 PE=1 SV=1	Fermt2	A0A0G2JWC7	20.5518	21.4839	19.4959	17.5681	23.9603	23.215	23.455	23.1713
1103	Fermitin family member 3 OS=Rattus norvegicus OX=10116 GN=Fermt3 PE=1 SV=1	Fermt3	B2GVB9	20.3735	19.6977	20.5898	20.7383	16.7466	16.6167	18.599	NaN
1104	Ferritin heavy chain OS=Rattus norvegicus OX=10116 GN=Fth1 PE=1 SV=3	Fth1	P19132	20.037	19.5443	19.8402	20.3123	20.3887	20.725	20.7058	20.9119
1105	Ferrochelatase OS=Rattus norvegicus OX=10116 GN=Fech PE=1 SV=1	Fech	D3ZBM3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1106	Fetub protein OS=Rattus norvegicus OX=10116 GN=Fetub PE=1 SV=1	Fetub	Q6IRS6	25.031	25.453	25.7298	25.1957	22.1242	21.7942	21.4625	22.1305
1107	Fibrillin 1 OS=Rattus norvegicus OX=10116 GN=Fbn1 PE=1 SV=1	Fbn1	G3V9M6	18.7414	17.3015	18.793	19.228	20.9988	21.5795	21.0007	21.3065
1108	Fibrillin 2 OS=Rattus norvegicus OX=10116 GN=Fbn2 PE=4 SV=3	Fbn2	F1M5Q4	20.1719	19.657	19.9118	20.4408	17.5499	16.1524	15.7153	18.1755
1109	Fibrinogen beta chain OS=Rattus norvegicus OX=10116 GN=Fgb PE=1 SV=4	Fgb	P14480	29.1805	28.9244	29.0046	29.3041	28.0247	27.7964	27.1388	28.0859
1110	Fibrinogen gamma chain OS=Rattus norvegicus OX=10116 GN=Fgg PE=1 SV=3	Fgg	P02680	28.7808	28.4815	28.4564	28.7027	27.5003	27.2336	26.6821	27.6648
1111	Fibrinogen-like 2 OS=Rattus norvegicus OX=10116 GN=Fgl2 PE=1 SV=1	Fgl2	G3V7P2	21.2398	20.3063	21.1355	20.19	19.9079	18.6542	20.612	20.5256

1112	Fibrinogen-like protein 1 OS=Rattus norvegicus OX=10116 GN=Fgl1 PE=2 SV=1	Fgl1	Q5M8C6	15.7172	16.9257	17.745	17.8221	NaN	14.7836	16.073	NaN
1113	Fibronectin OS=Rattus norvegicus OX=10116 GN=Fn1 PE=1 SV=2	Fn1	A0A096P6L8	19.9361	19.4133	20.2819	19.6095	17.5203	17.8681	NaN	17.4982
1114	Fibronectin OS=Rattus norvegicus OX=10116 GN=Fn1 PE=1 SV=3	Fn1	F1LST1	28.6795	28.4131	28.9167	29.1258	25.87	25.882	25.075	26.4019
1115	Fibulin 2 OS=Rattus norvegicus OX=10116 GN=Fbln2 PE=1 SV=1	Fbln2	G3V6X1	16.3587	16.709	18.0748	15.1259	19.6718	19.9003	19.7806	19.9216
1116	Fibulin-1 OS=Rattus norvegicus OX=10116 GN=Fbln1 PE=1 SV=1	Fbln1	B1WC21	18.9925	18.8867	19.6831	19.6565	22.0274	22.1982	21.4592	21.4336
1117	Fibulin-1 OS=Rattus norvegicus OX=10116 GN=Fbln1 PE=1 SV=1	Fbln1	D3ZQ25	21.6098	20.923	21.9923	21.2595	21.6797	21.7594	21.8953	21.8451
1118	Fibulin-5 OS=Rattus norvegicus OX=10116 GN=Fbln5 PE=2 SV=1	Fbln5	Q9WVH8	17.5472	17.0315	17.8375	16.2113	19.5545	20.3344	19.2976	19.7369
1119	Ficolin (Collagen/fibrinogen domain containing) 1 OS=Rattus norvegicus OX=10116 GN=Fcna PE=1 SV=1	Fcna	Q5M8B4	20.6378	20.8687	20.5436	19.4683	16.927	18.2987	18.5838	18.1687
1120	Filamin A OS=Rattus norvegicus OX=10116 GN=Flna PE=1 SV=1	Flna	C0JPT7	22.6911	23.1247	22.8961	22.0576	23.8103	24.5987	24.2041	24.151
1121	Filamin B OS=Rattus norvegicus OX=10116 GN=Flnb PE=1 SV=1	Flnb	A0A0G2JXT8	NaN	NaN	NaN	NaN	16.6776	19.1368	18.5241	15.8247
1122	Filamin binding LIM protein 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Fblim1 PE=4 SV=1	Fblim1	A0A0G2K995	NaN	14.783	NaN	14.5023	18.7089	19.8701	19.564	19.277
1123	Filamin-A-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Filip1 PE=1 SV=2	Filip1	F1LM79	18.0949	18.7673	18.2707	18.8138	19.4553	20.5879	19.7977	19.7753
1124	Filamin-C OS=Rattus norvegicus OX=10116 GN=Flnc PE=1 SV=1	Flnc	D3ZHA0	22.5852	22.7627	22.9997	23.32	26.5881	26.8787	26.8531	26.4491
1125	Flap endonuclease 1 OS=Rattus norvegicus OX=10116 GN=Fen1 PE=2 SV=1	Fen1	Q5XIP6	NaN	NaN	NaN	NaN	18.0477	NaN	NaN	NaN
1126	FLII, actin-remodeling protein OS=Rattus norvegicus OX=10116 GN=Flii PE=1 SV=1	Flii	Q5RKI5	16.7059	15.0742	14.1176	17.6666	20.2343	21.1503	21.0773	21.02
1127	FLN29 gene product, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Trafd1 PE=1 SV=1	Trafd1	G3V959	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1128	FMR1 autosomal homolog 2 OS=Rattus norvegicus OX=10116 GN=Fxr2 PE=1 SV=1	Fxr2	B1H2A6	NaN	NaN	NaN	NaN	17.7368	19.6773	17.4996	18.2482
1129	Focal adhesion kinase 1 OS=Rattus norvegicus OX=10116 GN=Ptk2 PE=1 SV=1	Ptk2	A0A0G2KAT5	14.9639	15.0494	15.5452	NaN	18.4739	17.887	16.2379	18.1279
1130	Folliculin OS=Rattus norvegicus OX=10116 GN=Flcn PE=1 SV=1	Flcn	Q76JQ2	NaN	NaN	NaN	NaN	17.5186	16.4421	NaN	17.0467
1131	Follistatin-related protein 1 OS=Rattus norvegicus OX=10116 GN=Fstl1 PE=4 SV=3	Fstl1	F8WG88	18.0767	15.2888	18.1635	15.1533	NaN	16.8541	NaN	16.9737
1132	Forkhead box K1 OS=Rattus norvegicus OX=10116 GN=Foxk1 PE=1 SV=2	Foxk1	D3ZU55	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1133	Formin-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Fnbp1 PE=1 SV=3	Fnbp1	F1LZF2	NaN	NaN	14.911	NaN	16.9755	16.1682	15.9159	NaN
1134	Formin-like 3 OS=Rattus norvegicus OX=10116 GN=Fmnl3 PE=1 SV=1	Fmnl3	A0A0G2JXC2	NaN	NaN	NaN	NaN	17.0969	17.1109	NaN	13.99
1135	Four and a half LIM domains 1 OS=Rattus norvegicus OX=10116 GN=Fhl1 PE=1 SV=1	Fhl1	Q6P792	20.1478	20.2524	20.8268	19.7063	22.4787	23.7283	23.8569	22.7479
1136	Four and a half LIM domains protein 2 OS=Rattus norvegicus OX=10116 GN=Fhl2 PE=1 SV=1	Fhl2	O35115	NaN	15.9116	NaN	NaN	20.4499	20.3381	20.2028	19.8826
1137	Fragile X mental retardation syndrome-related protein 1 OS=Rattus norvegicus OX=10116 GN=Fxr1 PE=1 SV=1	Fxr1	Q5XI81	NaN	16.2435	16.0526	15.9412	21.1119	22.0799	21.0847	21.0094
1138	Fructose-bisphosphate aldolase A OS=Rattus norvegicus OX=10116 GN=Aldoa PE=1 SV=2	Aldoa	P05065	22.7817	23.4674	23.4398	22.967	25.9831	25.8841	25.9748	25.6977
1139	Fructose-bisphosphate aldolase B OS=Rattus norvegicus OX=10116 GN=Aldob PE=1 SV=2	Aldob	P00884	15.9222	16.5539	16.0528	15.7782	18.3922	NaN	NaN	17.7906
1140	FRY microtubule-binding protein OS=Rattus norvegicus OX=10116 GN=Fry PE=1 SV=3	Fry	E9PTY6	21.3702	21.46	20.9473	20.6177	21.4528	22.8284	22.5964	22.0752
1141	FRY-like transcription coactivator OS=Rattus norvegicus OX=10116 GN=Fryl PE=1 SV=2	Fryl	D3ZQY4	NaN	NaN	NaN	NaN	17.8107	19.4754	18.5321	17.9928
1142	FTS and Hook-interacting protein OS=Rattus norvegicus OX=10116 GN=Fam160a2 PE=1 SV=1	Fhip1b	Q66H54	NaN	NaN	NaN	NaN	16.2029	17.4337	16.9071	16.17
1143	Fucokinase OS=Rattus norvegicus OX=10116 GN=Fuk PE=1 SV=1	Fcsk	A0A0G2JVI4	NaN	NaN	NaN	NaN	19.1698	19.3137	19.1245	18.1143
1144	Fumarate hydratase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Fh PE=1 SV=1	Fh	P14408	17.2619	17.4934	NaN	14.6712	20.4402	22.1217	22.1425	23.2125
1145	FUS RNA-binding protein OS=Rattus norvegicus OX=10116 GN=Fus PE=1 SV=1	Fus	Q5PQK2	14.2645	NaN	NaN	14.1945	21.0053	20.716	19.713	20.8197
1146	FXYD domain-containing ion transport regulator OS=Rattus norvegicus OX=10116 GN=Fxyd1 PE=1 SV=1	Fxyd1	A0A0H2UHS8	15.3052	17.1151	15.7835	15.7925	20.7158	21.3819	20.6561	20.7343
1147	FYVE and coiled-coil domain containing 1 (Predicted) OS=Rattus norvegicus OX=10116 GN=Fyco1 PE=1 SV=1	Fyco1	D3Z9D2	15.0257	16.5426	NaN	17.0879	15.3449	17.2262	17.1495	17.032
1148	G kinase-anchoring protein 1 OS=Rattus norvegicus OX=10116 GN=Gkap1 PE=1 SV=1	Gkap1	Q5XIG5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1149	G protein beta subunit-like, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Mlst8 PE=1 SV=1	Mlst8	G3V7F1	NaN	14.7864	14.6458	15.5987	NaN	16.5987	17.4487	16.6799
1150	G protein-coupled receptor 21 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Rabgap1 PE=1 SV=1	Rabgap1	D3ZX42	16.8538	17.0165	18.3779	NaN	20.392	19.9907	20.0274	19.5973
1151	G protein-coupled receptor kinase interacting ArfGAP 2 OS=Rattus norvegicus OX=10116 GN=Git2 PE=1 SV=1	Git2	Q66H91	18.9168	19.7526	20.1134	18.3812	21.4398	22.0837	21.9836	21.7303
1152	G3BP stress granule assembly factor 1 OS=Rattus norvegicus OX=10116 GN=G3bp1 PE=1 SV=1	G3bp1	D3ZYS7	17.7149	16.6165	15.899	17.3659	21.7546	22.8635	21.8742	21.6306
1153	G3BP stress granule assembly factor 2 OS=Rattus norvegicus OX=10116 GN=G3bp2 PE=1 SV=1	G3bp2	Q6AY21	NaN	NaN	NaN	NaN	20.8756	21.6157	20.5904	20.4518
1154	Galactokinase 1 OS=Rattus norvegicus OX=10116 GN=Galk1 PE=1 SV=1	Galk1	Q5RKH2	19.4249	15.2956	19.6763	19.5726	22.1443	22.2127	22.8719	22.7324
1155	Galactose-4-epimerase, UDP, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Gale PE=1 SV=1	Gale	Q4QRB0	NaN	NaN	NaN	NaN	NaN	NaN	17.1247	16.8419
1156	Galanin peptides OS=Rattus norvegicus OX=10116 GN=Gal PE=1 SV=1	Gal	P10683	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1157	Galectin OS=Rattus norvegicus OX=10116 GN=Lgals9 PE=1 SV=1	Lgals9	G3V7N8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1158	Galectin OS=Rattus norvegicus OX=10116 GN=Lgalsl PE=1 SV=1	Lgalsl	B4F7A3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1159	Galectin-1 OS=Rattus norvegicus OX=10116 GN=Lgals1 PE=1 SV=2	Lgals1	P11762	20.6851	21.1018	21.0689	21.4727	23.195	23.562	23.7198	23.41
1160	Galectin-3-binding protein OS=Rattus norvegicus OX=10116 GN=Lgals3bp PE=1 SV=2	Lgals3bp	O70513	16.0964	16.1361	17.9209	17.0714	15.1583	NaN	NaN	NaN
1161	Gamma-enolase OS=Rattus norvegicus OX=10116 GN=Eno2 PE=1 SV=2	Eno2	P07323	NaN	16.8176	15.2231	15.6402	NaN	19.1683	19.8324	18.9923
1162	Gamma-glutamyl cyclotransferase OS=Rattus norvegicus OX=10116 GN=Ggct PE=1 SV=1	Ggct	D3ZPV8	NaN	18.1933	15.4	15.5969	NaN	NaN	NaN	NaN
1163	Gamma-tubulin complex component OS=Rattus norvegicus OX=10116 GN=Tubgcp2 PE=1 SV=1	Tubgcp2	B2RYP8	16.3006	15.3362	15.6846	16.9049	17.6511	18.7369	18.5672	16.7987
1164	Gamma-tubulin complex component OS=Rattus norvegicus OX=10116 GN=Tubgcp3 PE=1 SV=1	Tubgcp3	A0A0G2JUU7	NaN	NaN	NaN	NaN	20.2071	19.6256	19.2985	19.6582

1165	Gap junction alpha-1 protein OS=Rattus norvegicus OX=10116 GN=Gja1 PE=1 SV=2	Gja1	P08050	NaN	NaN	NaN	16.9207	19.0944	19.1868	18.1588	18.9951
1166	Gasdermin A OS=Rattus norvegicus OX=10116 GN=Gsdma PE=4 SV=1	Gsdma	D3ZA32	14.5757	17.9657	14.2836	17.0602	NaN	15.5972	NaN	NaN
1167	GCN1 eIF2 alpha kinase activator-like 1 OS=Rattus norvegicus OX=10116 GN=Gcn1 PE=1 SV=3	Gcn1	F1LRI5	18.5031	18.8388	18.3135	18.6484	22.8119	22.8562	22.8859	22.8158
1168	GDP-mannose pyrophosphorylase B OS=Rattus norvegicus OX=10116 GN=Gmppb PE=1 SV=1	Gmppb	D4A746	NaN	NaN	NaN	NaN	NaN	15.8795	NaN	NaN
1169	Gelsolin OS=Rattus norvegicus OX=10116 GN=Gsn PE=1 SV=1	Gsn	Q68FP1	25.1015	24.2164	25.2172	25.2519	25.669	25.1947	25.2636	25.0977
1170	Gem (nuclear organelle)-associated protein 5 OS=Rattus norvegicus OX=10116 GN=Gemin5 PE=1 SV=2	Gemin5	D3ZGD0	NaN	NaN	NaN	NaN	16.4935	17.3612	16.8518	16.8094
1171	General transcription factor IIF subunit 1 OS=Rattus norvegicus OX=10116 GN=Gtf2f1 PE=1 SV=1	Gtf2f1	Q6AY96	NaN	NaN	NaN	NaN	15.1736	13.7658	14.2174	14.5038
1172	General vesicular transport factor p115 OS=Rattus norvegicus OX=10116 GN=Uso1 PE=1 SV=1	Uso1	P41542	16.518	17.4561	15.6058	13.7111	20.2413	19.7215	20.7088	20.2447
1173	Gephyrin OS=Rattus norvegicus OX=10116 GN=Gphn PE=1 SV=3	Gphn	Q03555	18.1022	18.4209	18.4154	16.7553	19.2789	20.3961	20.0156	19.6987
1174	Geranylgeranyl transferase type-1 subunit beta OS=Rattus norvegicus OX=10116 GN=Pggt1b PE=1 SV=1	Pggt1b	P53610	NaN	NaN	NaN	NaN	NaN	16.6862	16.7224	16.6511
1175	Geranylgeranyl transferase type-2 subunit alpha OS=Rattus norvegicus OX=10116 GN=Rabggta PE=1 SV=1	Rabggta	Q08602	20.2906	19.5812	19.5988	19.4617	20.0344	22.4396	22.8628	22.7357
1176	Geranylgeranyl transferase type-2 subunit beta OS=Rattus norvegicus OX=10116 GN=Rabggtb PE=1 SV=1	Rabggtb	F1LSM6	NaN	NaN	NaN	NaN	16.719	17.9421	17.635	16.6693
1177	GIMAP4 OS=Rattus norvegicus OX=10116 GN=Gimap4 PE=1 SV=1	Gimap4	Q0R3X4	NaN	NaN	NaN	NaN	19.0897	16.0163	17.0657	16.7647
1178	GLI pathogenesis-related 2 OS=Rattus norvegicus OX=10116 GN=Glipr2 PE=1 SV=3	Glipr2	F1M5V2	19.3956	20.1525	19.765	19.5178	21.8981	22.2541	21.8629	22.1929
1179	Glia maturation factor beta OS=Rattus norvegicus OX=10116 GN=Gmfb PE=1 SV=2	Gmfb	Q63228	NaN	NaN	NaN	NaN	17.9647	16.9993	17.6361	NaN
1180	Glioblastoma amplified sequence OS=Rattus norvegicus OX=10116 GN=Nipsnap2 PE=1 SV=1	Nipsnap2	Q5RK08	NaN	15.8582	NaN	NaN	16.7242	19.6575	18.6223	19.1209
1181	Globin a1 OS=Rattus norvegicus OX=10116 GN=LOC103694855 PE=1 SV=1	Hbb-b1	Q62669	25.7118	25.4656	25.9393	25.9364	23.3082	22.726	23.1175	22.9879
1182	Globin a4 OS=Rattus norvegicus OX=10116 GN=Hbb PE=1 SV=1	Hbb	A0A0G2JSW3	24.5058	24.0538	24.3588	21.1965	21.2107	21.5885	20.5805	NaN
1183	Globin c2 OS=Rattus norvegicus OX=10116 GN=Hba-a2 PE=1 SV=1	Hba-a2	A0A0G2JSV6	28.7459	28.4253	28.6163	28.5708	26.3693	26.242	26.0998	26.1992
1184	Globin e1 OS=Rattus norvegicus OX=10116 GN=Hbz PE=3 SV=1	Hbz	G3V8R3	NaN	16.0278	15.7259	16.0281	17.0305	NaN	17.1472	17.1512
1185	Glucan (1,4-alpha-), branching enzyme 1 (Fragment) OS=Rattus norvegicus OX=10116 GN=Gbe1 PE=1 SV=1	Gbe1	A0A096MJY6	NaN	NaN	NaN	NaN	18.4688	17.5651	17.6983	18.5311
1186	Glucocorticoid receptor OS=Rattus norvegicus OX=10116 GN=Nr3c1 PE=1 SV=2	Nr3c1	P06536	14.7693	13.7162	NaN	NaN	17.9294	18.4931	17.232	17.9408
1187	Glucokinase regulatory protein OS=Rattus norvegicus OX=10116 GN=Gckr PE=1 SV=3	Gckr	Q07071	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1188	Glucose-6-phosphate 1-dehydrogenase OS=Rattus norvegicus OX=10116 GN=G6pdx PE=1 SV=3	G6pd	P05370	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1189	Glucose-6-phosphate isomerase OS=Rattus norvegicus OX=10116 GN=Gpi PE=1 SV=1	Gpi	Q6P6V0	18.4777	19.1222	19.2825	18.4472	21.4924	21.897	21.7758	21.5693
1190	Glutamate dehydrogenase 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Glud1 PE=1 SV=2	Glud1	P10860	18.1804	18.0187	18.764	18.797	15.3541	18.226	17.4617	NaN
1191	Glutamate--cysteine ligase regulatory subunit OS=Rattus norvegicus OX=10116 GN=Gclm PE=1 SV=1	Gclm	P48508	18.2464	18.1969	16.4128	19.6206	22.1776	21.2354	20.9166	20.7994
1192	Glutamate-rich WD repeat-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Grwd1 PE=1 SV=1	Grwd1	A0A140TAH3	NaN	NaN	NaN	NaN	NaN	NaN	15.4713	16.1849
1193	Glutamine fructose-6-phosphate transaminase 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Gfpt1 PE=1 SV=1	Gfpt1	A0A0G2KB56	18.8395	16.5756	19.0731	18.8985	21.5313	21.1018	21.3308	21.3496
1194	Glutamine synthetase OS=Rattus norvegicus OX=10116 GN=Glul PE=1 SV=3	Glul	P09606	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1195	Glutamine-rich 1 OS=Rattus norvegicus OX=10116 GN=Qrich1 PE=1 SV=1	Qrich1	A0A0G2JX16	NaN	NaN	NaN	NaN	20.9441	20.5976	20.855	20.461
1196	Glutamine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Qars PE=1 SV=1	Qars1	Q66H61	19.3964	19.6931	18.5329	19.0967	23.6914	23.0461	23.4312	23.364
1197	Glutamyl aminopeptidase OS=Rattus norvegicus OX=10116 GN=Enpep PE=1 SV=2	Enpep	P50123	18.9332	17.9842	17.8703	17.3484	20.9029	19.9525	20.2066	20.4264
1198	Glutamyl-prolyl-tRNA synthetase OS=Rattus norvegicus OX=10116 GN=Eprs PE=1 SV=1	Eprs	A0A0G2JZI2	20.7441	20.6073	20.7011	19.8596	25.8304	25.395	25.6587	25.6569
1199	Glutaredoxin-1 OS=Rattus norvegicus OX=10116 GN=Glrx PE=3 SV=3	Glrx	Q9ESH6	14.2984	NaN	NaN	NaN	16.8462	NaN	17.1399	16.1253
1200	Glutaredoxin-3 OS=Rattus norvegicus OX=10116 GN=Glrx3 PE=1 SV=2	Glrx3	Q9JLZ1	17.6949	17.6272	18.636	16.1549	22.4691	22.9419	23.1173	22.6515
1201	Glutathione peroxidase 1 OS=Rattus norvegicus OX=10116 GN=Gpx1 PE=1 SV=4	Gpx1	P04041	19.1286	19.1832	19.2173	19.8308	19.9303	19.8598	19.9771	19.5377
1202	Glutathione peroxidase 3 OS=Rattus norvegicus OX=10116 GN=Gpx3 PE=2 SV=2	Gpx3	P23764	22.9719	22.5711	23.2484	24.9103	18.326	17.018	18.2408	17.0785
1203	Glutathione peroxidase OS=Rattus norvegicus OX=10116 GN=Gpx4 PE=1 SV=2	Gpx4	F8WFK6	22.0733	21.9398	22.6759	23.0218	22.3167	21.3607	21.4887	21.3042
1204	Glutathione S-transferase Mu 5 OS=Rattus norvegicus OX=10116 GN=Gstm5 PE=1 SV=3	Gstm5	Q9Z1B2	20.5851	20.6043	20.1145	19.4423	20.6164	20.9096	22.2967	22.0341
1205	Glutathione S-transferase P OS=Rattus norvegicus OX=10116 GN=Gstp1 PE=1 SV=2	Gstp1	P04906	18.4493	19.1813	18.2978	20.6367	20.906	20.837	20.9051	20.3613
1206	Glutathione S-transferase theta-2 OS=Rattus norvegicus OX=10116 GN=Gstt2 PE=1 SV=3	Gstt2	P30713	NaN	NaN	NaN	NaN	18.4816	17.9978	17.711	18.5461
1207	Glutathione S-transferase Yb-3 OS=Rattus norvegicus OX=10116 GN=Gstm3 PE=1 SV=2	Gstm7	P08009	NaN	16.1427	NaN	NaN	18.9097	17.9947	18.5026	18.3564
1208	Glutathione S-transferase, mu 7 OS=Rattus norvegicus OX=10116 GN=Gstm7 PE=1 SV=1	Gstm7	A0A0G2K4U2	NaN	NaN	NaN	NaN	16.1094	NaN	17.1746	16.9943
1209	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus OX=10116 GN=Gapdh PE=1 SV=3	Gapdh	P04797	27.5709	27.0421	27.4043	27.4227	30.2582	30.2318	30.6174	30.6947
1210	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus OX=10116 PE=1 SV=1	)A0G2K7M1_R	A0A0G2K7M1	16.8372	20.0767	16.6344	19.536	17.1274	17.9575	NaN	16.4708
1211	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus OX=10116 PE=1 SV=1	M0R660_RAT	M0R660	20.0729	19.52	19.8757	21.3681	24.0443	24.6855	24.837	25.5194
1212	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus OX=10116 PE=1 SV=2	E9PTV9_RAT	E9PTV9	NaN	NaN	16.8595	NaN	18.4841	18.0073	18.6285	18.4715
1213	Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Rattus norvegicus OX=10116 GN=Gpd1l PE=1 SV=1	Gpd1l	D3ZAP9	16.0443	15.7069	NaN	15.7118	19.7563	21.99	22.5158	21.9616
1214	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Rattus norvegicus OX=10116 GN=Gpd1 PE=1 SV=4	Gpd1	O35077	19.3984	18.6501	19.9666	19.6628	20.3569	21.5898	21.6777	21.0195
1215	Glycine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Gars PE=1 SV=1	Gars1	G3V7G8	17.9388	18.3834	17.5719	18.6874	23.9675	23.0726	23.6794	23.8074
1216	Glycogen [starch] synthase, muscle OS=Rattus norvegicus OX=10116 GN=Gys1 PE=1 SV=1	Gys1	A2RRU1	17.3023	16.3219	17.6265	17.2249	22.9831	21.92	22.6364	23.2159
1217	Glycogen phosphorylase, brain form (Fragment) OS=Rattus norvegicus OX=10116 GN=Pygb PE=1 SV=3	Pygb	P53534	NaN	NaN	NaN	NaN	16.7178	21.3649	21.3474	NaN

1218	Glycogen synthase kinase 3 beta, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Gsk3b PE=1 SV=1	Gsk3b	A0A0G2JSH4	NaN	NaN	14.1371	NaN	18.9475	18.8317	18.5235	18.6124
1219	Glycogen synthase kinase-3 alpha OS=Rattus norvegicus OX=10116 GN=Gsk3a PE=1 SV=1	Gsk3a	P18265	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1220	Glycogenin-1 OS=Rattus norvegicus OX=10116 GN=Gyg1 PE=2 SV=4	Gyg1	O08730	17.9578	15.5303	15.6219	NaN	25.5905	23.8934	25.1136	25.6287
1221	Glycolipid transfer protein OS=Rattus norvegicus OX=10116 GN=GLTP PE=2 SV=1	Gltp	B0BNM9	NaN	NaN	14.2708	15.6416	18.4413	NaN	18.5183	NaN
1222	Glycophorin-C OS=Rattus norvegicus OX=10116 GN=Gypc PE=1 SV=1	Gypc	Q6XFR6	18.6412	18.2613	17.7609	18.5526	17.9534	17.606	19.3971	15.4612
1223	Glycoprotein 5, platelet OS=Rattus norvegicus OX=10116 GN=NEWGENE_2724 PE=4 SV=1	Gp5	G3V9H9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1224	Glycoprotein 9 OS=Rattus norvegicus OX=10116 GN=Gp9 PE=2 SV=1	Gp9	Q4AEG0	17.3043	16.7512	17.4979	NaN	NaN	NaN	NaN	NaN
1225	Glycoprotein Ib platelet subunit alpha OS=Rattus norvegicus OX=10116 GN=Gp1ba PE=1 SV=1	Gp1ba	D3ZQU7	16.9443	16.7357	16.7612	15.9873	NaN	NaN	NaN	NaN
1226	Glycosylation dependent cell adhesion molecule 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Glycam1 PE=4 SV=	Glycam1	G3V9L4	15.7112	15.7584	16.5003	19.93	NaN	NaN	NaN	NaN
1227	Glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Gpld1 PE=1 S	Gpld1	G3V8B1	24.3105	23.5568	23.2861	23.3629	20.7774	20.8036	20.9953	21.0592
1228	Glypican 4 OS=Rattus norvegicus OX=10116 GN=Gpc4 PE=1 SV=1	Gpc4	Q642B0	NaN	NaN	NaN	NaN	18.0228	18.5492	NaN	17.8147
1229	Glypican-1 OS=Rattus norvegicus OX=10116 GN=Gpc1 PE=1 SV=1	Gpc1	P35053	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1230	GM2 ganglioside activator OS=Rattus norvegicus OX=10116 GN=Gm2a PE=1 SV=1	Gm2a	Q6IN37	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1231	GMP reductase OS=Rattus norvegicus OX=10116 GN=Gmpr PE=3 SV=1	Gmpr	F1LRV6	16.8272	18.3773	18.0261	17.6099	20.1939	20.0068	19.8127	20.2055
1232	GMP synthase [glutamine-hydrolyzing] OS=Rattus norvegicus OX=10116 GN=Gmps PE=1 SV=1	Gmps	Q4V7C6	17.3921	17.858	18.2479	15.5486	21.8111	21.6862	22.2649	22.7858
1233	Golgi apparatus protein 1 OS=Rattus norvegicus OX=10116 GN=Glg1 PE=1 SV=1	Glg1	G3V8G5	15.4255	17.6727	16.7704	15.9203	20.9506	21.6854	21.3875	21.396
1234	Golgi associated, gamma adaptin ear containing, ARF binding protein 2, isoform CRA_a OS=Rattus norvegicus OX=10116 GI	Gga2	G3V8F7	NaN	NaN	NaN	NaN	17.6687	17.8662	17.9357	18.0702
1235	Golgi brefeldin A-resistant guanine nucleotide exchange factor 1 OS=Rattus norvegicus OX=10116 GN=Gbf1 PE=1 SV=2	Gbf1	F1M8X9	19.2215	19.1319	18.9491	17.6298	20.5016	21.1401	21.0633	21.0425
1236	Golgi membrane protein 1 OS=Rattus norvegicus OX=10116 GN=Golm1 PE=1 SV=2	Golm1	D4AEL2	NaN	NaN	NaN	NaN	17.217	NaN	17.4047	NaN
1237	Golgi phosphoprotein 3 OS=Rattus norvegicus OX=10116 GN=Golph3 PE=1 SV=1	Golph3	Q569C9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1238	Golgi reassembly-stacking protein 2 OS=Rattus norvegicus OX=10116 GN=Gorasp2 PE=1 SV=1	Gorasp2	Q68G33	17.1294	20.7256	17.7387	15.0933	22.4861	22.2325	22.485	22.5213
1239	Golgi SNAP receptor complex member 2 OS=Rattus norvegicus OX=10116 GN=Gosr2 PE=1 SV=2	Gosr2	O35165	17.2072	NaN	NaN	18.1546	17.796	17.7626	17.2819	17.394
1240	Golgi to ER traffic protein 4 OS=Rattus norvegicus OX=10116 GN=Get4 PE=1 SV=2	Get4	F1LXF5	16.6621	18.0084	18.3698	14.2846	21.2552	20.6263	21.0247	20.5911
1241	Golgi-associated, gamma adaptin ear-containing, ARF-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Gga1 PE=1 S	Gga1	Q5FVF3	16.4223	15.6658	NaN	17.1308	21.3621	21.2703	20.9228	20.9314
1242	Golgin A3 OS=Rattus norvegicus OX=10116 GN=Golga3 PE=1 SV=1	Golga3	D3ZLD5	NaN	10.7169	NaN	NaN	NaN	13.5677	NaN	13.8227
1243	GPN-loop GTPase OS=Rattus norvegicus OX=10116 GN=Gpn1 PE=1 SV=1	Gpn1	B1WBZ7	NaN	NaN	14.1134	NaN	NaN	NaN	NaN	17.3878
1244	G-protein coupled receptor-associated sorting protein 1 OS=Rattus norvegicus OX=10116 GN=Gprasp1 PE=1 SV=1	Gprasp1	M0R9R0	NaN	NaN	NaN	NaN	NaN	16.3895	15.8821	NaN
1245	G-protein signalling modulator 1 (AGS3-like, C. elegans), isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Gpsm1 PE=	Gpsm1	G3V9X2	NaN	14.437	NaN	NaN	18.8731	19.2921	19.5147	19.7121
1246	Grancalcin OS=Rattus norvegicus OX=10116 GN=Gca PE=1 SV=2	Gca	D3ZYI0	NaN	NaN	NaN	NaN	18.5147	17.3331	17.7167	17.872
1247	Granulin, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Grn PE=4 SV=1	Grn	G3V8V1	16.8407	16.8303	17.572	18.3455	18.8266	18.727	NaN	NaN
1248	GRB10-interacting GYF protein 1 OS=Rattus norvegicus OX=10116 GN=Gigyf1 PE=1 SV=1	Gigyf1	D3ZQJ3	NaN	NaN	NaN	NaN	16.8692	16.4284	15.9282	16.5936
1249	GRB2-associated-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Gab1 PE=1 SV=1	Gab1	A0A0G2JZD5	16.1007	NaN	NaN	NaN	19.5882	20.3393	20.1118	19.3475
1250	G-rich RNA sequence-binding factor 1 OS=Rattus norvegicus OX=10116 GN=Grsf1 PE=1 SV=2	Grsf1	F1LRK4	NaN	NaN	16.1844	16.3352	20.7501	22.3597	21.9716	21.5699
1251	Group specific component OS=Rattus norvegicus OX=10116 GN=Gc PE=1 SV=1	Gc	Q68FY4	25.2028	24.9437	25.5013	25.2873	21.4549	21.3256	21.1159	21.355
1252	Growth factor receptor-bound protein 10 OS=Rattus norvegicus OX=10116 GN=Grb10 PE=4 SV=1	Grb10	A0A0G2JYJ1	15.7902	16.6412	17.0381	16.1531	20.8195	21.1998	20.6527	20.2641
1253	Growth factor receptor-bound protein 14 OS=Rattus norvegicus OX=10116 GN=Grb14 PE=1 SV=1	Grb14	O88900	NaN	NaN	NaN	NaN	16.6239	17.4508	17.2769	16.8417
1254	Growth factor receptor-bound protein 2 OS=Rattus norvegicus OX=10116 GN=Grb2 PE=1 SV=1	Grb2	P62994	NaN	NaN	15.4781	NaN	19.5655	19.3735	19.5335	19.2245
1255	GTPase KRas OS=Rattus norvegicus OX=10116 GN=Kras PE=1 SV=3	Kras	P08644	15.7423	18.0296	16.4741	17.6286	18.8313	19.174	16.986	18.6381
1256	GTPase, IMAP family member 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=ian2 PE=1 SV=1	ian2	Q3LF76	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1257	GTPase-activating protein and VPS9 domains 1 OS=Rattus norvegicus OX=10116 GN=Gapvd1 PE=1 SV=3	Gapvd1	D4A022	17.769	17.4165	18.0342	17.6994	20.0209	19.6348	19.3634	20.0622
1258	GTP-binding nuclear protein Ran OS=Rattus norvegicus OX=10116 GN=Ran PE=1 SV=3	Ran	P62828	21.2189	20.5915	21.4181	21.2865	23.409	22.7055	23.2715	23.1015
1259	GTP-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Gtpbp1 PE=1 SV=1	Gtpbp1	D2XV59	17.5247	NaN	NaN	13.897	19.4131	19.4763	20.2017	20.9299
1260	GTP-binding protein OS=Rattus norvegicus OX=10116 GN=Rem1 PE=2 SV=1	Rem1	Q4KLY1	NaN	NaN	NaN	NaN	17.1171	NaN	NaN	16.9565
1261	GTP-binding protein OS=Rattus norvegicus OX=10116 GN=Rrad PE=3 SV=1	Rrad	G3V7K9	15.0269	NaN	16.4037	17.8001	22.7503	22.3828	22.1277	21.8699
1262	GTP-binding protein Rheb OS=Rattus norvegicus OX=10116 GN=Rheb PE=1 SV=1	Rheb	Q62639	15.2935	15.154	15.6997	16.6933	22.3021	21.6362	21.8084	21.4752
1263	GTP-binding protein SAR1b OS=Rattus norvegicus OX=10116 GN=Sar1b PE=2 SV=1	Sar1b	Q5HZY2	15.1269	18.7146	18.0376	16.9365	22.4135	22.0423	22.3909	22.4876
1264	Guanine nucleotide binding protein, alpha 11 OS=Rattus norvegicus OX=10116 GN=Gna11 PE=1 SV=1	Gna11	G3V6Q6	17.8297	16.7796	16.6487	18.3801	19.8054	19.266	19.2045	19.3576
1265	Guanine nucleotide binding protein, alpha q polypeptide, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Gnaq PE=1	Gnaq	D4AE68	NaN	NaN	15.7221	NaN	17.8433	18.4919	17.7166	18.3796
1266	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Rattus norvegicus OX=10116 GN=Gnai2 PE=1 SV=3	Gnai2	P04897	22.0991	22.1355	22.0999	22.162	24.2404	23.9674	23.8795	23.9876
1267	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Rattus norvegicus OX=10116 GN=Gng5 PE=3 SV	Gng5	P63219	19.4185	19.7589	20.0898	19.1102	22.1397	22.0718	21.723	21.8192
1268	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Gnb1 PE=1 SV=4	Gnb1	P54311	21.6235	21.8886	21.8363	21.2201	24.0599	24.0161	23.7631	23.9478
1269	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Rattus norvegicus OX=10116 GN=Gnb2 PE=1 SV=4	Gnb2	P54313	21.051	20.9542	20.7781	20.5383	22.175	22.7688	22.4039	22.573
1270	Guanine nucleotide-binding protein G(k) subunit alpha OS=Rattus norvegicus OX=10116 GN=Gnai3 PE=1 SV=3	Gnai3	P08753	17.8621	18.5113	18.5112	16.6087	19.855	19.8551	19.7321	19.8371

1271	Guanine nucleotide-binding protein G(o) subunit alpha OS=Rattus norvegicus OX=10116 GN=Gnao1 PE=1 SV=2	Gnao1	P59215	16.7976	17.7784	16.1887	16.6882	21.9507	21.7705	21.6231	21.6197
1272	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Rattus norvegicus OX=10116 GN=Gnas PE=1 SV=	Gnas	Q63803	18.6373	18.7861	19.2884	19.0083	20.1093	19.9208	20.2812	20.4079
1273	Guanine nucleotide-binding protein subunit beta-4 OS=Rattus norvegicus OX=10116 GN=Gnb4 PE=2 SV=4	Gnb4	O35353	16.3477	15.7478	16.5973	16.4129	18.1142	18.192	17.6419	NaN
1274	Guanine nucleotide-binding protein subunit gamma OS=Rattus norvegicus OX=10116 GN=Gng10 PE=1 SV=1	Gng10	Q3KRE3	18.2668	18.9576	18.7276	16.9217	20.5507	20.7349	20.3241	20.2693
1275	Guanine nucleotide-binding protein subunit gamma OS=Rattus norvegicus OX=10116 GN=Gng12 PE=1 SV=1	Gng12	G3V6P8	19.9138	19.6292	19.3748	19.2442	21.6499	21.5897	21.0512	21.4996
1276	Guanine nucleotide-binding protein subunit gamma OS=Rattus norvegicus OX=10116 GN=Gng2 PE=1 SV=2	Gng2	M0RBJ0	15.6721	16.3673	16.3377	16.2625	18.3003	18.2411	17.9987	18.3276
1277	Guanylate kinase 1 OS=Rattus norvegicus OX=10116 GN=Guk1 PE=1 SV=2	Guk1	E9PTV0	16.2827	16.1783	16.5818	16.8999	15.7166	16.0876	17.0421	17.167
1278	Gup1, glycerol uptake/transporter homolog (Yeast) (Predicted) OS=Rattus norvegicus OX=10116 GN=Hhatl PE=3 SV=1	Hhatl	D4A9P9	NaN	NaN	NaN	NaN	NaN	16.8275	16.3829	NaN
1279	H2-K region expressed gene 2, rat orthologue OS=Rattus norvegicus OX=10116 GN=Pfdn6 PE=1 SV=1	Pfdn6	Q6MGC4	15.2566	15.4317	15.8901	NaN	19.7395	17.1206	18.4858	19.5141
1280	Haloacid dehalogenase-like hydrolase domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Hdhd2 PE=1 SV=	Hdhd2	Q6QI86	16.5209	15.6693	NaN	15.7399	18.2254	18.631	NaN	17.4313
1281	Hamartin OS=Rattus norvegicus OX=10116 GN=Tsc1 PE=1 SV=1	Tsc1	Q9Z136	NaN	16.248	NaN	14.8935	18.522	19.0872	18.9091	17.4125
1282	Haptoglobin OS=Rattus norvegicus OX=10116 GN=Hp PE=1 SV=3	Hp	P06866	24.3552	23.7958	24.8452	25.3943	20.8572	20.4157	19.6479	19.562
1283	HAUS augmin-like complex, subunit 7 OS=Rattus norvegicus OX=10116 GN=Haus7 PE=1 SV=1	Haus7	B0BN53	15.8582	16.2517	17.3592	15.9092	18.2546	17.6868	15.9034	18.0756
1284	HBS1-like protein OS=Rattus norvegicus OX=10116 GN=Hbs1l PE=1 SV=1	Hbs1l	A0A0G2K2P6	14.5427	16.1326	15.8568	16.8298	20.5531	21.0036	21.1874	20.4746
1285	Heart development protein with EGF-like domains 1 OS=Rattus norvegicus OX=10116 GN=Heg1 PE=1 SV=3	Heg1	F1M9I4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1286	Heat shock 27kD protein family, member 7 (Cardiovascular) OS=Rattus norvegicus OX=10116 GN=Hspb7 PE=2 SV=1	Hspb7	B5DFG4	17.8907	16.3936	17.852	17.6256	23.5856	22.6392	23.031	23.1221
1287	Heat shock 27kDa protein 1 OS=Rattus norvegicus OX=10116 GN=Hspb1 PE=1 SV=1	Hspb1	G3V913	23.1485	22.4421	22.7928	22.9454	27.7431	27.0628	27.7816	27.7406
1288	Heat shock 27kDa protein 3 OS=Rattus norvegicus OX=10116 GN=Hspb3 PE=3 SV=1	Hspb3	G3V7G6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1289	Heat shock 70 kDa protein 14 OS=Rattus norvegicus OX=10116 GN=Hspa14 PE=2 SV=1	Hspa14	Q6AYB4	17.5269	18.7994	15.5308	15.5283	18.2056	19.1566	19.596	19.6228
1290	Heat shock 70 kDa protein 1A OS=Rattus norvegicus OX=10116 GN=Hspa1a PE=2 SV=1	Hspa1a	P0DMW0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1291	Heat shock 70 kDa protein 1-like OS=Rattus norvegicus OX=10116 GN=Hspa1l PE=2 SV=2	Hspa1l	P55063	NaN	15.8319	15.2717	NaN	NaN	NaN	NaN	NaN
1292	Heat shock 70 kDa protein 4 OS=Rattus norvegicus OX=10116 GN=Hspa4 PE=1 SV=1	Hspa4	F1LRV4	21.534	21.3563	22.0268	21.3523	21.4038	21.3452	21.6242	21.6003
1293	Heat shock cognate 71 kDa protein OS=Rattus norvegicus OX=10116 GN=Hspa8 PE=1 SV=1	Hspa8	P63018	23.1811	22.4607	23.0619	23.2135	26.33	26.1728	26.0207	26.0959
1294	Heat shock factor-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Hsbp1 PE=3 SV=1	Hsbp1	Q8K3X8	NaN	NaN	NaN	NaN	17.769	18.1947	17.4199	18.441
1295	Heat shock protein 75 kDa, mitochondrial OS=Rattus norvegicus OX=10116 GN=Trap1 PE=1 SV=1	Trap1	Q5XHZ0	14.528	NaN	17.3885	NaN	NaN	17.1062	NaN	NaN
1296	Heat shock protein beta-2 OS=Rattus norvegicus OX=10116 GN=Hspb2 PE=3 SV=1	Hspb2	O35878	NaN	14.1658	14.4008	NaN	20.0255	19.3857	20.5893	20.8869
1297	Heat shock protein beta-6 OS=Rattus norvegicus OX=10116 GN=Hspb6 PE=1 SV=1	Hspb6	P97541	20.4189	20.4796	20.6107	16.9488	24.1503	23.571	24.1023	24.0271
1298	Heat shock protein beta-8 OS=Rattus norvegicus OX=10116 GN=Hspb8 PE=1 SV=1	Hspb8	Q9EPX0	NaN	NaN	NaN	14.1566	22.5327	22.7145	21.7496	21.4615
1299	Heat shock protein HSP 90-alpha OS=Rattus norvegicus OX=10116 GN=Hsp90aa1 PE=1 SV=3	Hsp90aa1	P82995	20.6273	20.7272	20.85	20.7811	25.5883	24.7207	25.2869	25.3192
1300	Heat shock protein HSP 90-beta OS=Rattus norvegicus OX=10116 GN=Hsp90ab1 PE=1 SV=4	Hsp90ab1	P34058	24.2206	24.0377	24.1149	23.9432	28.4387	27.634	28.1332	28.1342
1301	Hebp1 protein OS=Rattus norvegicus OX=10116 GN=Hebp1 PE=1 SV=1	Hebp1	B4F7C7	NaN	15.7065	15.8598	NaN	17.146	16.6445	17.4962	15.8529
1302	HECT domain E3 ubiquitin protein ligase 1 OS=Rattus norvegicus OX=10116 GN=Hectd1 PE=1 SV=3	Hectd1	D3ZLS5	21.3336	21.3663	20.7094	20.5804	22.3432	21.6813	22.0172	22.129
1303	HECT domain E3 ubiquitin protein ligase 4 OS=Rattus norvegicus OX=10116 GN=Hectd4 PE=1 SV=3	Hectd4	F1LZX5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1304	Heme oxygenase 1 OS=Rattus norvegicus OX=10116 GN=Hmox1 PE=1 SV=1	Hmox1	P06762	16.808	NaN	15.4608	NaN	16.8058	16.8739	NaN	NaN
1305	Heme oxygenase 2 OS=Rattus norvegicus OX=10116 GN=Hmox2 PE=1 SV=1	Hmox2	P23711	NaN	NaN	NaN	NaN	15.7245	16.3699	16.5502	17.1098
1306	Hemoglobin subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Hbb PE=1 SV=3	Hbb	P02091	29.0192	28.5895	28.9111	28.5724	26.4323	26.221	26.0466	25.9806
1307	Hemoglobin subunit beta-2 OS=Rattus norvegicus OX=10116 PE=1 SV=2	Hbb-bs	P11517	26.6304	25.9919	26.5602	26.2464	23.4957	23.4263	23.4567	22.8942
1308	Hemopexin OS=Rattus norvegicus OX=10116 GN=Hpx PE=1 SV=3	Hpx	P20059	23.2918	24.6554	23.8012	22.8321	19.0551	19.7593	18.2352	18.5286
1309	Heparin cofactor 2 OS=Rattus norvegicus OX=10116 GN=Serpind1 PE=1 SV=1	Serpind1	A0A0G2K8K3	23.4582	22.9539	23.3824	23.4407	21.5449	20.5457	21.405	21.8582
1310	Hepatitis B virus x interacting protein (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Lamtor5 PE=1 SV=	Lamtor5	D3ZF11	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1311	Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Rattus norvegicus OX=10116 GN=Hgs PE=1 SV=1	Hgs	A0A140TAH1	19.5376	19.2919	19.3668	18.844	22.5264	21.9494	21.7453	21.7307
1312	Hepatoma-derived growth factor-related protein 2 OS=Rattus norvegicus OX=10116 GN=Hdgfl2 PE=1 SV=2	Hdgfl2	Q925G1	25.62	25.0766	25.6573	26.2303	23.4449	22.6092	22.7915	22.8462
1313	Hermansky-Pudlak syndrome 5 protein homolog OS=Rattus norvegicus OX=10116 GN=Saa4 PE=1 SV=1	Hps5	Q7TMC3	23.6317	23.5171	23.5406	23.1812	20.2531	20.0942	20.5852	20.6383
1314	Heterogeneous nuclear ribonucleoprotein A1 OS=Rattus norvegicus OX=10116 GN=Hnrnpa1 PE=1 SV=3	Hnrnpa1	P04256	15.7837	17.084	NaN	NaN	19.4051	19.6183	19.1752	19.0207
1315	Heterogeneous nuclear ribonucleoprotein A3 OS=Rattus norvegicus OX=10116 GN=Hnrnpa3 PE=1 SV=1	Hnrnpa3	Q6URK4	NaN	NaN	NaN	NaN	19.8626	17.4912	NaN	17.918
1316	Heterogeneous nuclear ribonucleoprotein C OS=Rattus norvegicus OX=10116 GN=Hnrnpc PE=1 SV=2	Hnrnpc	G3V9R8	NaN	NaN	NaN	NaN	18.8909	19.2849	18.6974	18.4433
1317	Heterogeneous nuclear ribonucleoprotein D0 OS=Rattus norvegicus OX=10116 GN=Hnrnpd PE=1 SV=2	Hnrnpd	Q9JJ54	18.8138	19.426	18.8355	18.8474	21.6709	19.8926	19.9869	19.4948
1318	Heterogeneous nuclear ribonucleoprotein D-like OS=Rattus norvegicus OX=10116 GN=Hnrnpdl PE=1 SV=1	Hnrnpdl	A0A0G2KAZ7	NaN	NaN	NaN	NaN	17.8974	16.8815	16.3725	16.6742
1319	Heterogeneous nuclear ribonucleoprotein F OS=Rattus norvegicus OX=10116 GN=Hnrnpf PE=1 SV=3	Hnrnpf	Q794E4	18.191	18.1452	14.8674	16.079	23.1887	22.1891	22.4299	22.3919
1320	Heterogeneous nuclear ribonucleoprotein H OS=Rattus norvegicus OX=10116 GN=Hnrnph1 PE=1 SV=1	Hnrnph1	A0A0G2JTG7	17.855	18.1937	17.4963	18.1861	22.1901	21.6042	21.4815	21.5165
1321	Heterogeneous nuclear ribonucleoprotein H2 OS=Rattus norvegicus OX=10116 GN=Hnrnph2 PE=1 SV=1	Hnrnph2	Q6AY09	NaN	NaN	NaN	NaN	17.9819	18.7716	17.7397	18.4734
1322	Heterogeneous nuclear ribonucleoprotein K OS=Rattus norvegicus OX=10116 GN=Hnrnpk PE=1 SV=1	Hnrnpk	Q5D059	18.5456	18.6331	18.7392	19.2979	24.7173	24.3011	24.5794	24.5232
1323	Heterogeneous nuclear ribonucleoprotein L OS=Rattus norvegicus OX=10116 GN=Hnrnpl PE=1 SV=2	Fblim1	F1LQ48	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

1324	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus OX=10116 GN=Hnrnpm PE=1 SV=1	Hnrnpm	F1M3D3	22.7078	22.2211	22.4954	22.0449	25.1901	24.8909	24.7614	24.6292
1325	Heterogeneous nuclear ribonucleoprotein Q OS=Rattus norvegicus OX=10116 GN=Syncrip PE=1 SV=2	Syncrip	M0R735	19.3777	19.17	19.0391	19.6695	21.9084	22.7658	22.3153	22.5242
1326	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus OX=10116 GN=Hnrnpu PE=1 SV=1	Hnrnpu	Q6IMY8	18.3369	18.4885	18.2621	22.6879	22.1049	22.6655	22.416	22.5974
1327	Heterogeneous nuclear ribonucleoprotein U-like 2 OS=Rattus norvegicus OX=10116 GN=Hnrnpul2 PE=1 SV=1	Hnrnpul2	D4ABT8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1328	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus OX=10116 GN=Hnrnpa2b1 PE=1 SV=1	Hnrnpa2b1	A7VJC2	16.4977	17.823	16.7945	17.6129	20.053	18.6826	18.7224	18.7624
1329	Hexokinase-1 OS=Rattus norvegicus OX=10116 GN=Hk1 PE=1 SV=2	Hk1	M0RAQ6	NaN	NaN	NaN	NaN	17.9905	18.5809	19.216	19.3885
1330	Hexokinase-1 OS=Rattus norvegicus OX=10116 GN=Hk1 PE=1 SV=4	Hk1	P05708	20.9748	20.6189	20.7093	20.5566	22.4832	23.1038	23.4752	23.2745
1331	Hexokinase-2 OS=Rattus norvegicus OX=10116 GN=Hk2 PE=1 SV=1	Hk2	P27881	16.5604	16.8088	17.4901	17.9442	19.3493	20.3557	21.2906	21.3149
1332	HGF activator OS=Rattus norvegicus OX=10116 GN=Hgfac PE=1 SV=1	Hgfac	Q5EBA7	18.8473	18.4884	20.3499	19.7736	17.259	16.252	17.3517	15.6262
1333	Hif1an protein OS=Rattus norvegicus OX=10116 GN=Hif1an PE=2 SV=1	Hif1an	B0BNG5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1334	HIG1 domain family, member 2A OS=Rattus norvegicus OX=10116 GN=Higd2a PE=2 SV=1	Higd2a	B2GV65	NaN	NaN	NaN	NaN	NaN	17.0308	16.6894	16.9376
1335	High density lipoprotein binding protein (Vigilin) OS=Rattus norvegicus OX=10116 GN=Hdlbp PE=1 SV=1	Hdlbp	Q3KRF2	17.8512	17.7912	16.0273	16.1353	22.2034	22.2095	22.1045	22.0978
1336	High mobility group protein B1 OS=Rattus norvegicus OX=10116 GN=Hmgb1 PE=1 SV=2	Hmgb1	P63159	NaN	NaN	NaN	14.6316	23.4314	21.8391	21.6966	21.3642
1337	High mobility group protein B2 OS=Rattus norvegicus OX=10116 GN=Hmgb2 PE=2 SV=2	Hmgb2	P52925	NaN	NaN	15.5334	NaN	22.2623	21.1024	20.922	NaN
1338	Hippocalcin-like protein 1 OS=Rattus norvegicus OX=10116 GN=Hpcal1 PE=1 SV=2	Hpcal1	P62749	15.1413	NaN	16.112	NaN	20.3549	20.053	19.7726	19.6909
1339	Histidine ammonia-lyase OS=Rattus norvegicus OX=10116 GN=Hal PE=1 SV=1	Hal	P21213	17.7334	20.6652	16.4201	18.3001	NaN	17.6522	NaN	NaN
1340	Histidine rich calcium binding protein, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Hrc PE=1 SV=1	Hrc	G3V8S6	14.563	16.1922	NaN	NaN	17.7603	18.9217	17.5184	17.4831
1341	Histidine triad nucleotide-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Hint1 PE=1 SV=5	Hint1	P62959	14.6583	NaN	NaN	13.8391	18.59	18.0435	18.0612	18.5104
1342	Histidine-rich glycoprotein OS=Rattus norvegicus OX=10116 GN=Hrg PE=1 SV=1	Hrg	A0A0G2K3G0	24.0429	23.9506	23.9677	22.9644	20.429	19.7959	18.7299	19.6496
1343	Histone acetyltransferase type B catalytic subunit OS=Rattus norvegicus OX=10116 GN=Hat1 PE=2 SV=1	Hat1	Q5M939	NaN	NaN	14.7068	16.3598	18.7295	19.5166	19.5333	19.233
1344	Histone cluster 1 H1 family member c OS=Rattus norvegicus OX=10116 GN=Hist1h1c PE=1 SV=1	H1f2	A0A0G2K654	NaN	NaN	NaN	14.4976	19.8429	21.4619	20.7687	20.9593
1345	Histone deacetylase 1 OS=Rattus norvegicus OX=10116 GN=Hdac1 PE=1 SV=1	Hdac1	Q4QQW4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1346	Histone deacetylase OS=Rattus norvegicus OX=10116 GN=Hdac5 PE=1 SV=3	Hdac5	F1LM64	16.6994	NaN	NaN	NaN	17.4869	NaN	NaN	NaN
1347	Histone deacetylase OS=Rattus norvegicus OX=10116 GN=Hdac6 PE=1 SV=1	Hdac6	A0A0G2QC41	NaN	15.781	16.1671	NaN	18.625	18.9447	17.3724	18.249
1348	Histone H2A OS=Rattus norvegicus OX=10116 GN=H2afv PE=3 SV=1	H2az2	D4AEC0	NaN	NaN	NaN	NaN	14.8249	17.1932	16.7156	16.75
1349	Histone H2A OS=Rattus norvegicus OX=10116 GN=Hist1h2ak PE=3 SV=1	H2ac4	D3ZVK7	20.7661	19.9356	18.7557	19.8718	20.2998	22.408	21.9433	21.9399
1350	Histone H2B OS=Rattus norvegicus OX=10116 GN=Hist1h2bd PE=3 SV=2	Hist1h2bd	D3ZWM5	20.7662	20.5883	19.9445	20.8011	21.1159	22.5471	22.112	22.1348
1351	Histone H3 OS=Rattus norvegicus OX=10116 GN=Hist2h3c2 PE=1 SV=1	LOC102549173	D3ZJ08	19.8221	20.0563	18.8694	18.9891	20.2754	21.5088	21.1357	20.9475
1352	Histone H4 OS=Rattus norvegicus OX=10116 GN=Hist1h4b PE=1 SV=2	Hist2h4	P62804	20.6254	20.2948	19.0996	20.4915	21.2805	21.6265	21.2052	20.9039
1353	Histone-arginine methyltransferase CARM1 OS=Rattus norvegicus OX=10116 GN=Carm1 PE=1 SV=1	Carm1	Q4AE70	NaN	16.0461	NaN	NaN	20.071	20.9573	20.8173	20.9999
1354	Histone-binding protein RBBP7 OS=Rattus norvegicus OX=10116 GN=Rbbp7 PE=2 SV=1	Rbbp7	Q71UF4	NaN	15.9603	NaN	15.568	18.9924	18.9626	19.0038	18.1231
1355	Hmgb3 protein OS=Rattus norvegicus OX=10116 GN=Hmgb3 PE=1 SV=1	Hmgb3	B0BN99	16.0237	NaN	NaN	15.0748	20.4142	19.3364	19.1791	19.1284
1356	Homer protein homolog 3 OS=Rattus norvegicus OX=10116 GN=Homer3 PE=1 SV=2	Homer3	Q9Z2X5	22.1572	20.268	23.5721	21.647	20.6948	19.353	20.1409	19.4979
1357	Hormone-sensitive lipase OS=Rattus norvegicus OX=10116 GN=Lipe PE=1 SV=3	Lipe	P15304	19.698	19.7097	20.9193	19.591	20.678	20.4829	20.8085	20.8532
1358	Host cell factor C1 OS=Rattus norvegicus OX=10116 GN=Hcfc1 PE=1 SV=1	Hcfc1	D3ZN95	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1359	Hsc70-interacting protein OS=Rattus norvegicus OX=10116 GN=St13 PE=1 SV=1	St13	P50503	18.483	17.9386	19.4369	18.6281	23.486	22.3678	22.7729	22.7937
1360	Hsd17b4 protein OS=Rattus norvegicus OX=10116 GN=Hsd17b4 PE=1 SV=1	Hsd17b4	Q6IN39	15.8835	17.55	15.6069	17.3298	19.9371	19.9673	19.6539	19.8921
1361	Hsp70-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Hspbp1 PE=1 SV=1	Hspbp1	Q6IMX7	NaN	NaN	NaN	NaN	19.1372	NaN	18.6077	18.4475
1362	Hsp90 co-chaperone Cdc37 OS=Rattus norvegicus OX=10116 GN=Cdc37 PE=1 SV=2	Cdc37	Q63692	21.082	20.3223	20.9316	20.9303	23.1207	22.3932	22.8387	22.8426
1363	Hsp90 co-chaperone Cdc37-like 1 OS=Rattus norvegicus OX=10116 GN=Cdc37l1 PE=2 SV=1	Cdc37l1	Q5XIC3	NaN	NaN	NaN	NaN	17.5018	16.3855	16.248	16.5201
1364	Huntingtin interacting protein 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Hip1 PE=1 SV=1	Hip1	G3V8Y8	20.6153	20.8977	21.2231	20.2593	20.1332	19.8128	19.3843	19.3634
1365	Huntingtin interacting protein 2 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ube2k PE=1 SV=1	Ube2k	D3ZXS8	14.7775	18.1349	15.1506	17.7336	21.8752	20.4489	21.569	21.904
1366	Huntingtin OS=Rattus norvegicus OX=10116 GN=Htt PE=1 SV=1	Htt	G3V9P7	18.8812	NaN	18.855	19.0023	NaN	NaN	NaN	16.3068
1367	Huntingtin-interacting protein K OS=Rattus norvegicus OX=10116 GN=Hypk PE=1 SV=1	Hypk	F1M8A5	17.0348	17.4627	17.6364	15.2671	NaN	17.7785	17.1444	17.5043
1368	Hyaluronan-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Habp2 PE=1 SV=1	Habp2	F1M8H8	19.8089	19.064	19.3092	18.0968	17.1134	17.7655	NaN	NaN
1369	Hyaluronan-mediated motility receptor OS=Rattus norvegicus OX=10116 GN=Hmmr PE=4 SV=1	Hmmr	A0A0G2JXY1	NaN	NaN	NaN	NaN	NaN	16.944	17.7892	NaN
1370	Hydroxyacyl glutathione hydrolase OS=Rattus norvegicus OX=10116 GN=Hagh PE=1 SV=2	Hagh	F1LQI1	15.4485	NaN	NaN	NaN	15.5696	15.7549	16.639	NaN
1371	Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Hmgcs1 PE=1 SV=1	Hmgcs1	P17425	20.9642	19.337	20.0124	NaN	19.7883	20.014	20.5681	20.1552
1372	Hydroxysteroid dehydrogenase-like protein 2 OS=Rattus norvegicus OX=10116 GN=Hsdl2 PE=2 SV=1	Hsdl2	Q4V8F9	NaN	16.1419	NaN	NaN	18.4757	20.9872	19.7998	18.9207
1373	Hypothetical protein LOC681410 OS=Rattus norvegicus OX=10116 GN=LOC681410 PE=1 SV=3	LOC681410	F1M3H8	15.0459	15.841	NaN	NaN	20.7348	21.5109	20.921	21.2832
1374	Hypothetical protein LOC688282 OS=Rattus norvegicus OX=10116 GN=LOC688282 PE=4 SV=2	LOC688282	M0RB05	15.9773	15.4493	NaN	15.9873	NaN	NaN	NaN	18.0788
1375	Hypoxanthine-guanine phosphoribosyltransferase OS=Rattus norvegicus OX=10116 GN=Hprt1 PE=1 SV=1	Hprt1	P27605	17.4794	17.6119	17.874	18.6539	21.3794	21.7878	21.7105	21.6729
1376	Hypoxia up-regulated protein 1 OS=Rattus norvegicus OX=10116 GN=Hyou1 PE=1 SV=1	Hyou1	Q63617	16.6033	15.2787	16.9174	13.8904	20.0739	20.6839	19.6691	20.549

1377	Ig gamma-2A chain C region OS=Rattus norvegicus OX=10116 GN=Igg-2a PE=1 SV=1	LOC679045	P20760	26.6568	26.4948	26.4024	25.3315	22.0695	21.3445	20.6332	20.3275
1378	Ig gamma-2B chain C region OS=Rattus norvegicus OX=10116 GN=Igh-1a PE=1 SV=1	Igh-6	P20761	24.2552	24.2362	24.3895	24.6324	20.0371	19.0166	19.6822	19.7616
1379	Ig gamma-2C chain C region OS=Rattus norvegicus OX=10116 PE=2 SV=1	IGG2C_RAT	P20762	20.8011	20.5098	21.6359	22.8404	18.3083	16.4813	15.9191	17.0232
1380	Ig kappa chain C region, A allele OS=Rattus norvegicus OX=10116 PE=1 SV=1	Igkc	P01836	21.1609	16.8134	21.2801	22.2835	17.5428	17.2742	16.7475	16.6811
1381	Ig kappa chain V region S211 OS=Rattus norvegicus OX=10116 PE=1 SV=1	LOC500374	P01681	16.1662	17.3551	NaN	NaN	NaN	15.1438	15.1263	15.0304
1382	Ig lambda-2 chain C region OS=Rattus norvegicus OX=10116 PE=4 SV=1	LAC2_RAT	P20767	23.0009	23.009	21.837	21.4451	17.3214	17.6554	16.9071	16.1715
1383	Ilf2 protein OS=Rattus norvegicus OX=10116 GN=Ilf2 PE=1 SV=1	Ilf2	B2RZC6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1384	Immunoglobulin joining chain OS=Rattus norvegicus OX=10116 GN=Jchain PE=1 SV=1	Jchain	G3V6G1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1385	Immunoglobulin superfamily member 1 OS=Rattus norvegicus OX=10116 GN=Igsf1 PE=1 SV=1	Igsf1	Q925N6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1386	Immunoglobulin superfamily-containing leucine-rich repeat OS=Rattus norvegicus OX=10116 GN=Islr PE=1 SV=1	Islr	B1H232	17.3485	17.2546	17.1707	17.7296	15.2476	NaN	NaN	16.2644
1387	Immunoglobulin-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Igbp1 PE=2 SV=2	Igbp1	O08836	14.8033	15.1445	15.1657	NaN	20.1014	19.4062	19.5687	19.4723
1388	Importin 11 OS=Rattus norvegicus OX=10116 GN=Ipo11 PE=1 SV=2	Ipo11	M0R8E8	NaN	16.7387	NaN	NaN	19.2155	18.9673	18.7946	18.4012
1389	Importin 4 OS=Rattus norvegicus OX=10116 GN=Ipo4 PE=1 SV=2	Ipo4	D4A2D7	19.6913	18.4177	18.2735	19.013	21.7063	21.3405	21.4132	21.7825
1390	Importin 5 OS=Rattus norvegicus OX=10116 GN=Ipo5 PE=1 SV=1	Ipo5	D4A781	18.6616	16.8968	17.1063	16.4358	22.0709	22.4246	22.6882	22.2509
1391	Importin 7 OS=Rattus norvegicus OX=10116 GN=Ipo7 PE=1 SV=1	Ipo7	D4AE96	15.9409	16.015	NaN	NaN	20.5595	19.1018	20.139	20.018
1392	Importin 9 OS=Rattus norvegicus OX=10116 GN=Ipo9 PE=1 SV=2	Ipo9	D4A857	18.0866	17.8733	16.9253	16.8876	22.2922	21.8949	22.2992	21.9753
1393	Importin subunit alpha OS=Rattus norvegicus OX=10116 GN=Kpna3 PE=1 SV=1	Kpna3	Q56R18	NaN	NaN	NaN	15.187	20.4235	19.2771	20.1615	20.1223
1394	Importin subunit alpha OS=Rattus norvegicus OX=10116 GN=Kpna4 PE=1 SV=1	Kpna4	Q56R17	NaN	NaN	NaN	NaN	18.8624	18.1779	18.6752	18.8302
1395	Importin subunit alpha OS=Rattus norvegicus OX=10116 GN=Kpna6 PE=1 SV=3	Kpna6	F1LT58	20.7183	20.6513	20.7143	21.1573	21.1984	20.4552	20.7459	20.8785
1396	Importin subunit alpha OS=Rattus norvegicus OX=10116 GN=LOC100359600 PE=3 SV=1	LOC100359600	M0R7I0	19.6448	18.1762	16.4615	18.405	22.7734	22.0534	22.1074	22.1662
1397	Importin subunit alpha-5 OS=Rattus norvegicus OX=10116 GN=Kpna1 PE=1 SV=1	Kpna1	P83953	NaN	NaN	NaN	NaN	19.6852	19.7192	19.4507	19.5836
1398	Importin subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Kpnb1 PE=1 SV=1	Kpnb1	F2Z3Q8	24.6467	24.5408	25.0337	23.9864	24.4443	23.9374	24.3282	24.1208
1399	Inducible T-cell co-stimulator ligand OS=Rattus norvegicus OX=10116 GN=Icoslg PE=1 SV=3	Icoslg	F1LVL2	17.6508	17.7629	NaN	14.0183	18.0467	18.4209	18.2487	17.8096
1400	Inhibitor of kappaB kinase beta, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Ikbkb PE=1 SV=1	Ikbkb	G3V8H5	17.3452	NaN	NaN	NaN	NaN	NaN	17.7315	17.5214
1401	Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Rattus norvegicus OX=10116 GN=Ikbip PE=2 SV=1	Ikbip	Q5EAJ6	16.7339	15.9382	16.9002	16.5376	NaN	17.4613	17.1249	NaN
1402	Inosine triphosphate pyrophosphatase OS=Rattus norvegicus OX=10116 GN=Itpa PE=3 SV=1	Itpa	D3ZW55	NaN	16.3336	16.6072	16.9094	20.5858	20.3866	20.8589	20.6332
1403	Inosine-5'-monophosphate dehydrogenase 2 OS=Rattus norvegicus OX=10116 GN=Impdh2 PE=1 SV=1	Impdh2	E9PU28	18.5763	20.1409	17.852	20.3524	22.9105	21.2	21.7194	21.5312
1404	Inosine-5'-monophosphate dehydrogenase OS=Rattus norvegicus OX=10116 GN=Impdh1 PE=3 SV=1	Impdh1	A0A0A0MXZ8	NaN	NaN	NaN	NaN	17.6924	17.3788	17.645	16.4972
1405	Inositol 1,4,5-trisphosphate receptor type 1 OS=Rattus norvegicus OX=10116 GN=Itpr1 PE=1 SV=3	Itpr1	F1LNT1	NaN	16.9812	17.8691	NaN	15.1008	14.9852	NaN	15.3141
1406	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase (Fragment) OS=Rattus norvegicus OX=10116 GN	Ppip5k2	A0A096MK18	NaN	NaN	NaN	NaN	16.7368	16.2359	NaN	NaN
1407	Inositol monophosphatase 2 OS=Rattus norvegicus OX=10116 GN=Impa2 PE=2 SV=1	Impa2	Q8CIN7	NaN	NaN	NaN	NaN	18.9061	NaN	18.7509	18.8309
1408	Inositol polyphosphate-1-phosphatase OS=Rattus norvegicus OX=10116 GN=Inpp1 PE=1 SV=1	Inpp1	Q5RJK6	NaN	NaN	NaN	NaN	17.4015	17.0391	17.8274	NaN
1409	Inositol polyphosphate-5-phosphatase F OS=Rattus norvegicus OX=10116 GN=Inpp5f PE=1 SV=1	Inpp5f	D3ZKG7	NaN	NaN	NaN	NaN	16.5217	NaN	16.0094	NaN
1410	Inositol-1-monophosphatase OS=Rattus norvegicus OX=10116 GN=Impa1 PE=1 SV=1	Impa1	F1M978	NaN	15.5255	15.0457	16.466	19.7358	18.5252	18.8929	18.9557
1411	Insulin receptor substrate 2 OS=Rattus norvegicus OX=10116 GN=Irs2 PE=1 SV=2	Irs2	F1MAL5	NaN	NaN	NaN	14.02	17.1819	15.5694	15.2967	NaN
1412	Insulin-degrading enzyme OS=Rattus norvegicus OX=10116 GN=Ide PE=1 SV=1	Ide	P35559	14.651	16.4034	NaN	20.3281	17.8968	18.8138	18.0211	18.3127
1413	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Igf2bp1 PE=1 SV=1	Igf2bp1	Q8CGX0	NaN	NaN	NaN	NaN	20.1958	21.3602	20.7648	20.4822
1414	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Igf2bp2 PE=1 SV=3	Igf2bp2	D3ZWZ6	15.3394	NaN	14.6131	NaN	19.9064	20.7203	20.083	19.875
1415	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Igf2bp3 PE=1 SV=1	Igf2bp3	A0A0G2K0Y2	17.6435	19.002	18.496	18.9349	20.708	21.781	20.8687	21.0946
1416	Insulin-like growth factor 2 receptor OS=Rattus norvegicus OX=10116 GN=Igf2r PE=1 SV=1	Igf2r	G3V824	23.5497	23.6501	24.0008	23.4781	27.037	27.2058	26.8685	26.9878
1417	Insulin-like growth factor 2, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Igf2 PE=3 SV=1	Igf2	A0A0G2JTA6	19.8741	19.237	20.4977	19.4597	18.5934	19.271	18.5814	17.6506
1418	Insulin-like growth factor-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Igfbp1 PE=1 SV=2	Igfbp1	P21743	NaN	17.0916	18.0727	17.2847	NaN	14.8767	15.1165	15.8169
1419	Insulin-like growth factor-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Igfbp2 PE=1 SV=3	Igfbp2	P12843	21.0555	20.1079	21.3022	20.95	17.5019	18.2675	16.3969	15.4473
1420	Insulin-like growth factor-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Igfbp3 PE=1 SV=2	Igfbp3	P15473	16.7816	NaN	NaN	17.3236	NaN	NaN	NaN	NaN
1421	Insulin-like growth factor-binding protein 4 OS=Rattus norvegicus OX=10116 GN=Igfbp4 PE=1 SV=2	Igfbp4	P21744	18.9558	18.9992	19.465	18.8337	16.6142	NaN	NaN	17.1513
1422	Integrin alpha 5 (Mapped) OS=Rattus norvegicus OX=10116 GN=Itga5 PE=1 SV=1	Itga5	A0A0G2K1E2	15.1976	15.0822	15.052	17.9133	20.8521	20.8851	20.7863	20.8956
1423	Integrin beta 1 binding protein 2 (Predicted) OS=Rattus norvegicus OX=10116 GN=Itgb1bp2 PE=4 SV=1	Itgb1bp2	D3ZW59	16.6314	NaN	14.2662	17.0037	18.5327	17.9003	19.013	18.6123
1424	Integrin beta OS=Rattus norvegicus OX=10116 GN=Itgb1 PE=1 SV=1	Itgb1	A0A0G2JSK5	21.4849	21.5736	21.2336	21.2973	23.7783	23.8556	23.5972	23.8629
1425	Integrin beta OS=Rattus norvegicus OX=10116 GN=Itgb2 PE=1 SV=1	Itgb2	B2RYB8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1426	Integrin beta OS=Rattus norvegicus OX=10116 GN=Itgb3 PE=1 SV=2	Itgb3	M0RCF3	23.0459	22.5636	23.1137	22.6355	20.6973	20.1327	19.9763	20.3965
1427	Integrin subunit alpha 2b OS=Rattus norvegicus OX=10116 GN=Itga2b PE=1 SV=2	Itga2b	D3ZAC0	22.8848	22.5419	22.997	22.8642	19.9054	19.5787	20.193	20.5193
1428	Integrin subunit alpha 6 OS=Rattus norvegicus OX=10116 GN=Itga6 PE=1 SV=1	Itga6	G3V667	15.6779	15.9189	15.8724	NaN	16.9128	16.7942	17.877	16.1976
1429	Integrin subunit alpha V OS=Rattus norvegicus OX=10116 GN=Itgav PE=1 SV=1	Itgav	A0A0G2JVZ6	17.6221	17.7917	18.6746	18.9896	20.6387	20.2146	20.1828	20.7706

1430	Integrin-linked protein kinase OS=Rattus norvegicus OX=10116 GN=Ilk PE=2 SV=1	Ilk	Q99J82	20.9609	19.2674	19.7196	19.1046	23.3354	23.5071	23.7826	23.3704
1431	Inter alpha-trypsin inhibitor, heavy chain 4 OS=Rattus norvegicus OX=10116 GN=Itih4 PE=1 SV=1	Itih4	Q5EBC0	25.1294	25.5854	25.1922	24.6811	22.4206	22.0022	21.2772	21.5345
1432	Inter-alpha trypsin inhibitor, heavy chain 1 OS=Rattus norvegicus OX=10116 GN=Itih1 PE=1 SV=1	Itih1	B2RYM3	23.432	23.4575	23.9087	23.835	20.9035	19.7779	20.2433	20.8131
1433	Inter-alpha-trypsin inhibitor heavy chain 2 OS=Rattus norvegicus OX=10116 GN=Itih2 PE=1 SV=3	Itih2	D3ZFH5	25.2915	25.149	25.4959	25.6234	22.3913	22.0727	21.9461	22.1715
1434	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Rattus norvegicus OX=10116 GN=Itih3 PE=1 SV=3	Itih3	D3ZBS2	25.4579	24.9648	25.6578	25.6621	22.8122	22.608	22.3679	22.6112
1435	Intercellular adhesion molecule 2 OS=Rattus norvegicus OX=10116 GN=Icam2 PE=1 SV=1	Icam2	Q6AXM6	NaN	NaN	NaN	NaN	17.3736	16.787	16.6347	16.6177
1436	Interferon regulatory factor 2 binding protein 1 (Predicted) OS=Rattus norvegicus OX=10116 GN=Irf2bp1 PE=1 SV=1	Irf2bp1	D4AAZ8	16.5063	NaN	NaN	17.6446	18.8065	16.9132	17.8562	17.6707
1437	Interferon regulatory factor 2-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Irf2bp2 PE=1 SV=1	Irf2bp2	M0R9Z5	NaN	NaN	NaN	NaN	19.8651	18.4667	18.1271	18.4183
1438	Interferon regulatory factor 2-binding protein-like OS=Rattus norvegicus OX=10116 GN=Irf2bpl PE=1 SV=1	Irf2bpl	Q5EIC4	NaN	16.3727	15.6385	16.0596	19.8962	19.4834	19.0346	19.2888
1439	Interferon-induced transmembrane protein 2 OS=Rattus norvegicus OX=10116 GN=Ifitm2 PE=1 SV=1	Ifitm2	Q9R175	16.3758	16.9561	17.1472	17.1139	15.9509	18.0901	18.1752	19.0422
1440	Interferon-induced transmembrane protein 3 OS=Rattus norvegicus OX=10116 GN=ifitm3 PE=2 SV=1	Ifitm3	P26376	16.8902	NaN	16.4382	14.0685	19.5413	20.1656	19.6234	19.6149
1441	Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Rattus norvegicus OX=10116 GN=Prkr	Prkra	G3V7J2	NaN	NaN	NaN	NaN	19.9647	21.1864	20.4414	20.3816
1442	Interleukin 1 receptor accessory protein b OS=Rattus norvegicus OX=10116 GN=Il1rap PE=1 SV=1	Il1rap	D1M8S3	18.768	17.708	19.1792	19.381	18.2391	19.9934	18.8394	19.4018
1443	Interleukin-1 receptor-associated kinase 1 OS=Rattus norvegicus OX=10116 GN=Irak1 PE=1 SV=1	Irak1	B2RYH5	NaN	NaN	NaN	NaN	17.4929	NaN	17.2698	NaN
1444	Intersectin 2 OS=Rattus norvegicus OX=10116 GN=Itsn2 PE=1 SV=2	Itsn2	M0R7A6	15.2268	NaN	NaN	NaN	16.3324	NaN	17.7423	17.0649
1445	Intersectin-1 OS=Rattus norvegicus OX=10116 GN=Itsn1 PE=1 SV=2	Itsn1	Q9WVE9	NaN	NaN	12.0606	NaN	18.9878	18.8905	19.4453	19.2425
1446	IQ motif and Sec7 domain 1 OS=Rattus norvegicus OX=10116 GN=Iqsec1 PE=1 SV=1	Iqsec1	A0A0G2JUG7	NaN	NaN	15.0092	NaN	NaN	18.3955	17.9868	16.8513
1447	IQ motif containing GTPase activating protein 1 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Iqgap1 P	Iqgap1	G3V7Q7	21.5819	20.2976	20.6099	21.1505	23.2263	22.562	22.6677	22.7423
1448	IQ motif-containing GTPase-activating protein 3 OS=Rattus norvegicus OX=10116 GN=Iqgap3 PE=1 SV=1	Iqgap3	D3ZCS4	19.5475	18.6212	19.088	18.6541	20.3339	20.4853	20.4332	19.961
1449	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Rattus norvegicus OX=10116 GN=Iah1 PE=2 SV=2	Iah1	Q711G3	15.6585	15.1024	15.5415	17.2625	16.9345	16.9271	17.2017	NaN
1450	Isochorismatase domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=LOC103694869 PE=1 SV=1	Isoc1	F2Z3T7	NaN	NaN	NaN	NaN	19.1318	18.3519	18.694	18.3448
1451	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Idh3B PE=2 SV=1	Idh3b	Q68FX0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1452	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Idh3g PE=1 SV=2	Idh3g	P41565	NaN	NaN	NaN	NaN	NaN	17.864	NaN	17.606
1453	Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Idh3a PE=1 SV=2	Idh3a	F1LNF7	18.509	17.8285	17.7004	17.651	21.9541	23.0075	22.5482	22.5322
1454	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Rattus norvegicus OX=10116 GN=Idh1 PE=1 SV=1	Idh1	P41562	NaN	NaN	16.618	16.7554	17.2373	NaN	NaN	NaN
1455	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus OX=10116 GN=Idh2 PE=1 SV=2	Idh2	P56574	20.3906	20.9576	21.4495	19.9361	21.8306	24.1246	23.5556	24.0698
1456	Isoleucine-tRNA synthetase (Predicted) OS=Rattus norvegicus OX=10116 GN=Iars PE=1 SV=2	Iars1	F1LS86	18.5568	20.1398	18.4012	18.8337	23.0777	22.5424	22.9557	22.7078
1457	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ivd PE=1 SV=2	Ivd	P12007	15.2595	NaN	NaN	NaN	NaN	17.7141	17.8471	17.7999
1458	IST1 homolog OS=Rattus norvegicus OX=10116 GN=Ist1 PE=2 SV=1	Ist1	Q568Z6	NaN	NaN	NaN	15.2972	20.0039	19.5621	19.9415	19.5899
1459	Itfg1 protein OS=Rattus norvegicus OX=10116 GN=Itfg1 PE=1 SV=1	Itfg1	Q5U355	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1460	Junction plakoglobin OS=Rattus norvegicus OX=10116 GN=Jup PE=1 SV=1	Jup	Q6P0K8	23.1087	24.4393	22.4427	23.6683	23.398	23.8198	23.0725	22.8595
1461	Junctional adhesion molecule A OS=Rattus norvegicus OX=10116 GN=F11r PE=1 SV=1	F11r	Q9JHY1	NaN	NaN	NaN	NaN	18.3927	18.0777	18.6885	18.2987
1462	Junctophilin-2 OS=Rattus norvegicus OX=10116 GN=Jph2 PE=1 SV=1	Jph2	Q2PS20	18.7945	17.5476	17.7411	15.5154	18.8113	19.3026	18.7652	18.9705
1463	Jupiter microtubule associated homolog 1 OS=Rattus norvegicus OX=10116 GN=JPT1 PE=1 SV=3	Jpt1	Q6AXU6	16.6675	17.354	16.6535	NaN	16.3692	18.7881	16.0989	17.0483
1464	Kappa-casein OS=Rattus norvegicus OX=10116 GN=Csn3 PE=2 SV=1	Csn3	P04468	19.2102	15.8835	16.2827	NaN	16.7709	NaN	NaN	16.7947
1465	Kelch repeat and BTB (POZ) domain containing 2 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Kbtbd2	Kbtbd2	D3ZVS6	NaN	NaN	NaN	NaN	NaN	16.4573	NaN	16.0135
1466	Kelch-like family member 31 OS=Rattus norvegicus OX=10116 GN=Klhl31 PE=4 SV=1	Klhl31	D3ZLT6	18.1373	17.3282	15.6414	17.6168	20.978	21.4231	21.5904	21.425
1467	Kelch-like protein 41 OS=Rattus norvegicus OX=10116 GN=Klhl41 PE=1 SV=1	Klhl41	Q9ER30	NaN	NaN	NaN	NaN	19.7177	19.5388	20.0286	19.5998
1468	Keratin 16 OS=Rattus norvegicus OX=10116 GN=Krt16 PE=1 SV=1	Krt16	Q6IFU9	22.2491	23.092	17.3708	21.3982	23.4237	23.208	22.1326	21.2831
1469	Keratin 76 OS=Rattus norvegicus OX=10116 GN=Krt76 PE=2 SV=1	Krt76	Q6IFZ5	26.7116	26.5421	25.9581	25.7137	26.6059	25.5972	26.1281	26.3223
1470	Keratin 78 OS=Rattus norvegicus OX=10116 GN=Krt78 PE=3 SV=1	Krt78	A0A0G2K4H7	18.8646	21.1203	19.3394	19.5579	18.0108	18.5749	18.8776	19.009
1471	Keratin 84 OS=Rattus norvegicus OX=10116 GN=Krt84 PE=3 SV=1	Krt84	A0A0G2K0I4	15.9202	17.5062	16.0938	16.2897	17.9023	18.6606	17.9628	14.7779
1472	Keratin, type I cytoskeletal 10 OS=Rattus norvegicus OX=10116 GN=Krt10 PE=1 SV=1	Krt10	A0A0G2K2V6	27.127	28.6307	26.7763	27.3938	26.3745	26.8646	26.4632	26.1624
1473	Keratin, type I cytoskeletal 12 OS=Rattus norvegicus OX=10116 GN=Krt12 PE=3 SV=1	Krt12	A0A0G2K4H9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1474	Keratin, type I cytoskeletal 13 OS=Rattus norvegicus OX=10116 GN=Krt13 PE=3 SV=1	Krt13	Q6IFV4	20.1955	21.5846	15.4626	20.8978	20.6067	18.192	20.2092	20.2067
1475	Keratin, type I cytoskeletal 14 OS=Rattus norvegicus OX=10116 GN=Krt14 PE=2 SV=1	Krt14	Q6IFV1	26.7304	28.0949	26.2826	26.9487	26.6019	26.8141	26.1621	25.8718
1476	Keratin, type I cytoskeletal 15 OS=Rattus norvegicus OX=10116 GN=Krt15 PE=1 SV=1	Krt15	Q6IFV3	20.6355	20.9408	18.4132	19.5254	20.4466	18.5533	19.6657	19.3617
1477	Keratin, type I cytoskeletal 17 OS=Rattus norvegicus OX=10116 GN=Krt17 PE=1 SV=1	Krt17	A0A0G2K9Q9	24.8033	26.3269	24.3715	25.1223	24.7008	24.8242	24.4504	24.3079
1478	Keratin, type I cytoskeletal 17 OS=Rattus norvegicus OX=10116 GN=Krt17 PE=1 SV=1	Krt17	Q6IFU8	NaN	18.9235	16.004	16.4873	18.976	16.6379	16.48	NaN
1479	Keratin, type I cytoskeletal 19 OS=Rattus norvegicus OX=10116 GN=Krt19 PE=1 SV=2	Krt19	Q63279	17.0974	17.2733	NaN	NaN	18.7981	17.9343	18.7605	NaN
1480	Keratin, type I cytoskeletal 40 OS=Rattus norvegicus OX=10116 GN=Krt40 PE=3 SV=1	Krt40	Q6IFW2	16.2687	17.2739	NaN	17.6305	NaN	16.8587	NaN	NaN
1481	Keratin, type I cytoskeletal 42 OS=Rattus norvegicus OX=10116 GN=Krt42 PE=3 SV=1	Krt42	Q6IFU7	23.6754	24.2954	23.0902	23.4234	23.4464	23.7073	22.6589	22.427
1482	Keratin, type II cytoskeletal 1 OS=Rattus norvegicus OX=10116 GN=Krt1 PE=1 SV=1	Krt1	A0A0G2JST3	26.2263	27.8568	25.7697	26.0348	25.8657	26.3819	25.7878	25.32

1483	Keratin, type II cytoskeletal 1b OS=Rattus norvegicus OX=10116 GN=Krt77 PE=3 SV=1	Krt77	A0A0G2JZQ9	19.0455	23.3938	19.5863	18.7507	20.2858	19.5658	20.345	19.7107
1484	Keratin, type II cytoskeletal 2 epidermal OS=Rattus norvegicus OX=10116 GN=Krt2 PE=3 SV=1	Krt2	Q6IG02	26.1304	26.5457	25.095	25.6076	24.3706	25.0855	24.6653	24.8448
1485	Keratin, type II cytoskeletal 4 OS=Rattus norvegicus OX=10116 GN=Krt4 PE=3 SV=1	Krt4	Q6IG00	16.1564	15.6288	NaN	16.9856	NaN	NaN	NaN	14.6322
1486	Keratin, type II cytoskeletal 5 OS=Rattus norvegicus OX=10116 GN=Krt5 PE=1 SV=1	Krt5	A0A0G2K509	27.9164	29.0711	27.3967	28.1541	27.2536	27.4731	26.8071	26.6479
1487	Keratin, type II cytoskeletal 5 OS=Rattus norvegicus OX=10116 GN=Krt5 PE=1 SV=1	Krt5	Q6P6Q2	23.8846	25.5851	23.5957	25.1434	24.3263	24.5628	23.5763	23.0734
1488	Keratin, type II cytoskeletal 6A OS=Rattus norvegicus OX=10116 GN=Krt6a PE=1 SV=1	LOC683313	Q4FZU2	25.0195	26.2469	25.0324	23.4571	25.2818	25.3211	24.6922	24.5416
1489	Keratin, type II cytoskeletal 7 OS=Rattus norvegicus OX=10116 GN=Krt7 PE=3 SV=1	Krt7	Q6IG12	NaN	NaN	16.8198	NaN	NaN	NaN	15.3014	NaN
1490	Keratin, type II cytoskeletal 72 OS=Rattus norvegicus OX=10116 GN=Krt72 PE=3 SV=1	Krt72	A0A0G2K7N1	NaN	18.5484	NaN	18.129	NaN	17.134	NaN	NaN
1491	Keratin, type II cytoskeletal 73 OS=Rattus norvegicus OX=10116 GN=Krt73 PE=1 SV=1	Krt73	Q6IG03	26.0657	27.2736	25.8137	26.8807	25.8049	25.8935	25.3514	25.2139
1492	Keratin, type II cytoskeletal 75 OS=Rattus norvegicus OX=10116 GN=Krt75 PE=1 SV=1	Krt75	A0A0H2UHH5	20.6698	21.9725	19.6356	20.193	22.0679	22.1572	20.9098	19.9971
1493	Keratin, type II cytoskeletal 8 OS=Rattus norvegicus OX=10116 GN=Krt8 PE=1 SV=3	Krt8	Q10758	22.151	23.5906	21.5433	22.2325	21.4135	22.0082	21.018	20.9516
1494	Keratin, type II cytoskeletal 80 OS=Rattus norvegicus OX=10116 GN=Krt80 PE=3 SV=1	Krt80	Q6IMF1	NaN	20.1351	NaN	16.9922	16.5785	18.3476	17.1014	15.6353
1495	Keratinocyte differentiation-associated protein OS=Rattus norvegicus OX=10116 GN=Krtdap PE=2 SV=1	Krtdap	P85411	23.3831	22.8987	23.1751	23.3661	18.4761	18.4011	18.0127	18.3549
1496	Keratinocyte proline-rich protein OS=Rattus norvegicus OX=10116 GN=Kprp PE=4 SV=1	Kprp	G3V9A5	18.5268	18.0926	17.4234	14.5551	NaN	18.3949	17.211	NaN
1497	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Khdrb	Khdrbs1	Q91V33	16.6802	16.5556	NaN	NaN	19.5992	20.5203	19.8443	19.8533
1498	Kinectin 1 OS=Rattus norvegicus OX=10116 GN=Ktn1 PE=1 SV=2	Ktn1	D4A4Z9	NaN	NaN	NaN	NaN	19.1777	18.8444	17.042	18.6256
1499	Kinesin family member 11 OS=Rattus norvegicus OX=10116 GN=Kif11 PE=1 SV=1	Kif11	F1MAB8	17.9363	15.2411	17.2024	15.2839	19.5511	20.3249	19.5456	19.4002
1500	Kinesin family member 13A OS=Rattus norvegicus OX=10116 GN=Kif13a PE=1 SV=1	Kif13a	D3ZM20	18.2081	17.6166	17.9002	16.6491	19.5421	19.4943	19.4979	19.3803
1501	Kinesin family member 13B OS=Rattus norvegicus OX=10116 GN=Kif13b PE=1 SV=1	Kif13b	A0A0G2K8Z9	NaN	NaN	13.3985	NaN	19.9799	20.7109	19.9683	19.7841
1502	Kinesin family member 4A OS=Rattus norvegicus OX=10116 GN=Kif4a PE=1 SV=1	Kif4a	E9PSJ3	18.799	18.0409	18.3009	17.3656	NaN	17.4997	17.3093	17.7379
1503	Kinesin light chain 1 OS=Rattus norvegicus OX=10116 GN=Klc1 PE=1 SV=2	Klc1	P37285	19.797	18.3618	19.1939	17.1237	23.103	23.6283	23.6232	23.0482
1504	Kinesin light chain 2 OS=Rattus norvegicus OX=10116 GN=Klc2 PE=1 SV=1	Klc2	B2GV74	20.3447	20.5242	20.125	18.6259	23.5417	23.7009	23.5995	23.2905
1505	Kinesin light chain 4 OS=Rattus norvegicus OX=10116 GN=Klc4 PE=1 SV=1	Klc4	Q5PQM2	19.9141	20.5954	19.5282	18.6729	23.0211	23.0932	22.9189	22.6083
1506	Kinesin-1 heavy chain OS=Rattus norvegicus OX=10116 GN=Kif5b PE=1 SV=1	Kif5b	Q2PQA9	23.7412	23.4238	24.1789	23.9082	25.6315	26.1186	26.0652	25.6435
1507	Kinesin-like protein KIF15 OS=Rattus norvegicus OX=10116 GN=Kif15 PE=2 SV=1	Kif15	Q7TSP2	19.2321	18.3818	18.987	16.4882	19.4734	21.1804	20.8217	20.4102
1508	Kinesin-like protein KIF1B OS=Rattus norvegicus OX=10116 GN=Kif1b PE=1 SV=2	Kif1b	O88658	16.3792	18.24	16.3711	15.7084	20.8078	21.1793	20.7066	20.5841
1509	Kinesin-like protein KIF1C OS=Rattus norvegicus OX=10116 GN=Kif1c PE=1 SV=1	Kif1c	F1M9C8	19.8585	20.5115	20.1215	20.1324	18.0795	19.7115	19.4822	19.0459
1510	Kinetochore associated 1 (Predicted) OS=Rattus norvegicus OX=10116 GN=Kntc1 PE=4 SV=2	Kntc1	D3ZVJ3	15.6027	NaN	15.2003	14.3887	18.525	19.6291	19.1353	19.1357
1511	Kinetochore protein Nuf2 OS=Rattus norvegicus OX=10116 GN=Nuf2 PE=2 SV=1	Nuf2	Q6AYL9	21.2319	21.1815	21.8084	21.3622	17.3349	17.0869	17.0495	17.2182
1512	Kinetochore protein Spc25 OS=Rattus norvegicus OX=10116 GN=Spc25 PE=2 SV=1	Spc25	Q5M856	19.4219	21.3615	18.5742	19.8308	20.7298	19.9868	19.6466	17.9137
1513	Kininogen-1 OS=Rattus norvegicus OX=10116 GN=Kng1 PE=1 SV=1	Kng1	A0A0G2KA54	16.0455	NaN	17.3115	NaN	NaN	NaN	NaN	NaN
1514	Kininogen-1 OS=Rattus norvegicus OX=10116 GN=Kng1 PE=2 SV=1	Kng2l1	P08934	25.0533	24.7674	25.1377	24.8661	22.7692	21.8839	22.0044	22.6872
1515	KN motif and ankyrin repeat domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Kank2 PE=1 SV=2	Kank2	D3ZD05	16.7227	17.0688	16.4413	14.0907	19.594	20.662	19.7197	19.2091
1516	KN motif and ankyrin repeat domains 1 OS=Rattus norvegicus OX=10116 GN=Kank1 PE=1 SV=2	Kank1	D4AE58	NaN	NaN	NaN	NaN	18.8864	19.1569	19.8244	19.5558
1517	La ribonucleoprotein domain family, member 1 OS=Rattus norvegicus OX=10116 GN=Larp1 PE=1 SV=3	Larp1	F1M062	NaN	NaN	NaN	NaN	17.9376	18.7949	18.6793	18.2559
1518	La ribonucleoprotein domain family, member 4B OS=Rattus norvegicus OX=10116 GN=Larp4b PE=1 SV=2	Larp4b	D3ZF45	NaN	NaN	NaN	NaN	18.1631	17.9312	16.4843	15.9247
1519	Lactadherin OS=Rattus norvegicus OX=10116 GN=Mfge8 PE=1 SV=1	Mfge8	Q1PBJ1	22.9151	22.5574	22.3972	22.4901	20.2097	21.3235	20.8061	20.4669
1520	Lactoylglutathione lyase OS=Rattus norvegicus OX=10116 GN=Glo1 PE=1 SV=3	Glo1	Q6P7Q4	16.2072	15.4014	NaN	NaN	18.443	19.5158	19.6822	19.1745
1521	Lamin A, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Lmna PE=1 SV=1	Lmna	G3V8L3	16.3785	17.4605	16.8079	19.9994	20.5261	18.9302	18.8292	19.2793
1522	Lamina-associated polypeptide 2, isoform beta OS=Rattus norvegicus OX=10116 GN=Tmpo PE=1 SV=3	Tmpo	Q62733	17.0452	NaN	16.8808	17.3461	17.2843	17.2264	17.289	16.8881
1523	Laminin subunit alpha 2 OS=Rattus norvegicus OX=10116 GN=Lama2 PE=1 SV=3	Lama2	F1M614	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1524	Laminin subunit beta 1 OS=Rattus norvegicus OX=10116 GN=Lamb1 PE=1 SV=3	Lamb1	D3ZQN7	19.2041	20.4401	18.7988	18.2434	19.8772	19.8356	19.554	19.8425
1525	Laminin subunit beta-2 OS=Rattus norvegicus OX=10116 GN=Lamb2 PE=1 SV=1	Lamb2	M0R6K0	NaN	NaN	NaN	17.8036	17.14	18.5883	18.1977	16.5909
1526	Laminin subunit gamma 1 OS=Rattus norvegicus OX=10116 GN=Lamc1 PE=1 SV=1	Lamc1	F1MAA7	16.3939	19.099	18.4118	17.7022	21.0866	19.9329	19.8934	20.306
1527	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase OS=Rattus norvegicus OX=10116 GN=Aasdh	Aasdhppt	B2RYJ4	NaN	NaN	NaN	NaN	19.6557	16.8926	18.7646	18.2465
1528	Large neutral amino acids transporter small subunit 1 OS=Rattus norvegicus OX=10116 GN=Slc7a5 PE=1 SV=2	Slc7a5	Q63016	18.2287	18.1217	18.3531	17.6072	17.9944	17.8019	17.5779	18.0449
1529	Large proline-rich protein BAG6 OS=Rattus norvegicus OX=10116 GN=Bag6 PE=1 SV=2	Bag6	Q6MG49	21.0263	17.7617	15.2168	21.062	22.7824	21.9856	22.3742	21.7945
1530	Late endosomal/lysosomal adaptor, MAPK and MTOR activator 2 OS=Rattus norvegicus OX=10116 GN=Lamtor2 PE=1 SV=	Lamtor2	D4A465	15.3165	15.6998	16.8552	16.0626	19.6169	19.1064	19.3843	19.5315
1531	Latent transforming growth factor beta binding protein 2, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ltbp2 PE=1	Ltbp2	A0A0G2K1G5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1532	Latent-transforming growth factor beta-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ltbp1 PE=1 SV=2	Ltbp1	D3ZAA3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1533	Latent-transforming growth factor beta-binding protein 4 OS=Rattus norvegicus OX=10116 GN=Ltbp4 PE=1 SV=2	Ltbp4	D4A917	17.2993	16.7904	15.9867	NaN	19.0598	20.6805	18.6147	19.1209
1534	LDL receptor-related protein 1 OS=Rattus norvegicus OX=10116 GN=Lrp1 PE=1 SV=1	Lrp1	G3V928	21.7152	23.6262	21.9945	22.5712	18.1195	21.5593	21.3766	21.1386
1535	Lecithin cholesterol acyltransferase OS=Rattus norvegicus OX=10116 GN=Lcat PE=1 SV=1	Lcat	O35849	19.8938	18.7495	19.7925	19.3699	16.7802	16.4143	NaN	16.406

1536	Lectin, mannose-binding 2 OS=Rattus norvegicus OX=10116 GN=Lman2 PE=1 SV=1	Lman2	B0BNG3	19.8227	19.324	18.7616	19.599	20.9086	22.2514	21.7456	21.7807
1537	Leiomodin-2-like OS=Rattus norvegicus OX=10116 GN=LOC100909784 PE=1 SV=1	LOC100909784	A0A0G2K918	NaN	NaN	NaN	NaN	18.2543	18.3279	17.9264	18.6257
1538	Leprecan 1, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=P3h1 PE=1 SV=1	P3h1	A0A0G2K199	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1539	Lethal(2) giant larvae protein homolog 1 OS=Rattus norvegicus OX=10116 GN=Llgl1 PE=1 SV=1	Llgl1	Q8K4K5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1540	Leucine repeat adapter protein 25 OS=Rattus norvegicus OX=10116 GN=Fam89b PE=1 SV=1	Fam89b	Q566R4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1541	Leucine rich repeat and fibronectin type III domain containing 2 OS=Rattus norvegicus OX=10116 GN=Lrfn2 PE=4 SV=1	Lrfn2	G3V7J3	16.4245	17.0077	16.8119	20.9836	NaN	NaN	NaN	NaN
1542	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Lrpprc PE=1 SV=2	Lrpprc	F1LM33	NaN	NaN	NaN	NaN	17.0356	19.5567	18.624	18.3183
1543	Leucine-rich repeat flightless-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Lrrfip1 PE=1 SV=1	Lrrfip1	Q66HF9	14.2	14.1801	15.5905	NaN	21.2952	21.9588	21.8405	21.4879
1544	Leucine-rich repeat flightless-interacting protein 2 OS=Rattus norvegicus OX=10116 GN=Lrrfip2 PE=1 SV=1	Lrrfip2	Q4V7E8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1545	Leucine-rich repeat-containing 40 OS=Rattus norvegicus OX=10116 GN=Lrrc40 PE=1 SV=3	Lrrc40	G3V7I7	16.7516	15.8602	16.0765	NaN	21.1632	20.8465	21.3714	21.3639
1546	Leucine-rich repeat-containing 47 OS=Rattus norvegicus OX=10116 GN=Lrrc47 PE=1 SV=2	Lrrc47	F1LT49	15.7364	NaN	NaN	NaN	19.4836	20.2155	20.5977	20.7783
1547	Leucine-rich repeat-containing protein 41 OS=Rattus norvegicus OX=10116 GN=Lrrc41 PE=2 SV=1	Lrrc41	Q5M9H1	NaN	NaN	NaN	NaN	16.1163	NaN	16.5158	16.3373
1548	Leucine-rich repeat-containing protein 57 OS=Rattus norvegicus OX=10116 GN=Lrrc57 PE=2 SV=1	Lrrc57	Q5FVI3	NaN	NaN	15.1452	NaN	18.6452	17.2098	17.9045	16.4779
1549	Leucine-rich repeat-containing protein 59 OS=Rattus norvegicus OX=10116 GN=Lrrc59 PE=1 SV=1	Lrrc59	Q5RJR8	19.7221	NaN	15.3127	NaN	20.504	21.4022	19.7361	20.5321
1550	Leucine-rich repeats and calponin homology domain-containing 3 OS=Rattus norvegicus OX=10116 GN=Lrch3 PE=1 SV=2	Lrch3	D4A8M4	15.253	13.4018	NaN	16.1272	17.2949	18.5898	18.3263	17.8017
1551	Leucyl-cystinyl aminopeptidase OS=Rattus norvegicus OX=10116 GN=Lnpep PE=1 SV=1	Lnpep	P97629	18.3216	17.5172	17.5114	17.4403	21.9997	22.5977	22.3276	22.2848
1552	Leucyl-tRNA synthetase OS=Rattus norvegicus OX=10116 GN=Lars PE=1 SV=1	Lars1	Q5PPJ6	15.7565	18.7293	16.9208	16.0957	22.6765	22.0982	22.6689	22.3012
1553	Leukocyte cell-derived chemotaxin 1 OS=Rattus norvegicus OX=10116 GN=Cnmd PE=2 SV=1	Cnmd	A0JPL7	18.6267	NaN	NaN	NaN	16.8099	14.5096	NaN	NaN
1554	Leukocyte surface antigen CD47 OS=Rattus norvegicus OX=10116 GN=Cd47 PE=1 SV=1	Cd47	A0A0G2JTH4	19.4892	18.9929	18.4871	19.522	19.1686	18.817	18.2861	19.0963
1555	Leukosialin OS=Rattus norvegicus OX=10116 GN=Spn PE=1 SV=2	Spn	R9PXZ7	16.0312	16.4683	16.5011	16.3943	16.416	15.2705	NaN	15.355
1556	Leukotriene A(4) hydrolase OS=Rattus norvegicus OX=10116 GN=Lta4h PE=1 SV=1	Lta4h	Q499P2	19.5109	18.081	18.3379	18.3417	17.2227	21.4043	21.3231	20.9924
1557	LIM and cysteine-rich domains 1 OS=Rattus norvegicus OX=10116 GN=Lmcd1 PE=1 SV=1	Lmcd1	Q6AYF2	18.1879	18.3776	17.1659	17.2373	22.7025	23.1209	23.5561	23.1679
1558	LIM and senescent cell antigen-like-containing domain protein OS=Rattus norvegicus OX=10116 GN=Lims1 PE=1 SV=1	Lims1	C0KUC6	19.0273	18.9782	17.4959	16.9398	22.7467	23.3134	22.9624	22.8984
1559	LIM and SH3 domain protein 1 OS=Rattus norvegicus OX=10116 GN=Lasp1 PE=1 SV=1	Lasp1	Q99MZ8	17.4214	18.0655	NaN	17.855	17.0671	17.7322	NaN	15.9755
1560	LIM domain 7 OS=Rattus norvegicus OX=10116 GN=Lmo7 PE=1 SV=1	Lmo7	A0A0G2K174	16.439	16.5382	16.3919	17.4386	22.7976	23.7202	23.2069	23.0836
1561	LIM domain and actin-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Lima1 PE=1 SV=2	Lima1	F1LR10	NaN	NaN	NaN	NaN	17.7561	17.1039	NaN	17.5251
1562	LIM domain-binding 3 OS=Rattus norvegicus OX=10116 GN=Ldb3 PE=1 SV=1	Ldb3	A0A096MJ01	19.6041	19.3918	19.4835	19.7563	27.0839	26.6992	27.0293	26.6233
1563	LIM domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Limd1 PE=1 SV=1	Limd1	B5DEH0	18.6992	18.4279	18.9372	18.3879	21.5971	22.533	21.9732	21.6304
1564	LIM domain-containing protein ajuba OS=Rattus norvegicus OX=10116 GN=Ajuba PE=1 SV=1	Ajuba	Q5U2Z2	NaN	NaN	NaN	NaN	16.6383	NaN	NaN	NaN
1565	Limbic system-associated membrane protein OS=Rattus norvegicus OX=10116 GN=Lsamp PE=1 SV=1	Lsamp	Q62813	NaN	NaN	NaN	NaN	18.0664	NaN	NaN	17.9132
1566	Lipase OS=Rattus norvegicus OX=10116 GN=Lipo1 PE=3 SV=1	Lipo1	D3ZUQ1	NaN	18.172	16.7373	NaN	NaN	NaN	15.8879	15.0591
1567	Lipin 1 OS=Rattus norvegicus OX=10116 GN=Lpin1 PE=1 SV=1	Lpin1	A0A0G2JW03	NaN	NaN	NaN	NaN	16.2344	14.5544	14.9917	NaN
1568	Lipoma-preferred partner homolog OS=Rattus norvegicus OX=10116 GN=Lpp PE=1 SV=1	Lpp	Q5XI07	17.8671	18.5153	18.115	17.5013	23.2169	23.8679	23.2963	22.9001
1569	Lipopolysaccharide-binding protein OS=Rattus norvegicus OX=10116 GN=Lbp PE=1 SV=1	Lbp	Q3MID7	21.4796	21.0635	20.5402	20.7403	19.231	18.0449	18.1933	17.6201
1570	Lipoprotein lipase OS=Rattus norvegicus OX=10116 GN=Lpl PE=1 SV=1	Lpl	Q06000	18.8225	18.5844	18.7145	19.1336	19.9771	19.972	19.8274	19.8609
1571	L-lactate dehydrogenase A chain OS=Rattus norvegicus OX=10116 GN=Ldha PE=1 SV=1	Ldha	P04642	21.517	22.0248	22.1294	21.0769	24.8993	25.3607	25.5372	25.3501
1572	L-lactate dehydrogenase B chain OS=Rattus norvegicus OX=10116 GN=Ldhb PE=1 SV=2	Ldhb	P42123	21.0519	21.1592	20.9179	20.1252	25.2909	26.7269	27.1767	26.9051
1573	LOC683667 protein OS=Rattus norvegicus OX=10116 GN=Sri PE=1 SV=1	Sri	B0BNJ1	18.0046	17.8629	17.9902	16.7789	22.6459	22.2613	22.4346	22.557
1574	LOC685144 protein OS=Rattus norvegicus OX=10116 GN=Sec24c PE=1 SV=1	Sec24c	B5DEG8	14.7492	NaN	16.3393	16.1231	20.4722	20.1471	19.8508	20.4501
1575	LOC689226 protein OS=Rattus norvegicus OX=10116 GN=Ube2r2 PE=1 SV=1	Ube2r2	B2RZ96	NaN	NaN	NaN	NaN	18.0821	17.5389	17.9994	17.2866
1576	Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acadl PE=1 SV=1	Acadl	P15650	19.6371	19.3758	18.04	20.6563	20.5118	21.8111	21.0691	21.3643
1577	Long-chain-fatty-acid--CoA ligase 1 OS=Rattus norvegicus OX=10116 GN=Acsl1 PE=1 SV=1	Acsl1	P18163	23.2689	23.0262	23.3484	22.7921	22.3221	22.4994	21.8402	22.0015
1578	Low molecular weight phosphotyrosine protein phosphatase OS=Rattus norvegicus OX=10116 GN=Acp1 PE=1 SV=2	Acp1	Z4YNF4	17.4951	15.7455	17.4494	17.2918	NaN	17.0736	16.8756	16.693
1579	LPS-responsive beige-like anchor protein OS=Rattus norvegicus OX=10116 GN=Lrba PE=1 SV=1	Lrba	A0A0G2JYI0	17.2713	18.6174	17.6542	17.0726	19.0133	18.2329	18.4859	17.896
1580	LRP chaperone MESD OS=Rattus norvegicus OX=10116 GN=Mesd PE=2 SV=1	Mesd	Q5U2R7	20.6806	20.7019	21.1763	19.4555	20.045	20.488	20.5249	20.505
1581	LRP16 protein OS=Rattus norvegicus OX=10116 GN=Macrod1 PE=1 SV=1	Macrod1	A0A0G2K5F1	15.8521	15.7741	15.6275	NaN	19.183	19.8443	20.219	19.8104
1582	LRRGT00052 OS=Rattus norvegicus OX=10116 PE=2 SV=1	Grtp1	Q6TXE7	17.4	NaN	NaN	14.4402	17.1619	15.7777	15.3219	15.6952
1583	LRRGT00199 OS=Rattus norvegicus OX=10116 GN=Taf3 PE=1 SV=1	Atp5f1c	Q6QI09	18.3118	18.8863	16.8166	17.3759	21.0802	22.7059	22.4394	22.5056
1584	LSM family member 14B OS=Rattus norvegicus OX=10116 GN=Lsm14b PE=1 SV=1	Lsm14b	A0A0G2JZY0	NaN	18.635	16.7996	NaN	16.3134	17.3512	17.3545	17.6506
1585	LSM12 homolog OS=Rattus norvegicus OX=10116 GN=Lsm12 PE=1 SV=1	Lsm12	D4A8G0	NaN	NaN	NaN	NaN	19.6787	20.3396	19.8408	19.5353
1586	LSM14A mRNA-processing body assembly factor OS=Rattus norvegicus OX=10116 GN=Lsm14a PE=1 SV=1	Lsm14a	B2GV58	NaN	NaN	NaN	NaN	17.369	16.6914	17.4462	17.4439
1587	LSM6 homolog, U6 small nuclear RNA and mRNA degradation-associated OS=Rattus norvegicus OX=10116 GN=Lsm6 PE=1	LOC100360750	D3ZG07	NaN	16.5899	15.323	NaN	19.6268	18.7361	18.1817	19.0008
1588	LUC7-like 2 (S. cerevisiae) OS=Rattus norvegicus OX=10116 GN=Luc7l2 PE=1 SV=1	Luc7l2	B2RYP6	17.4805	17.8859	14.3021	12.8307	22.5889	21.8357	21.4616	21.4465

1589	LUC7-like 3 pre-mRNA-splicing factor OS=Rattus norvegicus OX=10116 GN=Luc7l3 PE=1 SV=1	Luc7l3	D3ZFB2	NaN	NaN	NaN	NaN	19.1212	18.255	17.2019	15.9711
1590	Lumican OS=Rattus norvegicus OX=10116 GN=Lum PE=1 SV=1	Lum	P51886	22.8892	21.9718	22.3226	22.6969	21.9333	21.0748	21.006	21.6256
1591	Lupus La protein homolog OS=Rattus norvegicus OX=10116 GN=Ssb PE=1 SV=1	Ssb	Q66HM7	21.0881	20.867	21.1682	19.41	20.9874	22.1627	21.1668	21.597
1592	Ly6/Plaur domain containing 2 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Lypd2 PE=4 SV=3	Lypd2	D4A707	19.4549	20.2043	19.4902	17.5458	16.427	NaN	15.8851	NaN
1593	Lymphocyte cytosolic protein 1 OS=Rattus norvegicus OX=10116 GN=Lcp1 PE=1 SV=1	Lcp1	A0A0G2K014	16.044	16.716	15.7185	16.9033	16.4068	NaN	16.7399	16.0447
1594	Lys-63-specific deubiquitinase BRCC36 OS=Rattus norvegicus OX=10116 GN=Brcc3 PE=2 SV=1	Brcc3	B2RYM5	21.8942	23.2078	21.4343	23.3592	21.394	21.2331	20.8897	20.7186
1595	Lysine demethylase 3B OS=Rattus norvegicus OX=10116 GN=Kdm3b PE=1 SV=2	Kdm3b	M0RDF1	NaN	15.4036	15.4587	15.8474	19.017	16.8914	18.3147	17.853
1596	Lysine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Kars PE=1 SV=1	Kars1	Q5XIM7	20.4284	20.2943	20.3375	19.1988	23.4772	22.965	23.5451	23.1989
1597	LysM domain-containing 2 OS=Rattus norvegicus OX=10116 GN=Lysmd2 PE=1 SV=1	Lysmd2	A0A0G2K146	NaN	NaN	NaN	NaN	16.7855	15.7288	15.6905	15.8812
1598	Lysophospholipid acyltransferase 5 OS=Rattus norvegicus OX=10116 GN=Lpcat3 PE=2 SV=1	Lpcat3	Q5FVN0	19.3725	19.009	18.9708	18.9507	20.4907	21.0725	20.5617	20.9211
1599	Lysosome membrane protein 2 OS=Rattus norvegicus OX=10116 GN=Scarb2 PE=1 SV=2	Scarb2	P27615	NaN	16.3216	17.1568	14.3171	18.6388	19.7544	18.52	19.213
1600	Lysosome-associated membrane glycoprotein 1 OS=Rattus norvegicus OX=10116 GN=Lamp1 PE=1 SV=1	Lamp1	P14562	20.0658	20.4758	20.0975	19.2726	23.1576	23.0345	23.0543	22.9968
1601	Lysosome-associated membrane glycoprotein 2 OS=Rattus norvegicus OX=10116 GN=Lamp2 PE=1 SV=3	Lamp2	P17046	18.316	17.6758	18.2065	17.7104	19.3055	20.0932	19.7881	20.0379
1602	Lysozyme OS=Rattus norvegicus OX=10116 GN=Lyz2 PE=1 SV=1	Lyz2	F1M8E9	17.651	18.5457	19.7754	18.8475	15.1608	16.7896	16.5479	NaN
1603	Lysyl oxidase-like 1 OS=Rattus norvegicus OX=10116 GN=Loxl1 PE=2 SV=1	Loxl1	Q5FWS5	20.6345	19.9623	19.8357	20.2887	17.9197	18.5766	18.0062	18.2952
1604	Macrophage colony-stimulating factor 1 receptor OS=Rattus norvegicus OX=10116 GN=Csf1r PE=1 SV=2	Csf1r	D4ACA7	17.3958	17.0437	17.9166	17.8203	18.0189	18.4621	17.3424	17.1672
1605	Macrophage migration inhibitory factor OS=Rattus norvegicus OX=10116 GN=Mif PE=1 SV=4	Mif	P30904	19.4619	18.0014	18.9539	19.2194	21.115	20.6123	21.2986	21.2415
1606	Macrophage scavenger receptor 1 OS=Rattus norvegicus OX=10116 GN=Msr1 PE=1 SV=3	Msr1	D3ZDS2	18.0682	17.9498	17.5833	16.8352	NaN	NaN	17.5017	17.0394
1607	Macrophage-capping protein OS=Rattus norvegicus OX=10116 GN=Capg PE=1 SV=1	Capg	Q6AYC4	NaN	NaN	NaN	NaN	16.9758	17.4533	NaN	NaN
1608	Macrophage-stimulating 1 OS=Rattus norvegicus OX=10116 GN=Mst1 PE=3 SV=1	Mst1	F7FMS0	15.6299	15.6935	16.3472	16.4473	NaN	NaN	NaN	NaN
1609	MAD2 (Mitotic arrest deficient, homolog)-like 1 (Yeast) (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=M	Mad2l1	D4ACM2	NaN	NaN	NaN	NaN	23.0255	22.6183	23.136	23.0605
1610	MAGE family member D2 OS=Rattus norvegicus OX=10116 GN=Maged2 PE=1 SV=1	Maged2	Q3B7U1	19.1678	18.5964	18.3934	18.6477	22.6725	21.9708	21.9829	21.8319
1611	Magnesium-dependent phosphatase 1 OS=Rattus norvegicus OX=10116 GN=Mdp1 PE=1 SV=1	Mdp1	D4A4U3	NaN	NaN	NaN	NaN	18.299	17.4845	18.0185	17.4235
1612	Major vault protein OS=Rattus norvegicus OX=10116 GN=Mvp PE=1 SV=1	Mvp	A0A140TAE0	18.8596	20.5405	18.5296	18.5569	21.4859	21.9728	21.8791	24.2501
1613	MAL2A OS=Rattus norvegicus OX=10116 GN=Mal2 PE=2 SV=1	Mal2	Q7TPB7	15.9181	17.1334	16.567	15.9087	NaN	13.7358	NaN	NaN
1614	Malate dehydrogenase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Mdh1 PE=1 SV=3	Mdh1	O88989	19.6824	20.0161	19.9984	20.3119	24.4255	24.5451	24.6511	24.4677
1615	Malate dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mdh2 PE=1 SV=2	Mdh2	P04636	20.8359	21.5441	19.3227	20.7189	21.8681	24.3354	23.4415	23.7109
1616	Maleylacetoacetate isomerase OS=Rattus norvegicus OX=10116 GN=Gstz1 PE=1 SV=2	Gstz1	P57113	NaN	NaN	NaN	NaN	16.7341	17.1405	18.1572	17.07
1617	Malignant T-cell-amplified sequence 1 OS=Rattus norvegicus OX=10116 GN=Mcts1 PE=2 SV=1	Mcts1	Q4G009	NaN	16.6269	NaN	NaN	18.1696	18.0034	18.0019	18.2992
1618	Mammary tumor virus receptor 2, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Sssca1 PE=1 SV=1	Znrd2	D3ZG88	17.5618	NaN	NaN	18.328	20.2608	20.8451	20.7085	20.4633
1619	Mannan-binding lectin serine peptidase 2 OS=Rattus norvegicus OX=10116 GN=Masp2 PE=1 SV=1	Masp2	A2VCV7	22.1213	21.2896	21.7343	22.087	16.8429	17.0276	NaN	15.0247
1620	Mannan-binding lectin serine protease 1 OS=Rattus norvegicus OX=10116 GN=Masp1 PE=1 SV=1	Masp1	A0A0H2UHA1	21.175	20.9093	21.1628	20.7686	19.6778	17.6273	18.7592	19.1376
1621	Mannose receptor, C type 1 OS=Rattus norvegicus OX=10116 GN=Mrc1 PE=1 SV=3	Mrc1	D3ZD31	21.8901	21.9125	21.7794	21.7274	21.0111	21.1513	20.8495	20.9972
1622	Mannose-1-phosphate guanyltransferase alpha OS=Rattus norvegicus OX=10116 GN=Gmppa PE=2 SV=1	Gmppa	Q5XIC1	NaN	NaN	NaN	NaN	19.9498	18.5673	18.8115	18.8061
1623	Mannose-6-phosphate isomerase OS=Rattus norvegicus OX=10116 GN=Mpi PE=2 SV=1	Mpi	Q68FX1	NaN	16.5781	16.0577	15.9457	17.5563	18.4653	19.2307	17.4677
1624	Mannose-binding protein A OS=Rattus norvegicus OX=10116 GN=Mbl1 PE=1 SV=1	Mbl1	P19999	20.2239	20.2597	20.3629	20.0929	16.9643	17.8159	17.5977	17.7635
1625	Mannose-P-dolichol utilization defect 1 OS=Rattus norvegicus OX=10116 GN=Mpdu1 PE=1 SV=1	Mpdu1	D3Z865	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1626	Map2k3 protein OS=Rattus norvegicus OX=10116 GN=Map2k3 PE=1 SV=1	Map2k3	B1H230	NaN	16.4951	17.8094	NaN	20.0713	20.1691	20.5969	20.2154
1627	Map3k3 protein OS=Rattus norvegicus OX=10116 GN=Map3k3 PE=1 SV=1	Map3k3	B5DF98	NaN	NaN	14.7872	NaN	17.1866	18.3705	17.8505	17.7811
1628	MAP7 domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Map7d1 PE=1 SV=1	Map7d1	D4A644	19.7246	19.7475	19.1523	NaN	22.727	23.7647	23.1415	22.8735
1629	Mapk1ip1l protein OS=Rattus norvegicus OX=10116 GN=Mapk1ip1l PE=1 SV=1	Mapk1ip1l	B2RZ29	NaN	NaN	14.6782	NaN	20.2913	16.5642	18.0977	18.0339
1630	MAPK-regulated co-repressor-interacting protein 2 OS=Rattus norvegicus OX=10116 GN=Mcrip2 PE=1 SV=1	Mcrip2	D3ZM07	NaN	NaN	NaN	NaN	18.591	19.6688	19.4102	19.2191
1631	Matrin-3 OS=Rattus norvegicus OX=10116 GN=Matr3 PE=1 SV=1	Matr3	A0A0G2JSR7	16.6848	15.9592	16.6881	15.8657	19.3384	19.0901	18.2531	17.2745
1632	Matrix metallopeptidase 19 OS=Rattus norvegicus OX=10116 GN=Mmp19 PE=2 SV=1	Mmp19	C0M4B0	18.1396	16.5188	16.5414	16.6186	NaN	NaN	NaN	NaN
1633	Matrix-remodeling-associated 7 OS=Rattus norvegicus OX=10116 GN=Mxra7 PE=1 SV=1	Mxra7	M0RA39	14.4435	NaN	NaN	NaN	15.4429	16.9938	16.7275	16.9128
1634	MCC, WNT-signaling pathway regulator OS=Rattus norvegicus OX=10116 GN=Mcc PE=1 SV=1	Mcc	A0A0G2K098	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1635	Megakaryoblastic leukemia (translocation) 1 OS=Rattus norvegicus OX=10116 GN=Mrtfa PE=1 SV=1	Mrtfa	A0A0G2JXC5	NaN	15.906	16.06	NaN	18.2776	18.6747	17.7547	17.7595
1636	Melanoma-associated antigen D1 OS=Rattus norvegicus OX=10116 GN=Maged1 PE=1 SV=3	Maged1	Q9ES73	NaN	NaN	NaN	NaN	17.6856	NaN	18.2272	17.8202
1637	Membrane-associated progesterone receptor component 1 OS=Rattus norvegicus OX=10116 GN=Pgrmc1 PE=1 SV=1	Pgrmc1	A0A0H2UHK2	NaN	15.6262	15.7857	15.925	18.6881	18.8994	18.4766	19.0739
1638	Membrane-associated progesterone receptor component 2 OS=Rattus norvegicus OX=10116 GN=Pgrmc2 PE=1 SV=1	Pgrmc2	Q5XIU9	17.1915	16.5151	16.9538	15.9045	20.7595	21.4348	21.0272	21.3914
1639	Membrane-bound O-acyltransferase domain-containing 7-like 1 OS=Rattus norvegicus OX=10116 GN=Mboat7l1 PE=1 SV=1	Mboat7l1	G3V7N6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1640	Metalloendopeptidase OS=Rattus norvegicus OX=10116 GN=Bmp1 PE=4 SV=2	Bmp1	F1M798	16.774	NaN	NaN	16.442	16.0215	NaN	NaN	NaN
1641	Metalloproteinase inhibitor 3 OS=Rattus norvegicus OX=10116 GN=Timp3 PE=2 SV=1	Timp3	P48032	21.0761	20.6678	20.862	20.0808	17.6045	16.7034	15.9517	NaN

1642	Metalloreductase STEAP3 OS=Rattus norvegicus OX=10116 GN=Steap3 PE=1 SV=1	Steap3	A0A0H2UI26	18.3284	16.0012	17.8012	18.6536	NaN	17.5021	17.3081	17.4407
1643	Metallothionein OS=Rattus norvegicus OX=10116 GN=Mt1m PE=3 SV=1	Mt1m	D3ZHV3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1644	Metallothionein-1 OS=Rattus norvegicus OX=10116 GN=Mt1 PE=1 SV=1	Mt1	P02803	NaN	NaN	NaN	NaN	NaN	17.0041	17.1331	NaN
1645	Metaxin 2 OS=Rattus norvegicus OX=10116 GN=Mtx2 PE=1 SV=1	Mtx2	Q5U1Z9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1646	Methanethiol oxidase OS=Rattus norvegicus OX=10116 GN=Selenbp1 PE=1 SV=2	LOC103689947	F1LRJ9	NaN	15.4492	16.2294	15.4232	NaN	17.6455	16.6361	16.5912
1647	Methionine adenosyltransferase 2 subunit beta OS=Rattus norvegicus OX=10116 GN=Mat2b PE=2 SV=1	Mat2b	Q5U2R0	NaN	NaN	NaN	NaN	17.6367	NaN	18.6745	19.1495
1648	Methionine aminopeptidase 2 OS=Rattus norvegicus OX=10116 GN=Metap2 PE=1 SV=1	Metap2	Q6IRK1	NaN	NaN	NaN	NaN	17.6705	15.9767	17.5028	17.973
1649	Methionine aminopeptidase 2 OS=Rattus norvegicus OX=10116 GN=Metap2 PE=1 SV=2	Metap2	P38062	16.9973	16.6367	17.2684	17.2106	19.4847	19.4609	19.0649	18.5875
1650	Methionine aminopeptidase OS=Rattus norvegicus OX=10116 GN=Metap1 PE=1 SV=1	Metap1	D3ZE72	NaN	NaN	18.6809	NaN	17.5898	16.7407	NaN	16.6658
1651	Methionyl-tRNA synthetase OS=Rattus norvegicus OX=10116 GN=Mars PE=1 SV=1	Mars1	D3Z941	15.0142	NaN	16.5502	17.1422	22.7118	22.3886	22.798	22.8365
1652	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mccc2 PE=2 SV=1	Mccc2	Q5XIT9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1653	Methylthioribose-1-phosphate isomerase OS=Rattus norvegicus OX=10116 GN=Mri1 PE=1 SV=1	Mri1	Q5HZE4	20.7974	20.6068	20.6654	19.2144	21.1805	21.2428	21.3151	21.1894
1654	Methylthioribulose-1-phosphate dehydratase OS=Rattus norvegicus OX=10116 GN=Apip PE=1 SV=3	Apip	D3ZUI1	15.0331	12.7891	15.6179	NaN	16.1197	16.3097	18.7134	15.4205
1655	Methyltransferase-like 27 OS=Rattus norvegicus OX=10116 GN=Mettl27 PE=1 SV=1	Mettl27	D4AED6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1656	Methyltransferase-like 3 OS=Rattus norvegicus OX=10116 GN=Mettl3 PE=1 SV=1	Mettl3	Q4V8G6	20.3448	21.6337	19.485	19.5727	20.3782	20.6889	19.663	NaN
1657	Mevalonate kinase OS=Rattus norvegicus OX=10116 GN=Mvk PE=1 SV=1	Mvk	M0R5W4	NaN	NaN	NaN	NaN	17.9061	17.3077	NaN	18.1172
1658	MICAL-like protein 1 OS=Rattus norvegicus OX=10116 GN=Micall1 PE=1 SV=1	Micall1	D3ZQL6	NaN	NaN	NaN	NaN	17.8571	17.3207	17.1444	16.7266
1659	MICOS complex subunit MIC60 OS=Rattus norvegicus OX=10116 GN=Immt PE=1 SV=1	Immt	A0A0G2JVH4	20.344	19.9298	19.135	19.0698	20.1057	21.6084	21.0048	21.5051
1660	MICOS complex subunit OS=Rattus norvegicus OX=10116 GN=Chchd3 PE=1 SV=1	Chchd3	D3ZUX5	NaN	16.9419	NaN	NaN	17.2278	19.4433	18.2002	18.5506
1661	Microfibril-associated glycoprotein 4-like OS=Rattus norvegicus OX=10116 GN=LOC102553715 PE=1 SV=3	Mfap4	D4A7W8	19.1789	19.6819	19.791	19.0495	19.2896	18.9026	18.9755	19.1725
1662	Microsomal glutathione S-transferase 3 OS=Rattus norvegicus OX=10116 GN=Mgst3 PE=1 SV=1	Mgst3	D4ADS4	15.5372	NaN	15.847	NaN	17.9979	19.4724	18.8536	18.9692
1663	Microtubule-actin cross-linking factor 1 OS=Rattus norvegicus OX=10116 GN=Macf1 PE=1 SV=1	Macf1	A0A0G2K9T4	21.3193	22.0273	22.1828	22.5698	23.461	24.4935	23.808	23.7285
1664	Microtubule-associated protein 1A OS=Rattus norvegicus OX=10116 GN=Map1a PE=1 SV=1	Map1a	A0A0G2K5C6	16.033	16.8215	16.1374	NaN	18.2369	19.5138	19.6612	19.6629
1665	Microtubule-associated protein 1A OS=Rattus norvegicus OX=10116 GN=Map1a PE=1 SV=1	Map1a	P34926	20.0341	19.7103	18.5515	17.1935	22.2553	24.5244	24.0027	23.6226
1666	Microtubule-associated protein 1B OS=Rattus norvegicus OX=10116 GN=Map1b PE=1 SV=3	Map1b	P15205	19.2994	19.8108	19.1038	19.0512	21.9332	22.5379	22.1687	22.1375
1667	Microtubule-associated protein 1S OS=Rattus norvegicus OX=10116 GN=Map1s PE=1 SV=1	Map1s	P0C5W1	15.9078	NaN	NaN	NaN	18.5565	19.9474	19.3018	18.9819
1668	Microtubule-associated protein 4 OS=Rattus norvegicus OX=10116 GN=Map4 PE=1 SV=1	Map4	Q5M7W5	NaN	NaN	NaN	NaN	20.8904	22.2173	21.8104	21.5696
1669	Microtubule-associated protein OS=Rattus norvegicus OX=10116 GN=Map4 PE=1 SV=1	Map4	A0A0G2JW88	19.7855	20.3089	19.9613	19.7486	25.4497	26.563	26.1437	25.9189
1670	Microtubule-associated protein RP/EB family member 1 OS=Rattus norvegicus OX=10116 GN=Mapre1 PE=1 SV=3	Mapre1	Q66HR2	NaN	16.7687	15.8335	15.82	22.5756	22.3168	22.4172	22.0231
1671	Microtubule-associated protein RP/EB family member 2 OS=Rattus norvegicus OX=10116 GN=Mapre2 PE=1 SV=1	Mapre2	Q3B8Q0	15.7572	12.6657	15.6918	13.8896	21.0614	21.1546	21.6738	21.5174
1672	Microtubule-associated serine/threonine kinase family member 4 OS=Rattus norvegicus OX=10116 GN=Mast4 PE=1 SV=2	Mast4	M0R3L1	20.7533	22.1052	19.8938	20.9553	19.9886	21.1454	20.7575	20.9701
1673	Midkine OS=Rattus norvegicus OX=10116 GN=Mdk PE=2 SV=1	Mdk	Q9R1S9	NaN	NaN	16.0131	NaN	18.4497	20.4486	19.4925	19.7882
1674	Misato 1, mitochondrial distribution and morphology regulator OS=Rattus norvegicus OX=10116 GN=Msto1 PE=1 SV=1	Msto1	D3ZMW3	22.6104	21.9784	21.9965	21.3179	22.8461	22.3035	22.0217	22.2189
1675	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Rattus norvegicus OX=10116 GN=Slc25a11 PE=1 SV=3	Slc25a11	P97700	15.7163	17.43	NaN	NaN	17.9352	18.8476	19.1809	19.1619
1676	Mitochondrial brown fat uncoupling protein 1 OS=Rattus norvegicus OX=10116 GN=Ucp1 PE=1 SV=2	Ucp1	P04633	16.7101	19.0003	16.7969	15.8936	16.103	17.6348	16.2975	16.8603
1677	Mitochondrial carnitine/acylcarnitine carrier protein OS=Rattus norvegicus OX=10116 GN=Slc25a20 PE=1 SV=1	Slc25a20	P97521	18.9816	NaN	19.4765	18.9763	NaN	17.568	16.8975	17.0346
1678	Mitochondrial carrier 2 OS=Rattus norvegicus OX=10116 GN=Mtch2 PE=1 SV=1	Mtch2	A0A0G2K459	NaN	NaN	NaN	NaN	NaN	18.8358	18.0717	18.9026
1679	Mitochondrial fission 1 protein OS=Rattus norvegicus OX=10116 GN=Fis1 PE=1 SV=1	Fis1	P84817	17.7178	15.8054	17.3392	16.1815	21.8351	20.0117	21.6595	21.6836
1680	Mitochondrial fission regulator 1-like OS=Rattus norvegicus OX=10116 GN=Mtfr1l PE=1 SV=1	Mtfr1l	Q5XII9	NaN	NaN	NaN	NaN	16.9516	17.4578	17.1881	NaN
1681	Mitochondrial import inner membrane translocase subunit Tim13 OS=Rattus norvegicus OX=10116 GN=Timm13 PE=3 SV=	Timm13	P62076	NaN	NaN	NaN	NaN	17.911	17.6108	18.0363	17.9799
1682	Mitochondrial import receptor subunit TOM20 homolog OS=Rattus norvegicus OX=10116 GN=Tomm20 PE=1 SV=2	Tomm20	Q62760	NaN	NaN	16.5508	NaN	NaN	17.1506	NaN	NaN
1683	Mitochondrial import receptor subunit TOM22 homolog OS=Rattus norvegicus OX=10116 GN=Tomm22 PE=1 SV=1	Tomm22	Q75Q41	16.27	17.1189	15.6317	15.5342	16.8782	19.5247	18.8372	19.4081
1684	Mitochondrial import receptor subunit TOM34 OS=Rattus norvegicus OX=10116 GN=Tomm34 PE=1 SV=1	Tomm34	Q3KRD5	18.7174	17.9704	18.4895	18.4368	24.0566	23.4009	23.7289	23.7832
1685	Mitochondrial import receptor subunit TOM40 homolog OS=Rattus norvegicus OX=10116 GN=Tomm40 PE=1 SV=1	Tomm40	Q75Q40	NaN	NaN	NaN	NaN	16.2215	17.25	17.1941	17.2685
1686	Mitochondrial import receptor subunit TOM70 OS=Rattus norvegicus OX=10116 GN=Tomm70 PE=1 SV=1	Tomm70	Q75Q39	NaN	14.3445	14.9361	NaN	NaN	NaN	15.7927	15.991
1687	Mitochondrial peptide methionine sulfoxide reductase OS=Rattus norvegicus OX=10116 GN=Msra PE=1 SV=1	Msra	Q923M1	NaN	18.4571	NaN	NaN	17.7382	NaN	17.3542	NaN
1688	Mitochondrial proton/calcium exchanger protein OS=Rattus norvegicus OX=10116 GN=Letm1 PE=1 SV=1	Letm1	Q5XIN6	NaN	NaN	NaN	NaN	16.3306	16.7429	16.575	15.8455
1689	Mitochondrial ribosomal protein L12 OS=Rattus norvegicus OX=10116 GN=Mrpl12 PE=1 SV=1	Mrpl12	D3ZXF9	NaN	NaN	NaN	NaN	NaN	NaN	16.9751	17.3875
1690	Mitogen-activated protein kinase 1 OS=Rattus norvegicus OX=10116 GN=Mapk1 PE=1 SV=3	Mapk1	P63086	18.669	18.9944	17.9587	18.0132	23.5085	22.1337	22.6955	22.7258
1691	Mitogen-activated protein kinase 3 OS=Rattus norvegicus OX=10116 GN=Mapk3 PE=1 SV=5	Mapk3	P21708	NaN	NaN	NaN	13.4873	21.3371	20.4203	20.7072	20.3004
1692	Mitogen-activated protein kinase kinase 4 OS=Rattus norvegicus OX=10116 GN=Map2k4 PE=1 SV=3	Map2k4	F1LP57	19.0683	20.4031	19.2638	20.3779	21.1481	20.8758	21.0677	21.1595
1693	Mitogen-activated protein kinase kinase 6 OS=Rattus norvegicus OX=10116 GN=Map2k6 PE=1 SV=1	Map2k6	Q925D6	17.2926	17.3393	17.2777	17.5812	21.2379	20.2507	20.2292	20.2617
1694	Mitogen-activated protein kinase kinase kinase 20 OS=Rattus norvegicus OX=10116 GN=Map3k20 PE=1 SV=1	Map3k20	D4AE17	15.7333	NaN	14.8312	NaN	21.4746	21.323	21.2804	21.0645

1695	Mitogen-activated protein kinase kinase kinase kinase 4 OS=Rattus norvegicus OX=10116 GN=Map4k4 PE=1 SV=1	Map4k4	A0A0G2K7W4	14.6932	15.7838	14.969	16.5488	19.0309	18.4674	18.2765	18.188
1696	Mitogen-activated protein kinase kinase kinase kinase OS=Rattus norvegicus OX=10116 GN=Map4k1 PE=1 SV=1	Map4k1	D3Z8I4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1697	Mitogen-activated protein kinase OS=Rattus norvegicus OX=10116 GN=Mapk14 PE=1 SV=1	Mapk14	G3V617	17.2557	16.6583	16.8971	15.4581	21.3943	20.3066	20.1964	20.6792
1698	Mitogen-activated protein kinase OS=Rattus norvegicus OX=10116 GN=Mapk9 PE=1 SV=1	Mapk9	D4A5V8	15.3821	NaN	16.5864	NaN	19.1871	18.5584	18.8446	18.6838
1699	Mitogen-activated protein kinase-activated protein kinase 2 OS=Rattus norvegicus OX=10116 GN=Mapkapk2 PE=1 SV=3	Mapkapk2	F1M9C0	17.5648	16.5377	16.3804	16.3815	21.5871	20.8836	21.038	20.6982
1700	Mitotic spindle organizing protein 1 OS=Rattus norvegicus OX=10116 GN=Mzt1 PE=1 SV=3	Mzt1	D4A4N1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1701	Mitotic spindle organizing protein 2B OS=Rattus norvegicus OX=10116 GN=Mzt2b PE=4 SV=1	Mzt2b	D4AA02	NaN	NaN	NaN	NaN	16.2742	16.3312	16.5839	16.3682
1702	MMS19 homolog, cytosolic iron-sulfur assembly component OS=Rattus norvegicus OX=10116 GN=Mms19 PE=1 SV=1	Mms19	M0R6T4	14.4739	16.9193	14.9589	NaN	20.5305	21.5498	21.6016	21.6536
1703	MOB kinase activator 1B OS=Rattus norvegicus OX=10116 GN=Mob1b PE=1 SV=1	Mob1b	D4A1V7	16.163	16.5729	NaN	15.0987	22.1388	21.6667	22.1057	21.8277
1704	MOB kinase activator 2 OS=Rattus norvegicus OX=10116 GN=Mob2 PE=1 SV=2	Mob2	D3ZLX3	NaN	NaN	15.4352	NaN	18.2482	17.8039	17.9417	18.115
1705	MOB-like protein phocein OS=Rattus norvegicus OX=10116 GN=Mob4 PE=1 SV=1	Mob4	Q9QYW3	16.7904	17.4262	15.7446	NaN	20.5578	20.5481	20.638	20.4728
1706	Moesin OS=Rattus norvegicus OX=10116 GN=Msn PE=1 SV=1	Msn	A0A096MK30	21.8818	22.0774	21.6993	21.6781	24.1179	24.022	23.7398	23.9282
1707	MON2 homolog, regulator of endosome-to-Golgi-trafficking OS=Rattus norvegicus OX=10116 GN=Mon2 PE=1 SV=3	Mon2	D3ZCG3	15.8224	18.3888	NaN	16.7472	17.5255	18.6475	17.7718	NaN
1708	Monocarboxylate transporter 1 OS=Rattus norvegicus OX=10116 GN=Slc16a1 PE=1 SV=1	Slc16a1	P53987	20.0261	20.704	20.4402	20.5678	22.0883	23.1755	22.9102	22.7493
1709	Monocarboxylate transporter 10 OS=Rattus norvegicus OX=10116 GN=Slc16a10 PE=1 SV=1	Slc16a10	G3V621	17.3997	16.8266	NaN	NaN	NaN	NaN	NaN	NaN
1710	Monocarboxylate transporter 4 OS=Rattus norvegicus OX=10116 GN=Slc16a3 PE=1 SV=1	Slc16a3	O35910	17.1425	NaN	16.4773	15.873	18.0399	17.8953	17.6379	18.1018
1711	Monoglyceride lipase OS=Rattus norvegicus OX=10116 GN=Mgll PE=1 SV=1	Mgll	Q8R431	NaN	15.9664	NaN	NaN	20.4104	20.5399	19.9797	20.2472
1712	Mortality factor 4-like protein 1 OS=Rattus norvegicus OX=10116 GN=Morf4l1 PE=2 SV=1	Morf4l1	Q6AYU1	18.3561	18.6988	18.8717	18.3093	16.5123	17.9702	17.4861	17.0363
1713	Mothers against decapentaplegic homolog 2 OS=Rattus norvegicus OX=10116 GN=Smad2 PE=1 SV=1	Smad2	O70436	NaN	NaN	NaN	NaN	16.0654	16.8691	16.6445	16.2122
1714	mRNA decay activator protein ZFP36L1 OS=Rattus norvegicus OX=10116 GN=Zfp36l1 PE=1 SV=1	Zfp36l1	P17431	NaN	NaN	NaN	NaN	18.188	18.5687	17.9487	16.2349
1715	MTSS1, I-BAR domain-containing OS=Rattus norvegicus OX=10116 GN=Mtss1 PE=1 SV=2	Mtss1	D3ZYM5	NaN	NaN	16.9093	15.74	17.0111	NaN	16.4862	16.6856
1716	MTSS1L, I-BAR domain-containing OS=Rattus norvegicus OX=10116 GN=Mtss1l PE=1 SV=3	Mtss2	D4A3S6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1717	Muc1 protein OS=Rattus norvegicus OX=10116 GN=Muc1 PE=2 SV=1	Muc1	B2GV31	18.8484	19.7959	20.3254	19.2545	17.3934	17.5511	17.377	17.7025
1718	Multifunctional protein ADE2 OS=Rattus norvegicus OX=10116 GN=Paics PE=1 SV=3	Paics	P51583	21.6622	21.4409	21.108	21.3059	25.0091	22.9709	23.9591	23.931
1719	Multimerin 1 OS=Rattus norvegicus OX=10116 GN=Mmrn1 PE=4 SV=1	Mmrn1	D4A3E0	21.5905	21.0489	21.9194	21.3113	24.2749	24.0442	24.1597	24.3071
1720	Multiple inositol polyphosphate phosphatase 1 OS=Rattus norvegicus OX=10116 GN=Minpp1 PE=3 SV=1	Minpp1	G3V7H2	16.4855	15.9651	16.9096	17.5131	NaN	NaN	NaN	NaN
1721	Murinoglobulin-1 OS=Rattus norvegicus OX=10116 GN=LOC297568 PE=1 SV=1	LOC297568	A0A0G2K926	16.9745	14.2891	19.7911	20.6161	15.1177	NaN	15.5237	16.1486
1722	Murinoglobulin-1 OS=Rattus norvegicus OX=10116 GN=Mug1 PE=1 SV=2	Mug1	D4A6E3	17.425	NaN	19.6532	19.4899	16.9508	NaN	16.6162	NaN
1723	Murinoglobulin-1 OS=Rattus norvegicus OX=10116 GN=Mug1 PE=2 SV=1	Mug1	Q03626	26.1046	26.4962	26.752	26.2005	22.7227	21.6545	21.729	22.0363
1724	Murinoglobulin-2 OS=Rattus norvegicus OX=10116 GN=Mug2 PE=1 SV=1	Mug2	Q6IE52	16.234	16.2729	17.9179	16.0642	NaN	NaN	16.8838	NaN
1725	Musashi RNA-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Msi2 PE=1 SV=3	Msi2	F1LWE6	16.4807	NaN	16.5739	NaN	19.6552	20.0636	19.2387	19.3175
1726	Muscleblind-like protein 2 OS=Rattus norvegicus OX=10116 GN=Mbnl2 PE=1 SV=1	Mbnl2	F2Z3T4	NaN	NaN	18.6057	NaN	18.197	17.925	NaN	NaN
1727	Muscleblind-like-splicing regulator 1 OS=Rattus norvegicus OX=10116 GN=Mbnl1 PE=1 SV=1	Mbnl1	A0A0G2JX72	15.0837	NaN	NaN	NaN	20.1231	19.3196	18.8877	19.6064
1728	Muscular LMNA-interacting protein OS=Rattus norvegicus OX=10116 GN=Mlip PE=1 SV=1	Mlip	A0A096MK47	19.5848	19.2717	19.6787	18.0919	22.4795	22.5313	22.7091	22.3799
1729	Myadm protein OS=Rattus norvegicus OX=10116 GN=Myadm PE=1 SV=1	Myadm	Q05BA4	18.633	19.7022	18.8697	19.0532	22.2931	22.4874	22.0054	22.2298
1730	Myc box-dependent-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Bin1 PE=1 SV=2	Bin1	F1LMX1	16.2855	16.8542	16.6174	16.5414	16.5076	NaN	NaN	16.4559
1731	MYC-binding protein 2, E3 ubiquitin protein ligase OS=Rattus norvegicus OX=10116 GN=Mycbp2 PE=1 SV=3	Mycbp2	D4A2D3	NaN	15.0134	15.1458	NaN	17.8463	16.5118	17.2231	16.952
1732	Myc-binding protein OS=Rattus norvegicus OX=10116 GN=Mycbp PE=1 SV=1	Mycbp	D4A7F2	NaN	NaN	NaN	17.4755	19.7368	19.7266	20.0989	19.5112
1733	Myeloid leukemia factor 1 OS=Rattus norvegicus OX=10116 GN=Mlf1 PE=1 SV=1	Mlf1	D3ZCQ9	NaN	NaN	NaN	NaN	16.7184	17.7931	17.2885	17.049
1734	Myeloid leukemia factor 2 OS=Rattus norvegicus OX=10116 GN=Mlf2 PE=1 SV=1	Mlf2	D3ZPN3	NaN	NaN	NaN	NaN	16.0876	16.6154	16.3254	15.9523
1735	Myeloid-derived growth factor OS=Rattus norvegicus OX=10116 GN=Mydgf PE=1 SV=2	Mydgf	M0R3V4	NaN	NaN	NaN	NaN	NaN	17.0522	NaN	NaN
1736	Myl6 protein OS=Rattus norvegicus OX=10116 GN=Myl6 PE=2 SV=1	Myl6	B2GV99	20.2484	20.672	20.1562	18.5747	25.5207	25.4577	24.7467	24.8601
1737	Myl9 protein OS=Rattus norvegicus OX=10116 GN=Myl9 PE=1 SV=1	Myl9	B0BMS8	NaN	NaN	NaN	16.0772	19.5026	20.1251	19.5795	19.5751
1738	Myocardial ischemic preconditioning associated protein 7 OS=Rattus norvegicus OX=10116 GN=Pxn PE=1 SV=1	Pxn	Q1EG89	14.9752	NaN	16.5798	17.1634	21.5592	21.4084	21.2823	20.774
1739	Myocyte-specific enhancer factor 2A OS=Rattus norvegicus OX=10116 GN=Mef2a PE=1 SV=2	Mef2a	M0R6R7	18.2324	17.6701	17.5276	16.5224	17.9492	17.6972	17.6872	17.5479
1740	Myoglobin OS=Rattus norvegicus OX=10116 GN=Mb PE=1 SV=3	Mb	Q9QZ76	16.1004	15.3525	16.4147	NaN	23.8743	24.4678	24.114	23.5237
1741	Myopalladin OS=Rattus norvegicus OX=10116 GN=Mypn PE=1 SV=1	Mypn	A0A0G2K046	16.7679	15.6275	16.006	NaN	19.5254	19.7606	19.6335	18.7513
1742	Myosin heavy chain 14 OS=Rattus norvegicus OX=10116 GN=Myh14 PE=1 SV=1	Myh14	F1LNF0	16.2401	16.5696	17.0201	16.6667	16.9587	19.7391	17.2104	18.0176
1743	Myosin light chain 1/3, skeletal muscle isoform OS=Rattus norvegicus OX=10116 GN=Myl1 PE=1 SV=2	Myl1	P02600	16.7697	17.139	16.8698	16.2073	16.9528	NaN	NaN	NaN
1744	Myosin light chain 3 OS=Rattus norvegicus OX=10116 GN=Myl3 PE=1 SV=2	Myl3	P16409	20.0376	21.0307	19.4326	20.5858	25.8704	26.1736	25.2898	25.4325
1745	Myosin light chain 4 OS=Rattus norvegicus OX=10116 GN=Myl4 PE=1 SV=1	Myl4	M0R4E1	NaN	NaN	NaN	NaN	20.833	NaN	NaN	NaN
1746	Myosin light chain 4 OS=Rattus norvegicus OX=10116 GN=Myl4 PE=2 SV=2	Myl4	P17209	14.6065	NaN	15.1306	19.1951	24.5657	23.6453	23.3894	23.7996
1747	Myosin light chain 7 OS=Rattus norvegicus OX=10116 GN=Myl7 PE=1 SV=1	Myl7	A0A0G2K2W5	18.0068	17.4376	16.9222	16.3176	21.745	20.764	20.5456	21.0465

1748	Myosin light chain kinase 3 OS=Rattus norvegicus OX=10116 GN=Mylk3 PE=1 SV=1	Mylk3	E9PT87	20.7329	22.0904	20.3302	20.2896	23.3065	23.0463	23.173	22.9622
1749	Myosin light chain kinase OS=Rattus norvegicus OX=10116 GN=Mylk PE=1 SV=2	Mylk	D3ZFU9	NaN	NaN	18.3972	18.7041	18.0879	18.5765	16.3864	17.9955
1750	Myosin phosphatase Rho-interacting protein OS=Rattus norvegicus OX=10116 GN=Mprip PE=1 SV=1	Mprip	A0A0G2JUR5	16.5568	17.0047	17.0529	17.4925	15.7991	14.692	17.0908	NaN
1751	Myosin regulatory light chain 12B OS=Rattus norvegicus OX=10116 GN=Myl12b PE=4 SV=1	Myl12b	A0A0G2JSW0	NaN	NaN	NaN	NaN	18.5568	19.6973	16.9129	16.252
1752	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform OS=Rattus norvegicus OX=10116 GN=Myl2 PE=1 SV=2	Myl2	P08733	18.9047	18.2748	18.7691	18.2937	25.6325	25.9123	25.4304	25.5142
1753	Myosin regulatory light chain RLC-A OS=Rattus norvegicus OX=10116 GN=Rlc-a PE=2 SV=2	Myl12a	P13832	18.3405	18.6854	19.1799	18.2986	23.9324	24.6311	23.5839	23.5669
1754	Myosin VI OS=Rattus norvegicus OX=10116 GN=Myo6 PE=1 SV=3	Myo6	D4A5I9	NaN	NaN	NaN	NaN	15.0543	17.7058	17.698	16.1544
1755	Myosin XVIIIa OS=Rattus norvegicus OX=10116 GN=Myo18a PE=1 SV=1	Myo18a	A0A0G2JY08	19.7388	19.3029	20.018	19.5783	21.2028	22.0005	21.9195	21.9391
1756	Myosin XVIIIb OS=Rattus norvegicus OX=10116 GN=Myo18b PE=1 SV=2	Myo18b	M0R6Z9	17.8895	17.7055	18.7718	19.1419	19.04	19.2553	20.3203	19.9208
1757	Myosin, heavy polypeptide 10, non-muscle, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Myh10 PE=1 SV=1	Myh10	G3V9Y1	26.1102	25.7601	25.764	24.4792	26.8617	26.8241	25.8616	26.1997
1758	Myosin, heavy polypeptide 9, non-muscle OS=Rattus norvegicus OX=10116 GN=Myh9 PE=1 SV=1	Myh9	G3V6P7	23.2996	23.8839	23.531	24.0038	26.5384	27.5388	26.4812	26.5135
1759	Myosin-11 OS=Rattus norvegicus OX=10116 GN=Myh11 PE=1 SV=1	Myh11	A0A0G2K6S9	21.0132	20.02	20.0441	20.9499	22.4417	24.5662	23.9788	23.833
1760	Myosin-3 OS=Rattus norvegicus OX=10116 GN=Myh3 PE=1 SV=1	Myh3	G3V6D8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1761	Myosin-4 OS=Rattus norvegicus OX=10116 GN=Myh4 PE=1 SV=1	Myh4	Q29RW1	NaN	NaN	NaN	NaN	NaN	18.6231	16.8976	17.0023
1762	Myosin-6 OS=Rattus norvegicus OX=10116 GN=Myh6 PE=1 SV=2	Myh6	G3V885	24.0318	19.3326	19.8118	18.387	22.2356	24.9003	22.9148	22.8463
1763	Myosin-7 OS=Rattus norvegicus OX=10116 GN=Myh7 PE=1 SV=1	Myh7	G3V8B0	21.4846	21.2124	21.2262	21.3888	25.4917	28.7228	27.0926	27.1191
1764	Myosin-binding protein C, cardiac-type OS=Rattus norvegicus OX=10116 GN=Mybpc3 PE=1 SV=2	Mybpc3	P56741	19.3655	17.9828	19.5873	19.3727	23.5177	23.5578	23.2443	23.3439
1765	Myosin-binding protein C, slow-type OS=Rattus norvegicus OX=10116 GN=Mybpc1 PE=1 SV=1	Mybpc1	A0A0G2JUE5	17.5262	18.5902	19.4007	18.5528	18.4105	18.6385	14.9857	18.344
1766	Myotrophin OS=Rattus norvegicus OX=10116 GN=Mtpn PE=1 SV=2	Mtpn	P62775	NaN	NaN	NaN	NaN	NaN	16.5019	16.792	16.8473
1767	Myotubularin related protein 2 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Mtmr2 PE=1 SV=1	Mtmr2	D3ZA31	15.6612	15.4451	NaN	16.5481	16.3275	16.0973	16.1875	15.6934
1768	Myristoylated alanine-rich C-kinase substrate OS=Rattus norvegicus OX=10116 GN=Marcks PE=1 SV=2	Marcks	P30009	22.8182	23.3931	23.7964	22.9623	26.0149	26.1661	26.0266	26.0337
1769	N(alpha)-acetyltransferase 15, NatA auxiliary subunit OS=Rattus norvegicus OX=10116 GN=Naa15 PE=1 SV=2	Naa15	D3ZD89	NaN	NaN	NaN	NaN	18.2445	17.9862	19.1269	18.4429
1770	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Rattus norvegicus OX=10116 GN=Ddah1 PE=1 SV=3	Ddah1	O08557	NaN	14.2714	13.5586	17.656	20.4594	20.8254	20.8056	20.5402
1771	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Rattus norvegicus OX=10116 GN=Ddah2 PE=1 SV=1	Ddah2	Q6MG60	18.4504	18.7433	19.2024	18.5412	19.9903	20.8423	19.6227	20.1918
1772	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Rattus norvegicus OX=10116 GN=Slc9a3r1 PE=1 SV=3	Slc9a3r1	Q9JJ19	19.3942	19.1804	20.249	17.9969	17.6863	15.9125	NaN	17.4524
1773	N-acetylgalactosamine kinase OS=Rattus norvegicus OX=10116 GN=Galk2 PE=2 SV=1	Galk2	Q5XIG6	NaN	17.483	16.955	15.6457	NaN	18.2186	18.7741	18.4924
1774	N-acetylneuraminate lyase OS=Rattus norvegicus OX=10116 GN=Npl PE=2 SV=1	Npl	Q66H59	15.182	14.6326	NaN	NaN	16.5027	16.1221	16.5815	NaN
1775	N-acetylneuraminate synthase OS=Rattus norvegicus OX=10116 GN=Nans PE=1 SV=1	Nans	B1WC26	16.3741	18.5537	17.6185	15.7538	17.4471	21.0388	21.606	21.3326
1776	NAD(P)(+)--arginine ADP-ribosyltransferase OS=Rattus norvegicus OX=10116 GN=Art3 PE=3 SV=1	Art3	A0A0G2K8S9	NaN	15.9998	15.9428	NaN	15.8754	17.0247	16.2179	NaN
1777	NAD(P)(+)--arginine ADP-ribosyltransferase OS=Rattus norvegicus OX=10116 GN=Art4 PE=1 SV=2	Art4	F1MA10	NaN	NaN	16.1806	NaN	16.5351	16.9703	NaN	16.5218
1778	NAD-dependent protein deacetylase OS=Rattus norvegicus OX=10116 GN=Sirt2 PE=1 SV=1	Sirt2	A0A0G2JWM2	18.5287	17.1071	17.9679	18.9997	21.483	21.1437	21.4332	21.4421
1779	NAD-dependent protein deacylase sirtuin-5, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sirt5 PE=2 SV=1	Sirt5	Q68FX9	NaN	NaN	NaN	16.3293	20.3764	19.5691	20.0831	19.2879
1780	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 11 (Predicted) OS=Rattus norvegicus OX=10116 GN=Ndufb11 PE=	Ndufb11	D4A7L4	NaN	NaN	NaN	NaN	17.5505	19.3195	18.9054	19.1841
1781	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 5 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN	Ndufb5	D4A565	19.3789	19.0135	17.9842	17.2552	17.8098	19.3539	18.9741	19.1162
1782	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 7 (Predicted) OS=Rattus norvegicus OX=10116 GN=Ndufb7 PE=1 S	Ndufb7	D3ZLT1	NaN	NaN	15.4018	NaN	NaN	17.9513	17.9567	17.8361
1783	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 9 OS=Rattus norvegicus OX=10116 GN=Ndufb9 PE=1 SV=1	Ndufb9	B2RYW3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1784	NADH dehydrogenase (Ubiquinone) Fe-S protein 3 (Predicted), isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Nduf	Ndufs3	D3ZG43	NaN	NaN	NaN	NaN	18.6797	19.4275	19.0327	19.1407
1785	NADH dehydrogenase (Ubiquinone) Fe-S protein 5 OS=Rattus norvegicus OX=10116 GN=Ndufs5 PE=1 SV=1	Ndufs5	B5DEL8	NaN	NaN	NaN	NaN	NaN	16.9292	NaN	NaN
1786	NADH dehydrogenase (Ubiquinone) Fe-S protein 7 OS=Rattus norvegicus OX=10116 GN=Ndufs7 PE=1 SV=1	Ndufs7	Q5RJN0	NaN	17.401	NaN	17.6934	18.3722	20.4213	19.7669	20.2288
1787	NADH dehydrogenase (Ubiquinone) Fe-S protein 8 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Nduf	Ndufs8	B0BNE6	20.1947	20.9734	20.5513	19.9566	19.6021	20.2113	20.0164	20.2041
1788	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Rattus norvegicus OX=10116 GN=N	Ndufa10	Q561S0	18.6017	18.3016	18.7029	15.0526	18.4924	20.1563	17.6276	19.647
1789	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=Rattus norvegicus OX=10116 GN=Ndufa11 PE=2 SV	Ndufa11	Q80W89	NaN	NaN	NaN	NaN	NaN	17.3001	16.9527	17.3498
1790	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Rattus norvegicus OX=10116 GN=Ndufa12 PE=1 SV	Ndufa12	F1LXA0	16.951	16.8874	15.3194	15.1396	18.5213	19.9101	19.7746	19.8863
1791	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Rattus norvegicus OX=10116 GN=Ndufa2 PE=1 SV=	Ndufa2	D3ZS58	14.9526	NaN	14.1939	NaN	16.7215	19.475	17.6296	19.5493
1792	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Rattus norvegicus OX=10116 GN=Ndufa5 PE=1 SV=	Ndufa5	Q63362	NaN	NaN	NaN	NaN	18.3351	20.3899	19.8163	19.9616
1793	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Rattus norvegicus OX=10116 GN=Ndufa6 PE=1 SV=	Ndufa6	D4A3V2	19.4169	16.9144	18.7239	18.7582	18.5974	19.1194	18.8368	18.8509
1794	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Rattus norvegicus OX=10116 GN=Ndufa8 PE=1 SV=	Ndufa8	A0A0G2JVL6	16.9163	16.4891	15.8764	NaN	17.5676	20.618	20.244	19.8769
1795	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Rattus norvegicus OX=10116 GN=Nd	Ndufa9	Q5BK63	15.084	14.7798	15.4916	NaN	17.2545	19.0714	18.8329	19.0394
1796	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufv1 PE=1 SV=	Ndufv1	Q5XIH3	17.5471	17.311	17.0406	16.0983	19.2574	21.0909	20.2929	20.8237
1797	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufv2 PE=1 SV=	Ndufv2	P19234	19.1724	20.4171	18.6911	21.3443	20.0484	21.1885	20.4181	20.7755
1798	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufv3 PE=3 SV=	Ndufv3	Q6PCU8	NaN	NaN	11.2254	NaN	NaN	NaN	12.4023	13.5676
1799	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufs2 PE=	Ndufs2	Q641Y2	15.8171	16.1987	17.2349	16.6578	17.4071	19.9035	19.3963	19.6118
1800	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufs4 PE=	Ndufs4	Q5XIF3	17.8968	NaN	NaN	NaN	18.5649	19.5385	18.7449	19.2197

1801	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Rattus norvegicus OX=10116 GN=LOC100912	LOC679739	D3ZCZ9	15.9132	15.6064	15.9268	NaN	18.3523	19.9127	19.8605	19.887
1802	NADH:ubiquinone oxidoreductase subunit A13 OS=Rattus norvegicus OX=10116 GN=Ndufa13 PE=1 SV=1	Ndufa13	D3ZE15	19.7191	18.994	18.7838	18.4969	18.2421	17.5393	18.9447	15.7348
1803	NADH:ubiquinone oxidoreductase subunit A7 OS=Rattus norvegicus OX=10116 GN=Ndufa7 PE=1 SV=1	Ndufa7	A9UMV9	NaN	NaN	16.9226	NaN	18.7048	21.2276	20.8588	21.006
1804	NADH:ubiquinone oxidoreductase subunit B10 OS=Rattus norvegicus OX=10116 GN=Ndufb10 PE=1 SV=1	Ndufb10	D4A0T0	15.9574	17.9277	17.7399	16.5492	20.5553	21.6509	21.4925	21.6387
1805	NADH:ubiquinone oxidoreductase subunit B4 OS=Rattus norvegicus OX=10116 GN=Ndufb4 PE=1 SV=1	Ndufb4	F1LPG5	17.9462	NaN	NaN	NaN	17.1042	18.2399	18.2559	18.4015
1806	NADH-cytochrome b5 reductase 3 OS=Rattus norvegicus OX=10116 GN=Cyb5r3 PE=1 SV=2	Cyb5r3	P20070	15.3344	17.5639	17.0908	17.1744	20.1477	19.4994	18.3063	19.2992
1807	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufs1 PE=1 SV=	Ndufs1	Q66HF1	21.2256	21.4228	21.3062	19.0333	21.078	22.6078	22.2939	22.7206
1808	NADH-ubiquinone oxidoreductase chain 5 OS=Rattus norvegicus OX=10116 GN=Mtnd5 PE=3 SV=3	mt-Nd5	P11661	NaN	16.3878	NaN	NaN	17.944	19.0672	18.7754	19.0592
1809	NADP-dependent malic enzyme OS=Rattus norvegicus OX=10116 GN=Me1 PE=1 SV=2	Me1	P13697	NaN	17.3987	NaN	17.2759	18.5368	NaN	NaN	NaN
1810	NADPH--cytochrome P450 reductase OS=Rattus norvegicus OX=10116 GN=Por PE=1 SV=3	Por	P00388	NaN	NaN	NaN	NaN	17.1559	17.7495	16.5946	16.8062
1811	NADPH-dependent diflavin oxidoreductase 1 OS=Rattus norvegicus OX=10116 GN=Ndor1 PE=1 SV=1	Ndor1	D4ABT4	NaN	NaN	NaN	NaN	16.2071	16.7354	15.9632	NaN
1812	N-alpha-acetyltransferase 11 OS=Rattus norvegicus OX=10116 GN=Naa11 PE=2 SV=1	Naa11	Q4V8K3	NaN	15.6024	15.4961	15.3219	16.9439	20.0541	19.7008	19.9318
1813	Nardilysin OS=Rattus norvegicus OX=10116 GN=Nrdc PE=1 SV=1	Nrdc	D3ZQ59	NaN	NaN	NaN	NaN	NaN	16.4192	16.3592	16.1604
1814	Nascent polypeptide-associated complex subunit alpha OS=Rattus norvegicus OX=10116 GN=Naca PE=1 SV=1	Naca	M0R9L0	20.8864	20.229	20.2892	20.6017	24.9882	26.1244	25.3501	24.8763
1815	Natriuretic peptides A OS=Rattus norvegicus OX=10116 GN=Nppa PE=1 SV=1	Nppa	P01161	17.8177	17.7025	17.4803	17.3014	22.3593	23.3857	23.1711	22.9212
1816	Natriuretic peptides B OS=Rattus norvegicus OX=10116 GN=Nppb PE=1 SV=3	Nppb	P13205	NaN	NaN	NaN	NaN	15.4735	16.9414	16.2088	16.4408
1817	Nck-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Nckap1 PE=2 SV=1	Nckap1	P55161	20.4635	19.9046	20.0664	20.1228	20.684	21.0267	21.1172	20.5719
1818	NDUFA4, mitochondrial complex-associated OS=Rattus norvegicus OX=10116 GN=Ndufa4 PE=1 SV=1	Ndufa4	B2RZD6	19.1978	19.1048	18.291	16.9606	20.3206	22.1042	21.7747	21.9783
1819	Nebulette OS=Rattus norvegicus OX=10116 GN=Nebl PE=1 SV=2	Nebl	D4A164	19.9903	19.186	19.0726	16.8756	20.0197	21.4054	20.6514	19.6531
1820	Nebulin-related-anchoring protein OS=Rattus norvegicus OX=10116 GN=Nrap PE=1 SV=1	Nrap	D4A4K6	19.8927	20.0247	20.381	20.0756	22.7914	21.8409	22.8023	21.3665
1821	NEDD8-activating enzyme E1 catalytic subunit OS=Rattus norvegicus OX=10116 GN=Uba3 PE=1 SV=1	Uba3	Q99MI7	NaN	NaN	NaN	NaN	17.8463	16.4993	17.026	16.822
1822	NEDD8-activating enzyme E1 regulatory subunit OS=Rattus norvegicus OX=10116 GN=Nae1 PE=1 SV=3	Nae1	F1M7W7	NaN	NaN	NaN	NaN	17.7167	NaN	NaN	NaN
1823	NEDD8-conjugating enzyme UBE2F OS=Rattus norvegicus OX=10116 GN=Ube2f PE=2 SV=2	Ube2f	Q5U203	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1824	Negative regulator of ubiquitin-like proteins 1 OS=Rattus norvegicus OX=10116 GN=Nub1 PE=1 SV=1	Nub1	F7ES73	NaN	NaN	NaN	NaN	16.7306	16.4108	16.3323	NaN
1825	Neprilysin OS=Rattus norvegicus OX=10116 GN=Mme PE=1 SV=2	Mme	P07861	17.7524	17.1639	17.2857	17.7337	17.6035	15.9056	17.4422	17.4912
1826	Neudesin OS=Rattus norvegicus OX=10116 GN=Nenf PE=2 SV=1	Nenf	Q6IUR5	16.683	16.3498	15.5958	17.9303	19.4085	19.8978	18.8884	19.3822
1827	Neural cell adhesion molecule 1 OS=Rattus norvegicus OX=10116 GN=Ncam1 PE=1 SV=3	Ncam1	F1LUV9	18.8393	19.3806	19.5961	18.9885	22.4181	22.068	22.2571	22.4243
1828	Neural precursor cell-expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase OS=Rattus norvegicus OX	Nedd4l	A0A0G2JXP3	NaN	NaN	NaN	NaN	NaN	18.9287	NaN	NaN
1829	Neural Wiskott-Aldrich syndrome protein OS=Rattus norvegicus OX=10116 GN=Wasl PE=1 SV=2	Wasl	F1LSG0	NaN	NaN	NaN	NaN	18.4958	NaN	NaN	NaN
1830	Neuroendocrine secretory protein 55 OS=Rattus norvegicus OX=10116 GN=Gnas PE=2 SV=1	Gnas	Q792G6	18.1962	18.189	18.2342	17.7756	17.9828	16.3208	17.2685	17.8793
1831	Neurogenic locus notch homolog protein 3 OS=Rattus norvegicus OX=10116 GN=Notch3 PE=4 SV=2	Notch3	F1LQX7	NaN	NaN	16.2512	14.6093	NaN	NaN	NaN	NaN
1832	Neuromodulin OS=Rattus norvegicus OX=10116 GN=Gap43 PE=1 SV=1	Gap43	P07936	19.1424	19.3927	19.4524	19.3598	19.4604	19.4466	18.8232	19.3677
1833	Neuron navigator 1 OS=Rattus norvegicus OX=10116 GN=Nav1 PE=1 SV=3	Nav1	D4A5I4	NaN	10.9262	15.8182	NaN	19.9439	20.1026	20.3815	20.2791
1834	Neuron navigator 2 OS=Rattus norvegicus OX=10116 GN=Nav2 PE=1 SV=1	Nav2	A0A0G2K833	20.4195	20.0707	17.783	18.4561	19.9983	20.7959	20.4434	19.8938
1835	Neuronal calcium sensor 1 OS=Rattus norvegicus OX=10116 GN=Ncs1 PE=1 SV=2	Ncs1	P62168	NaN	15.5039	NaN	NaN	16.8408	16.5125	17.3538	16.4379
1836	Neuron-specific calcium-binding protein hippocalcin OS=Rattus norvegicus OX=10116 GN=Hpca PE=1 SV=2	Hpca	P84076	NaN	NaN	NaN	NaN	16.5478	15.1565	NaN	NaN
1837	Neuropilin-1 OS=Rattus norvegicus OX=10116 GN=Nrp1 PE=1 SV=1	Nrp1	Q9QWJ9	NaN	NaN	NaN	NaN	20.5371	21.4415	20.4574	20.5959
1838	Neuroplastin OS=Rattus norvegicus OX=10116 GN=Nptn PE=1 SV=2	Nptn	P97546	NaN	17.6888	17.4219	17.3234	17.4783	17.6801	17.2507	NaN
1839	Neutral amino acid transporter ASCT1 OS=Rattus norvegicus OX=10116 GN=Slc1a4 PE=1 SV=1	Slc1a4	Q76GL9	NaN	NaN	NaN	NaN	16.3787	16.3554	NaN	NaN
1840	Neutral cholesterol ester hydrolase 1 OS=Rattus norvegicus OX=10116 GN=Nceh1 PE=1 SV=1	Nceh1	B2GV54	NaN	NaN	NaN	NaN	18.4331	18.4272	18.3186	18.3204
1841	Nexilin OS=Rattus norvegicus OX=10116 GN=Nexn PE=1 SV=1	Nexn	A0A0G2K6I3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1842	NFKB inhibitor interacting Ras-like protein 2 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Nkiras2 PE	Nkiras2	D3ZCK2	16.3343	NaN	16.22	NaN	17.2068	NaN	17.0789	NaN
1843	NHL repeat containing 2 (Predicted) OS=Rattus norvegicus OX=10116 GN=Nhlrc2 PE=1 SV=1	Nhlrc2	D3ZLM5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1844	NHP2-like protein 1 OS=Rattus norvegicus OX=10116 GN=Snu13 PE=2 SV=4	Snu13	P55770	NaN	NaN	NaN	NaN	16.9086	NaN	17.4868	17.3286
1845	NHS actin-remodeling regulator OS=Rattus norvegicus OX=10116 GN=Nhs PE=1 SV=3	Nhs	F1LU76	NaN	NaN	NaN	NaN	18.1355	18.6116	18.594	18.498
1846	NHS-like 1 OS=Rattus norvegicus OX=10116 GN=Nhsl1 PE=4 SV=1	Nhsl1	A0A0G2JZL4	21.1662	21.0301	20.9999	20.5475	20.9014	20.4041	20.9924	21.0012
1847	Niban-like protein 1 OS=Rattus norvegicus OX=10116 GN=Fam129b PE=1 SV=1	Niban2	B4F7E8	18.2522	18.6848	18.0844	18.0833	20.4311	20.8239	21.1889	21.367
1848	Nicastrin OS=Rattus norvegicus OX=10116 GN=Ncstn PE=1 SV=1	Ncstn	Q8CGU6	15.7631	14.9112	16.212	NaN	17.6863	18.4418	17.6631	17.9605
1849	Nicotinamide nucleotide transhydrogenase OS=Rattus norvegicus OX=10116 GN=Nnt PE=1 SV=1	Nnt	Q5BJZ3	20.8632	20.4554	19.9252	19.8043	22.6983	23.6976	23.0716	23.2707
1850	Nicotinamide phosphoribosyltransferase OS=Rattus norvegicus OX=10116 GN=Nampt PE=1 SV=1	Nampt	Q80Z29	16.985	17.2469	17.5594	16.1503	19.7684	20.1405	20.759	20.8195
1851	Nidogen-1 OS=Rattus norvegicus OX=10116 GN=Nid1 PE=1 SV=1	Nid1	F1LM84	19.6755	18.5873	19.1671	19.4337	19.742	18.6262	19.2005	18.6891
1852	Nidogen-2 OS=Rattus norvegicus OX=10116 GN=Nid2 PE=4 SV=2	Nid2	W4VSR4	18.7956	17.7987	19.2563	18.8688	NaN	15.7927	NaN	15.6202
1853	NIMA-related kinase 9 OS=Rattus norvegicus OX=10116 GN=Nek9 PE=1 SV=1	Nek9	A0A0G2K8N9	16.5977	14.8676	NaN	16.8273	20.1156	20.6411	20.7216	20.5374

1854	Nischarin OS=Rattus norvegicus OX=10116 GN=Nisch PE=2 SV=2	Nisch	Q4G017	NaN	NaN	NaN	NaN	18.6392	18.9253	19.2153	19.0201
1855	Nitric oxide synthase OS=Rattus norvegicus OX=10116 GN=Nos3 PE=1 SV=1	Nos3	F1LQC7	NaN	NaN	NaN	NaN	19.68	19.4179	19.2617	19.1297
1856	Nitric oxide synthase-interacting protein OS=Rattus norvegicus OX=10116 GN=Nosip PE=1 SV=1	Nosip	D3ZH12	16.7487	NaN	16.7886	19.255	16.3528	16.5816	17.5124	17.2139
1857	N-lysine methyltransferase SMYD2 OS=Rattus norvegicus OX=10116 GN=Smyd2 PE=1 SV=1	Smyd2	Q7M6Z3	NaN	NaN	NaN	NaN	NaN	NaN	18.9777	18.4627
1858	NmrA-like family domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Nmral1 PE=1 SV=2	Nmral1	D3ZDB9	18.0216	15.2614	16.4552	16.6416	21.8573	21.0988	21.2938	21.2712
1859	N-myc downstream regulated gene 2, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Ndrg2 PE=1 SV=1	Ndrg2	A0A0G2JSU4	17.7052	16.6382	18.7408	16.9473	23.1461	23.469	23.9547	23.63
1860	Nodal modulator 1 OS=Rattus norvegicus OX=10116 GN=Nomo1 PE=1 SV=1	Nomo1	D3ZSA9	NaN	NaN	16.2448	16.1407	17.712	18.1551	17.562	18.1392
1861	Non-POU domain-containing octamer-binding protein OS=Rattus norvegicus OX=10116 GN=Nono PE=1 SV=3	Nono	Q5FVM4	NaN	16.1878	NaN	NaN	18.8343	18.3824	17.7302	18.1423
1862	Non-SMC condensin I complex, subunit G OS=Rattus norvegicus OX=10116 GN=Ncapg PE=1 SV=3	Ncapg	D3ZD72	17.3405	16.7612	16.7642	18.1191	16.1135	NaN	16.914	17.265
1863	Non-specific cytotoxic cell receptor protein 1 homolog (zebrafish) OS=Rattus norvegicus OX=10116 GN=Nccrp1 PE=4 SV=1	Nccrp1	D3ZQ18	NaN	16.1591	NaN	NaN	NaN	NaN	NaN	NaN
1864	Non-specific lipid-transfer protein OS=Rattus norvegicus OX=10116 GN=Scp2 PE=1 SV=3	Scp2	F1LQ55	15.6107	15.8694	NaN	NaN	18.2761	19.357	18.0545	19.0441
1865	Non-specific serine/threonine protein kinase OS=Rattus norvegicus OX=10116 GN=Akt2 PE=1 SV=1	Akt2	Q3HSE5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1866	Non-specific serine/threonine protein kinase OS=Rattus norvegicus OX=10116 GN=Mark2 PE=1 SV=1	Mark2	A0A0G2K6X6	15.8918	14.8899	16.263	14.2882	20.5646	21.3207	20.9697	20.3361
1867	Non-specific serine/threonine protein kinase OS=Rattus norvegicus OX=10116 GN=Mark3 PE=1 SV=1	Mark3	A0A0G2JU56	18.2061	17.8498	16.5022	16.3416	19.9233	20.6191	19.6182	19.3661
1868	Non-specific serine/threonine protein kinase OS=Rattus norvegicus OX=10116 GN=Pak4 PE=1 SV=1	Pak4	B5DF62	NaN	NaN	NaN	NaN	17.3197	16.966	17.1539	16.5989
1869	Non-specific serine/threonine protein kinase OS=Rattus norvegicus OX=10116 GN=Prkaa2 PE=1 SV=1	Prkaa2	G3V715	15.1612	14.9229	16.0057	18.043	22.8126	22.3074	22.5272	22.1829
1870	Non-specific serine/threonine protein kinase OS=Rattus norvegicus OX=10116 GN=Stk38 PE=1 SV=3	Stk38	G3V9Q4	17.2267	17.3621	16.6539	18.5041	18.6482	NaN	17.9789	18.4744
1871	NPC intracellular cholesterol transporter 2 OS=Rattus norvegicus OX=10116 GN=Npc2 PE=1 SV=1	Npc2	F7FJQ3	14.8349	NaN	15.6195	15.083	NaN	15.6889	NaN	NaN
1872	NSF attachment protein gamma OS=Rattus norvegicus OX=10116 GN=Napg PE=1 SV=1	Napg	A0A0G2K350	16.6791	15.5892	17.6524	16.5306	20.3298	19.8072	19.6312	19.5097
1873	NSFL1 cofactor p47 OS=Rattus norvegicus OX=10116 GN=Nsfl1c PE=1 SV=1	Nsfl1c	O35987	18.2195	18.8449	18.8278	17.4015	21.5965	21.5114	21.1941	22.0438
1874	N-terminal kinase-like protein OS=Rattus norvegicus OX=10116 GN=Scyl1 PE=2 SV=1	Scyl1	Q5M9F8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1875	N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Rattus norvegicus OX=10116 GN=Ntmt1 PE=2 SV=3	Ntmt1	Q5BJX0	NaN	NaN	NaN	NaN	18.3785	16.6648	17.2473	17.9827
1876	Nuclear autoantigenic sperm protein OS=Rattus norvegicus OX=10116 GN=Nasp PE=1 SV=1	Nasp	Q66HD3	20.5174	21.267	20.8387	20.6411	22.8826	22.2444	22.6738	22.4334
1877	Nuclear factor 1 A-type OS=Rattus norvegicus OX=10116 GN=Nfia PE=1 SV=2	Nfia	P09414	NaN	NaN	NaN	NaN	18.3616	19.0399	18.2964	18.1166
1878	Nuclear factor 1 OS=Rattus norvegicus OX=10116 GN=Nfib PE=1 SV=2	Nfib	O70185	18.3698	20.3038	17.6535	NaN	20.3183	20.0647	19.8728	19.7354
1879	Nuclear factor kappa B subunit 2 OS=Rattus norvegicus OX=10116 GN=Nfkb2 PE=1 SV=1	Nfkb2	Q5U2Z4	NaN	NaN	NaN	NaN	17.0956	NaN	17.3243	NaN
1880	Nuclear factor kappaB subunit p65 OS=Rattus norvegicus OX=10116 GN=Rela PE=1 SV=1	Rela	Q7TQN4	16.8544	17.8768	17.0508	NaN	20.3122	19.9251	20.177	20.1215
1881	Nuclear factor NF-kappa-B p105 subunit OS=Rattus norvegicus OX=10116 GN=Nfkb1 PE=1 SV=2	Nfkb1	F1LQH2	20.0149	20.1522	20.1457	20.2354	21.7296	21.3833	21.5897	21.3051
1882	Nuclear FMR1-interacting protein 2 OS=Rattus norvegicus OX=10116 GN=Nufip2 PE=1 SV=2	Nufip2	D3ZC82	NaN	NaN	14.3162	15.4467	17.4625	18.1913	18.0871	17.7697
1883	Nuclear migration protein nudC OS=Rattus norvegicus OX=10116 GN=Nudc PE=1 SV=1	Nudc	Q63525	19.355	19.5467	19.4459	19.0742	21.8749	20.5572	21.6639	21.4872
1884	Nuclear pore complex protein Nup54 OS=Rattus norvegicus OX=10116 GN=Nup54 PE=1 SV=1	Nup54	P70582	NaN	14.6415	NaN	16.2697	19.3916	NaN	17.3234	17.6361
1885	Nuclear pore complex protein Nup88 OS=Rattus norvegicus OX=10116 GN=Nup88 PE=1 SV=1	Nup88	O08658	15.5603	15.8401	15.1061	NaN	19.7805	19.7804	19.9007	19.9993
1886	Nuclear pore complex protein Nup93 OS=Rattus norvegicus OX=10116 GN=Nup93 PE=1 SV=1	Nup93	Q66HC5	NaN	13.3501	NaN	16.6519	21.2025	20.1191	21.0355	20.8487
1887	Nuclear pore glycoprotein p62 OS=Rattus norvegicus OX=10116 GN=Nup62 PE=1 SV=1	Nup62	P17955	17.9295	17.4827	18.4327	NaN	20.6292	18.9686	19.79	19.6077
1888	Nuclear protein localization protein 4 homolog OS=Rattus norvegicus OX=10116 GN=Nploc4 PE=1 SV=1	Nploc4	A0A0G2JU66	15.8902	16.035	15.9997	15.1063	21.1131	19.6028	20.5009	20.4688
1889	Nuclear receptor binding protein OS=Rattus norvegicus OX=10116 GN=Nrbp1 PE=1 SV=1	Nrbp1	Q3SWT7	NaN	NaN	15.4328	15.142	20.5239	19.939	20.2842	19.7518
1890	Nuclear receptor coactivator OS=Rattus norvegicus OX=10116 GN=Ncoa1 PE=1 SV=2	Ncoa1	D4A3Q3	NaN	NaN	NaN	NaN	15.5995	NaN	NaN	NaN
1891	Nuclear transport factor 2 OS=Rattus norvegicus OX=10116 GN=Nutf2 PE=1 SV=1	Nutf2	P61972	16.316	17.759	NaN	16.6038	18.5397	17.881	17.6747	17.7226
1892	Nuclease-sensitive element-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ybx1 PE=1 SV=1	Ybx1	Q3ZAV2	21.6352	21.8598	21.7841	18.5859	23.2543	24.7822	23.9936	24.0918
1893	Nucleobindin 2, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Nucb2 PE=1 SV=1	Nucb2	G3V8R1	17.5977	16.6651	16.1848	16.6343	16.28	17.7348	17.7066	18.2521
1894	Nucleobindin-1 OS=Rattus norvegicus OX=10116 GN=Nucb1 PE=1 SV=1	Nucb1	Q63083	17.956	17.4289	17.1388	16.5411	19.09	21.0893	20.0024	20.4297
1895	Nucleolin OS=Rattus norvegicus OX=10116 GN=Ncl PE=1 SV=1	Ncl	Q5U328	19.5213	18.7307	18.6154	19.2399	22.8729	23.959	23.5456	23.499
1896	Nucleophosmin OS=Rattus norvegicus OX=10116 GN=Npm1 PE=1 SV=1	Npm1	P13084	15.8411	NaN	15.4046	16.09	21.1675	18.939	17.0629	18.1547
1897	Nucleoporin 214 (Fragment) OS=Rattus norvegicus OX=10116 GN=Nup214 PE=1 SV=2	Nup214	D4ACK1	NaN	NaN	NaN	NaN	16.7114	16.6582	17.0051	16.9055
1898	Nucleoporin p58/p45 OS=Rattus norvegicus OX=10116 GN=Nup58 PE=1 SV=1	Nup58	P70581	NaN	NaN	NaN	NaN	16.7279	15.6714	16.053	16.3977
1899	Nucleoside diphosphate kinase A OS=Rattus norvegicus OX=10116 GN=Nme1 PE=1 SV=1	Nme1	Q05982	16.3908	16.0237	16.0055	16.916	18.4856	18.439	18.2215	17.9713
1900	Nucleoside diphosphate kinase B OS=Rattus norvegicus OX=10116 GN=Nme2 PE=1 SV=1	Nme2	P19804	20.9423	21.0958	21.3676	19.2444	23.5614	24.255	24.4692	24.0137
1901	Nucleoside-triphosphatase, cancer-related OS=Rattus norvegicus OX=10116 GN=Ntpcr PE=1 SV=1	Ntpcr	D4A478	NaN	NaN	NaN	NaN	19.0812	18.1574	18.9632	18.1386
1902	Nucleosome assembly protein 1-like 1 OS=Rattus norvegicus OX=10116 GN=Nap1l1 PE=1 SV=1	Nap1l1	G3V6H9	17.1767	16.5099	15.4512	18.3465	20.5728	19.3295	20.0415	20.2505
1903	Nucleosome assembly protein 1-like 4 OS=Rattus norvegicus OX=10116 GN=Nap1l4 PE=1 SV=1	Nap1l4	A0A0H2UHZ2	15.3439	14.8998	16.4028	17.3568	21.7821	21.1672	21.4186	21.2593
1904	NudC domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Nudcd1 PE=1 SV=1	Nudcd1	F7F163	NaN	NaN	NaN	17.3577	17.3267	17.1457	17.0057	17.3649
1905	NudC domain-containing 3 (Fragment) OS=Rattus norvegicus OX=10116 GN=Nudcd3 PE=1 SV=1	Nudcd3	A0A0G2K226	NaN	NaN	NaN	NaN	18.7887	NaN	17.4671	NaN
1906	NudC domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Nudcd2 PE=2 SV=1	Nudcd2	Q5M823	NaN	NaN	14.359	NaN	21.1846	19.7153	20.4407	20.76

1907	Obg-like ATPase 1 OS=Rattus norvegicus OX=10116 GN=Ola1 PE=2 SV=1	Ola1	A0JPJ7	18.101	17.9769	18.912	18.5022	21.8955	21.8545	22.4695	22.218
1908	Obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF OS=Rattus norvegicus OX=10116 GN=Obscn PE=1 SV=1	Obscn	A0A0G2JUP3	18.5267	18.2961	17.6727	19.3052	20.9876	21.0928	21.2857	20.852
1909	Obscurin-like protein 1 OS=Rattus norvegicus OX=10116 GN=Obsl1 PE=2 SV=3	Obsl1	D3ZZ80	20.6028	21.7273	21.0551	19.3298	19.3548	20.178	18.3206	18.636
1910	OCIA domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Ociad1 PE=1 SV=1	Ociad1	Q5XIG4	18.0523	17.8782	18.2885	19.7437	18.467	19.3444	18.324	18.6534
1911	Olfactomedin 4 OS=Rattus norvegicus OX=10116 GN=Olfm4 PE=4 SV=1	Olfm4	D3ZMI6	NaN	16.739	15.5601	NaN	NaN	NaN	NaN	NaN
1912	Olfactomedin-like 3 (Predicted) OS=Rattus norvegicus OX=10116 GN=Olfml3 PE=4 SV=1	Olfml3	G3V8H7	NaN	NaN	15.3064	NaN	NaN	NaN	16.2064	16.5636
1913	Oligosaccharyltransferase complex subunit OSTC OS=Rattus norvegicus OX=10116 GN=Ostc PE=2 SV=1	Ostc	B0K025	NaN	NaN	NaN	NaN	18.6462	18.4056	18.6112	18.7811
1914	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferas	Ogt	G3V6F4	17.9164	17.1081	17.5512	18.3328	20.7703	21.6203	21.6644	20.8506
1915	Omega-amidase NIT2 OS=Rattus norvegicus OX=10116 GN=Nit2 PE=1 SV=1	Nit2	Q497B0	18.2064	17.93	17.5376	18.1155	18.9443	19.838	19.1541	19.2978
1916	Oncoprotein-induced transcript 3 protein OS=Rattus norvegicus OX=10116 GN=Oit3 PE=2 SV=1	Oit3	Q6V0K7	21.4105	21.0613	19.6698	20.012	17.566	18.095	NaN	17.8024
1917	Osteoglycin OS=Rattus norvegicus OX=10116 GN=Ogn PE=1 SV=1	Ogn	D3ZVB7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1918	Osteopontin OS=Rattus norvegicus OX=10116 GN=Spp1 PE=1 SV=2	Spp1	P08721	17.7372	17.3528	18.2951	17.8794	17.744	NaN	15.6974	15.1534
1919	OTU deubiquitinase 7B OS=Rattus norvegicus OX=10116 GN=Otud7b PE=1 SV=1	Otud7b	D3ZH40	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1920	Out at first protein homolog OS=Rattus norvegicus OX=10116 GN=Oaf PE=2 SV=1	Oaf	Q6AYE5	16.4111	14.3698	17.1456	16.4868	17.6681	17.1998	17.527	17.7757
1921	Oxidation resistance protein 1 OS=Rattus norvegicus OX=10116 GN=Oxr1 PE=1 SV=3	Oxr1	Q4V8B0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1922	Oxidative stress-responsive kinase 1 OS=Rattus norvegicus OX=10116 GN=Oxsr1 PE=1 SV=1	Oxsr1	D3ZUC9	15.5567	NaN	17.4654	17.2666	22.2926	21.3222	21.8134	21.4546
1923	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cpox PE=1 SV=1	Cpox	Q3B7D0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1924	Oxysterol-binding protein OS=Rattus norvegicus OX=10116 GN=Osbp PE=1 SV=2	Osbp	D4A9D8	17.3374	NaN	17.2669	17.048	20.8758	20.8155	20.8331	20.7539
1925	Oxysterol-binding protein OS=Rattus norvegicus OX=10116 GN=Osbpl11 PE=1 SV=1	Osbpl11	B5DF74	14.7236	14.4194	NaN	16.2617	20.5123	19.7931	20.0325	20.0457
1926	Oxysterol-binding protein OS=Rattus norvegicus OX=10116 GN=Osbpl2 PE=1 SV=1	Osbpl2	Q5BK47	NaN	16.6015	NaN	NaN	16.6342	16.119	NaN	16.4937
1927	Oxysterol-binding protein OS=Rattus norvegicus OX=10116 GN=Osbpl3 PE=1 SV=2	Osbpl3	D3ZHZ3	15.4007	NaN	NaN	NaN	19.7784	18.3113	19.1464	19.4362
1928	Oxysterol-binding protein OS=Rattus norvegicus OX=10116 GN=Osbpl9 PE=1 SV=3	Osbpl9	F1LRE5	NaN	16.5522	NaN	NaN	17.9071	19.6693	17.3987	NaN
1929	Oxysterol-binding protein-related protein 1 OS=Rattus norvegicus OX=10116 GN=Osbpl1a PE=1 SV=1	Osbpl1a	Q8K4M9	NaN	NaN	NaN	NaN	19.2344	18.526	18.7974	18.9099
1930	Pachytene checkpoint protein 2 homolog OS=Rattus norvegicus OX=10116 GN=Trip13 PE=2 SV=1	Trip13	Q5XHZ9	NaN	15.9304	16.5477	16.8417	20.6507	20.4409	20.6037	20.2677
1931	Pancreatic secretory granule membrane major glycoprotein GP2 OS=Rattus norvegicus OX=10116 GN=Gp2 PE=4 SV=2	Gp2	F1M9X2	NaN	NaN	15.3537	15.84	15.619	17.4992	16.5218	16.5207
1932	Pantothenate kinase 4 OS=Rattus norvegicus OX=10116 GN=Pank4 PE=1 SV=1	Pank4	G3V7T3	18.1392	16.3438	16.6944	15.0765	21.344	20.894	21.404	21.5875
1933	Paralemmin 2 OS=Rattus norvegicus OX=10116 GN=Palm2 PE=1 SV=1	Palm2	A0A096MIZ1	15.0325	17.0851	14.1247	NaN	19.7099	20.0398	19.0954	19.5749
1934	Paralemmin-1 OS=Rattus norvegicus OX=10116 GN=Palm PE=1 SV=1	Palm	Q920Q0	19.2129	18.7014	19.2254	19.2734	18.5324	18.4416	17.5757	18.4128
1935	Parathymosin OS=Rattus norvegicus OX=10116 GN=Ptms PE=1 SV=2	Ptms	P04550	NaN	15.3351	NaN	NaN	17.8164	18.1154	18.2407	17.7555
1936	Parvin, beta OS=Rattus norvegicus OX=10116 GN=Parvb PE=1 SV=1	Parvb	D3ZKG5	18.1681	17.9728	19.4453	18.6652	21.1517	20.0228	21.2011	20.6767
1937	PAXX, non-homologous end joining factor OS=Rattus norvegicus OX=10116 GN=Paxx PE=1 SV=1	Paxx	A0A0G2QC22	NaN	NaN	NaN	NaN	NaN	NaN	16.7973	17.2314
1938	Pcbp2 protein OS=Rattus norvegicus OX=10116 GN=Pcbp2 PE=1 SV=1	Pcbp2	Q4V8F6	NaN	NaN	NaN	NaN	NaN	NaN	18.3424	17.4847
1939	Pcyox1l protein OS=Rattus norvegicus OX=10116 GN=Pcyox1l PE=2 SV=1	Pcyox1l	B5DEI0	NaN	NaN	NaN	NaN	NaN	16.6665	16.0122	NaN
1940	PDZ and LIM domain 3, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Pdlim3 PE=1 SV=1	Pdlim3	A0A0G2JSM3	17.7257	17.1905	15.6982	18.2952	23.3923	22.6516	23.0131	22.9781
1941	PDZ and LIM domain protein 1 OS=Rattus norvegicus OX=10116 GN=Pdlim1 PE=1 SV=4	Pdlim1	P52944	17.4431	15.2902	15.0952	15.8208	21.0546	20.0168	20.6989	20.5335
1942	PDZ and LIM domain protein 5 OS=Rattus norvegicus OX=10116 GN=Pdlim5 PE=1 SV=2	Pdlim5	Q62920	18.5672	17.1761	17.6764	16.2517	25.625	25.6863	25.8037	25.3524
1943	PDZ domain-containing protein GIPC1 OS=Rattus norvegicus OX=10116 GN=Gipc1 PE=1 SV=2	Gipc1	Q9Z254	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1944	PDZ-binding kinase OS=Rattus norvegicus OX=10116 GN=Pbk PE=1 SV=1	Pbk	A1L1J7	13.9743	NaN	NaN	NaN	17.2709	18.9797	18.7863	18.9535
1945	Peflin OS=Rattus norvegicus OX=10116 GN=Pef1 PE=2 SV=1	Pef1	Q641Z8	16.6793	16.8014	17.87	17.4032	19.9708	18.4255	17.343	18.9024
1946	Pentraxin 3 OS=Rattus norvegicus OX=10116 GN=Ptx3 PE=4 SV=1	Ptx3	D3ZT94	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1947	Peptidase inhibitor 16 OS=Rattus norvegicus OX=10116 GN=Pi16 PE=1 SV=1	Pi16	A0A1W2Q642	16.4821	16.7397	17.0818	17.6486	NaN	NaN	NaN	NaN
1948	Peptide-methionine (R)-S-oxide reductase OS=Rattus norvegicus OX=10116 GN=Msrb3 PE=1 SV=3	Msrb3	D4A650	18.3043	17.1	17.4482	18.0295	20.603	20.2166	20.3418	20.0852
1949	Peptidoglycan recognition protein 2 OS=Rattus norvegicus OX=10116 GN=Pglyrp2 PE=1 SV=2	Pglyrp2	M0R485	21.5916	21.2426	22.0824	22.127	18.8821	18.0971	16.245	18.0889
1950	Peptidyl-glycine alpha-amidating monooxygenase OS=Rattus norvegicus OX=10116 GN=Pam PE=1 SV=1	Pam	P14925	16.8054	16.9818	16.0081	16.6853	22.0198	22.3381	21.7783	21.9753
1951	Peptidyl-prolyl cis-trans isomerase A OS=Rattus norvegicus OX=10116 GN=Ppia PE=1 SV=2	Ppia	P10111	22.036	21.9866	22.2677	22.349	23.6638	24.0331	24.0577	23.9098
1952	Peptidyl-prolyl cis-trans isomerase B OS=Rattus norvegicus OX=10116 GN=Ppib PE=1 SV=3	Ppib	P24368	19.5212	20.0769	19.4951	19.4689	21.7929	22.3189	21.9609	22.1464
1953	Peptidyl-prolyl cis-trans isomerase D OS=Rattus norvegicus OX=10116 GN=Ppid PE=1 SV=3	Ppid	Q6DGG0	16.0835	17.5248	18.5068	18.2117	21.3323	20.8547	21.6544	21.4442
1954	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Rattus norvegicus OX=10116 GN=Fkbp1a PE=1 SV=3	Fkbp1a	Q62658	17.7097	17.9977	18.2207	17.9771	23.5817	23.0205	23.4822	23.5132
1955	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Rattus norvegicus OX=10116 GN=Fkbp4 PE=1 SV=3	Fkbp4	Q9QVC8	17.1385	NaN	15.3581	NaN	21.9184	20.5245	21.1965	21.4102
1956	Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Rattus norvegicus OX=10116 GN=Fkbp8 PE=2 SV=1	Fkbp8	Q3B7U9	NaN	NaN	NaN	NaN	17.5971	17.3564	17.2218	17.4626
1957	Peptidyl-prolyl cis-trans isomerase OS=Rattus norvegicus OX=10116 GN=Pin1 PE=1 SV=1	Pin1	B0BNL2	14.714	14.5328	NaN	NaN	18.5467	19.8712	20.4744	19.6109
1958	Peptidyl-prolyl cis-trans isomerase OS=Rattus norvegicus OX=10116 GN=Ppic PE=1 SV=1	Ppic	Q6AYQ9	21.8495	21.3823	21.7033	21.8902	19.7592	20.4754	19.0871	19.8808
1959	Peptidylprolyl isomerase OS=Rattus norvegicus OX=10116 GN=Fkbp10 PE=1 SV=1	Fkbp10	Q5U2V1	NaN	15.6821	NaN	15.3054	17.8972	19.2909	19.4484	19.742

1960	Peptidylprolyl isomerase OS=Rattus norvegicus OX=10116 GN=Fkbp2 PE=1 SV=1	Fkbp2	D3ZZR9	NaN	16.7856	NaN	16.9887	18.9832	19.1898	18.7482	19.0771
1961	Peptidylprolyl isomerase OS=Rattus norvegicus OX=10116 GN=Fkbp3 PE=1 SV=1	Fkbp3	G3V6L9	17.2362	17.5155	16.8772	17.6239	21.9074	20.9402	21.317	21.3038
1962	Peptidyl-tRNA hydrolase 2 OS=Rattus norvegicus OX=10116 GN=Ptrh2 PE=1 SV=1	Ptrh2	Q5XI86	NaN	NaN	NaN	NaN	17.5533	18.0346	17.7646	NaN
1963	Pericentriolar material 1 OS=Rattus norvegicus OX=10116 GN=Pcm1 PE=1 SV=1	Pcm1	A0A0G2K0X1	18.7451	19.9106	18.5209	18.745	19.653	21.5355	20.035	19.942
1964	Perilipin 4 OS=Rattus norvegicus OX=10116 GN=Plin4 PE=4 SV=2	Plin4	M0R7S5	20.2651	21.1958	19.3008	19.8338	21.7272	21.4877	21.3354	21.5874
1965	Perilipin OS=Rattus norvegicus OX=10116 GN=Plin1 PE=1 SV=1	Plin1	A0A0G2JTP6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1966	Perilipin OS=Rattus norvegicus OX=10116 GN=Plin2 PE=1 SV=1	Plin2	F6QBA3	NaN	17.0581	NaN	NaN	18.6389	21.4418	20.9589	20.4419
1967	Perilipin OS=Rattus norvegicus OX=10116 GN=Plin3 PE=1 SV=1	Plin3	M0RA08	21.3692	21.6929	21.5236	21.7771	24.5572	23.9898	24.4035	23.9824
1968	Periostin OS=Rattus norvegicus OX=10116 GN=Postn PE=1 SV=1	Postn	D3ZAF5	21.1611	21.2523	22.0879	21.9406	22.8902	22.2565	21.95	22.5527
1969	Peroxidasin OS=Rattus norvegicus OX=10116 GN=Pxdn PE=4 SV=1	Pxdn	A0A0G2JWB6	NaN	NaN	14.6405	15.7993	21.5007	21.2555	21.2574	21.58
1970	Peroxiredoxin 3 OS=Rattus norvegicus OX=10116 GN=Prdx3 PE=1 SV=1	Prdx3	G3V7I0	17.1646	NaN	15.1889	NaN	16.1161	19.4699	18.0273	19.1548
1971	Peroxiredoxin 5, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Prdx5 PE=1 SV=1	Prdx5	A0A0G2JSS8	18.4351	18.0037	18.2331	18.8175	18.4203	19.2011	19.3541	19.3084
1972	Peroxiredoxin-1 OS=Rattus norvegicus OX=10116 GN=Prdx1 PE=1 SV=1	Prdx1	Q63716	21.9075	22.3611	21.5012	22.3323	26.0408	25.1132	25.597	25.6868
1973	Peroxiredoxin-2 OS=Rattus norvegicus OX=10116 GN=Prdx2 PE=1 SV=1	Prdx2	A0A0G2JSH9	22.4896	22.5773	22.7706	23.2559	26.0486	25.4011	25.6073	25.6553
1974	Peroxiredoxin-4 OS=Rattus norvegicus OX=10116 GN=Prdx4 PE=2 SV=1	Prdx4	Q9Z0V5	19.1516	20.6342	19.3481	19.1617	19.6802	19.4309	19.7738	19.9734
1975	Peroxiredoxin-6 OS=Rattus norvegicus OX=10116 GN=Prdx6 PE=1 SV=3	Prdx6	O35244	18.2103	19.1864	19.1137	19.3958	21.5451	21.2819	21.702	21.4949
1976	Peroxiredoxin-like 2A OS=Rattus norvegicus OX=10116 GN=Prxl2a PE=1 SV=1	Prxl2a	Q6AXX6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1977	Peroxisomal biogenesis factor 19 OS=Rattus norvegicus OX=10116 GN=LOC100911356 PE=1 SV=1	Pex19	G3V907	16.2687	17.6454	16.3707	15.6866	22.1427	19.8835	20.7876	20.8622
1978	Peroxisomal targeting signal 1 receptor OS=Rattus norvegicus OX=10116 GN=Pex5 PE=1 SV=1	Pex5	A0A0A0MP84	NaN	NaN	NaN	NaN	18.7445	NaN	18.8833	19.3151
1979	Peroxisomal trans-2-enoyl-CoA reductase OS=Rattus norvegicus OX=10116 GN=Pecr PE=1 SV=1	Pecr	A0A0G2JVG4	NaN	NaN	NaN	NaN	NaN	16.3914	15.8836	16.1194
1980	PEST proteolytic signal-containing nuclear protein OS=Rattus norvegicus OX=10116 GN=Pcnp PE=1 SV=1	Pcnp	Q7TP40	15.2431	NaN	NaN	15.7509	20.2241	20.3652	19.9704	20.4118
1981	Phenylalanine--tRNA ligase alpha subunit OS=Rattus norvegicus OX=10116 GN=Farsa PE=1 SV=1	Farsa	Q505J8	20.3844	16.6426	17.1512	18.9677	19.838	22.1668	22.2941	21.9092
1982	Phenylalanyl-tRNA synthetase subunit beta OS=Rattus norvegicus OX=10116 GN=Farsb PE=1 SV=1	Farsb	Q68FT7	17.6696	NaN	NaN	NaN	18.657	18.4611	19.7087	18.8515
1983	Phosducin-like protein 3 OS=Rattus norvegicus OX=10116 GN=Pdcl3 PE=1 SV=1	Pdcl3	Q4KLJ8	19.2287	19.5696	19.7613	NaN	20.0797	18.1965	18.961	19.4886
1984	Phosphatase domain-containing, paladin 1 OS=Rattus norvegicus OX=10116 GN=Pald1 PE=1 SV=1	Pald1	D3ZCT5	17.2055	15.0885	16.2577	17.3639	19.0743	17.6075	18.9668	19.5197
1985	Phosphate carrier protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Slc25a3 PE=1 SV=1	Slc25a3	Q6IRH6	19.9178	21.0333	19.4157	18.4565	21.933	23.3758	22.9005	23.083
1986	Phosphatidate cytidylyltransferase OS=Rattus norvegicus OX=10116 GN=Cds2 PE=1 SV=1	Cds2	G3V8W2	NaN	NaN	NaN	NaN	NaN	16.3901	NaN	NaN
1987	Phosphatidylethanolamine-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Pebp1 PE=1 SV=3	Pebp1	P31044	19.068	18.9739	20.0129	17.9514	22.2758	22.512	22.5201	22.5019
1988	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Rattus norvegicus OX=10116 GN=Inppl1 PE=1 SV=1	Inppl1	Q9WVR3	18.3428	18.6476	18.1784	18.3655	22.3072	22.1733	22.1216	21.7768
1989	Phosphatidylinositol 4-kinase type 2-alpha OS=Rattus norvegicus OX=10116 GN=Pi4k2a PE=1 SV=1	Pi4k2a	Q99M64	18.6694	17.8928	18.3395	19.1056	18.7576	17.9105	18.4259	18.9037
1990	Phosphatidylinositol binding clathrin assembly protein, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Picalm PE=1 S	Picalm	A0A0G2JTT2	18.0482	21.23	17.8259	18.4369	22.5835	21.3385	21.4945	21.291
1991	Phosphatidylinositol transfer protein alpha isoform OS=Rattus norvegicus OX=10116 GN=Pitpna PE=1 SV=2	Pitpna	P16446	17.0286	15.6146	15.1549	16.235	21.0498	20.1749	21.1458	20.6998
1992	Phosphatidylinositol transfer protein beta isoform OS=Rattus norvegicus OX=10116 GN=Pitpnb PE=1 SV=2	Pitpnb	P53812	NaN	NaN	16.6088	17.2617	20.8933	19.5738	20.2062	19.7389
1993	Phosphodiesterase OS=Rattus norvegicus OX=10116 GN=Pde8b PE=2 SV=1	Pde8b	Q76KC5	24.0592	25.4726	24.0705	24.8727	23.5512	23.7896	23.1826	23.002
1994	Phosphofurin acidic cluster sorting protein 1 OS=Rattus norvegicus OX=10116 GN=Pacs1 PE=1 SV=1	Pacs1	F1LPG3	NaN	14.0503	14.6495	14.9629	19.9868	19.7506	19.9915	19.8152
1995	Phosphoglucomutase 1 OS=Rattus norvegicus OX=10116 GN=Pgm1 PE=1 SV=2	Pgm1	Q499Q4	14.7074	16.8996	17.4817	16.6644	22.7196	22.3661	22.1773	22.1732
1996	Phosphoglycerate kinase 1 OS=Rattus norvegicus OX=10116 GN=Pgk1 PE=1 SV=2	Pgk1	P16617	20.4032	20.4674	21.3049	20.4068	23.5101	24.2554	24.3609	23.9987
1997	Phosphoglycerate mutase 1 OS=Rattus norvegicus OX=10116 GN=Pgam1 PE=1 SV=4	Pgam1	P25113	19.7257	19.9101	19.6526	20.1435	23.4297	23.1258	23.6028	23.6334
1998	Phosphoglycerate mutase 2 OS=Rattus norvegicus OX=10116 GN=Pgam2 PE=1 SV=2	Pgam2	P16290	18.4978	18.3327	18.7318	18.823	19.4682	19.4994	20.0607	19.9491
1999	Phosphohistidine phosphatase 1 OS=Rattus norvegicus OX=10116 GN=Phpt1 PE=1 SV=1	Phpt1	D3ZP47	NaN	NaN	NaN	NaN	12.0287	11.118	NaN	NaN
2000	Phosphoinositide phospholipase C OS=Rattus norvegicus OX=10116 GN=Plcd1 PE=1 SV=1	Plcd1	G3V9D1	NaN	16.2006	16.4626	NaN	17.7058	16.8077	NaN	NaN
2001	Phosphoinositide phospholipase C OS=Rattus norvegicus OX=10116 GN=Plcd3 PE=1 SV=1	Plcd3	D4A978	19.8977	21.8401	19.5478	20.628	19.5335	20.1547	19.3112	19.1228
2002	Phospholipase A2, group XIIB OS=Rattus norvegicus OX=10116 GN=Pla2g12b PE=1 SV=1	Pla2g12b	M0RCI5	16.8407	15.177	16.7789	17.4751	17.5555	17.5086	17.2495	17.7247
2003	Phospholipase A2, membrane associated OS=Rattus norvegicus OX=10116 GN=Pla2g2a PE=1 SV=2	Pla2g2a	P14423	22.2354	21.0332	21.7435	20.2422	19.4137	16.142	17.4649	17.3561
2004	Phospholipase A-2-activating protein OS=Rattus norvegicus OX=10116 GN=Plaa PE=1 SV=3	Plaa	P54319	16.4262	16.7367	19.3317	17.1833	22.2966	22.8333	23.0331	22.8129
2005	Phospholipid scramblase 3 OS=Rattus norvegicus OX=10116 GN=Plscr3 PE=2 SV=1	Plscr3	Q6QBQ4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2006	Phospholipid transfer protein OS=Rattus norvegicus OX=10116 GN=Pltp PE=1 SV=1	Pltp	E9PSP1	22.0452	21.7203	21.6891	21.7832	17.5848	18.0052	17.7193	17.6278
2007	Phosphomannomutase OS=Rattus norvegicus OX=10116 GN=Pmm2 PE=1 SV=1	Pmm2	B5DF46	14.5644	16.9062	17.2021	16.5647	19.4914	19.325	19.7331	19.0357
2008	Phosphopantothenoylcysteine synthetase OS=Rattus norvegicus OX=10116 GN=Ppcs PE=1 SV=1	Ppcs	D4A6X7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2009	Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Prpsap1 PE=1 SV=1	Prpsap1	G3V7B5	NaN	16.26	17.156	NaN	19.709	19.4853	19.9885	19.395
2010	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Prpsap2 PE=1 SV=1	Prpsap2	O08618	NaN	13.7527	14.6106	16.671	20.3541	19.4473	20.3427	20.1195
2011	Phosphorylase b kinase gamma catalytic chain, liver/testis isoform OS=Rattus norvegicus OX=10116 GN=Phkg2 PE=1 SV=1	Phkg2	P31325	NaN	15.2253	15.4234	NaN	16.1427	16.9838	16.702	16.4243
2012	Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform OS=Rattus norvegicus OX=10116 GN=Phka1 PE=1 S	Phka1	Q64649	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

2013	Phosphorylase b kinase regulatory subunit OS=Rattus norvegicus OX=10116 GN=Phkb PE=1 SV=1	Phkb	Q5RKH5	16.8434	15.6311	16.9798	16.0681	19.3269	20.8586	20.8989	20.4779
2014	Phosphorylated adapter RNA export protein OS=Rattus norvegicus OX=10116 GN=Phax PE=1 SV=2	Phax	Q63068	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2015	Phytanoyl-CoA dioxygenase, peroxisomal OS=Rattus norvegicus OX=10116 GN=Phyh PE=1 SV=2	Phyh	P57093	17.519	18.5826	18.373	17.4576	19.8478	20.8671	20.5067	20.9779
2016	Placenta-specific 8 OS=Rattus norvegicus OX=10116 GN=Plac8 PE=1 SV=1	Plac8	B5DF36	NaN	NaN	19.8307	NaN	NaN	17.7195	17.2662	17.8929
2017	Plakophilin 1 OS=Rattus norvegicus OX=10116 GN=Pkp1 PE=4 SV=2	Pkp1	D3ZY51	18.5246	18.8375	15.7261	18.3878	17.5486	18.838	NaN	NaN
2018	Plasma kallikrein OS=Rattus norvegicus OX=10116 GN=Klkb1 PE=1 SV=1	Klkb1	P14272	23.1387	23.0471	23.6131	22.6592	21.2303	20.8417	20.7789	21.1115
2019	Plasma membrane calcium-transporting ATPase 1 OS=Rattus norvegicus OX=10116 GN=Atp2b1 PE=1 SV=3	Atp2b1	P11505	NaN	13.7164	13.8793	NaN	NaN	15.8005	NaN	NaN
2020	Plasma membrane calcium-transporting ATPase 4 OS=Rattus norvegicus OX=10116 GN=Atp2b4 PE=1 SV=1	Atp2b4	Q64542	18.7241	18.8889	15.9191	20.2536	18.1837	18.4545	18.7163	19.0953
2021	Plasma protease C1 inhibitor OS=Rattus norvegicus OX=10116 GN=Serping1 PE=2 SV=1	Serping1	Q6P734	22.2057	22.4024	22.435	22.0397	19.6041	18.0504	19.2188	19.2213
2022	Plasminogen activator inhibitor 1 RNA-binding protein OS=Rattus norvegicus OX=10116 GN=Serbp1 PE=1 SV=2	Serbp1	Q6AXS5	19.0587	18.5828	18.4122	18.4894	23.366	23.2235	22.8936	22.7706
2023	Plasminogen OS=Rattus norvegicus OX=10116 GN=Plg PE=2 SV=2	Plg	Q01177	26.004	25.5314	26.3834	26.413	22.2689	22.1734	21.6399	22.8429
2024	Plastin 3 (T-isoform), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Pls3 PE=1 SV=2	Pls3	F1LPK7	17.0043	17.9826	18.3678	17.978	20.9784	19.9436	20.2913	20.133
2025	Platelet endothelial cell adhesion molecule OS=Rattus norvegicus OX=10116 GN=Pecam1 PE=1 SV=1	Pecam1	Q3SWT0	17.7938	NaN	17.9834	14.7165	20.5754	20.5296	20.3258	20.6068
2026	Platelet factor 4 OS=Rattus norvegicus OX=10116 GN=Pf4 PE=1 SV=1	Pf4	P06765	23.7399	23.0583	24.0863	23.5261	18.9823	18.1116	18.0236	18.7225
2027	Platelet glycoprotein 4 OS=Rattus norvegicus OX=10116 GN=Cd36 PE=1 SV=3	Cd36	Q07969	20.1659	20.5537	20.4716	20.2516	22.0973	22.6044	21.8868	21.8591
2028	Platelet glycoprotein Ib beta chain OS=Rattus norvegicus OX=10116 GN=Gp1bb PE=1 SV=1	Gp1bb	Q9JJM7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2029	Platelet-activating factor acetylhydrolase 2, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Pafah2 PE=1 SV=2	Pafah2	P83006	NaN	NaN	NaN	15.6525	18.0459	16.9838	17.3894	16.6323
2030	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Rattus norvegicus OX=10116 GN=Pafah1b1 PE=1 SV=2	Pafah1b1	P63004	NaN	NaN	NaN	NaN	18.3274	18.0212	NaN	NaN
2031	Platelet-activating factor acetylhydrolase OS=Rattus norvegicus OX=10116 GN=Pla2g7 PE=2 SV=1	Pla2g7	Q5M7T7	19.6612	19.7073	19.7907	19.9008	18.0226	18.5246	18.929	18.1056
2032	Platelet-derived growth factor C OS=Rattus norvegicus OX=10116 GN=Pdgfc PE=1 SV=1	Pdgfc	Q9EQX6	16.907	NaN	NaN	16.8009	NaN	NaN	NaN	NaN
2033	Pleckstrin homology domain-containing A2 OS=Rattus norvegicus OX=10116 GN=Plekha2 PE=1 SV=2	Plekha2	F1LXA9	19.9573	18.5028	18.1518	18.2484	19.9676	18.9552	19.0967	18.9925
2034	Pleckstrin homology domain-containing family F member 1 OS=Rattus norvegicus OX=10116 GN=Plekhf1 PE=2 SV=1	Plekhf1	Q68FU1	15.3659	NaN	NaN	NaN	18.7529	18.9026	19.106	18.6396
2035	Pleckstrin homology domain-containing O2 OS=Rattus norvegicus OX=10116 GN=Plekho2 PE=1 SV=2	Plekho2	D3Z9K4	14.9437	NaN	NaN	15.5269	18.6874	17.7263	18.0188	17.7402
2036	Pleckstrin homology like domain, family B, member 2 OS=Rattus norvegicus OX=10116 GN=Phldb2 PE=1 SV=3	Phldb2	D4A779	16.6972	NaN	NaN	NaN	16.844	19.1629	19.4327	19.4465
2037	Pleckstrin homology-like domain family A member 3 OS=Rattus norvegicus OX=10116 GN=Phlda3 PE=2 SV=1	Phlda3	Q5PQT7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2038	Pleckstrin homology-like domain family B member 1 OS=Rattus norvegicus OX=10116 GN=Phldb1 PE=1 SV=2	Phldb1	D3ZNS1	16.8417	14.9232	15.8992	16.2475	20.1928	21.1654	20.8653	20.1969
2039	Pleckstrin OS=Rattus norvegicus OX=10116 GN=Plek PE=1 SV=1	Plek	Q4KM33	18.2149	16.6846	18.3138	17.3549	18.0601	18.6636	18.6727	18.2114
2040	Plectin OS=Rattus norvegicus OX=10116 GN=Plec PE=1 SV=1	Plec	Q6S3A0	19.8266	20.0378	20.0121	20.3129	20.7272	20.4808	20.4635	20.5772
2041	Pleiotrophin OS=Rattus norvegicus OX=10116 GN=Ptn PE=1 SV=1	Ptn	P63090	NaN	14.2756	NaN	NaN	18.1966	18.7051	18.3015	17.9277
2042	Plexin B2 OS=Rattus norvegicus OX=10116 GN=Plxnb2 PE=1 SV=1	Plxnb2	D3ZQ57	17.7726	17.5119	17.9143	18.099	19.9907	20.4981	20.4661	20.6767
2043	Pneumo secretory protein 1 OS=Rattus norvegicus OX=10116 GN=Scgb3a2 PE=2 SV=1	Scgb3a2	Q71MM7	17.4178	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2044	POF1B, actin-binding protein OS=Rattus norvegicus OX=10116 GN=Pof1b PE=1 SV=2	Pof1b	D3ZWE3	NaN	16.9074	NaN	19.09	18.0422	17.9593	17.8257	17.8586
2045	Poly (A) polymerase alpha OS=Rattus norvegicus OX=10116 GN=Papola PE=1 SV=1	Papola	A0A0G2K0C9	16.671	15.9534	16.4405	18.4428	16.6439	15.6447	15.7771	15.984
2046	Poly [ADP-ribose] polymerase (Fragment) OS=Rattus norvegicus OX=10116 PE=1 SV=1	0A096MJR6_RA	A0A096MJR6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2047	Poly [ADP-ribose] polymerase 1 OS=Rattus norvegicus OX=10116 GN=Parp1 PE=1 SV=4	Parp1	P27008	20.9094	20.2329	18.9235	19.9927	20.0023	19.7166	19.4073	19.6542
2048	Poly(A)-binding protein-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Paip1 PE=1 SV=1	Paip1	A0A0G2JVP5	NaN	16.1261	NaN	NaN	20.8021	19.7656	20.9887	20.1797
2049	Poly(rC)-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Pcbp2 PE=1 SV=1	Pcbp2	Q6AYU5	21.8693	21.612	21.1406	21.4946	25.9938	25.5017	25.7078	25.5902
2050	Poly(rC)-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Pcbp3 PE=1 SV=1	Pcbp3	Q6AY48	19.3335	18.5909	19.3216	NaN	20.518	19.5643	19.6942	20.2995
2051	Poly(rC)-binding protein 4 OS=Rattus norvegicus OX=10116 GN=Pcbp4 PE=4 SV=1	Pcbp4	D3ZCS3	18.9013	18.4437	18.495	19.6354	23.1819	22.7307	22.5751	22.889
2052	Poly(U)-binding-splicing factor PUF60 OS=Rattus norvegicus OX=10116 GN=Puf60 PE=2 SV=2	Puf60	Q9WV25	NaN	16.8025	15.7331	16.3187	21.4137	20.4148	20.9237	20.3499
2053	Polyadenylate-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Pabpc1 PE=1 SV=1	Pabpc1	Q9EPH8	22.3669	22.3236	22.5622	22.7761	24.3397	24.678	24.2743	24.0798
2054	Polyadenylate-binding protein OS=Rattus norvegicus OX=10116 GN=Pabpc4 PE=1 SV=2	Pabpc4	G3V9N0	17.8126	17.9506	17.8122	17.7201	22.1587	23.4476	22.5118	22.5319
2055	Polymerase (RNA) I polypeptide C OS=Rattus norvegicus OX=10116 GN=Polr1c PE=1 SV=1	Polr1c	Q5RJK9	15.5827	NaN	NaN	NaN	16.6473	16.4534	17.1251	16.6042
2056	Polymerase (RNA) II (DNA directed) polypeptide C, 33kDa OS=Rattus norvegicus OX=10116 GN=Polr2c PE=1 SV=1	Polr2c	Q5EB90	NaN	NaN	NaN	NaN	19.3964	19.3741	19.5969	19.2321
2057	Polymerase (RNA) II (DNA directed) polypeptide J (Predicted) OS=Rattus norvegicus OX=10116 GN=Polr2j PE=1 SV=1	Polr2j	D3ZQI0	NaN	NaN	NaN	NaN	18.6304	18.3952	17.4969	18.2205
2058	Polypyrimidine tract binding protein 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ptbp1 PE=1 SV=1	Ptbp1	Q6P736	16.246	19.5367	17.2579	20.0375	22.7561	22.7768	21.5355	21.5851
2059	Polysaccharide biosynthesis domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Pbdc1 PE=1 SV=1	Pbdc1	G3V6C3	18.5996	17.8738	18.3384	18.6046	22.8359	22.2986	22.3414	22.3158
2060	Popeye domain-containing 2 OS=Rattus norvegicus OX=10116 GN=Popdc2 PE=1 SV=1	Popdc2	Q6P722	NaN	NaN	NaN	NaN	18.4226	18.6169	15.796	17.7243
2061	Potassium channel modulatory factor 1 OS=Rattus norvegicus OX=10116 GN=Kcmf1 PE=1 SV=1	Kcmf1	A0A0G2JX46	14.8875	NaN	NaN	15.7303	18.2099	17.0479	17.6328	16.905
2062	PPFIA-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ppfibp1 PE=1 SV=1	Ppfibp1	A0A0G2K781	18.8775	19.3006	20.3288	20.1007	21.4763	21.7427	21.314	21.1692
2063	PPFIA-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ppfibp1 PE=1 SV=1	Ppfibp1	D3ZJW3	NaN	NaN	NaN	NaN	18.225	16.7691	NaN	16.0818
2064	Ppm1b protein OS=Rattus norvegicus OX=10116 GN=Ppm1b PE=1 SV=1	Ppm1b	Q99ND8	18.7817	18.8622	17.6971	18.8796	22.8022	21.8961	22.0655	22.0229
2065	PRA1 family protein OS=Rattus norvegicus OX=10116 GN=Arl6ip5 PE=1 SV=1	Arl6ip5	A0A0H2UHF6	18.1615	19.1133	18.0733	17.1504	20.189	20.5618	20.6199	20.2438

2066	Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Pbxip1 PE=1 SV=1	Pbxip1	A2VD12	17.2136	17.8564	15.7339	14.6545	19.8844	20.1313	19.5799	19.6597
2067	Preferentially-expressed antigen in melanoma-like 3 OS=Rattus norvegicus OX=10116 GN=LOC100912836 PE=4 SV=3	Pramel3	D4A8C3	19.1247	18.1526	18.746	18.2091	18.0085	NaN	18.0141	17.9406
2068	Prefoldin 1 (Predicted) OS=Rattus norvegicus OX=10116 GN=Pfdn1 PE=1 SV=1	Pfdn1	D3ZX38	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2069	Prefoldin 5 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Pfdn5 PE=1 SV=1	Pfdn5	B5DFN4	19.2334	18.2198	18.6038	17.4738	20.836	18.2437	19.1879	20.4354
2070	Prefoldin subunit 2 OS=Rattus norvegicus OX=10116 GN=Pfdn2 PE=2 SV=1	Pfdn2	B0BN18	15.2778	NaN	NaN	NaN	20.6411	18.757	19.7851	18.6995
2071	Prefoldin subunit 3 OS=Rattus norvegicus OX=10116 GN=Vbp1 PE=1 SV=2	Vbp1	M0R919	NaN	NaN	NaN	NaN	20.4107	19.3247	19.9447	20.1466
2072	Prefoldin subunit 4 OS=Rattus norvegicus OX=10116 GN=Pfdn4 PE=1 SV=2	Pfdn4	M0R5N4	NaN	15.6127	14.563	NaN	19.4762	18.2685	18.6271	19.3195
2073	Pre-mRNA-processing factor 19 OS=Rattus norvegicus OX=10116 GN=Prpf19 PE=1 SV=2	Prpf19	Q9JMJ4	NaN	NaN	NaN	NaN	18.3726	18.4909	18.4813	18.6132
2074	Prenylcysteine oxidase OS=Rattus norvegicus OX=10116 GN=Pcyox1 PE=1 SV=1	Pcyox1	Q99ML5	17.0814	16.799	16.9537	16.837	18.4349	17.2377	17.7189	17.9281
2075	Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Rattus norvegicus OX=10116 GN=Ciao1 PE=2 SV=1	Ciao1	Q5M7T1	15.2715	NaN	NaN	NaN	17.1	18.6963	18.7365	17.8771
2076	Probable E3 ubiquitin-protein ligase HERC4 OS=Rattus norvegicus OX=10116 GN=Herc4 PE=2 SV=1	Herc4	Q5PQN1	17.5187	14.9159	NaN	16.0343	19.2486	18.0736	18.2605	19.3226
2077	Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Rattus norvegicus OX=10116 GN=Osgep PE=2 SV=2	Osgep	Q9WVS2	NaN	NaN	NaN	NaN	18.5434	17.2161	18.7856	17.8529
2078	Pro-cathepsin H OS=Rattus norvegicus OX=10116 GN=Ctsh PE=1 SV=1	Ctsh	A0A0G2K8H6	NaN	NaN	NaN	NaN	16.7664	17.742	18.0167	18.2749
2079	Procollagen C-endopeptidase enhancer 1 OS=Rattus norvegicus OX=10116 GN=Pcolce PE=1 SV=1	Pcolce	O08628	21.1779	21.0899	21.3378	21.3691	21.2621	20.9744	20.9687	21.0216
2080	Profilin-1 OS=Rattus norvegicus OX=10116 GN=Pfn1 PE=1 SV=2	Pfn1	P62963	21.8822	21.9022	22.4344	23.2469	24.5894	23.908	24.4388	24.3672
2081	Programmed cell death 2-like OS=Rattus norvegicus OX=10116 GN=Pdcd2l PE=1 SV=1	Pdcd2l	D3ZSC2	NaN	NaN	NaN	NaN	17.9209	17.0072	17.2019	17.2211
2082	Programmed cell death 5 OS=Rattus norvegicus OX=10116 GN=Pdcd5 PE=1 SV=1	Pdcd5	D4ADF5	NaN	NaN	NaN	NaN	NaN	NaN	17.2124	NaN
2083	Programmed cell death 6-interacting protein OS=Rattus norvegicus OX=10116 GN=Pdcd6ip PE=1 SV=1	Pdcd6ip	A0A140TAA4	19.6763	19.2874	19.1651	19.5351	24.0502	23.6499	23.7945	23.7461
2084	Programmed cell death protein 10 OS=Rattus norvegicus OX=10116 GN=Pdcd10 PE=2 SV=1	Pdcd10	Q6NX65	16.9142	15.6197	15.354	15.2475	19.7653	18.9897	19.7114	19.6363
2085	Programmed cell death protein 2 OS=Rattus norvegicus OX=10116 GN=Pdcd2 PE=2 SV=2	Pdcd2	P47816	NaN	NaN	NaN	NaN	16.8197	17.2029	17.163	17.2223
2086	Programmed cell death protein 6 OS=Rattus norvegicus OX=10116 GN=Pdcd6 PE=2 SV=1	Pdcd6	G3V7W1	NaN	NaN	NaN	NaN	19.5876	18.742	18.8219	18.9523
2087	Prohibitin OS=Rattus norvegicus OX=10116 GN=Phb PE=1 SV=1	Phb1	P67779	19.5735	19.8758	18.2108	18.8339	20.1191	21.7324	21.1194	21.7141
2088	Prohibitin-2 OS=Rattus norvegicus OX=10116 GN=Phb2 PE=1 SV=1	Phb2	Q5XIH7	19.9289	20.1226	18.6449	17.6838	21.1672	21.8498	21.5403	21.8015
2089	Prolactin induced protein, isoform CRA_d OS=Rattus norvegicus OX=10116 GN=Pip PE=4 SV=1	Pip	G3V812	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2090	Proliferating cell nuclear antigen OS=Rattus norvegicus OX=10116 GN=Pcna PE=1 SV=1	Pcna	P04961	18.5022	18.4976	17.9853	17.5752	19.7282	19.3869	22.0851	22.9556
2091	Proliferation-associated protein 2G4 OS=Rattus norvegicus OX=10116 GN=Pa2g4 PE=1 SV=1	Pa2g4	Q6AYD3	16.6943	17.092	16.9355	16.2999	18.333	18.9682	19.3455	17.2714
2092	Proline-rich 4 OS=Rattus norvegicus OX=10116 GN=Prr4 PE=4 SV=3	Prr4	D4A0S3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2093	Prolyl endopeptidase OS=Rattus norvegicus OX=10116 GN=Prep PE=1 SV=1	Prep	O70196	NaN	16.0984	15.644	15.7594	16.3323	20.0805	20.0802	20.0322
2094	Proprotein convertase subtilisin/kexin type 9 OS=Rattus norvegicus OX=10116 GN=Pcsk9 PE=1 SV=1	Pcsk9	P59996	17.7431	14.7734	18.1156	20.2368	15.6232	NaN	NaN	NaN
2095	Prosaposin OS=Rattus norvegicus OX=10116 GN=Psap PE=1 SV=2	Psap	F7EPE0	21.2751	20.811	21.3965	21.1541	21.3918	21.1617	20.1523	20.4176
2096	Prostacyclin synthase OS=Rattus norvegicus OX=10116 GN=Ptgis PE=2 SV=1	Ptgis	Q62969	NaN	NaN	15.6714	15.7486	17.9418	17.7722	17.2837	17.9602
2097	Prostaglandin E synthase 3 OS=Rattus norvegicus OX=10116 GN=Ptges3 PE=1 SV=2	Ptges3	P83868	16.8536	16.7157	16.1507	NaN	21.1645	20.1257	21.2092	21.1788
2098	Prostaglandin reductase 1 OS=Rattus norvegicus OX=10116 GN=Ptgr1 PE=2 SV=3	Ptgr1	P97584	20.1637	19.7928	20.7412	20.849	19.075	19.3266	19.8995	19.9269
2099	Prostaglandin reductase 2 OS=Rattus norvegicus OX=10116 GN=Ptgr2 PE=2 SV=2	Ptgr2	Q5BK81	NaN	NaN	NaN	16.3118	18.4455	18.6825	18.7127	18.2649
2100	Prostaglandin-H2 D-isomerase OS=Rattus norvegicus OX=10116 GN=Ptgds PE=1 SV=2	Ptgds	P22057	17.1375	17.621	17.9395	16.3652	NaN	NaN	14.1612	NaN
2101	Prostamide/prostaglandin F synthase OS=Rattus norvegicus OX=10116 GN=Prxl2b PE=3 SV=1	Prxl2b	D3ZVR7	NaN	NaN	14.7546	NaN	NaN	16.8394	17.0002	16.9445
2102	Proteaseome (Prosome, macropain) 28 subunit, 3 OS=Rattus norvegicus OX=10116 GN=Psme3 PE=1 SV=1	Psme3	Q5FVM2	15.9687	NaN	17.1392	13.394	20.8215	19.4056	20.3578	20.2382
2103	Proteasomal ubiquitin receptor ADRM1 OS=Rattus norvegicus OX=10116 GN=Adrm1 PE=1 SV=2	Adrm1	Q9JMB5	20.6098	19.716	20.1037	21.7084	22.7298	20.9993	22.0469	22.1172
2104	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 12 OS=Rattus norvegicus OX=10116 GN=Psmd12 PE=1 SV=1	Psmd12	Q5XIC6	17.6395	18.2983	17.2077	17.1148	23.5999	22.5005	23.1502	23.0967
2105	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 14 OS=Rattus norvegicus OX=10116 GN=Psmd14 PE=1 SV=1	Psmd14	Q4V8E2	NaN	19.6916	13.1974	14.308	21.988	20.6209	21.6863	20.8608
2106	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 3 OS=Rattus norvegicus OX=10116 GN=Psmd3 PE=1 SV=1	Psmd3	Q5U2S7	16.825	18.2974	17.9853	17.8108	23.4398	22.482	23.1254	23.0131
2107	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 5 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116	Psmd5	G3V8G2	16.9355	15.0747	16.075	18.5848	21.3256	20.2326	20.452	20.4939
2108	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 6 OS=Rattus norvegicus OX=10116 GN=Psmd6 PE=1 SV=1	Psmd6	Q6PCT9	17.1509	16.8315	16.9881	16.8147	23.3516	22.1472	22.5526	22.6254
2109	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 7 (Predicted) OS=Rattus norvegicus OX=10116 GN=Psmd7 PE=	Psmd7	D4AEH3	16.2458	16.2812	16.6839	NaN	22.4087	21.2637	21.9007	21.3183
2110	Proteasome (Prosome, macropain) activator subunit 1 OS=Rattus norvegicus OX=10116 GN=Psme1 PE=1 SV=1	Psme1	Q6P9V7	26.718	26.331	26.1253	24.9369	26.9818	26.3992	26.7711	26.7708
2111	Proteasome 26S subunit, ATPase 6 OS=Rattus norvegicus OX=10116 GN=Psmc6 PE=1 SV=1	Psmc6	G3V6W6	22.7982	20.9221	21.513	21.5883	24.3134	24.3066	24.4497	24.3623
2112	Proteasome 26S subunit, non-ATPase 8 OS=Rattus norvegicus OX=10116 GN=Psmd8 PE=1 SV=1	Psmd8	F1LMQ3	22.2025	22.3086	22.0177	21.7307	22.1879	21.6534	22.1853	22.1653
2113	Proteasome activator complex subunit 2 OS=Rattus norvegicus OX=10116 GN=Psme2 PE=2 SV=3	Psme2	Q63798	17.9348	NaN	17.0648	17.5979	21.4058	21.9168	22.4577	22.3677
2114	Proteasome inhibitor PI31 subunit OS=Rattus norvegicus OX=10116 GN=Psmf1 PE=1 SV=2	Psmf1	F1M7S2	NaN	NaN	NaN	NaN	19.7717	17.8491	18.3813	18.1564
2115	Proteasome maturation protein OS=Rattus norvegicus OX=10116 GN=Pomp PE=1 SV=1	Pomp	A5HKJ3	17.2769	16.2428	16.2778	16.6743	19.3365	18.8492	18.9966	18.6607
2116	Proteasome subunit alpha type OS=Rattus norvegicus OX=10116 GN=Psma7 PE=1 SV=1	Psma7	A0A0G2K0W9	19.1787	20.0455	18.8394	19.0277	20.5491	19.8773	19.9155	20.4779
2117	Proteasome subunit alpha type-1 OS=Rattus norvegicus OX=10116 GN=Psma1 PE=1 SV=2	Psma1	P18420	20.0448	20.9066	20.5795	19.6285	20.8355	19.9419	20.2075	20.1248
2118	Proteasome subunit alpha type-2 OS=Rattus norvegicus OX=10116 GN=Psma2 PE=1 SV=3	Psma2	P17220	17.0726	17.1289	17.7086	17.72	18.0521	16.0795	17.2006	18.9357

2119	Proteasome subunit alpha type-3 OS=Rattus norvegicus OX=10116 GN=Psma3 PE=1 SV=3	Psma3	P18422	17.2644	19.1029	18.8228	18.6699	17.3263	19.5134	19.682	19.1374
2120	Proteasome subunit alpha type-4 OS=Rattus norvegicus OX=10116 GN=Psma4 PE=1 SV=1	Psma4	P21670	19.8384	20.1885	20.274	18.7352	21.288	21.5846	22.3278	21.9045
2121	Proteasome subunit alpha type-5 OS=Rattus norvegicus OX=10116 GN=Psma5 PE=1 SV=1	Psma5	P34064	18.3177	20.697	18.0383	18.4535	20.4167	20.0858	20.8226	20.2875
2122	Proteasome subunit alpha type-6 OS=Rattus norvegicus OX=10116 GN=Psma6 PE=1 SV=1	Psma6	P60901	19.1635	20.0759	19.0904	18.9393	21.5317	21.2129	21.5415	21.2274
2123	Proteasome subunit beta OS=Rattus norvegicus OX=10116 GN=LOC100360846 PE=3 SV=1	LOC100360846	A0A0G2JSL0	20.078	20.5269	19.0659	20.1174	19.8897	19.8226	20.0668	19.7259
2124	Proteasome subunit beta OS=Rattus norvegicus OX=10116 GN=Psmb5 PE=1 SV=1	Psmb5	G3V7Q6	18.5876	18.2938	18.9928	17.9432	19.8086	19.7025	19.3377	18.9922
2125	Proteasome subunit beta type-1 OS=Rattus norvegicus OX=10116 GN=Psmb1 PE=1 SV=3	Psmb1	P18421	19.1769	20.392	20.5597	21.6403	19.3436	19.9683	19.6088	19.5607
2126	Proteasome subunit beta type-2 OS=Rattus norvegicus OX=10116 GN=Psmb2 PE=1 SV=1	Psmb2	P40307	17.2466	18.6801	18.1451	17.9451	17.4869	17.9538	16.5084	16.5485
2127	Proteasome subunit beta type-3 OS=Rattus norvegicus OX=10116 GN=Psmb3 PE=1 SV=1	Psmb3	P40112	16.4964	17.184	16.6316	17.008	17.4688	17.6187	17.78	17.7423
2128	Proteasome subunit beta type-4 OS=Rattus norvegicus OX=10116 GN=Psmb4 PE=1 SV=2	Psmb4	P34067	17.3405	18.912	18.65	17.7812	18.6736	18.0726	18.7224	18.5782
2129	Proteasome subunit beta type-7 OS=Rattus norvegicus OX=10116 GN=Psmb7 PE=1 SV=1	Psmb7	Q9JHW0	17.0697	19.5939	17.1405	17.7561	19.2218	17.9307	17.6037	17.5236
2130	Protein AMBP OS=Rattus norvegicus OX=10116 GN=Ambp PE=1 SV=1	Ambp	Q64240	24.3792	23.8463	24.3893	24.7355	20.3543	18.8759	18.4816	19.9404
2131	Protein arginine methyltransferase 1-like OS=Rattus norvegicus OX=10116 GN=LOC100361025 PE=3 SV=1	LOC100361025	A0A0G2K9I8	NaN	17.8834	16.3896	17.5878	17.4881	18.8824	18.7855	19.5389
2132	Protein arginine N-methyltransferase 3 OS=Rattus norvegicus OX=10116 GN=Prmt3 PE=1 SV=1	Prmt3	A0A0G2JW52	16.9618	16.8107	17.0095	NaN	16.6087	16.6494	16.217	NaN
2133	Protein arginine N-methyltransferase 5 OS=Rattus norvegicus OX=10116 GN=Prmt5 PE=1 SV=1	Prmt5	D4A0E8	15.0588	15.8206	NaN	16.5098	NaN	17.5002	16.8336	16.3406
2134	Protein argonaute-2 OS=Rattus norvegicus OX=10116 GN=Ago2 PE=1 SV=2	Ago2	F1LRP7	20.5234	20.1496	20.0724	19.1008	20.5541	20.7666	20.6471	20.2645
2135	Protein ATP1B4 OS=Rattus norvegicus OX=10116 GN=Atp1b4 PE=1 SV=1	Atp1b4	Q9R193	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2136	Protein BEX1 OS=Rattus norvegicus OX=10116 GN=Bex1 PE=1 SV=2	Bex1	Q3MKQ2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2137	Protein C, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Proc PE=1 SV=1	Proc	F7FMY6	19.5585	19.2341	19.3858	19.3901	15.7298	NaN	NaN	17.7241
2138	Protein C10-like OS=Rattus norvegicus OX=10116 GN=LOC100911713 PE=1 SV=1	Grcc10	D3ZMS0	NaN	15.8888	NaN	16.1888	21.2563	20.1236	20.3712	20.7457
2139	Protein CDV3 homolog OS=Rattus norvegicus OX=10116 GN=Cdv3 PE=1 SV=1	Cdv3	A0A0G2K0B0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2140	Protein DEK OS=Rattus norvegicus OX=10116 GN=Dek PE=1 SV=1	Dek	Q6AXS3	20.0091	19.9431	20.3496	20.1531	17.7465	17.1684	16.9257	17.6574
2141	Protein delta homolog 1 OS=Rattus norvegicus OX=10116 GN=Dlk1 PE=1 SV=1	Dlk1	O70534	20.123	20.7975	21.191	20.1484	17.032	17.0902	16.8461	17.0404
2142	Protein diaphanous homolog 1 OS=Rattus norvegicus OX=10116 GN=Diaph1 PE=1 SV=3	Diaph1	F1M775	18.6785	17.8411	18.9882	18.1768	18.5096	18.1969	17.8731	18.0635
2143	Protein disulfide-isomerase A4 OS=Rattus norvegicus OX=10116 GN=Pdia4 PE=1 SV=1	Pdia4	G3V6T7	NaN	17.1969	15.2537	18.8924	20.0386	20.277	20.1903	20.6865
2144	Protein disulfide-isomerase A6 OS=Rattus norvegicus OX=10116 GN=Pdia6 PE=1 SV=1	Pdia6	A0A0G2JSZ5	20.0252	20.4442	19.4151	19.6607	22.9488	23.3559	22.9443	23.5918
2145	Protein disulfide-isomerase OS=Rattus norvegicus OX=10116 GN=P4hb PE=1 SV=2	P4hb	P04785	22.1376	22.5966	21.4833	20.4615	23.7076	24.3863	23.8488	24.3543
2146	Protein disulfide-isomerase OS=Rattus norvegicus OX=10116 GN=Pdia3 PE=1 SV=1	Pdia3	A0A0H2UHM5	22.0595	22.2681	21.7378	20.8588	24.2803	24.7963	24.2961	24.7417
2147	Protein Dr1 OS=Rattus norvegicus OX=10116 GN=Dr1 PE=2 SV=1	Dr1	Q5XI68	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2148	Protein ERGIC-53 OS=Rattus norvegicus OX=10116 GN=Lman1 PE=1 SV=1	Lman1	A0A0G2JXC1	18.3115	17.8778	18.3288	18.237	20.4368	20.9097	19.6214	20.0618
2149	Protein ERGIC-53 OS=Rattus norvegicus OX=10116 GN=Lman1 PE=1 SV=1	Lman1	Q62902	19.7106	19.7779	19.6097	19.5426	22.3103	22.9951	22.1387	22.0169
2150	Protein FAM210A OS=Rattus norvegicus OX=10116 GN=Fam210a PE=2 SV=1	Fam210a	Q5XIJ4	17.3279	18.8995	16.2156	18.8925	20.8658	19.9315	18.2479	16.7981
2151	Protein FAM3C OS=Rattus norvegicus OX=10116 GN=Fam3c PE=1 SV=1	Fam3c	A0A0G2JUB0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2152	Protein FAM50A-like OS=Rattus norvegicus OX=10116 GN=LOC100910130 PE=1 SV=1	Fam50a	G3V9M8	NaN	NaN	NaN	NaN	18.0649	NaN	NaN	NaN
2153	Protein FAM98A OS=Rattus norvegicus OX=10116 GN=Fam98a PE=2 SV=1	Fam98a	Q5FWT1	NaN	NaN	NaN	NaN	17.7898	17.9151	17.5394	17.5153
2154	Protein fem-1 homolog A OS=Rattus norvegicus OX=10116 GN=Fem1a PE=2 SV=1	Fem1a	Q4V890	NaN	NaN	NaN	NaN	17.0814	16.8631	16.7375	16.3762
2155	Protein Hikeshi OS=Rattus norvegicus OX=10116 GN=Hikeshi PE=2 SV=2	Hikeshi	Q5M808	NaN	NaN	NaN	NaN	19.8382	18.8243	19.2683	19.3453
2156	Protein kinase AMP-activated non-catalytic subunit gamma 2 OS=Rattus norvegicus OX=10116 GN=Prkag2 PE=1 SV=1	Prkag2	A0A140UHX4	20.87	20.2676	18.5174	20.4742	22.6298	21.1846	21.2021	21.4822
2157	Protein kinase C and casein kinase substrate in neurons 2 protein OS=Rattus norvegicus OX=10116 GN=Pacsin2 PE=1 SV=2	Pacsin2	Q9QY17	16.0662	16.9678	16.5953	16.6931	22.1481	21.8498	21.9066	21.6354
2158	Protein kinase C and casein kinase substrate in neurons 3 OS=Rattus norvegicus OX=10116 GN=Pacsin3 PE=1 SV=3	Pacsin3	G3V9N7	15.9224	15.9827	15.5791	16.2135	NaN	16.011	NaN	NaN
2159	Protein kinase C delta type OS=Rattus norvegicus OX=10116 GN=Prkcd PE=1 SV=1	Prkcd	A0A140UHX0	17.9037	19.2959	19.2858	17.3803	23.2325	22.9505	23.2787	23.1425
2160	Protein kinase C epsilon type OS=Rattus norvegicus OX=10116 GN=Prkce PE=1 SV=1	Prkce	P09216	NaN	NaN	NaN	NaN	15.172	15.2862	15.1663	15.4859
2161	Protein kinase C OS=Rattus norvegicus OX=10116 GN=Prkca PE=1 SV=3	Prkca	F1LS98	17.9317	18.7387	17.5431	16.0481	20.2828	22.131	22.2516	22.3495
2162	Protein kinase C substrate 80K-H OS=Rattus norvegicus OX=10116 GN=Prkcsh PE=1 SV=1	Prkcsh	B1WC34	16.7077	18.0227	17.2649	14.9373	21.3583	21.9126	21.325	21.5851
2163	Protein kinase C-binding protein Beta15, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Rbck1 PE=1 SV=1	Rbck1	A0A0G2K9L6	NaN	NaN	NaN	17.5337	17.0393	17.8767	17.5165	NaN
2164	Protein kinase, cAMP-dependent, catalytic, alpha OS=Rattus norvegicus OX=10116 GN=Prkaca PE=1 SV=1	Prkaca	A1L1M0	17.2627	14.4904	16.7801	16.9435	23.2956	23.1719	23.1809	22.825
2165	Protein kish OS=Rattus norvegicus OX=10116 GN=Tmem167a PE=3 SV=2	Tmem167a	D3ZKR8	15.8643	15.8925	15.9731	16.4549	18.1838	18.5209	18.026	18.1072
2166	Protein KTI12 homolog OS=Rattus norvegicus OX=10116 GN=Kti12 PE=1 SV=1	Kti12	Q5I0L7	NaN	NaN	NaN	16.4814	18.6237	18.3806	19.0353	19.3493
2167	Protein LBH OS=Rattus norvegicus OX=10116 GN=Lbh PE=1 SV=1	Lbh	A0A0G2KAD4	NaN	NaN	NaN	NaN	18.2792	17.6716	17.85	17.2873
2168	Protein LTV1 homolog OS=Rattus norvegicus OX=10116 GN=Ltv1 PE=2 SV=1	Ltv1	Q68FR7	NaN	NaN	NaN	NaN	17.2538	15.9493	17.3735	NaN
2169	Protein LYRIC OS=Rattus norvegicus OX=10116 GN=Mtdh PE=1 SV=2	Mtdh	Q9Z1W6	NaN	NaN	NaN	NaN	16.232	17.9591	NaN	NaN
2170	Protein LZIC OS=Rattus norvegicus OX=10116 GN=Lzic PE=2 SV=1	Lzic	Q5PQN7	19.5881	NaN	NaN	NaN	21.4057	NaN	16.4458	19.9918
2171	Protein MEMO1 OS=Rattus norvegicus OX=10116 GN=Memo1 PE=1 SV=1	Memo1	Q4QQR9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

2172	Protein NDRG1 OS=Rattus norvegicus OX=10116 GN=Ndrg1 PE=1 SV=1	Ndrg1	Q6JE36	16.3622	16.2831	15.6289	16.4736	20.7898	20.7384	20.5244	20.788
2173	Protein NDRG4 OS=Rattus norvegicus OX=10116 GN=Ndrg4 PE=1 SV=1	Ndrg4	D3ZUT8	NaN	17.7268	15.4875	14.6204	19.9603	19.8851	20.5359	19.8925
2174	Protein numb homolog OS=Rattus norvegicus OX=10116 GN=Numb PE=1 SV=3	Numb	F1LNZ2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2175	Protein O-GlcNAcase OS=Rattus norvegicus OX=10116 GN=Oga PE=1 SV=1	Oga	A0A0H2UI10	NaN	NaN	14.7422	15.1503	19.9889	19.3827	19.9296	19.7982
2176	Protein PAT1 homolog 1 OS=Rattus norvegicus OX=10116 GN=Patl1 PE=2 SV=1	Patl1	B5DF93	NaN	NaN	NaN	NaN	17.6289	17.5884	17.3285	17.8746
2177	Protein pelota homolog OS=Rattus norvegicus OX=10116 GN=Pelo PE=1 SV=1	Pelo	Q5XIP1	NaN	NaN	NaN	NaN	NaN	17.8024	NaN	NaN
2178	Protein phosphatase 1 regulatory subunit 12A OS=Rattus norvegicus OX=10116 GN=Ppp1r12a PE=1 SV=1	Ppp1r12a	A0A0G2JWJ0	15.2717	NaN	15.3355	17.019	20.2645	20.384	20.2866	19.7849
2179	Protein phosphatase 1 regulatory subunit 14B OS=Rattus norvegicus OX=10116 GN=Ppp1r14b PE=2 SV=1	Ppp1r14b	Q8K3F3	NaN	NaN	NaN	NaN	18.9415	18.1916	18.7266	18.3066
2180	Protein phosphatase 1 regulatory subunit 14C OS=Rattus norvegicus OX=10116 GN=Ppp1r14c PE=1 SV=1	Ppp1r14c	Q8R4R9	15.235	18.1993	18.2946	NaN	17.139	16.9581	17.4566	16.9635
2181	Protein phosphatase 1 regulatory subunit 36 OS=Rattus norvegicus OX=10116 GN=Ppp1r36 PE=2 SV=1	Ppp1r36	Q68FW6	17.6269	16.7519	17.009	NaN	NaN	16.143	16.2375	16.7594
2182	Protein phosphatase 1 regulatory subunit 3B OS=Rattus norvegicus OX=10116 GN=Ppp1r3b PE=1 SV=1	Ppp1r3b	Q6IN01	18.1018	18.1166	17.8062	NaN	16.7253	18.1392	17.2197	17.1619
2183	Protein phosphatase 1 regulatory subunit 7 OS=Rattus norvegicus OX=10116 GN=Ppp1r7 PE=1 SV=1	Ppp1r7	Q5HZV9	16.6163	18.7617	NaN	NaN	18.905	18.0472	18.9813	18.7791
2184	Protein phosphatase 1 regulatory subunit OS=Rattus norvegicus OX=10116 GN=Ppp1r3d PE=1 SV=1	Ppp1r3d	D3ZZ26	18.3665	16.4731	NaN	NaN	24.3534	22.9862	23.2939	23.2987
2185	Protein phosphatase 1, regulatory (Inhibitor) subunit 12B (Predicted) OS=Rattus norvegicus OX=10116 GN=Ppp1r12b PE=1	Ppp1r12b	D3ZIC4	NaN	NaN	NaN	NaN	18.4142	18.6651	18.078	17.7433
2186	Protein phosphatase 1, regulatory subunit 12C OS=Rattus norvegicus OX=10116 GN=Ppp1r12c PE=1 SV=1	Ppp1r12c	A0A0G2K4R1	21.2464	21.4381	21.2882	21.6653	19.7219	19.7066	18.8816	20.02
2187	Protein phosphatase 1, regulatory subunit 13-like OS=Rattus norvegicus OX=10116 GN=Ppp1r13l PE=1 SV=2	Ppp1r13l	F1LW07	NaN	NaN	17.3128	15.0687	20.0563	19.4603	19.9431	19.9095
2188	Protein phosphatase 1, regulatory subunit 3A OS=Rattus norvegicus OX=10116 GN=Ppp1r3a PE=1 SV=1	Ppp1r3a	D3ZM60	17.1142	16.6021	17.2786	17.3561	NaN	NaN	17.6501	18.0356
2189	Protein phosphatase 1A OS=Rattus norvegicus OX=10116 GN=Ppm1a PE=1 SV=1	Ppm1a	A0A0H2UHE5	15.9314	16.2407	16.0737	16.3095	21.4571	19.9394	20.4723	19.5789
2190	Protein phosphatase 1E OS=Rattus norvegicus OX=10116 GN=Ppm1e PE=1 SV=1	Ppm1e	Q80Z30	NaN	NaN	NaN	NaN	NaN	16.4625	17.3824	NaN
2191	Protein phosphatase 1F OS=Rattus norvegicus OX=10116 GN=Ppm1f PE=2 SV=1	Ppm1f	Q9WVR7	17.8702	20.2963	16.6808	18.2548	19.5208	18.3372	19.8269	19.4782
2192	Protein phosphatase 1G OS=Rattus norvegicus OX=10116 GN=Ppm1g PE=1 SV=1	Ppm1g	A0A0H2UHT5	NaN	NaN	14.4599	NaN	19.1818	18.4161	18.6411	18.8104
2193	Protein phosphatase 2 (Formerly 2A), regulatory subunit A (PR 65), alpha isoform, isoform CRA_a OS=Rattus norvegicus OX	Ppp2r1a	Q5XI34	18.7461	19.2692	19.9603	19.2444	24.4942	24.3947	24.7521	24.6806
2194	Protein phosphatase 2 (Formerly 2A), regulatory subunit B", alpha OS=Rattus norvegicus OX=10116 GN=Ppp2r3a PE=2 SV=	Ppp2r3a	Q5PQN8	19.0903	17.6835	18.5121	19.3807	20.6978	21.8497	21.6971	21.3355
2195	Protein phosphatase 2 (Formerly 2A), regulatory subunit B", alpha, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Pp	Ppp2r3a	D3ZLD7	20.7778	19.6946	20.0719	21.0402	21.1732	20.4408	21.0814	20.9608
2196	Protein phosphatase 6, regulatory subunit 1 OS=Rattus norvegicus OX=10116 GN=Ppp6r1 PE=1 SV=1	Ppp6r1	A0A0G2JTK4	NaN	NaN	NaN	NaN	20.0585	19.2585	20.0725	19.4418
2197	Protein phosphatase 6, regulatory subunit 3 OS=Rattus norvegicus OX=10116 GN=Ppp6r3 PE=1 SV=3	Ppp6r3	F1MAH5	17.9418	17.9939	17.8768	17.1831	21.5688	20.7938	21.5547	21.5773
2198	Protein phosphatase inhibitor 2 OS=Rattus norvegicus OX=10116 GN=Ppp1r2 PE=1 SV=2	Ppp1r2	P50411	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2199	Protein phosphatase methylesterase 1 OS=Rattus norvegicus OX=10116 GN=Ppme1 PE=1 SV=2	Ppme1	Q4FZT2	NaN	NaN	NaN	NaN	21.0713	20.2164	20.5936	20.899
2200	Protein PRRC1 OS=Rattus norvegicus OX=10116 GN=Prrc1 PE=1 SV=1	Prrc1	G3V834	20.8241	19.4231	20.4112	20.5106	21.1674	20.3096	19.7119	20.5915
2201	Protein PRRC2A OS=Rattus norvegicus OX=10116 GN=Prrc2a PE=1 SV=1	Prrc2a	A0A0U1RRZ5	17.7424	18.0673	17.4769	16.8128	17.9435	19.0436	18.2159	17.3567
2202	Protein quaking-like OS=Rattus norvegicus OX=10116 GN=LOC108348175 PE=4 SV=1	Qk	A0A0G2JXZ5	19.2022	18.8322	19.3735	19.2699	24.0687	23.0734	23.3266	23.1306
2203	Protein regulator of cytokinesis 1 OS=Rattus norvegicus OX=10116 GN=Prc1 PE=4 SV=1	Prc1	D3ZES9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2204	Protein RER1 OS=Rattus norvegicus OX=10116 GN=Rer1 PE=1 SV=1	Rer1	Q498C8	16.6953	NaN	17.2676	NaN	19.5083	19.9414	19.4802	19.5319
2205	Protein RUFY3 OS=Rattus norvegicus OX=10116 GN=Rufy3 PE=1 SV=1	Rufy3	A0A0G2K6A9	NaN	NaN	NaN	NaN	18.0935	13.9573	NaN	14.491
2206	Protein S (Alpha), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Pros1 PE=1 SV=1	Pros1	M0R5R0	22.4627	21.7457	22.1313	22.4219	21.0286	20.5296	20.4386	20.5475
2207	Protein S100-A10 OS=Rattus norvegicus OX=10116 GN=S100a10 PE=1 SV=2	S100a10	P05943	18.1358	18.9836	18.7108	18.3685	21.6032	21.4273	21.888	21.7689
2208	Protein S100-A11 OS=Rattus norvegicus OX=10116 GN=S100a11 PE=3 SV=1	S100a11	Q6B345	18.0554	18.8323	18.4977	18.8412	21.9998	22.0748	22.3335	22.0268
2209	Protein S100-A4 OS=Rattus norvegicus OX=10116 GN=S100a4 PE=2 SV=1	S100a4	P05942	15.112	14.9119	15.8121	16.5849	20.5714	21.3676	21.2542	21.4894
2210	Protein S100-A8 OS=Rattus norvegicus OX=10116 GN=S100a8 PE=1 SV=3	S100a8	P50115	16.538	17.0602	16.4182	NaN	NaN	NaN	NaN	NaN
2211	Protein SEC13 homolog OS=Rattus norvegicus OX=10116 GN=Sec13 PE=1 SV=1	Sec13	Q5XFW8	18.0102	17.2109	17.509	16.7201	23.4723	23.412	23.3764	23.2419
2212	Protein SGT1 homolog OS=Rattus norvegicus OX=10116 GN=Sugt1 PE=2 SV=1	Sugt1	B0BN85	17.663	17.2028	17.575	18.0708	23.4256	22.2908	22.6765	22.7644
2213	Protein Smaug homolog 1 OS=Rattus norvegicus OX=10116 GN=Samd4a PE=1 SV=1	Samd4a	A0A0G2JUK8	17.6288	NaN	NaN	NaN	16.2202	18.4312	16.2882	NaN
2214	Protein TANC1 OS=Rattus norvegicus OX=10116 GN=Tanc1 PE=1 SV=3	Tanc1	G3V917	17.2816	16.821	17.4664	17.6547	19.8802	19.7545	19.9973	19.5847
2215	Protein transport protein sec16 OS=Rattus norvegicus OX=10116 GN=Sec16a PE=1 SV=1	Sec16a	D3ZN76	NaN	NaN	NaN	NaN	20.8857	21.7444	21.2738	21.0096
2216	Protein transport protein SEC23 OS=Rattus norvegicus OX=10116 GN=Sec23a PE=1 SV=1	Sec23a	A0A0G2JZM2	18.8634	19.8757	19.2643	18.2075	22.5302	22.1166	22.0836	22.2246
2217	Protein transport protein SEC23 OS=Rattus norvegicus OX=10116 GN=Sec23b PE=1 SV=2	Sec23b	D3ZCT7	NaN	NaN	NaN	15.2759	18.9936	18.0286	18.6716	18.9424
2218	Protein transport protein Sec31A OS=Rattus norvegicus OX=10116 GN=Sec31a PE=1 SV=1	Sec31a	G3V699	18.8645	19.0874	18.5582	19.0624	24.4807	24.3526	24.1942	24.0414
2219	Protein transport protein Sec61 subunit beta OS=Rattus norvegicus OX=10116 GN=Sec61b PE=1 SV=1	Sec61b	B2RZD1	NaN	NaN	NaN	NaN	20.0102	21.1043	19.4106	20.2624
2220	Protein tyrosine kinase 7 OS=Rattus norvegicus OX=10116 GN=Ptk7 PE=3 SV=3	Ptk7	D3ZHG3	NaN	NaN	16.0204	NaN	18.8565	19.6639	18.9265	19.4761
2221	Protein tyrosine kinase 9-like (A6-related protein) (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Twf2 P	Twf2	B0BMY7	16.0755	17.9744	17.1663	16.6578	20.6488	18.9826	19.9612	19.8358
2222	Protein VAC14 homolog OS=Rattus norvegicus OX=10116 GN=Vac14 PE=1 SV=1	Vac14	Q80W92	NaN	NaN	NaN	NaN	18.4072	17.4962	NaN	NaN
2223	Protein YIF1B OS=Rattus norvegicus OX=10116 GN=Yif1b PE=1 SV=2	Yif1b	G3V9N6	NaN	NaN	NaN	NaN	18.2339	19.3741	18.6971	18.3267
2224	Protein YIPF4 OS=Rattus norvegicus OX=10116 GN=Yipf4 PE=2 SV=1	Yipf4	Q5M7T4	NaN	NaN	NaN	NaN	16.2044	16.6694	16.2093	NaN

2225	Protein YIPF6 OS=Rattus norvegicus OX=10116 GN=Yipf6 PE=1 SV=1	Yipf6	Q4QQU5	NaN	NaN	NaN	NaN	NaN	15.9484	15.7836	NaN
2226	Protein Z, vitamin K-dependent plasma glycoprotein OS=Rattus norvegicus OX=10116 GN=Proz PE=3 SV=4	Proz	G3V8K8	21.343	21.2649	20.7007	20.5682	19.4493	17.0957	18.6797	19.5658
2227	Protein Z-dependent protease inhibitor OS=Rattus norvegicus OX=10116 GN=Serpina10 PE=2 SV=2	Serpina10	Q62975	21.5392	21.1856	20.7815	20.8279	20.0355	19.264	19.9334	19.865
2228	Protein/nucleic acid deglycase DJ-1 OS=Rattus norvegicus OX=10116 GN=Park7 PE=1 SV=1	Park7	O88767	19.203	19.6117	19.3549	19.093	21.4552	21.6992	21.6464	21.415
2229	Protein-glutamate O-methyltransferase OS=Rattus norvegicus OX=10116 GN=Armt1 PE=1 SV=1	Armt1	Q6AYT5	16.5344	16.4629	NaN	NaN	21.9592	21.8814	22.3087	22.3275
2230	Protein-glutamine gamma-glutamyltransferase E OS=Rattus norvegicus OX=10116 GN=Tgm3 PE=3 SV=1	Tgm3	D4A5U3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2231	Protein-glutamine gamma-glutamyltransferase K OS=Rattus norvegicus OX=10116 GN=Tgm1 PE=1 SV=1	Tgm1	P23606	18.8107	21.0414	17.4426	18.836	18.3196	19.4829	18.6526	18.7048
2232	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Rattus norvegicus OX=10116 GN=Pcmt1 PE=1 SV=2	Pcmt1	P22062	20.6972	21.0083	21.4871	21.9587	22.1471	21.106	21.7963	21.6764
2233	Proteolipid protein 2 OS=Rattus norvegicus OX=10116 GN=Plp2 PE=2 SV=1	Plp2	Q6P742	17.0433	17.32	17.2984	17.304	21.1935	20.9311	20.6462	20.7501
2234	Prothrombin OS=Rattus norvegicus OX=10116 GN=F2 PE=1 SV=1	F2	G3V843	25.2306	25.1069	25.9332	25.5817	23.5319	22.652	22.9518	23.299
2235	Prothymosin alpha OS=Rattus norvegicus OX=10116 GN=Ptma PE=1 SV=2	Ptma	P06302	15.6041	NaN	16.11	NaN	18.1725	19.5087	18.701	18.9535
2236	Protocadherin 12 OS=Rattus norvegicus OX=10116 GN=Pcdh12 PE=1 SV=2	Pcdh12	F1MA46	20.2693	18.8391	18.6913	18.6158	19.5559	18.5286	18.5217	18.7702
2237	Protocadherin 7 OS=Rattus norvegicus OX=10116 GN=Pcdh7 PE=1 SV=1	Pcdh7	Q68HB8	NaN	NaN	NaN	NaN	NaN	15.2441	16.8358	NaN
2238	PRP31 pre-mRNA processing factor 31 homolog (Yeast) (Predicted) OS=Rattus norvegicus OX=10116 GN=Prpf31 PE=1 SV=	Prpf31	D3ZI68	NaN	15.6062	NaN	NaN	17.371	17.4898	19.4533	18.1204
2239	PTPRF-interacting protein alpha 1 OS=Rattus norvegicus OX=10116 GN=Ppfia1 PE=1 SV=1	Ppfia1	A0A0G2K3L9	16.9105	18.7688	15.9462	18.3676	17.236	18.0067	17.2995	17.1895
2240	Pulmonary surfactant-associated protein B OS=Rattus norvegicus OX=10116 GN=Sftpb PE=2 SV=1	Sftpb	P22355	19.3258	18.4574	18.3865	19.4655	NaN	16.5964	16.3085	15.5412
2241	Pulmonary surfactant-associated protein D OS=Rattus norvegicus OX=10116 GN=Sftpd PE=1 SV=1	Sftpd	A0A0G2JUF5	18.3687	18.5723	17.5291	16.8158	15.6967	NaN	NaN	NaN
2242	Pumilio RNA-binding family member 1 OS=Rattus norvegicus OX=10116 GN=Pum1 PE=1 SV=2	Pum1	D3Z8L5	NaN	NaN	NaN	NaN	18.5471	19.0411	18.7898	18.2522
2243	Purine nucleoside phosphorylase OS=Rattus norvegicus OX=10116 GN=Pnp PE=1 SV=1	Pnp	P85973	NaN	17.474	17.3807	16.896	16.3413	16.1271	16.4833	15.9573
2244	Putatative 28 kDa protein, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Pno1 PE=1 SV=1	Pno1	R9PXS8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2245	PYM homolog 1, exon junction complex-associated factor OS=Rattus norvegicus OX=10116 GN=Pym1 PE=1 SV=1	Pym1	D3ZGY1	NaN	NaN	NaN	NaN	NaN	18.959	17.4064	17.8354
2246	Pyridoxal-dependent decarboxylase domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Pdxdc1 PE=1 SV=1	Pdxdc1	G3V6B0	17.2456	17.563	17.0113	17.323	20.9107	20.8925	20.8594	20.6505
2247	Pyrophosphatase (inorganic) 1 OS=Rattus norvegicus OX=10116 GN=Ppa1 PE=1 SV=1	Ppa1	F7EPH4	19.4754	18.8095	19.0292	19.5944	20.9874	20.804	21.4757	20.9514
2248	Pyrroline-5-carboxylate reductase 3 OS=Rattus norvegicus OX=10116 GN=Pycr3 PE=2 SV=1	Pycr3	Q5PQJ6	17.8945	18.6059	18.4719	18.8531	24.7881	24.1328	24.3364	24.1332
2249	Pyruvate dehydrogenase E1 component subunit alpha OS=Rattus norvegicus OX=10116 GN=Pdha1 PE=1 SV=1	Pdha1	A0A0G2JW90	18.1621	18.3711	18.2057	18.377	18.6986	21.0878	20.7708	20.8166
2250	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pdhb PE=1 SV=1	Pdhb	A0A0G2KAM3	18.2987	18.1326	18.4815	19.0321	19.5568	21.1992	20.9821	20.6757
2251	Pyruvate kinase OS=Rattus norvegicus OX=10116 GN=Pkm PE=1 SV=1	Pkm	A0A0G2JVG3	17.8739	18.1425	18.5875	18.728	20.6053	19.1302	19.5731	19.7182
2252	Pyruvate kinase PKLR OS=Rattus norvegicus OX=10116 GN=Pklr PE=1 SV=2	Pklr	P12928	20.7957	19.3432	20.0982	19.9943	17.259	16.9914	16.7378	16.889
2253	Pyruvate kinase PKM OS=Rattus norvegicus OX=10116 GN=Pkm PE=1 SV=3	Pkm	P11980	22.5241	22.5492	22.5472	22.6965	25.2502	24.5065	24.9767	24.8964
2254	R3H domain-containing 1 OS=Rattus norvegicus OX=10116 GN=R3hdm1 PE=1 SV=1	R3hdm1	F1LNT3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2255	R3H domain-containing 2 OS=Rattus norvegicus OX=10116 GN=R3hdm2 PE=1 SV=1	R3hdm2	A0A0G2K4E8	NaN	NaN	NaN	NaN	17.8083	18.0542	18.1264	17.7426
2256	Rab GDP dissociation inhibitor alpha OS=Rattus norvegicus OX=10116 GN=Gdi1 PE=1 SV=1	Gdi1	P50398	NaN	16.567	16.9598	NaN	17.5271	18.5965	18.0507	18.0707
2257	Rab GDP dissociation inhibitor beta OS=Rattus norvegicus OX=10116 GN=Gdi2 PE=1 SV=2	Gdi2	P50399	19.3668	20.4569	19.8862	19.3515	21.8878	21.8202	21.9114	21.8627
2258	RAB GTPase-activating protein 1-like OS=Rattus norvegicus OX=10116 GN=Rabgap1l PE=1 SV=1	Rabgap1l	D3ZKH6	NaN	NaN	NaN	14.8871	17.7729	17.216	18.2665	17.6975
2259	Rab GTPase-binding effector protein 1 OS=Rattus norvegicus OX=10116 GN=Rabep1 PE=1 SV=1	Rabep1	G3V9J7	15.2177	NaN	NaN	NaN	NaN	18.4123	18.4982	NaN
2260	Rab GTPase-binding effector protein 2 OS=Rattus norvegicus OX=10116 GN=Rabep2 PE=1 SV=1	Rabep2	Q5EBC7	20.952	20.3975	21.0862	20.6451	18.5907	18.7842	17.5799	17.2828
2261	RAB, member RAS oncogene family-like 6 OS=Rattus norvegicus OX=10116 GN=Rabl6 PE=1 SV=1	Rabl6	D3ZKQ4	14.6201	13.8783	NaN	NaN	20.2485	19.4016	19.4696	18.859
2262	RAB10, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab10 PE=1 SV=1	Rab10	Q5RKJ9	19.0743	19.493	20.0681	19.1544	23.8498	23.4497	23.636	23.4335
2263	RAB11 family-interacting protein 5 OS=Rattus norvegicus OX=10116 GN=Rab11fip5 PE=1 SV=1	Rab11fip5	A0A0G2K1W1	NaN	NaN	NaN	NaN	19.32	19.0758	18.6592	16.328
2264	RAB14, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab14 PE=1 SV=1	Rab14	B0BMW0	18.7354	18.8692	17.9442	18.9734	23.4478	22.4501	22.6268	22.3664
2265	RAB2, member RAS oncogene family-like OS=Rattus norvegicus OX=10116 GN=Rgl2 PE=1 SV=1	Rgl2	Q6MGC5	NaN	NaN	NaN	NaN	19.1875	19.2874	19.3881	17.894
2266	RAB22A, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab22a PE=1 SV=1	Rab22a	B0BN19	16.1614	16.0711	16.0284	19.1593	21.1859	20.7047	21.0945	20.6052
2267	RAB23, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab23 PE=4 SV=1	Rab23	D3ZRM5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2268	RAB2B, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab2b PE=1 SV=1	Rab2b	Q3B7V5	NaN	NaN	NaN	NaN	16.8574	18.7742	19.2188	19.19
2269	RAB3A interacting protein (Rabin3) OS=Rattus norvegicus OX=10116 GN=Rab3ip PE=1 SV=1	Rab3ip	A1L127	16.0655	15.5845	16.5086	NaN	18.5431	19.6482	19.4114	19.6401
2270	RAB5B, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab5b PE=1 SV=1	Rab5b	A1L1J8	18.4427	19.0675	19.2695	19.5648	24.0055	23.1467	23.4766	23.4438
2271	RAB5C, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab5c PE=1 SV=1	Rab5c	B0BNK1	NaN	NaN	16.1782	NaN	22.4377	21.7603	22.0537	21.9858
2272	Rac family small GTPase 2 OS=Rattus norvegicus OX=10116 GN=Rac2 PE=1 SV=1	Rac2	Q5U1Y2	17.8764	16.8768	17.8	17.3486	20.146	20.1385	19.9969	19.8557
2273	RAC-alpha serine/threonine-protein kinase OS=Rattus norvegicus OX=10116 GN=Akt1 PE=1 SV=1	Akt1	P47196	16.7353	16.805	14.3368	15.2034	21.3056	21.2848	21.1714	21.148
2274	RAD23 homolog A, nucleotide excision repair protein OS=Rattus norvegicus OX=10116 GN=Rad23a PE=1 SV=1	Rad23a	A0A0G2K7M2	15.8921	NaN	NaN	14.7645	20.0859	18.8217	19.4616	19.3299
2275	Radixin OS=Rattus norvegicus OX=10116 GN=Rdx PE=1 SV=2	Rdx	E9PT65	20.6494	22.1292	19.9005	20.8724	21.6734	21.8771	21.4809	21.7311
2276	RAF proto-oncogene serine/threonine-protein kinase OS=Rattus norvegicus OX=10116 GN=Raf1 PE=1 SV=1	Raf1	P11345	NaN	NaN	NaN	NaN	19.9	20.0816	20.1723	19.3128
2277	Ragulator complex protein LAMTOR1 OS=Rattus norvegicus OX=10116 GN=Lamtor1 PE=1 SV=1	Lamtor1	Q6P791	20.4436	20.2145	19.9456	19.8203	18.7348	19.3315	18.5727	18.708

2278	Ragulator complex protein LAMTOR3 OS=Rattus norvegicus OX=10116 GN=Lamtor3 PE=2 SV=1	Lamtor3	Q5U204	NaN	NaN	NaN	NaN	17.0851	16.337	17.2259	17.1343
2279	Ral GTPase-activating protein subunit beta OS=Rattus norvegicus OX=10116 GN=Ralgapb PE=1 SV=2	Ralgapb	R9PXV2	NaN	15.0216	14.447	NaN	17.7848	16.9648	17.592	17.2467
2280	RALBP1-associated Eps domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Reps1 PE=1 SV=1	Reps1	A0A0G2JZY3	NaN	14.9955	NaN	NaN	NaN	16.8938	NaN	16.0093
2281	RAN GTPase-activating protein 1 OS=Rattus norvegicus OX=10116 GN=Rangap1 PE=1 SV=2	Rangap1	F1MAA5	16.8853	15.1804	16.853	17.5399	21.5164	21.1407	21.701	21.7972
2282	RAN-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ranbp1 PE=1 SV=1	Ranbp1	D4A2G9	16.4766	18.1879	17.0012	17.606	21.5917	20.8739	21.5192	21.4094
2283	RAN-binding protein 10 OS=Rattus norvegicus OX=10116 GN=Ranbp10 PE=1 SV=2	Ranbp10	D3Z7Z5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2284	RAN-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Ranbp3 PE=1 SV=2	Ranbp3	M0R5Q3	NaN	15.9431	16.2849	16.5083	21.6784	21.5467	21.5748	20.9252
2285	Rap guanine nucleotide exchange factor 1 OS=Rattus norvegicus OX=10116 GN=Rapgef1 PE=1 SV=3	Rapgef1	F1M8L9	14.4185	14.2146	15.2005	NaN	18.1982	18.3752	18.3247	18.266
2286	RAP1 GTPase-activating protein 2 OS=Rattus norvegicus OX=10116 GN=Rap1gap2 PE=1 SV=1	Rap1gap2	A0A0G2K0S7	14.295	14.4341	NaN	NaN	18.1966	16.8017	17.7415	17.54
2287	RAP1, GTP-GDP dissociation stimulator 1 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Rap1gds1 PE=	Rap1gds1	A0A0G2K1D2	18.1281	19.3053	17.8483	19.0264	19.0122	20.3017	21.0169	20.4834
2288	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 OS=Rattus norvegicus OX=10116 GN=Raph1 PE=1 SV=2	Raph1	D4ADX8	20.9531	21.7307	20.6192	19.5507	21.6414	22.527	22.1585	22.2826
2289	Ras GTPase-activating protein 1 OS=Rattus norvegicus OX=10116 GN=Rasa1 PE=3 SV=1	Rasa1	P50904	16.9352	NaN	16.8163	NaN	16.1635	16.5808	16.8562	16.442
2290	Ras homolog family member C OS=Rattus norvegicus OX=10116 GN=Rhoc PE=1 SV=1	Rhoc	B2RYP0	14.8562	NaN	NaN	NaN	17.6846	18.5029	18.8604	18.5511
2291	Ras homolog family member G OS=Rattus norvegicus OX=10116 GN=Rhog PE=1 SV=1	Rhog	Q32PX6	18.1378	18.1569	17.6134	17.2989	19.8252	20.305	19.798	20.1386
2292	Ras interacting protein 1 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Rasip1 PE=1 SV=1	Rasip1	B5DF05	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2293	RAS protein activator-like 2 OS=Rattus norvegicus OX=10116 GN=Rasal2 PE=1 SV=1	Rasal2	A0A0G2JTA7	18.0978	17.867	18.8526	16.4065	20.9992	22.0456	21.5036	21.2456
2294	RAS related protein 2a OS=Rattus norvegicus OX=10116 GN=Rap2a PE=4 SV=1	Rap2a	A0A0G2JTW1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2295	Ras suppressor protein 1 OS=Rattus norvegicus OX=10116 GN=Rsu1 PE=1 SV=3	Rsu1	D4A8F2	18.9108	18.2513	18.1233	17.6903	22.251	21.6308	21.6422	21.6694
2296	RAS-related 2 OS=Rattus norvegicus OX=10116 GN=Rras2 PE=1 SV=1	Rras2	Q5BJU0	17.6784	16.8824	17.7977	18.1517	21.1671	21.268	21.11	20.6343
2297	Ras-related C3 botulinum toxin substrate 1 OS=Rattus norvegicus OX=10116 GN=Rac1 PE=1 SV=1	Rac1	Q6RUV5	21.8796	21.8864	21.8488	21.4155	23.4758	22.7754	22.702	22.7497
2298	Ras-related GTP-binding protein B OS=Rattus norvegicus OX=10116 GN=RragB PE=1 SV=1	RragB	Q63487	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2299	Ras-related protein Rab-11A OS=Rattus norvegicus OX=10116 GN=Rab11a PE=1 SV=3	Rab11a	P62494	NaN	NaN	15.5626	NaN	17.2092	16.6682	17.1106	17.036
2300	Ras-related protein Rab-11B OS=Rattus norvegicus OX=10116 GN=Rab11b PE=1 SV=4	Rab11b	O35509	20.8861	20.8074	20.0191	19.7316	25.2231	24.8428	24.8788	24.7303
2301	Ras-related protein Rab-12 OS=Rattus norvegicus OX=10116 GN=Rab12 PE=1 SV=2	Rab12	P35284	17.0632	17.3339	17.41	16.618	21.3313	20.568	20.4211	20.6878
2302	Ras-related protein Rab-13 OS=Rattus norvegicus OX=10116 GN=Rab13 PE=1 SV=2	Rab13	P35286	18.6804	14.9739	17.0721	NaN	20.4815	19.3108	19.1414	18.9415
2303	Ras-related protein Rab-18 OS=Rattus norvegicus OX=10116 GN=Rab18 PE=2 SV=1	Rab18	Q5EB77	18.1256	17.4472	16.7018	17.9754	21.2584	21.4266	20.7138	20.1517
2304	Ras-related protein Rab-1A OS=Rattus norvegicus OX=10116 GN=Rab1A PE=1 SV=3	Rab1a	Q6NYB7	21.8653	22.0795	21.4411	22.0776	25.6287	25.1486	25.4422	25.4655
2305	Ras-related protein Rab-21 OS=Rattus norvegicus OX=10116 GN=Rab21 PE=2 SV=1	Rab21	Q6AXT5	NaN	14.6394	14.2442	15.9636	21.4994	21.0998	21.4556	19.9516
2306	Ras-related protein Rab-27B OS=Rattus norvegicus OX=10116 GN=Rab27b PE=2 SV=3	Rab27b	Q99P74	NaN	16.5389	16.6677	16.7397	NaN	NaN	NaN	NaN
2307	Ras-related protein Rab-28 OS=Rattus norvegicus OX=10116 GN=Rab28 PE=2 SV=1	Rab28	P51158	NaN	NaN	NaN	NaN	19.8786	18.3137	19.0393	19.0031
2308	Ras-related protein Rab-2A OS=Rattus norvegicus OX=10116 GN=Rab2a PE=2 SV=1	Rab2a	P05712	18.952	18.2942	17.8483	19.585	22.5715	21.9304	22.3689	22.4726
2309	Ras-related protein Rab-34 OS=Rattus norvegicus OX=10116 GN=Rab34 PE=2 SV=1	Rab34	Q5U1Y1	NaN	NaN	NaN	NaN	15.6195	NaN	15.3938	15.8439
2310	Ras-related protein Rab-35 OS=Rattus norvegicus OX=10116 GN=Rab35 PE=1 SV=1	Rab35	Q5U316	18.7486	18.8704	19.4095	19.3336	20.7153	20.3013	20.8917	20.4746
2311	Ras-related protein Rab-3A OS=Rattus norvegicus OX=10116 GN=Rab3a PE=1 SV=1	Rab3a	P63012	19.6116	17.6967	NaN	16.0427	21.255	20.6681	21.1557	21.0437
2312	Ras-related protein Rab-4A OS=Rattus norvegicus OX=10116 GN=Rab4a PE=1 SV=3	Rab4a	P05714	17.9029	18.1319	18.2233	17.4312	20.9989	21.2093	20.6662	20.7158
2313	Ras-related protein Rab-5A OS=Rattus norvegicus OX=10116 GN=Rab5a PE=2 SV=1	Rab5a	M0RC99	15.5741	16.2144	16.726	NaN	21.4923	20.5264	21.0204	21.0188
2314	Ras-related protein Rab-6A OS=Rattus norvegicus OX=10116 GN=Rab6a PE=1 SV=2	Rab6a	Q9WVB1	19.5381	18.5753	18.8397	18.539	22.9235	23.0443	22.9993	23.0728
2315	Ras-related protein Rab-7a OS=Rattus norvegicus OX=10116 GN=Rab7a PE=1 SV=2	Rab7a	P09527	18.8718	19.7428	19.2101	19.0687	24.0061	23.6588	23.6404	23.4814
2316	Ras-related protein Rab-8A OS=Rattus norvegicus OX=10116 GN=Rab8a PE=1 SV=2	Rab8a	P35280	18.8014	17.9426	18.6044	17.5895	21.4171	20.9	20.8012	21.0026
2317	Ras-related protein Rab-8B OS=Rattus norvegicus OX=10116 GN=Rab8b PE=1 SV=1	Rab8b	P70550	16.7746	17.8281	18.2841	17.1892	18.5385	19.2471	18.0039	18.4516
2318	Ras-related protein Rab-9A OS=Rattus norvegicus OX=10116 GN=Rab9a PE=1 SV=2	Rab9a	Q99P75	NaN	17.9424	NaN	18.3571	17.6258	17.1783	17.3854	17.0105
2319	Ras-related protein Ral-A OS=Rattus norvegicus OX=10116 GN=Rala PE=1 SV=1	Rala	P63322	18.2724	18.7116	18.7771	18.7767	21.4323	21.9682	21.5201	21.0148
2320	Ras-related protein Ral-B OS=Rattus norvegicus OX=10116 GN=Ralb PE=2 SV=1	Ralb	P36860	18.748	18.4401	18.4949	18.4774	19.3897	20.7011	20.2495	20.5292
2321	Ras-related protein Rap-1A OS=Rattus norvegicus OX=10116 GN=Rap1a PE=1 SV=1	Rap1a	P62836	16.5461	17.3065	17.21	18.9382	20.2367	19.8666	19.1948	20.2781
2322	Ras-related protein Rap-1b OS=Rattus norvegicus OX=10116 GN=Rap1b PE=1 SV=2	Rap1b	Q62636	21.7648	21.9195	21.981	21.9406	22.8941	23.0829	23.0015	23.1274
2323	Ras-related protein R-Ras OS=Rattus norvegicus OX=10116 GN=Rras PE=1 SV=1	Rras	D3Z8L7	NaN	NaN	14.9934	NaN	18.7971	18.8177	17.7673	18.6679
2324	RBR-type E3 ubiquitin transferase OS=Rattus norvegicus OX=10116 GN=Arih1 PE=1 SV=1	Arih1	D3ZXL1	18.6576	NaN	NaN	NaN	17.1108	16.0657	17.6495	NaN
2325	RBR-type E3 ubiquitin transferase OS=Rattus norvegicus OX=10116 GN=Rnf14 PE=1 SV=1	Rnf14	Q3ZAU6	NaN	15.3941	15.2217	NaN	19.5154	19.272	19.6134	19.392
2326	RCG20041, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tceal5 PE=4 SV=1	Tceal5	M0RDJ7	NaN	NaN	NaN	NaN	18.9289	18.7621	18.5942	17.9526
2327	RCG20603 OS=Rattus norvegicus OX=10116 GN=Serpina3c PE=3 SV=1	Serpina3c	A0A0G2JSK1	24.5278	24.6972	25.2626	25.3004	21.9572	20.7859	21.2668	21.6792
2328	RCG20801, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Vipas39 PE=1 SV=1	Vipas39	A0A0G2K5Y1	17.85	17.0354	17.175	17.4151	15.1175	15.5431	14.6862	13.9309
2329	RCG23282, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Sec61g PE=1 SV=1	Sec61g	B5DEL7	NaN	NaN	NaN	NaN	NaN	18.2491	NaN	NaN
2330	RCG25591, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Stt3b PE=1 SV=1	Stt3b	B2RYD7	NaN	13.6725	NaN	NaN	18.1371	17.3829	16.6901	NaN

2331	RCG25684, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tmod3 PE=1 SV=1	Tmod3	Q6AXW2	NaN	NaN	NaN	NaN	17.7017	17.9097	17.2361	17.3207
2332	RCG27500, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Snrpb2 PE=1 SV=1	Snrpb2	B5DEQ4	NaN	NaN	NaN	NaN	19.7646	18.1421	18.8013	18.7844
2333	RCG30099, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tex52 PE=4 SV=1	Tex52	D4ABA3	19.4892	19.0752	19.335	19.8971	17.9416	16.836	17.7146	17.3695
2334	RCG31049, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Smim1 PE=1 SV=2	Smim1	F1M654	17.1508	NaN	16.4171	NaN	17.6834	18.4077	17.6012	18.0576
2335	RCG31390 OS=Rattus norvegicus OX=10116 GN=Sfn PE=3 SV=1	Sfn	G3V9A3	NaN	17.5008	NaN	14.0026	NaN	NaN	NaN	NaN
2336	RCG31562, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Tardbp PE=1 SV=1	Tardbp	I6L9G6	17.8321	16.3814	16.6679	18.0667	21.767	20.7442	20.8672	21.1262
2337	RCG32249 OS=Rattus norvegicus OX=10116 GN=Ube2c PE=3 SV=1	Ube2c	D3ZUW6	NaN	14.368	NaN	NaN	19.6977	18.762	19.7792	19.3371
2338	RCG33491, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Zfp207 PE=1 SV=1	Zfp207	Q498C9	NaN	NaN	NaN	NaN	NaN	16.8403	18.2336	16.5146
2339	RCG35421, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Tnip1 PE=4 SV=1	Tnip1	D3ZHV1	NaN	NaN	NaN	NaN	17.9989	17.2371	17.5261	17.3036
2340	RCG35999, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Smtn PE=1 SV=1	Smtn	D4ABA5	15.3188	NaN	15.7138	NaN	19.5911	19.027	19.2108	19.1889
2341	RCG37250, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Romo1 PE=1 SV=1	Romo1	D4A742	NaN	NaN	NaN	NaN	17.0129	17.279	17.5033	17.2577
2342	RCG37481, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Rbm12 PE=1 SV=1	Rbm12	Q6XLI7	NaN	14.9426	NaN	17.9869	19.58	18.2336	18.0597	16.8267
2343	RCG39455, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tsku PE=4 SV=1	Tsku	G3V8X6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2344	RCG39700, isoform CRA_d OS=Rattus norvegicus OX=10116 GN=Rab6a PE=1 SV=1	Rab6a	A0A0H2UHP9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2345	RCG40648, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Sec23ip PE=1 SV=1	Sec23ip	G3V8Q8	19.9739	19.3786	18.6366	20.1676	22.6854	22.2005	22.1236	22.1353
2346	RCG41580, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Rpl22l1 PE=2 SV=1	Rpl22l1	B2RZD5	15.7289	15.9427	NaN	NaN	20.4066	20.4366	20.1626	20.1697
2347	RCG43947 OS=Rattus norvegicus OX=10116 GN=Txndc5 PE=1 SV=1	Txndc5	D3ZZC1	16.0527	16.0815	16.6087	17.2502	19.1753	20.393	19.6829	20.854
2348	RCG45489, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Stom PE=1 SV=1	Stom	Q5XI04	19.0993	19.0818	18.4234	19.0436	17.8928	17.7235	16.6865	17.8544
2349	RCG48149, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=LOC100363782 PE=1 SV=1	Rab1b	G3V6H0	18.5813	18.2595	19.2207	17.9928	23.0833	22.7021	22.6416	22.7252
2350	RCG48672 OS=Rattus norvegicus OX=10116 GN=Snrpf PE=1 SV=1	Snrpf	D4AAT4	NaN	NaN	NaN	NaN	18.6853	18.0388	18.4729	NaN
2351	RCG49713 OS=Rattus norvegicus OX=10116 GN=Tceanc PE=4 SV=1	Tceanc	D4AEK4	19.8085	NaN	NaN	NaN	18.0529	17.0805	17.7702	17.2246
2352	RCG49849 OS=Rattus norvegicus OX=10116 GN=Vasn PE=1 SV=1	Vasn	D3ZAE6	17.7375	15.4142	15.5882	NaN	NaN	NaN	NaN	NaN
2353	RCG52686 OS=Rattus norvegicus OX=10116 GN=Upk1b PE=3 SV=1	Upk1b	A0A0H2UHB6	NaN	NaN	NaN	NaN	18.9886	18.4979	18.3175	16.3732
2354	RCG52996, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tfg PE=1 SV=1	Tfg	Q6AYR1	18.5299	18.1534	18.5858	17.4554	22.0993	21.0394	21.2823	22.1949
2355	RCG53953, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=LOC103690005 PE=1 SV=1	Tbcb	Q1RP74	17.2092	17.5024	18.1661	17.4658	21.866	21.1822	21.7099	21.6559
2356	RCG55135, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Tln1 PE=1 SV=1	Tln1	G3V852	23.8504	23.7877	24.346	23.7249	26.1471	26.3274	26.4518	26.1819
2357	RCG55706 OS=Rattus norvegicus OX=10116 GN=Stam PE=1 SV=1	Stam	B5DF55	15.9088	13.5703	16.0423	15.6161	21.2491	20.4903	20.545	20.508
2358	RCG56113, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Smyd1 PE=4 SV=1	Smyd1	D4A3D2	14.9665	15.0842	16.1493	16.1532	NaN	18.5704	19.1219	18.5373
2359	RCG57812, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Slk PE=1 SV=1	Slk	G3V7I8	20.506	20.0419	20.5598	20.9994	22.4403	22.8342	22.7123	22.5985
2360	RCG58353, isoform CRA_e OS=Rattus norvegicus OX=10116 GN=Trappc4 PE=1 SV=1	Trappc4	A0A0G2JSL2	13.7281	NaN	NaN	NaN	16.3212	16.185	NaN	NaN
2361	RCG59826 OS=Rattus norvegicus OX=10116 GN=Tab1 PE=1 SV=1	Tab1	A0A0U1RRU5	NaN	14.276	NaN	15.6863	18.5725	17.5808	17.9559	18.1191
2362	RCG61099, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Srsf3 PE=1 SV=1	Srsf3	Q0ZFS8	NaN	NaN	NaN	NaN	18.156	19.7625	18.845	18.8808
2363	RCG61894, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Strn PE=1 SV=1	Strn	G3V6L8	13.8063	15.2651	15.2215	NaN	20.229	20.3871	20.3997	20.1471
2364	RCG62582, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Ubap2l PE=1 SV=2	Ubap2l	E9PTR4	NaN	NaN	NaN	16.2446	20.9919	20.4348	20.4846	20.4808
2365	RCG63041 OS=Rattus norvegicus OX=10116 GN=LOC684509 PE=4 SV=1	LOC684509	M0RB63	NaN	NaN	NaN	NaN	16.6378	18.4776	18.0781	17.7674
2366	RCSD domain containing 1 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Rcsd1 PE=1 SV=1	Rcsd1	A0A0G2K7I4	16.8179	17.3684	17.1258	17.553	23.0102	21.6487	21.9855	21.909
2367	Receptor expression-enhancing protein 5 OS=Rattus norvegicus OX=10116 GN=Reep5 PE=1 SV=1	Reep5	B2RZ37	19.6161	20.0849	19.6614	17.3729	21.7412	22.0574	21.6051	21.9148
2368	Receptor of activated protein C kinase 1 OS=Rattus norvegicus OX=10116 GN=Rack1 PE=1 SV=3	Rack1	P63245	18.5895	18.9544	18.222	19.438	19.8185	23.7237	23.5502	23.4229
2369	Receptor protein-tyrosine kinase OS=Rattus norvegicus OX=10116 GN=Egfr PE=1 SV=1	Egfr	G3V6K6	18.274	18.7034	18.7441	17.9519	18.2866	18.5334	18.0016	18.5981
2370	Receptor-type tyrosine-protein phosphatase alpha OS=Rattus norvegicus OX=10116 GN=Ptpra PE=1 SV=1	Ptpra	A0A0G2JVR0	NaN	14.1267	14.3337	NaN	16.4609	15.806	15.6557	15.8101
2371	Receptor-type tyrosine-protein phosphatase C OS=Rattus norvegicus OX=10116 GN=Ptprc PE=1 SV=2	Ptprc	P04157	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2372	Reelin OS=Rattus norvegicus OX=10116 GN=Reln PE=4 SV=3	Reln	F1LZI7	19.3853	19.3854	19.1076	19.1715	18.7569	17.963	18.7459	18.3207
2373	Regulation of nuclear pre-mRNA domain-containing 1A OS=Rattus norvegicus OX=10116 GN=Rprd1a PE=1 SV=1	Rprd1a	D4AAU4	NaN	NaN	NaN	NaN	14.1608	13.8552	14.7626	13.8531
2374	Regulation of nuclear pre-mRNA domain-containing 1B OS=Rattus norvegicus OX=10116 GN=Rprd1b PE=1 SV=1	Rprd1b	B5DEK0	17.0317	15.6769	NaN	NaN	17.9733	16.394	16.7184	16.9998
2375	Regulator of G-protein signalling 3, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Rgs3 PE=1 SV=3	Rgs3	G3V9Q2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2376	Regulatory-associated protein of MTOR, complex 1 OS=Rattus norvegicus OX=10116 GN=Rptor PE=1 SV=2	Rptor	D3ZDU2	16.3893	16.4095	17.4858	16.3839	18.9857	19.2901	19.7684	19.7655
2377	Renin receptor OS=Rattus norvegicus OX=10116 GN=Atp6ap2 PE=2 SV=1	Atp6ap2	Q6AXS4	19.1479	15.7682	19.2502	18.7943	NaN	17.6325	17.1568	NaN
2378	Replication factor C (Activator 1) 3 OS=Rattus norvegicus OX=10116 GN=Rfc3 PE=1 SV=1	Rfc3	Q5M830	NaN	NaN	NaN	NaN	17.1723	NaN	17.277	NaN
2379	Replication factor C (Activator 1) 5 OS=Rattus norvegicus OX=10116 GN=Rfc5 PE=1 SV=1	Rfc5	B5DF29	NaN	NaN	NaN	NaN	17.2979	17.0722	16.7627	16.2887
2380	Replication factor C subunit 2 OS=Rattus norvegicus OX=10116 GN=Rfc2 PE=2 SV=1	Rfc2	Q641W4	NaN	NaN	NaN	NaN	17.7582	17.0814	17.9019	16.9993
2381	Replication protein A 32 kDa subunit OS=Rattus norvegicus OX=10116 GN=Rpa2 PE=2 SV=2	Rpa2	Q63528	NaN	15.5428	NaN	NaN	20.2094	18.4795	19.2314	19.7688
2382	Replication protein A subunit OS=Rattus norvegicus OX=10116 GN=Rpa1 PE=1 SV=1	Rpa1	A0A0G2KAT3	16.4043	16.3581	16.4765	NaN	21.3146	20.9223	21.168	20.4803
2383	Resistance to inhibitors of cholinesterase 8 homolog A (C. elegans) OS=Rattus norvegicus OX=10116 GN=Ric8a PE=1 SV=1	Ric8a	B1H241	NaN	NaN	NaN	NaN	18.199	17.8555	17.2666	17.9637

2384	Resistin OS=Rattus norvegicus OX=10116 GN=Retn PE=2 SV=1	Retn	Q8K4J7	19.8802	19.2442	18.1855	17.3762	15.6237	15.9473	16.275	15.8047
2385	Resistin-like gamma OS=Rattus norvegicus OX=10116 GN=Retnlg PE=2 SV=1	Retnlg	G3V686	17.0862	15.1526	16.9261	NaN	NaN	NaN	16.4747	NaN
2386	Reticulocalbin 1 OS=Rattus norvegicus OX=10116 GN=Rcn1 PE=1 SV=1	Rcn1	D3ZUB0	19.839	19.8694	20.0155	19.0477	19.1659	19.9072	20.0659	20.4454
2387	Reticulocalbin-3 OS=Rattus norvegicus OX=10116 GN=Rcn3 PE=1 SV=1	Rcn3	A0A0G2K022	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2388	Reticulon OS=Rattus norvegicus OX=10116 GN=Rtn4 PE=1 SV=1	Rtn4	F1LQN3	19.1797	19.9401	19.8684	19.6359	23.2648	24.1367	23.4256	23.5556
2389	Reticulon-1 OS=Rattus norvegicus OX=10116 GN=Rtn1 PE=1 SV=1	Rtn1	Q64548	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2390	Reticulon-3 OS=Rattus norvegicus OX=10116 GN=Rtn3 PE=1 SV=1	Rtn3	Q6RJR6	17.8942	17.8604	17.4432	17.2933	20.0629	20.9798	19.8913	20.0073
2391	Retinal dehydrogenase 1 OS=Rattus norvegicus OX=10116 GN=Aldh1a1 PE=1 SV=3	Aldh1a1	P51647	16.4548	17.8918	15.2638	NaN	16.5517	16.8003	NaN	NaN
2392	Retinal dehydrogenase 2 OS=Rattus norvegicus OX=10116 GN=Aldh1a2 PE=1 SV=2	Aldh1a2	Q63639	15.0055	14.5769	NaN	NaN	16.4176	16.7052	NaN	17.0648
2393	Retinol-binding protein 4 OS=Rattus norvegicus OX=10116 GN=Rbp4 PE=1 SV=1	Rbp4	P04916	22.7249	22.1527	22.9329	22.25	23.535	19.4187	19.6477	17.6904
2394	RGD1563325 protein OS=Rattus norvegicus OX=10116 GN=Tmem263 PE=1 SV=1	Tmem263	B2RZ08	20.6076	20.7269	21.0194	20.6406	23.1219	23.4039	23.5337	23.3709
2395	Rho family-interacting cell polarization regulator 1 OS=Rattus norvegicus OX=10116 GN=Ripor1 PE=1 SV=1	Ripor1	A0A0G2JVR9	16.5394	16.6356	14.499	16.4048	20.7978	20.9784	20.384	19.4578
2396	Rho family-interacting cell polarization regulator 2 OS=Rattus norvegicus OX=10116 GN=Ripor2 PE=1 SV=1	Ripor2	Q7TP54	20.9376	20.4024	20.2757	20.7946	21.4686	20.9882	21.0564	20.7435
2397	Rho GDP dissociation inhibitor beta OS=Rattus norvegicus OX=10116 GN=Arhgdib PE=1 SV=1	Arhgdib	Q5M860	15.7829	16.122	14.5588	15.2891	NaN	NaN	NaN	NaN
2398	Rho GDP-dissociation inhibitor 1 OS=Rattus norvegicus OX=10116 GN=Arhgdia PE=1 SV=1	Arhgdia	Q5XI73	20.3007	20.2444	20.5949	20.4583	23.746	22.9987	23.2639	23.4348
2399	Rho GTPase activating protein 18 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Arhgap18 PE=1 SV=2	Arhgap18	F1LXP8	NaN	15.7786	16.5215	NaN	19.9694	19.8425	20.0727	19.9789
2400	Rho GTPase-activating protein 1 OS=Rattus norvegicus OX=10116 GN=Arhgap1 PE=1 SV=1	Arhgap1	D4A6C5	17.4534	18.3508	16.0722	17.018	25.1031	24.5245	24.9147	24.8532
2401	Rho GTPase-activating protein 17 OS=Rattus norvegicus OX=10116 GN=Arhgap17 PE=1 SV=3	Arhgap17	F1M6X7	NaN	15.3305	NaN	NaN	18.0112	18.1318	18.614	16.7396
2402	Rho GTPase-activating protein 27 OS=Rattus norvegicus OX=10116 GN=Arhgap27 PE=1 SV=1	Arhgap27	F1LQ24	NaN	NaN	NaN	NaN	NaN	NaN	16.8127	16.3869
2403	Rho GTPase-activating protein 35 OS=Rattus norvegicus OX=10116 GN=Arhgap35 PE=1 SV=3	Arhgap35	D4AD82	NaN	NaN	NaN	NaN	17.7956	18.1132	16.7235	17.2218
2404	Rho guanine nucleotide exchange factor (GEF) 17 OS=Rattus norvegicus OX=10116 GN=Arhgef17 PE=1 SV=1	℄WGENE_13098	A0A0G2JXT9	21.291	20.5663	20.7398	18.8318	21.0226	19.7673	20.4494	20.4866
2405	Rho guanine nucleotide exchange factor 1 OS=Rattus norvegicus OX=10116 GN=Arhgef1 PE=2 SV=1	Arhgef1	Q9Z1I6	16.5243	14.0109	14.3252	NaN	20.0543	19.7153	19.5078	18.6263
2406	Rho guanine nucleotide exchange factor 12 OS=Rattus norvegicus OX=10116 GN=Arhgef12 PE=1 SV=1	Arhgef12	A0A0G2K860	18.5033	17.6439	19.0992	18.9883	17.2601	18.005	18.109	16.8406
2407	Rho guanine nucleotide exchange factor 2 OS=Rattus norvegicus OX=10116 GN=Arhgef2 PE=1 SV=1	Arhgef2	A0A0G2K0V4	18.6412	18.0699	19.6579	18.9219	20.7522	20.888	20.7376	20.0922
2408	Rho guanine nucleotide exchange factor 6 OS=Rattus norvegicus OX=10116 GN=Arhgef6 PE=1 SV=3	Arhgef6	D3ZWQ8	14.5282	15.0858	NaN	16.4004	19.3837	20.662	20.5694	20.034
2409	Rho guanine nucleotide exchange factor 7 OS=Rattus norvegicus OX=10116 GN=Arhgef7 PE=1 SV=1	Arhgef7	A0A0G2QC21	22.0109	22.0093	22.0251	21.5097	25.3747	25.3799	25.6966	25.2933
2410	Rho-associated protein kinase OS=Rattus norvegicus OX=10116 GN=Rock1 PE=1 SV=3	Rock1	D4A5S0	16.6781	NaN	15.1838	NaN	18.8636	17.8052	18.9226	18.6672
2411	Rho-associated protein kinase OS=Rattus norvegicus OX=10116 GN=Rock2 PE=1 SV=1	Rock2	A0A0G2K5N6	22.0734	22.8339	22.3591	21.8064	23.2574	23.0514	23.2038	22.9367
2412	Ribonuclease 4 OS=Rattus norvegicus OX=10116 GN=Rnase4 PE=1 SV=1	Rnase4	O55004	NaN	15.9041	16.3616	NaN	15.0769	NaN	15.0248	NaN
2413	Ribonuclease inhibitor OS=Rattus norvegicus OX=10116 GN=Rnh1 PE=1 SV=1	Rnh1	E2RUH2	19.5754	20.0927	20.6215	15.1494	21.8769	23.8528	24.0185	23.8372
2414	Ribonucleoside-diphosphate reductase OS=Rattus norvegicus OX=10116 GN=Rrm1 PE=1 SV=1	Rrm1	Q5U2Q5	18.4092	17.8281	18.1208	18.3876	22.8682	21.9173	22.5522	22.4383
2415	Ribonucleotide reductase M2 polypeptide OS=Rattus norvegicus OX=10116 GN=LOC100359539 PE=1 SV=1	LOC100359539	D4A7M6	NaN	NaN	NaN	NaN	19.1888	18.1498	18.4608	16.8652
2416	Ribose-phosphate pyrophosphokinase I -like OS=Rattus norvegicus OX=10116 GN=LOC314140 PE=1 SV=1	LOC314140	A0A0G2JSV3	17.1604	17.4868	17.9211	17.7869	21.8149	21.6799	22.0458	21.5875
2417	Ribosomal protein L37 OS=Rattus norvegicus OX=10116 PE=3 SV=2	D4A7Z2_RAT	D4A7Z2	16.9763	17.8005	17.875	17.1314	20.7322	21.3134	21.0778	21.0238
2418	Ribosomal protein S19-like2 OS=Rattus norvegicus OX=10116 GN=Rps19l2 PE=4 SV=1	Rps19	A0A0H2UI38	20.1709	20.6778	20.7707	19.9779	23.7145	25.2372	24.9544	24.9083
2419	Ribosomal protein S27-like OS=Rattus norvegicus OX=10116 GN=LOC100362987 PE=3 SV=1	LOC100362987	M0RA26	NaN	NaN	NaN	NaN	22.9593	22.1751	21.8243	21.777
2420	Ribosomal protein S6 kinase beta-1 OS=Rattus norvegicus OX=10116 GN=Rps6kb1 PE=1 SV=1	Rps6kb1	P67999	17.4262	NaN	17.1627	18.0471	17.8402	19.6182	19.6201	19.5493
2421	Ribosomal protein S6 kinase OS=Rattus norvegicus OX=10116 GN=Rps6ka3 PE=1 SV=2	Rps6ka3	D3Z8E0	19.2648	20.2022	17.8443	18.9622	22.0542	21.396	22.0065	21.6329
2422	Ribosomal protein S6 kinase OS=Rattus norvegicus OX=10116 GN=Rps6ka5 PE=1 SV=1	Rps6ka5	A0A0G2K366	20.0665	18.7068	18.9164	20.4531	19.075	18.6618	18.569	18.9492
2423	Ribosomal protein S6 kinase OS=Rattus norvegicus OX=10116 GN=Rps6kb2 PE=1 SV=1	Rps6kb2	D4AE24	NaN	NaN	NaN	NaN	16.7685	16.7876	16.6954	16.2438
2424	Ribosome-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Rrbp1 PE=1 SV=3	Rrbp1	F1M853	19.1836	19.2787	19.3437	18.3148	21.3043	21.8658	21.1282	21.294
2425	RIKEN cDNA 2310050C09 gene OS=Rattus norvegicus OX=10116 GN=LOC686143 PE=4 SV=3	LOC686143	F1M6N0	19.103	19.2634	17.7151	16.2989	NaN	16.7335	NaN	NaN
2426	RILP-like protein 1 OS=Rattus norvegicus OX=10116 GN=Rilpl1 PE=1 SV=1	Rilpl1	D3ZUQ0	18.5974	18.2399	18.2487	18.4623	21.2994	21.2505	21.2821	21.1979
2427	Ring finger protein 115 OS=Rattus norvegicus OX=10116 GN=Rnf115 PE=1 SV=2	Rnf115	D3ZB96	NaN	NaN	NaN	NaN	17.0823	17.5111	NaN	17.383
2428	Ring finger protein 126 OS=Rattus norvegicus OX=10116 GN=Rnf126 PE=1 SV=1	Rnf126	F7ESD4	NaN	NaN	NaN	NaN	19.9249	18.4196	18.7869	19.2219
2429	Ring finger protein 214 OS=Rattus norvegicus OX=10116 GN=Rnf214 PE=1 SV=3	Rnf214	D4A3V4	NaN	NaN	NaN	NaN	18.7791	16.9995	17.864	17.7999
2430	Ring finger protein 31 OS=Rattus norvegicus OX=10116 GN=Rnf31 PE=1 SV=2	Rnf31	E9PU29	16.9808	15.7684	15.4615	NaN	17.8415	18.4679	19.1395	18.4589
2431	Ring-box 1 OS=Rattus norvegicus OX=10116 GN=Rbx1 PE=1 SV=1	Rbx1	Q498D8	NaN	NaN	NaN	NaN	18.6618	18.5673	18.4878	18.399
2432	RNA 3'-terminal phosphate cyclase OS=Rattus norvegicus OX=10116 GN=Rtca PE=1 SV=1	Rtca	Q68FS8	15.0149	18.9472	14.9173	NaN	21.8662	23.1078	23.0223	22.6711
2433	RNA binding protein fox-1 homolog 2 OS=Rattus norvegicus OX=10116 GN=Rbfox2 PE=2 SV=1	Rbfox2	A1A5R1	NaN	NaN	16.0758	16.2027	17.0519	14.4361	16.7543	NaN
2434	RNA polymerase II subunit A C-terminal domain phosphatase SSU72 OS=Rattus norvegicus OX=10116 GN=Ssu72 PE=2 SV=	Ssu72	Q4KLK9	NaN	NaN	NaN	NaN	NaN	NaN	18.0369	15.8607
2435	RNA polymerase II-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Rpap1 PE=1 SV=1	Rpap1	Q3T1I9	18.9404	NaN	17.6866	NaN	18.2415	20.9435	18.3931	19.1264
2436	RNA polymerase II-associated protein 3 OS=Rattus norvegicus OX=10116 GN=Rpap3 PE=1 SV=1	Rpap3	Q68FQ7	NaN	15.8123	15.1996	NaN	18.2398	18.2626	19.678	17.8988

2437	RNA transcription, translation and transport factor OS=Rattus norvegicus OX=10116 GN=Rtraf PE=1 SV=1	Rtraf	F7EMB2	NaN	NaN	14.3742	NaN	21.3136	20.2717	20.1433	20.4605
2438	RNA-binding motif protein 38 OS=Rattus norvegicus OX=10116 GN=Rbm38 PE=1 SV=3	Rbm38	D3ZGE9	16.4855	15.9064	16.0785	NaN	17.6456	18.8807	17.5166	17.3142
2439	RNA-binding motif protein 39 OS=Rattus norvegicus OX=10116 GN=Rbm39 PE=1 SV=1	Rbm39	Q5BJP4	NaN	NaN	NaN	15.5427	18.4915	17.9506	16.8925	16.8709
2440	RNA-binding motif, single stranded-interacting protein 2 OS=Rattus norvegicus OX=10116 GN=Rbms2 PE=1 SV=1	Rbms2	A0A0G2JYJ7	NaN	NaN	16.6373	14.1019	20.6091	20.4831	20.108	20.4549
2441	RNA-binding motif, single-stranded-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Rbms1 PE=2 SV=1	Rbms1	Q5PQP1	NaN	NaN	NaN	NaN	17.4939	NaN	16.9565	17.1589
2442	RNA-binding protein 20 OS=Rattus norvegicus OX=10116 GN=Rbm20 PE=1 SV=1	Rbm20	E9PT37	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2443	RNA-binding protein 8A OS=Rattus norvegicus OX=10116 GN=Rbm8a PE=1 SV=1	Rbm8a	Q27W01	NaN	NaN	NaN	NaN	16.1537	NaN	NaN	NaN
2444	RNA-binding protein EWS-like OS=Rattus norvegicus OX=10116 GN=Ewsr1 PE=1 SV=1	Ewsr1	A0A140UHY3	NaN	NaN	NaN	NaN	20.4828	19.8565	19.4295	20.7808
2445	RNA-binding protein NOB1 OS=Rattus norvegicus OX=10116 GN=Nob1 PE=2 SV=1	Nob1	Q6VEU1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2446	RNA-binding protein, mRNA-processing factor 2 OS=Rattus norvegicus OX=10116 GN=Rbpms2 PE=1 SV=1	Rbpms2	B5DFF2	NaN	NaN	NaN	NaN	19.8776	19.7953	19.767	19.7154
2447	RNA-binding protein, mRNA-processing factor OS=Rattus norvegicus OX=10116 GN=Rbpms PE=1 SV=2	Rbpms	F1M9Y9	NaN	NaN	NaN	16.849	22.5635	21.9295	22.2714	22.0265
2448	RT1 class I histocompatibility antigen, AA alpha chain OS=Rattus norvegicus OX=10116 PE=1 SV=2	RT1-EC2	P16391	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2449	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) OS=Rattus norvegicus OX=10116 GN=Rtf1 PE=1	Rtf1	D3ZLH8	NaN	NaN	NaN	NaN	18.7697	17.8741	19.3044	19.2169
2450	RuvB-like 1 OS=Rattus norvegicus OX=10116 GN=Ruvbl1 PE=1 SV=1	Ruvbl1	P60123	14.9159	13.612	14.8625	14.4416	20.8347	20.2882	20.4832	20.6876
2451	RuvB-like helicase OS=Rattus norvegicus OX=10116 GN=Ruvbl2 PE=1 SV=1	Ruvbl2	G3V8T5	21.2644	21.3821	19.3079	22.0912	25.2195	21.7257	22.0523	21.9861
2452	Ryanodine receptor 2 OS=Rattus norvegicus OX=10116 GN=Ryr2 PE=1 SV=2	Ryr2	B0LPN4	20.4981	21.2021	19.4409	19.9049	21.3709	21.1545	20.6198	20.294
2453	S100 calcium binding protein A16 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=S100a16 PE=1 SV=1	S100a16	B0BMX3	NaN	NaN	NaN	NaN	18.3794	NaN	NaN	NaN
2454	Saccharopine dehydrogenase-like oxidoreductase OS=Rattus norvegicus OX=10116 GN=Sccpdh PE=1 SV=1	Sccpdh	Q6AY30	14.6423	14.9868	NaN	NaN	19.8241	20.5026	20.1044	20.1821
2455	Sacsin molecular chaperone OS=Rattus norvegicus OX=10116 GN=Sacs PE=1 SV=2	Sacs	D4A1D3	NaN	NaN	NaN	NaN	NaN	16.0179	15.8535	NaN
2456	S-adenosylhomocysteine hydrolase-like protein 1 OS=Rattus norvegicus OX=10116 GN=Ahcyl1 PE=1 SV=2	Ahcyl1	B5DFN2	NaN	NaN	NaN	NaN	18.191	NaN	NaN	17.3957
2457	S-adenosylmethionine synthase OS=Rattus norvegicus OX=10116 GN=Mat2a PE=1 SV=2	Mat2a	F1LRB8	19.1101	18.5798	19.0138	19.7094	22.3205	21.9314	22.7382	22.6751
2458	SAP domain-containing ribonucleoprotein OS=Rattus norvegicus OX=10116 GN=Sarnp PE=1 SV=3	Sarnp	Q498U4	19.8887	19.6952	19.7956	18.8136	21.0801	19.4938	20.0984	19.8564
2459	SAR1 gene homolog A (S. cerevisiae), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Sar1a PE=1 SV=1	Sar1a	Q6AY18	21.6821	21.5325	21.726	21.7111	24.6624	24.647	24.5648	24.7713
2460	Sarcalumenin OS=Rattus norvegicus OX=10116 GN=Srl PE=1 SV=3	Srl	F1LWG8	19.8642	20.7617	20.11	18.8568	24.1544	24.4705	23.7334	23.7787
2461	Sarcoglycan, delta OS=Rattus norvegicus OX=10116 GN=Sgcd PE=4 SV=3	Sgcd	F1LYS7	NaN	NaN	14.8607	NaN	16.7067	16.7132	16.3751	16.528
2462	Sarcoglycan, gamma OS=Rattus norvegicus OX=10116 GN=Sgcg PE=2 SV=1	Sgcg	Q5XID6	NaN	NaN	NaN	NaN	15.9636	16.6229	17.3795	17.4414
2463	Sarcolemmal membrane-associated protein OS=Rattus norvegicus OX=10116 GN=Slmap PE=1 SV=1	Slmap	A0A0G2JWA5	20.9528	20.7732	20.8327	21.2661	23.4185	23.6078	23.0397	23.3829
2464	Sarcolemmal membrane-associated protein OS=Rattus norvegicus OX=10116 GN=Slmap PE=1 SV=1	Slmap	B5DF63	NaN	NaN	16.0146	NaN	19.3869	19.6707	18.8054	19.1426
2465	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Rattus norvegicus OX=10116 GN=Atp2a1 PE=1 SV=1	Atp2a1	Q64578	22.2778	23.4743	22.9036	22.044	19.5574	19.555	19.7727	19.8187
2466	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Rattus norvegicus OX=10116 GN=Atp2a2 PE=1 SV=1	Atp2a2	P11507	23.1574	23.343	22.5497	22.2071	27.7286	27.9118	27.262	27.5286
2467	SCY1-like pseudokinase 2 OS=Rattus norvegicus OX=10116 GN=Scyl2 PE=1 SV=1	Scyl2	A0A0G2JVC2	18.6127	17.6804	18.0494	18.0294	20.3053	17.2434	19.3274	19.6796
2468	Sec1 family domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Scfd1 PE=1 SV=1	Scfd1	Q62991	14.6277	NaN	14.3601	NaN	19.5737	19.6679	19.7558	19.3529
2469	SEC14 and spectrin domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Sestd1 PE=1 SV=1	Sestd1	B5DFL9	NaN	NaN	NaN	NaN	18.3424	18.3627	16.8157	15.0239
2470	SEC24 homolog A, COPII coat complex component OS=Rattus norvegicus OX=10116 GN=Sec24a PE=1 SV=1	Sec24a	D3ZZA8	NaN	NaN	NaN	15.4679	16.483	NaN	15.4475	15.5965
2471	SEC24 homolog B, COPII coat complex component OS=Rattus norvegicus OX=10116 GN=Sec24b PE=1 SV=1	Sec24b	D3ZW15	NaN	NaN	14.7392	NaN	17.1226	NaN	16.0249	15.6379
2472	SEC24 homolog D, COPII coat complex component OS=Rattus norvegicus OX=10116 GN=Sec24d PE=1 SV=3	Sec24d	G3V9S9	NaN	NaN	NaN	NaN	20.7007	19.8487	19.713	19.933
2473	SECIS binding protein 2, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Secisbp2 PE=1 SV=2	Secisbp2	F1LPQ8	23.0945	22.5991	21.8246	22.9781	22.8101	22.777	22.0123	22.2716
2474	Secreted frizzled-related protein 1 OS=Rattus norvegicus OX=10116 GN=Sfrp1 PE=4 SV=1	Sfrp1	F1LLX7	NaN	NaN	NaN	NaN	18.1082	17.9735	17.6153	19.165
2475	Secreted phosphoprotein 24 OS=Rattus norvegicus OX=10116 GN=Spp2 PE=1 SV=2	Spp2	Q62740	21.2309	20.9643	20.9964	20.1273	16.4366	17.5934	17.16	16.765
2476	Secretin OS=Rattus norvegicus OX=10116 GN=Sct PE=1 SV=2	Sct	P11384	16.2965	NaN	NaN	14.9116	NaN	16.1362	NaN	NaN
2477	Secretoglobin, family 3A, member 1 OS=Rattus norvegicus OX=10116 GN=Scgb3a1 PE=4 SV=1	Scgb3a1	E9PU36	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2478	Secretory carrier-associated membrane protein 1 OS=Rattus norvegicus OX=10116 GN=Scamp1 PE=1 SV=1	Scamp1	P56603	17.3404	19.6724	19.1791	19.3159	21.4603	21.4777	20.9772	20.7803
2479	Secretory carrier-associated membrane protein OS=Rattus norvegicus OX=10116 GN=Scamp2 PE=1 SV=1	Scamp2	Q5U2U4	16.41	17.598	16.4895	16.8871	19.0531	19.481	19.0477	19.0881
2480	Secretory carrier-associated membrane protein OS=Rattus norvegicus OX=10116 GN=Scamp3 PE=1 SV=2	Scamp3	E9PTW1	16.5773	16.4121	17.1807	NaN	20.5435	21.4192	20.734	20.546
2481	Selenophosphate synthetase 1 OS=Rattus norvegicus OX=10116 GN=Sephs1 PE=1 SV=1	Sephs1	D3ZFY0	NaN	NaN	NaN	NaN	17.6691	16.9581	17.2654	17.1592
2482	Selenoprotein P OS=Rattus norvegicus OX=10116 GN=Selenop PE=1 SV=2	Selenop	P25236	19.8991	19.4131	19.8534	19.4986	17.5267	15.7755	NaN	15.4039
2483	Selenoprotein T OS=Rattus norvegicus OX=10116 GN=Selenot PE=1 SV=1	Selenot	A0A0G2K3B2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2484	Sepiapterin reductase OS=Rattus norvegicus OX=10116 GN=Spr PE=1 SV=1	Spr	P18297	16.6494	18.2775	18.138	17.9942	19.0682	17.0502	19.6871	20.2841
2485	Septin 6 OS=Rattus norvegicus OX=10116 GN=Sept6 PE=1 SV=1	Septin6	A0A0U1RRT8	NaN	NaN	15.3509	NaN	20.4928	20.6017	20.3294	19.6329
2486	Septin-11 OS=Rattus norvegicus OX=10116 GN=Sept11 PE=1 SV=1	Septin11	B3GNI6	18.7879	20.3938	19.0769	17.2171	22.3776	22.3239	22.332	22.2022
2487	Septin-2 OS=Rattus norvegicus OX=10116 GN=Sept2 PE=1 SV=1	Septin2	Q91Y81	18.2319	16.3019	18.1859	18.4926	22.7417	23.1248	23.1247	22.8597
2488	Septin-7 OS=Rattus norvegicus OX=10116 GN=Sept7 PE=1 SV=3	Septin7	F1LMC7	17.5923	18.5535	17.6636	18.0836	23.3428	23.6476	23.4329	23.2381
2489	Septin-8 OS=Rattus norvegicus OX=10116 GN=Sept8 PE=1 SV=1	Septin8	A0A0G2K7G7	14.3267	15.986	14.3654	14.8133	19.2903	19.7757	19.3289	18.3907

2490	Septin-9 OS=Rattus norvegicus OX=10116 GN=Sept9 PE=1 SV=1	Septin9	Q9QZR6	NaN	NaN	NaN	NaN	19.8535	20.4203	20.2836	20.2401
2491	Septin-9 OS=Rattus norvegicus OX=10116 GN=Sept9 PE=1 SV=3	Septin9	F1LN75	17.9389	16.4534	16.4397	16.9241	21.9285	22.368	22.2703	21.9578
2492	Sequestosome-1 OS=Rattus norvegicus OX=10116 GN=Sqstm1 PE=1 SV=1	Sqstm1	O08623	NaN	NaN	NaN	NaN	17.1698	17.2974	16.3399	16.6974
2493	Serine (Or cysteine) peptidase inhibitor, clade B (Ovalbumin), member 13 (Predicted) OS=Rattus norvegicus OX=10116 GN=	Serpinb13	D3ZKA0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2494	Serine (Or cysteine) peptidase inhibitor, clade B, member 6a OS=Rattus norvegicus OX=10116 GN=Serpinb6a PE=1 SV=1	Serpinb6a	Q6P9U0	17.7428	17.2011	17.1709	15.6494	20.8769	21.2908	21.645	21.3034
2495	Serine (Or cysteine) peptidase inhibitor, clade C (Antithrombin), member 1 OS=Rattus norvegicus OX=10116 GN=Serpinc1 P	Serpinc1	Q5M7T5	24.3579	24.186	24.7244	24.5562	21.282	21.4648	21.4999	21.6597
2496	Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 4 OS=Rattus norvegicus OX=	Serpina4	Q5M8C3	22.581	22.0535	22.3552	22.3695	19.1373	17.5981	20.1766	17.7349
2497	Serine (Or cysteine) proteinase inhibitor, clade H, member 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Serpinh1	Serpinh1	Q5RJR9	NaN	NaN	NaN	NaN	17.6665	19.1396	18.141	17.7606
2498	Serine protease inhibitor A3K OS=Rattus norvegicus OX=10116 GN=Serpina3k PE=1 SV=3	Serpina3c	P05545	21.0211	20.0248	21.1631	20.8138	18.8475	18.1153	17.8273	17.3233
2499	Serine protease inhibitor A3L OS=Rattus norvegicus OX=10116 GN=Serpina3l PE=1 SV=3	LOC299282	P05544	18.1508	17.4135	19.2179	19.0948	NaN	15.4995	15.2809	NaN
2500	Serine protease inhibitor A3N OS=Rattus norvegicus OX=10116 GN=LOC299282 PE=1 SV=1	LOC299282	A0A0G2K1T8	23.4509	23.5566	23.3638	22.5294	19.4468	19.5372	19.5545	20.6682
2501	Serine protease inhibitor A3N OS=Rattus norvegicus OX=10116 GN=LOC299282 PE=1 SV=1	LOC299282	F1LM05	26.6578	26.3521	26.9771	26.7559	23.0469	22.2687	22.5591	23.2715
2502	Serine protease inhibitor A3N OS=Rattus norvegicus OX=10116 GN=Serpina3n PE=1 SV=3	Serpina3n	P09006	23.6017	23.8552	23.8019	23.6542	20.586	19.2634	20.1489	20.5902
2503	Serine racemase OS=Rattus norvegicus OX=10116 GN=Srr PE=1 SV=1	Srr	Q76EQ0	15.6874	14.6261	16.2688	NaN	18.3582	18.3744	18.659	18.7678
2504	Serine/arginine-rich splicing factor 2 OS=Rattus norvegicus OX=10116 GN=Srsf2 PE=1 SV=3	Srsf2	Q6PDU1	16.7468	17.1222	19.9062	18.3504	20.748	21.577	21.643	21.6742
2505	Serine/arginine-rich splicing factor 6 OS=Rattus norvegicus OX=10116 GN=Srsf6 PE=1 SV=1	Srsf6	G3V6S8	NaN	15.8847	NaN	NaN	17.6565	17.9263	18.0765	18.1316
2506	Serine/threonine kinase 26 OS=Rattus norvegicus OX=10116 GN=Stk26 PE=1 SV=2	Stk26	F1LXV3	NaN	NaN	NaN	NaN	19.0067	17.8732	18.9203	18.2856
2507	Serine/threonine kinase 3 (STE20 homolog, yeast) OS=Rattus norvegicus OX=10116 GN=Stk3 PE=1 SV=1	Stk3	B1WBQ5	17.3034	17.8274	18.5317	17.4361	20.0991	19.3191	19.6431	19.5439
2508	Serine/threonine kinase 4 OS=Rattus norvegicus OX=10116 GN=Stk4 PE=1 SV=1	Stk4	D4A648	NaN	NaN	NaN	NaN	17.7453	16.2576	15.8759	17.4815
2509	Serine/threonine-protein kinase 24 OS=Rattus norvegicus OX=10116 GN=Stk24 PE=2 SV=1	Stk24	B0LT89	13.9635	NaN	NaN	NaN	19.9299	19.6079	19.6672	19.57
2510	Serine/threonine-protein kinase A-Raf OS=Rattus norvegicus OX=10116 GN=Araf PE=1 SV=1	Araf	P14056	14.7396	15.032	NaN	NaN	18.4525	18.0638	19.1109	18.9019
2511	Serine/threonine-protein kinase D1 OS=Rattus norvegicus OX=10116 GN=Prkd1 PE=1 SV=2	Prkd1	Q9WTQ1	NaN	NaN	NaN	13.6888	18.7105	NaN	18.6246	18.6481
2512	Serine/threonine-protein kinase MARK1 OS=Rattus norvegicus OX=10116 GN=Mark1 PE=1 SV=1	Mark1	O08678	16.8984	15.8711	17.345	18.5468	NaN	NaN	NaN	17.0518
2513	Serine/threonine-protein kinase MRCK beta OS=Rattus norvegicus OX=10116 GN=Cdc42bpb PE=1 SV=1	Cdc42bpb	Q7TT49	16.107	16.2643	16.6495	16.0907	20.3042	20.3674	20.0617	20.1546
2514	Serine/threonine-protein kinase mTOR OS=Rattus norvegicus OX=10116 GN=Mtor PE=1 SV=1	Mtor	P42346	NaN	14.9513	NaN	16.0729	18.1039	19.3027	19.295	19.0009
2515	Serine/threonine-protein kinase N1 OS=Rattus norvegicus OX=10116 GN=Pkn1 PE=1 SV=2	Pkn1	Q63433	16.4052	NaN	NaN	NaN	20.7793	19.4844	20.286	20.2367
2516	Serine/threonine-protein kinase N2 OS=Rattus norvegicus OX=10116 GN=Pkn2 PE=1 SV=2	Pkn2	O08874	16.7865	15.6789	17.4471	NaN	21.7079	20.9704	21.3562	19.3196
2517	Serine/threonine-protein kinase Nek6 OS=Rattus norvegicus OX=10116 GN=Nek6 PE=1 SV=1	Nek6	P59895	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2518	Serine/threonine-protein kinase Nek7 OS=Rattus norvegicus OX=10116 GN=Nek7 PE=1 SV=1	Nek7	A0A0G2JUP0	NaN	13.3406	NaN	NaN	19.2099	17.306	19.0744	18.655
2519	Serine/threonine-protein kinase PAK 2 OS=Rattus norvegicus OX=10116 GN=Pak2 PE=1 SV=1	Pak2	Q64303	18.3161	18.3728	18.2976	17.7037	22.9721	21.9257	22.4352	22.2735
2520	Serine/threonine-protein kinase RIO3 OS=Rattus norvegicus OX=10116 GN=Riok3 PE=1 SV=1	Riok3	D3ZND9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2521	Serine/threonine-protein kinase TNNI3K OS=Rattus norvegicus OX=10116 GN=Tnni3k PE=4 SV=2	Tnni3k	F1LPM9	NaN	NaN	NaN	NaN	19.9603	20.2599	19.5962	18.9252
2522	Serine/threonine-protein kinase WNK1 OS=Rattus norvegicus OX=10116 GN=Wnk1 PE=1 SV=1	Wnk1	A0A0G2K3A0	16.624	18.9994	18.116	16.1283	22.9565	22.8039	22.7685	22.4861
2523	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Rattus norvegicus OX=10116 GN=P	Ppp2r2a	P36876	18.7127	18.1998	18.8782	18.6061	22.0088	22.2509	22.5984	21.9386
2524	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B OS=Rattus norvegicus OX=10116 GN=Ppp2r2d PE=1 S	Ppp2r2d	A0A0G2JSQ0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2525	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit OS=Rattus norvegicus OX=10116 GN=Ppp2r5a PE=1 SV	Ppp2r5a	D3ZDI7	17.5399	16.9078	16.8393	NaN	18.7062	19.7215	19.4003	18.9334
2526	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit OS=Rattus norvegicus OX=10116 GN=Ppp2r5c PE=1 SV	Ppp2r5c	D4A1A5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2527	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit OS=Rattus norvegicus OX=10116 GN=Ppp2r5d PE=1 SV	Ppp2r5d	F1MAA3	NaN	17.3983	NaN	15.3111	20.9366	20.7264	21.376	20.8146
2528	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit OS=Rattus norvegicus OX=10116 GN=Ppp2r5e PE=1 SV	Ppp2r5e	A0A0G2JTA1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2529	Serine/threonine-protein phosphatase 2A activator OS=Rattus norvegicus OX=10116 GN=Ptpa PE=1 SV=1	Ptpa	B2RYQ2	15.4623	16.4893	16.9123	16.8912	20.9961	19.6618	20.6791	20.4151
2530	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Rattus norvegicus OX=10116 GN=Ppp3ca PE=1	Ppp3ca	P63329	16.8281	15.4788	15.6012	14.3842	19.3828	18.3126	18.9732	19.1341
2531	Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Rattus norvegicus OX=10116 GN=Ppp4r1 PE=1 SV=1	Ppp4r1	Q8VI02	17.4851	17.3391	16.5547	16.6638	18.6823	18.5279	18.5807	18.4083
2532	Serine/threonine-protein phosphatase 5 OS=Rattus norvegicus OX=10116 GN=Ppp5c PE=1 SV=1	Ppp5c	P53042	NaN	NaN	NaN	NaN	19.6149	16.8346	17.9909	18.1937
2533	Serine/threonine-protein phosphatase 6 catalytic subunit OS=Rattus norvegicus OX=10116 GN=Ppp6c PE=2 SV=2	Ppp6c	Q64620	NaN	NaN	15.3712	15.0572	19.6278	19.4221	19.4501	19.1687
2534	Serine/threonine-protein phosphatase OS=Rattus norvegicus OX=10116 GN=LOC100362453 PE=3 SV=1	LOC100362453	A0A0G2JYA4	17.5067	16.5661	16.2324	19.2711	20.7339	21.205	20.9922	20.8171
2535	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Rattus norvegicus OX=10116 GN=Ppp1ca PE=1 SV=1	Ppp1ca	P62138	15.4044	15.5008	14.9608	NaN	19.1768	18.9579	19.1414	19.2304
2536	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Rattus norvegicus OX=10116 GN=Ppp1cb PE=1 SV=3	Ppp1cb	P62142	22.058	21.7928	22.3137	22.1828	22.0296	22.3839	22.0395	22.0846
2537	Serine-threonine kinase receptor-associated protein OS=Rattus norvegicus OX=10116 GN=Strap PE=1 SV=1	Strap	Q5XIG8	17.389	17.1328	16.7535	14.1946	20.2011	20.1281	20.7739	20.1198
2538	Serine--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Sars PE=1 SV=1	Sars1	A0A0G2JZG7	15.5473	16.0434	16.6052	15.8303	19.9844	18.6374	18.7044	19.3996
2539	Serotransferrin OS=Rattus norvegicus OX=10116 GN=Tf PE=1 SV=1	Tf	A0A0G2QC06	29.3884	29.3965	29.7714	29.4303	25.586	25.4823	24.9495	25.139
2540	Serotransferrin OS=Rattus norvegicus OX=10116 GN=Tf PE=1 SV=3	Tf	P12346	24.6465	24.9334	24.9162	23.5944	21.8045	21.6252	20.9429	21.198
2541	Serpin family F member 2 OS=Rattus norvegicus OX=10116 GN=Serpinf2 PE=1 SV=1	Serpinf2	F7FHF3	24.1666	24.1389	24.3878	23.8829	21.01	19.915	19.8478	20.8832
2542	Serpin H1 OS=Rattus norvegicus OX=10116 GN=Serpinh1 PE=1 SV=1	Serpinh1	P29457	21.734	21.8333	21.7217	21.0323	24.4654	24.8511	24.56	24.8286

2543	Serum albumin OS=Rattus norvegicus OX=10116 GN=Alb PE=1 SV=1	Alb	A0A0G2JSH5	24.265	26.3487	25.1855	26.4119	22.2182	22.0764	21.0618	21.7295
2544	Serum albumin OS=Rattus norvegicus OX=10116 GN=Alb PE=1 SV=2	Alb	P02770	31.5013	31.4632	31.5614	31.5005	28.1127	27.742	27.4202	27.6775
2545	Serum amyloid P-component OS=Rattus norvegicus OX=10116 GN=Apcs PE=1 SV=1	Apcs	A0A0H2UHH2	22.6719	23.14	23.1406	22.8285	15.4954	17.2887	15.4987	16.9178
2546	Serum paraoxonase/arylesterase 1 OS=Rattus norvegicus OX=10116 GN=Pon1 PE=1 SV=3	Pon1	P55159	21.0073	21.5558	20.5062	21.3123	19.3559	19.0543	18.8144	19.3408
2547	Serum response factor OS=Rattus norvegicus OX=10116 GN=Srf PE=1 SV=2	Srf	D3ZHH8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2548	S-formylglutathione hydrolase OS=Rattus norvegicus OX=10116 GN=Esd PE=2 SV=1	Esd	B0BNE5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2549	SH2B adapter protein 1 OS=Rattus norvegicus OX=10116 GN=Sh2b1 PE=1 SV=1	Sh2b1	Q62985	15.9238	15.8476	16.6626	15.0902	19.8454	20.2594	19.985	19.734
2550	SH3 and multiple ankyrin repeat domains protein 3 (Fragment) OS=Rattus norvegicus OX=10116 GN=Shank3 PE=1 SV=2	Shank3	A0A0U1RS13	16.5871	16.9259	NaN	16.9071	NaN	NaN	NaN	15.2464
2551	SH3 and PX domains 2A OS=Rattus norvegicus OX=10116 GN=Sh3pxd2a PE=1 SV=1	Sh3pxd2a	A0A0G2JX92	18.6347	18.4318	18.1967	17.8794	20.1831	20.8839	20.5198	20.2671
2552	SH3 and PX domains 2B OS=Rattus norvegicus OX=10116 GN=Sh3pxd2b PE=1 SV=2	Sh3pxd2b	D3ZAF9	15.4186	NaN	NaN	15.9647	NaN	17.1289	NaN	NaN
2553	SH3 domain binding glutamic acid-rich protein-like 3 OS=Rattus norvegicus OX=10116 GN=Sh3bgrl3 PE=1 SV=1	Sh3bgrl3	B2RZ27	15.525	17.1706	15.9792	17.1747	13.814	17.3942	16.4171	16.3864
2554	SH3 domain-binding glutamate-rich protein OS=Rattus norvegicus OX=10116 GN=Sh3bgr PE=1 SV=1	Sh3bgr	D3ZU20	NaN	NaN	NaN	16.5933	19.9423	19.4311	19.8751	19.7587
2555	SH3 domain-binding glutamic acid-rich-like protein OS=Rattus norvegicus OX=10116 GN=Sh3bgrl PE=1 SV=1	Sh3bgrl	B5DFD8	NaN	NaN	NaN	17.3513	16.4478	16.8475	NaN	16.6988
2556	SH3 domain-binding protein 4 OS=Rattus norvegicus OX=10116 GN=Sh3bp4 PE=1 SV=1	Sh3bp4	G3V8J0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2557	SH3 domain-containing kinase-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Sh3kbp1 PE=1 SV=2	Sh3kbp1	Q925Q9	17.7952	18.9289	17.1574	16.3749	20.514	19.9413	19.5672	20.1862
2558	SHC-transforming protein 1 OS=Rattus norvegicus OX=10116 GN=Shc1 PE=1 SV=1	Shc1	Q5M824	NaN	15.8959	NaN	17.3918	NaN	17.0208	16.6186	16.0507
2559	Shroom family member 3 OS=Rattus norvegicus OX=10116 GN=Shroom3 PE=1 SV=3	Shroom3	F1LP26	NaN	NaN	15.3278	NaN	16.4979	17.1906	16.2997	NaN
2560	Signal peptidase complex subunit 2 OS=Rattus norvegicus OX=10116 GN=Spcs2 PE=1 SV=1	Spcs2	D3ZD11	NaN	14.6062	NaN	NaN	16.1296	16.8329	16.9901	17.0793
2561	Signal recognition particle 19 OS=Rattus norvegicus OX=10116 GN=Srp19 PE=1 SV=1	Srp19	B2RZ66	NaN	NaN	NaN	NaN	16.4699	NaN	NaN	16.2698
2562	Signal recognition particle 54 kDa protein OS=Rattus norvegicus OX=10116 GN=Srp54 PE=2 SV=1	Srp54a	Q6AYB5	18.9469	18.2536	19.1515	17.9263	22.5489	22.214	22.0244	21.712
2563	Signal recognition particle 9 kDa protein OS=Rattus norvegicus OX=10116 GN=Srp9 PE=1 SV=1	Srp9	D4A511	NaN	NaN	NaN	NaN	16.291	16.608	16.2314	16.7856
2564	Signal recognition particle subunit SRP68 OS=Rattus norvegicus OX=10116 GN=Srp68 PE=1 SV=1	Srp68	B2RYI2	17.038	17.5046	17.1801	17.5282	20.322	20.7196	20.2066	20.4183
2565	Signal recognition particle subunit SRP72 OS=Rattus norvegicus OX=10116 GN=LOC108348180 PE=1 SV=2	Srp72	D4A7R0	15.6026	15.6087	15.8095	NaN	19.3907	18.9401	19.6395	19.2949
2566	Signal recognition particle subunit SRP72-like OS=Rattus norvegicus OX=10116 GN=LOC108348180 PE=1 SV=1	Srp72	B0BND9	NaN	NaN	NaN	14.0061	18.891	19.4974	19.1027	19.2925
2567	Signal transducer and activator of transcription 3 OS=Rattus norvegicus OX=10116 GN=Stat3 PE=1 SV=1	Stat3	P52631	18.5124	17.9617	18.2306	17.5898	22.7221	23.3703	23.1323	23.0109
2568	Signal transducer and activator of transcription OS=Rattus norvegicus OX=10116 GN=Stat1 PE=1 SV=2	Stat1	F1M9D6	15.205	18.4166	15.8958	17.5307	20.4032	20.3534	20.8647	20.2803
2569	Signal transducer and activator of transcription OS=Rattus norvegicus OX=10116 GN=Stat2 PE=1 SV=1	Stat2	Q5XI26	18.7846	19.9635	18.9886	NaN	15.3237	16.9474	16.9262	17.1732
2570	Signal transducer and activator of transcription OS=Rattus norvegicus OX=10116 GN=Stat5b PE=1 SV=1	Stat5b	A0A0G2JSR4	NaN	NaN	NaN	NaN	20.2047	19.9366	19.8768	19.6657
2571	Signal transducing adapter molecule 2 OS=Rattus norvegicus OX=10116 GN=Stam2 PE=2 SV=1	Stam2	Q5XHY7	14.9926	14.9756	15.3415	NaN	17.1939	18.317	17.8904	17.9315
2572	Signal-induced proliferation-associated 1-like protein 2 OS=Rattus norvegicus OX=10116 GN=Sipa1l2 PE=1 SV=3	Sipa1l2	F1M8G8	NaN	NaN	NaN	NaN	17.513	17.3897	17.4346	17.2382
2573	SIK family kinase 3 OS=Rattus norvegicus OX=10116 GN=Sik3 PE=1 SV=2	Sik3	M0RD40	NaN	NaN	NaN	NaN	19.8315	19.8893	19.7164	19.5004
2574	Similar to 60S ribosomal protein L23a OS=Rattus norvegicus OX=10116 GN=LOC689899 PE=3 SV=1	LOC689899	D3ZTH8	19.6408	19.7157	18.8187	19.3207	22.7033	23.9412	23.5553	23.4383
2575	Similar to 60S ribosomal protein L27a OS=Rattus norvegicus OX=10116 GN=RGD1562402 PE=3 SV=1	RGD1562402	A0A0G2K7W6	NaN	NaN	NaN	16.2847	21.619	23.2198	22.7651	22.6052
2576	Similar to alpha-fetoprotein OS=Rattus norvegicus OX=10116 GN=LOC360919 PE=1 SV=1	LOC360919	F7FAY5	18.3927	18.8993	19.1441	17.5307	18.6753	17.6972	18.5754	18.261
2577	Similar to CG3740-PA OS=Rattus norvegicus OX=10116 GN=LOC690000 PE=1 SV=1	LOC690000	D3ZWS2	NaN	15.9379	14.3713	17.0017	20.5087	20.2642	20.6622	20.2855
2578	Similar to D7Wsu128e protein OS=Rattus norvegicus OX=10116 GN=Ubfd1 PE=1 SV=3	Ubfd1	G3V8E4	NaN	NaN	16.4842	17.2831	19.8153	20.3604	19.714	19.9904
2579	Similar to DNA segment, Chr 8, ERATO Doi 531, expressed, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Vps37a P	Vps37a	Q4V794	18.0973	17.7708	16.3077	15.6108	18.5513	20.5133	20.9637	20.8269
2580	Similar to GTPase-activating protein testicular GAP1 OS=Rattus norvegicus OX=10116 GN=RGD1563562 PE=4 SV=2	LOC103691539	D3ZH11	18.1182	17.8387	17.6902	17.9402	NaN	16.6742	NaN	NaN
2581	Similar to RIKEN cDNA 0610038D11 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Trmt112 PE=1 SV=	Trmt112	B2RYS9	19.2701	18.849	18.6371	14.7098	20.0809	20.7368	20.4187	20.3097
2582	Similar to RIKEN cDNA 1110059P08 OS=Rattus norvegicus OX=10116 GN=Vta1 PE=1 SV=1	Vta1	A0A096MKH2	NaN	NaN	NaN	NaN	NaN	17.4605	18.1538	18.0728
2583	Similar to RIKEN cDNA 1300017J02 OS=Rattus norvegicus OX=10116 GN=RGD1310507 PE=1 SV=1	Inhca	A0A0G2K896	23.6999	23.4738	24.404	23.8076	19.3253	20.2194	19.4928	20.3319
2584	Similar to RIKEN cDNA 2310022B05 OS=Rattus norvegicus OX=10116 GN=RGD1559896 PE=1 SV=1	RGD1559896	D3ZY47	14.8615	14.6365	14.6026	NaN	20.2329	19.7828	19.9339	19.9826
2585	Similar to RIKEN cDNA 2610002M06 OS=Rattus norvegicus OX=10116 GN=RGD1566265 PE=1 SV=1	RGD1566265	G3V6A6	14.896	15.1259	NaN	NaN	19.158	15.6842	18.6334	19.0895
2586	Similar to RIKEN cDNA 2810055F11 (Predicted) OS=Rattus norvegicus OX=10116 GN=L3hypdh PE=1 SV=1	L3hypdh	D3ZV91	17.0246	19.7766	19.6073	18.7961	19.6896	20.6615	21.0384	20.5087
2587	Similar to RIKEN cDNA 5730449L18 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tsen15 PE=1 SV=1	Tsen15	A0A0G2K1V3	NaN	NaN	NaN	NaN	18.2717	NaN	18.492	18.5077
2588	Similar to RIKEN cDNA 5730469D23 (Predicted) OS=Rattus norvegicus OX=10116 GN=Uba6 PE=1 SV=1	Uba6	D4A8H3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2589	Similar to RIKEN cDNA 5830475I06 OS=Rattus norvegicus OX=10116 GN=RGD1311744 PE=1 SV=3	RGD1311744	D4A1U8	NaN	15.5791	15.3361	17.1581	18.5661	17.699	18.0237	17.7049
2590	Similar to RIKEN cDNA 6430548M08 OS=Rattus norvegicus OX=10116 GN=RGD1304884 PE=1 SV=1	RGD1304884	D4A3C2	NaN	16.8914	16.4941	NaN	21.5961	20.5244	21.4257	20.1034
2591	Similar to TANK-binding kinase 1 OS=Rattus norvegicus OX=10116 GN=Tbk1 PE=1 SV=1	Tbk1	D4A7D3	14.8271	NaN	NaN	NaN	NaN	18.7439	16.7507	16.5307
2592	Similar to TBC1 domain family, member 8;BUB2-like protein 1;vascular Rab-GAP/TBC-containing (Predicted), isoform CRA	Tbc1d9b	F1LRL4	21.4233	21.0865	21.5914	21.1419	20.3106	20.0453	20.5974	20.6333
2593	Similar to THUMP domain containing 3 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Thumpd3 PE=1	Thumpd3	D3ZSV7	17.3484	14.8214	15.238	NaN	18.1586	15.4726	18.0345	18.3947
2594	Similar to Tripartite motif protein 47 OS=Rattus norvegicus OX=10116 GN=Trim47 PE=1 SV=1	Trim47	D3ZA22	18.0084	17.9596	17.7413	17.486	20.9585	22.3563	22.1222	21.5636
2595	Similar to TTF-I interacting peptide 20;TIP20;Transcription Termination Factor I Interacting Peptide 20 (Predicted) OS=Ratt	Zfp787	D3ZDN6	NaN	NaN	NaN	NaN	NaN	15.7972	16.0682	NaN

2596	Similar to Vanin-3 (Predicted) OS=Rattus norvegicus OX=10116 GN=Vnn3 PE=1 SV=1	Vnn3	D4A183	16.7374	16.3898	16.4117	18.1468	15.5965	NaN	NaN	NaN
2597	Similar to zinc finger protein (Predicted) OS=Rattus norvegicus OX=10116 GN=Zpr1 PE=1 SV=1	Zpr1	D3ZWN1	NaN	NaN	NaN	NaN	16.7121	17.1682	14.8563	15.6323
2598	SLAIN motif family, member 2 OS=Rattus norvegicus OX=10116 GN=Slain2 PE=1 SV=1	Slain2	G3V6A2	21.9809	22.3176	22.4055	22.0391	21.0761	21.9878	21.1704	20.6897
2599	SLIT-ROBO Rho GTPase-activating protein 2 OS=Rattus norvegicus OX=10116 GN=Srgap2 PE=1 SV=1	Srgap2	D4A208	21.5294	19.2053	20.5016	20.6514	21.1036	20.4188	20.4623	19.9894
2600	Small ArfGAP 1 OS=Rattus norvegicus OX=10116 GN=Smap1 PE=1 SV=1	Smap1	M0RC57	NaN	NaN	NaN	NaN	19.2484	17.2044	17.9752	18.268
2601	Small ArfGAP2 OS=Rattus norvegicus OX=10116 GN=Smap2 PE=1 SV=1	Smap2	B1WBX6	NaN	NaN	12.2803	NaN	19.5127	16.306	18.8527	19.0638
2602	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Rattus norvegicus OX=10116 GN=Sgta PE=1 SV=	Sgta	O70593	16.8883	16.9103	17.2902	20.1722	22.8696	21.1813	21.6643	22.2629
2603	Small muscular protein OS=Rattus norvegicus OX=10116 GN=Smpx PE=1 SV=1	Smpx	Q925F0	NaN	NaN	15.0717	NaN	21.4875	21.5034	21.4675	21.4924
2604	Small nuclear ribonucleoprotein Sm D2 OS=Rattus norvegicus OX=10116 GN=Snrpd2 PE=1 SV=1	Snrpd2	B5DES0	NaN	NaN	NaN	NaN	18.2978	NaN	NaN	17.5791
2605	Small nuclear ribonucleoprotein Sm D3 OS=Rattus norvegicus OX=10116 GN=Snrpd3 PE=1 SV=1	Snrpd3	M0R907	NaN	16.7463	NaN	NaN	19.7941	18.601	19.2203	18.1157
2606	Small proline-rich protein 2D OS=Rattus norvegicus OX=10116 GN=Sprr2d PE=4 SV=2	Sprr2d	D3ZAR3	NaN	17.5054	16.3762	14.3338	17.4452	19.2707	NaN	16.4262
2607	Small ubiquitin-related modifier 3 OS=Rattus norvegicus OX=10116 GN=Sumo3 PE=3 SV=1	Sumo3	Q5XIF4	NaN	15.603	NaN	NaN	17.9219	17.3065	NaN	17.6426
2608	S-methyl-5'-thioadenosine phosphorylase OS=Rattus norvegicus OX=10116 GN=Mtap PE=1 SV=1	Mtap	Q7TP15	NaN	16.0478	NaN	14.8394	16.8787	17.6069	17.6637	17.4329
2609	Smoothelin-like 2 OS=Rattus norvegicus OX=10116 GN=Smtnl2 PE=1 SV=1	Smtnl2	D3ZUC1	NaN	15.3203	NaN	14.654	21.9739	22.1001	22.3671	22.2266
2610	SNAP-29 protein OS=Rattus norvegicus OX=10116 GN=Snap29 PE=1 SV=1	Snap29	Q9JI56	NaN	NaN	NaN	NaN	16.888	16.7664	16.7441	16.9705
2611	SNARE-associated protein Snapin OS=Rattus norvegicus OX=10116 GN=Snapin PE=1 SV=1	Snapin	P60192	NaN	NaN	NaN	NaN	19.5806	18.3661	18.4247	18.553
2612	Snta1 protein OS=Rattus norvegicus OX=10116 GN=Snta1 PE=1 SV=1	Snta1	B5DFL0	15.6322	NaN	NaN	NaN	NaN	16.7238	NaN	NaN
2613	Sodium/calcium exchanger 1 OS=Rattus norvegicus OX=10116 GN=Slc8a1 PE=1 SV=3	Slc8a1	Q01728	22.8862	22.9473	23.0455	21.3833	23.5619	23.208	23.107	22.7465
2614	Sodium/hydrogen exchanger OS=Rattus norvegicus OX=10116 GN=Slc9a6 PE=1 SV=2	Slc9a6	D3ZJ86	NaN	NaN	17.739	NaN	16.5739	16.1378	NaN	16.0955
2615	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Rattus norvegicus OX=10116 GN=Atp1a1 PE=1 SV=1	Atp1a1	P06685	22.0023	22.0374	21.6959	21.5915	25.72	25.6195	25.228	25.313
2616	Sodium/potassium-transporting ATPase subunit alpha-3 OS=Rattus norvegicus OX=10116 GN=Atp1a3 PE=1 SV=2	Atp1a3	P06687	16.8841	18.343	17.7899	14.6318	21.8497	21.7654	21.4411	20.9458
2617	Sodium/potassium-transporting ATPase subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Atp1b1 PE=1 SV=1	Atp1b1	P07340	18.3782	18.1683	17.2777	16.3568	23.7047	23.5772	23.2154	23.2546
2618	Sodium/potassium-transporting ATPase subunit beta-3 OS=Rattus norvegicus OX=10116 GN=Atp1b3 PE=2 SV=1	Atp1b3	Q63377	18.5192	15.6993	18.0912	17.9236	19.4199	19.5862	18.1535	19.3879
2619	Sodium-dependent neutral amino acid transporter SLC6A17 OS=Rattus norvegicus OX=10116 GN=Slc6a17 PE=1 SV=1	Slc6a17	P31662	NaN	NaN	NaN	NaN	NaN	15.9328	NaN	NaN
2620	Sodium-dependent phosphate transporter 2 OS=Rattus norvegicus OX=10116 GN=Slc20a2 PE=1 SV=1	Slc20a2	Q63488	17.5796	16.0354	15.99	NaN	20.2347	20.5999	19.9825	20.1468
2621	Solute carrier family 12 member 4 OS=Rattus norvegicus OX=10116 GN=Slc12a4 PE=1 SV=1	Slc12a4	Q63632	17.6272	17.1876	17.2706	17.9928	16.9767	18.1624	17.0963	16.9754
2622	Solute carrier family 12 member 7 OS=Rattus norvegicus OX=10116 GN=Slc12a7 PE=1 SV=1	Slc12a7	A0A0G2K8S1	NaN	NaN	NaN	NaN	NaN	18.3672	17.5928	NaN
2623	Solute carrier family 18 (Vesicular acetylcholine), member 3 OS=Rattus norvegicus OX=10116 GN=Slc18a3 PE=4 SV=1	Slc18a3	A0A1B0GWU4	16.4781	17.2932	17.9863	NaN	17.3976	18.0817	17.3211	17.5772
2624	Solute carrier family 2, facilitated glucose transporter member 1 OS=Rattus norvegicus OX=10116 GN=Slc2a1 PE=1 SV=1	Slc2a1	P11167	18.4657	NaN	16.7545	18.1115	21.3907	21.0687	21.2674	21.3773
2625	Solute carrier family 2, facilitated glucose transporter member 3 OS=Rattus norvegicus OX=10116 GN=Slc2a3 PE=1 SV=1	Slc2a3	A0A0G2JVB0	18.029	20.2764	19.3351	17.9121	18.5434	16.7052	16.9865	18.7593
2626	Solute carrier family 2, facilitated glucose transporter member 4 OS=Rattus norvegicus OX=10116 GN=Slc2a4 PE=1 SV=1	Slc2a4	P19357	NaN	16.0075	15.2913	NaN	19.4704	19.7739	19.7079	19.6654
2627	Solute carrier family 25 member 12 OS=Rattus norvegicus OX=10116 GN=Slc25a12 PE=1 SV=3	Slc25a12	F1LX07	NaN	NaN	NaN	NaN	NaN	17.0538	NaN	NaN
2628	Solute carrier family 43 member 1 OS=Rattus norvegicus OX=10116 GN=Slc43a1 PE=1 SV=2	Slc43a1	F7FL53	18.8682	18.3909	17.7985	20.7963	18.4762	17.1728	NaN	NaN
2629	Sorbin and SH3 domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Sorbs2 PE=1 SV=2	Sorbs2	F1LPM3	20.0087	19.4634	19.9134	20.0111	23.6293	24.3715	24.3436	23.5671
2630	Sorting and assembly machinery component 50 homolog OS=Rattus norvegicus OX=10116 GN=Samm50 PE=1 SV=1	Samm50	Q6AXV4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2631	Sorting nexin 2 OS=Rattus norvegicus OX=10116 GN=Snx2 PE=1 SV=1	Snx2	B2RYP4	17.4071	17.3363	16.0416	18.2334	21.0485	21.2684	21.5736	21.245
2632	Sorting nexin 4 OS=Rattus norvegicus OX=10116 GN=Snx4 PE=1 SV=1	Snx4	E9PU13	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2633	Sorting nexin OS=Rattus norvegicus OX=10116 GN=Snx6 PE=1 SV=1	Snx6	B5DEY8	19.6315	19.5762	20.2424	17.598	18.8207	18.7621	18.7083	19.3005
2634	Sorting nexin OS=Rattus norvegicus OX=10116 GN=Snx9 PE=1 SV=2	Snx9	M0R9L3	18.789	15.8074	18.0873	16.5249	16.9607	16.7147	15.9452	NaN
2635	Sorting nexin-1 OS=Rattus norvegicus OX=10116 GN=Snx1 PE=1 SV=1	Snx1	Q99N27	16.9596	16.0533	15.4221	NaN	20.6448	20.9406	20.1319	20.2718
2636	Sorting nexin-15 OS=Rattus norvegicus OX=10116 GN=Snx15 PE=2 SV=1	Snx15	Q4V896	NaN	NaN	NaN	NaN	16.723	NaN	16.786	NaN
2637	Sorting nexin-17 OS=Rattus norvegicus OX=10116 GN=Snx17 PE=1 SV=1	Snx17	Q6AYS6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2638	Sorting nexin-3 OS=Rattus norvegicus OX=10116 GN=Snx3 PE=1 SV=1	Snx3	Q5U211	16.7944	16.173	16.868	13.4474	21.6866	20.6818	21.3835	21.3853
2639	Sorting nexin-5 OS=Rattus norvegicus OX=10116 GN=Snx5 PE=1 SV=1	Snx5	B1H267	18.0695	17.2547	18.3808	18.3972	22.0165	20.4472	20.6422	21.3035
2640	SOS Ras/Rac guanine nucleotide exchange factor 1 OS=Rattus norvegicus OX=10116 GN=Sos1 PE=1 SV=2	Sos1	D4A3T0	NaN	15.4613	15.5722	15.7045	16.295	18.0705	17.9904	18.069
2641	Sp3 transcription factor OS=Rattus norvegicus OX=10116 GN=Sp3 PE=1 SV=1	Sp3	A0A0G2K5M1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2642	SPARC OS=Rattus norvegicus OX=10116 GN=Sparc PE=1 SV=4	Sparc	P16975	19.5704	19.8878	19.9441	18.0988	19.1196	20.042	19.2228	19.1802
2643	SPARC-like 1 (Mast9, hevin), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Sparcl1 PE=1 SV=1	Sparcl1	G3V7X5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2644	Spartin OS=Rattus norvegicus OX=10116 GN=Spart PE=1 SV=3	Spart	E9PT90	20.6094	20.6686	20.6803	20.7032	21.2528	21.1675	21.2481	21.1171
2645	SPATS2-like protein OS=Rattus norvegicus OX=10116 GN=Spats2l PE=4 SV=1	Spats2l	A0A0G2JVT4	NaN	NaN	NaN	NaN	16.6034	18.3318	17.7364	15.9218
2646	SPC24, NDC80 kinetochore complex component OS=Rattus norvegicus OX=10116 GN=Spc24 PE=4 SV=3	Spc24	D4A1C5	19.2358	18.743	18.8128	19.1999	20.4478	19.8104	20.0657	19.8805
2647	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus OX=10116 GN=Sptan1 PE=1 SV=1	Sptan1	A0A0G2K1Y8	19.3399	18.624	18.413	20.1105	23.7617	23.4481	23.6792	23.5131
2648	Spectrin beta chain OS=Rattus norvegicus OX=10116 GN=Sptb PE=1 SV=1	Sptb	A0A140UHX6	22.7259	23.2636	22.4579	23.7832	21.4714	22.0832	22.2863	21.9376

2649	Spectrin beta chain OS=Rattus norvegicus OX=10116 GN=Sptbn1 PE=1 SV=1	Sptbn1	A0A0G2K8W9	20.8074	20.4712	20.2144	19.9383	23.0894	23.4991	23.5554	23.3474
2650	Spectrin beta chain OS=Rattus norvegicus OX=10116 GN=Sptbn2 PE=1 SV=2	Sptbn2	F1MA36	NaN	NaN	NaN	NaN	17.4925	17.2614	17.4859	NaN
2651	Spectrin, alpha, erythrocytic 1 OS=Rattus norvegicus OX=10116 GN=Spta1 PE=1 SV=3	Spta1	D4A678	22.1631	22.5032	21.0303	22.0484	20.9579	21.1678	21.0138	20.8415
2652	Sperm-associated antigen 7 OS=Rattus norvegicus OX=10116 GN=Spag7 PE=1 SV=1	Spag7	D3ZCG4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2653	Sperm-associated antigen 9 OS=Rattus norvegicus OX=10116 GN=Spag9 PE=1 SV=1	Spag9	A0A0G2K6E8	18.8053	18.6763	19.2416	18.9439	20.9517	20.2151	20.6626	20.4911
2654	Spermatogenesis-associated 5 OS=Rattus norvegicus OX=10116 GN=Spata5 PE=1 SV=1	Spata5	A0A0G2K0I1	NaN	NaN	NaN	NaN	NaN	16.6024	16.2441	15.8274
2655	Spermidine synthase OS=Rattus norvegicus OX=10116 GN=LOC100912604 PE=1 SV=1	Srm	Q99MI5	17.7386	17.4017	17.4381	17.5176	19.6748	19.9935	20.8921	20.9922
2656	Spermine synthase OS=Rattus norvegicus OX=10116 GN=Sms PE=1 SV=1	Sms	Q3MIE9	NaN	NaN	NaN	NaN	18.4839	17.3627	19.2818	19.4978
2657	S-phase kinase-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Skp1 PE=1 SV=1	Skp1	A0A0G2K4X8	NaN	16.8581	16.0936	16.7186	22.8633	22.5802	22.5716	22.4011
2658	Spliceosome RNA helicase Ddx39b OS=Rattus norvegicus OX=10116 GN=Ddx39b PE=2 SV=3	Ddx39b	Q63413	14.106	NaN	16.9041	NaN	21.602	19.201	20.4517	20.6393
2659	Spliceosome-associated factor 3, U4/U6 recycling protein OS=Rattus norvegicus OX=10116 GN=Sart3 PE=1 SV=1	Sart3	D3ZAS8	NaN	NaN	NaN	NaN	16.5213	17.453	17.8489	17.3766
2660	Splicing factor 1 OS=Rattus norvegicus OX=10116 GN=Sf1 PE=1 SV=2	Sf1	F1LSC3	NaN	NaN	NaN	16.4766	20.2075	19.6227	19.4386	19.4353
2661	Splicing factor 3A subunit 2 OS=Rattus norvegicus OX=10116 GN=Sf3a2 PE=2 SV=1	Sf3a2	Q6AXT8	NaN	NaN	NaN	NaN	16.7923	16.8451	NaN	NaN
2662	Splicing factor 3b, subunit 2 OS=Rattus norvegicus OX=10116 GN=Sf3b2 PE=1 SV=3	Sf3b2	D3ZMS1	17.0907	16.8611	16.6509	15.6139	NaN	17.5568	NaN	NaN
2663	Splicing factor 3b, subunit 3 OS=Rattus norvegicus OX=10116 GN=Sf3b3 PE=1 SV=2	Sf3b3	E9PT66	NaN	NaN	NaN	NaN	15.5696	15.7906	NaN	NaN
2664	Splicing factor proline and glutamine rich OS=Rattus norvegicus OX=10116 GN=Sfpq PE=1 SV=1	Sfpq	A0A0G2K8K0	17.1703	19.1485	17.4341	NaN	19.1365	18.0789	18.2096	18.4692
2665	Spondin-2 OS=Rattus norvegicus OX=10116 GN=Spon2 PE=2 SV=1	Spon2	Q9WV75	16.7422	NaN	16.0947	NaN	NaN	NaN	15.0528	NaN
2666	SPRY domain-containing protein 7 OS=Rattus norvegicus OX=10116 GN=Spryd7 PE=2 SV=1	Spryd7	Q5M7T2	NaN	14.5037	14.2834	16.5861	19.8236	20.3129	19.9383	19.7074
2667	STAM-binding protein OS=Rattus norvegicus OX=10116 GN=Stambp PE=2 SV=1	Stambp	Q8R424	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2668	Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Snd1 PE=1 SV=1	Snd1	Q66X93	NaN	NaN	NaN	NaN	16.1733	15.986	15.7486	16.0907
2669	Stathmin OS=Rattus norvegicus OX=10116 GN=Stmn1 PE=1 SV=2	Stmn1	P13668	19.7477	19.8026	20.0205	19.7748	21.824	21.567	21.3324	21.5381
2670	Staufen double-stranded RNA-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Stau1 PE=1 SV=1	Stau1	Q9ET50	NaN	NaN	NaN	NaN	16.2558	17.4662	NaN	NaN
2671	STE20/SPS1-related proline-alanine-rich protein kinase OS=Rattus norvegicus OX=10116 GN=Stk39 PE=1 SV=2	Stk39	O88506	14.4921	14.8027	NaN	15.6288	23.271	23.5584	23.884	23.6811
2672	STE20-like serine/threonine-protein kinase OS=Rattus norvegicus OX=10116 GN=Slk PE=1 SV=1	Slk	O08815	NaN	NaN	15.1365	15.6281	18.4662	18.4075	18.4551	18.2383
2673	STIP1 homology and U-Box containing protein 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Stub1 PE=1 SV=1	Stub1	D4A4T0	16.2776	17.1452	17.0268	16.6016	21.2202	20.7586	21.1341	20.5478
2674	Stress-70 protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hspa9 PE=1 SV=1	Hspa9	F1M953	21.1015	20.4001	18.7097	19.7919	21.1108	23.1712	22.6946	22.9869
2675	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus OX=10116 GN=Stip1 PE=1 SV=1	Stip1	O35814	22.1588	22.0217	22.2819	20.8576	26.0256	23.9164	24.7243	24.8215
2676	Striated muscle-specific serine/threonine-protein kinase OS=Rattus norvegicus OX=10116 GN=Speg PE=1 SV=2	Speg	Q63638	22.9823	23.4517	23.1975	23.3712	22.7677	23.4274	22.8103	22.6745
2677	Striatin 4 OS=Rattus norvegicus OX=10116 GN=Strn4 PE=1 SV=1	Strn4	F1M6V8	19.2491	18.7064	18.7062	18.4559	19.716	20.1835	19.9954	19.9727
2678	Striatin-3 OS=Rattus norvegicus OX=10116 GN=Strn3 PE=1 SV=2	Strn3	P58405	NaN	NaN	15.9306	NaN	18.3651	18.8467	NaN	18.3776
2679	Structural maintenance of chromosomes protein OS=Rattus norvegicus OX=10116 GN=Smc2 PE=1 SV=1	Smc2	D4A5Q2	19.4757	NaN	18.7331	17.2182	19.6949	19.9079	20.4174	20.0883
2680	Structural maintenance of chromosomes protein OS=Rattus norvegicus OX=10116 GN=Smc4 PE=1 SV=1	Smc4	F1MAD9	20.4427	20.527	19.5148	20.6532	23.8964	23.5471	23.5779	23.9007
2681	STT3A, catalytic subunit of the oligosaccharyltransferase complex OS=Rattus norvegicus OX=10116 GN=Stt3a PE=1 SV=1	Stt3a	A0A0G2JWH5	15.6713	15.8012	15.4619	16.456	17.5487	18.9213	17.6538	18.2869
2682	Submandibular gland protein C OS=Rattus norvegicus OX=10116 GN=Smgc PE=4 SV=3	Smgc	E9PTP9	24.1359	23.5342	24.0392	25.2867	18.0283	18.0035	17.5884	18.1621
2683	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sdha PE=1	Sdha	Q920L2	19.2638	19.6684	16.3717	17.3504	21.6229	23.0282	22.5565	22.7753
2684	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sdhb PE=2	Sdhb	P21913	16.5424	16.5043	NaN	16.9788	19.4805	20.732	20.3144	20.4472
2685	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Rattus norvegicus OX=10116 GN=Suclg1 PE=	Suclg1	A0A0H2UHE1	16.9496	18.9208	NaN	NaN	16.2655	20.1225	18.5784	19.574
2686	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sucla2 PE=1 SV=1	Sucla2	F1LM47	17.2737	NaN	NaN	NaN	18.5263	19.591	18.3702	18.7732
2687	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Suclg2 PE=1 SV=2	Suclg2	F1LPV8	NaN	NaN	NaN	NaN	16.8523	18.3936	17.8477	17.9552
2688	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Oxct1 PE=1 SV=1	Oxct1	B2GV06	21.0758	20.9935	21.4932	21.0815	18.9095	20.7348	20.17	20.4413
2689	Sulfhydryl oxidase 1 OS=Rattus norvegicus OX=10116 GN=Qsox1 PE=1 SV=1	Qsox1	Q6IUU3	22.2918	21.8925	21.8739	22.015	19.3084	19.2535	18.7829	18.318
2690	SUMO-activating enzyme subunit 1 OS=Rattus norvegicus OX=10116 GN=Sae1 PE=2 SV=1	Sae1	Q6AXQ0	15.716	15.4044	NaN	NaN	19.5151	18.858	19.6374	19.7982
2691	Superoxide dismutase [Cu-Zn] OS=Rattus norvegicus OX=10116 GN=Sod1 PE=1 SV=2	Sod1	P07632	20.239	19.5589	20.7882	19.1896	21.2833	21.6238	21.173	20.8007
2692	Superoxide dismutase [Mn], mitochondrial OS=Rattus norvegicus OX=10116 GN=Sod2 PE=1 SV=2	Sod2	P07895	NaN	16.4984	NaN	NaN	NaN	NaN	NaN	NaN
2693	Suppressor of glucose, autophagy-associated 1 OS=Rattus norvegicus OX=10116 GN=Soga1 PE=4 SV=1	Soga1	A0A0G2KA88	NaN	NaN	NaN	NaN	NaN	17.8443	17.6703	17.1934
2694	Suppressor of IKBKE 1 OS=Rattus norvegicus OX=10116 GN=Sike1 PE=2 SV=1	Sike1	Q5FWT9	NaN	NaN	NaN	NaN	17.4799	16.7139	16.5971	NaN
2695	Suprabasin OS=Rattus norvegicus OX=10116 GN=Sbsn PE=1 SV=1	Sbsn	F7FEM5	21.4729	20.2173	20.8454	19.4092	19.827	19.8115	19.8868	19.6194
2696	Survival motor neuron protein OS=Rattus norvegicus OX=10116 GN=Smn1 PE=1 SV=1	Smn1	O35876	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2697	Survival of motor neuron-related-splicing factor 30 OS=Rattus norvegicus OX=10116 GN=Smndc1 PE=1 SV=1	Smndc1	A0A096MKB9	NaN	NaN	NaN	NaN	17.6896	NaN	17.2715	NaN
2698	SWAP complex protein (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Swap70 PE=1 SV=1	Swap70	D3ZRE7	NaN	16.9416	15.6954	NaN	20.5793	19.9687	19.7897	19.9156
2699	Swi5-dependent recombination DNA repair protein 1 homolog OS=Rattus norvegicus OX=10116 GN=Sfr1 PE=1 SV=1	Sfr1	A0A0H2UHK0	15.9114	NaN	NaN	17.0787	20.2731	18.0148	19.3864	18.3683
2700	Synapse associated protein 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Syap1 PE=1 SV=1	Syap1	F7F350	14.196	14.6095	17.2194	NaN	21.642	21.3907	22.2616	21.7878
2701	Synaptic functional regulator FMR1 OS=Rattus norvegicus OX=10116 GN=Fmr1 PE=1 SV=1	Fmr1	A0A0G2JZV8	NaN	NaN	NaN	NaN	17.9352	18.2057	16.6835	16.7304

2702	Synaptic vesicle membrane protein VAT-1 homolog OS=Rattus norvegicus OX=10116 GN=Vat1 PE=1 SV=1	Vat1	Q3MIE4	21.4803	21.5783	20.9582	21.0637	24.0544	23.5012	23.4839	23.3847
2703	Synaptobrevin homolog YKT6 OS=Rattus norvegicus OX=10116 GN=Ykt6 PE=1 SV=1	Ykt6	Q5EGY4	16.9766	NaN	NaN	17.1835	21.9007	20.961	21.4466	21.5079
2704	Synaptogyrin-1 (Fragment) OS=Rattus norvegicus OX=10116 GN=Syngr1 PE=4 SV=2	Syngr1	A0A0G2K3P9	NaN	NaN	NaN	15.4557	17.3491	18.1305	17.0222	16.5847
2705	Synaptogyrin-2 OS=Rattus norvegicus OX=10116 GN=Syngr2 PE=1 SV=2	Syngr2	O54980	NaN	NaN	NaN	NaN	19.2412	17.9585	18.0198	18.4863
2706	Synaptophysin-like 1 OS=Rattus norvegicus OX=10116 GN=Sypl1 PE=1 SV=1	Sypl1	A0A0G2KA82	17.2673	18.9709	16.9112	17.2581	21.5492	21.5188	21.2786	21.2756
2707	Synaptopodin 2-like OS=Rattus norvegicus OX=10116 GN=Synpo2l PE=1 SV=1	Synpo2l	D3ZZ68	19.9375	21.2722	19.3865	19.4939	21.7873	22.3215	21.8509	21.4336
2708	Synaptopodin-2 OS=Rattus norvegicus OX=10116 GN=Synpo2 PE=1 SV=2	Synpo2	D4A702	18.6408	18.1543	18.3734	18.198	20.0572	19.8871	18.8262	18.4267
2709	Synaptosomal-associated protein OS=Rattus norvegicus OX=10116 PE=3 SV=2	Snap23	M0R4V3	NaN	NaN	NaN	NaN	18.7081	17.9086	17.5855	18.1115
2710	Synergin gamma OS=Rattus norvegicus OX=10116 GN=Synrg PE=1 SV=3	Synrg	Q9JKC9	17.6463	18.428	17.9633	NaN	18.7061	18.8346	19.0557	18.7551
2711	Syntaxin 16 OS=Rattus norvegicus OX=10116 GN=Stx16 PE=1 SV=1	Stx16	A0A0G2K528	19.5967	18.9817	19.6421	NaN	19.7907	19.5738	18.3992	18.87
2712	Syntaxin-12 OS=Rattus norvegicus OX=10116 GN=Stx12 PE=1 SV=1	Stx12	A0A0G2JVB6	18.6991	18.5543	17.5828	19.9608	22.6977	23.0098	22.5091	22.4206
2713	Syntaxin-17 OS=Rattus norvegicus OX=10116 GN=Stx17 PE=1 SV=1	Stx17	Q9Z158	NaN	17.0317	NaN	17.0761	NaN	NaN	17.9258	17.6433
2714	Syntaxin-5 OS=Rattus norvegicus OX=10116 GN=Stx5 PE=1 SV=2	Stx5	Q08851	NaN	NaN	NaN	NaN	NaN	15.7466	15.754	16.0708
2715	Syntaxin-6 OS=Rattus norvegicus OX=10116 GN=Stx6 PE=1 SV=1	Stx6	Q63635	15.7414	15.3332	NaN	NaN	19.7009	19.5403	19.3879	19.0557
2716	Syntaxin-7 OS=Rattus norvegicus OX=10116 GN=Stx7 PE=1 SV=4	Stx7	O70257	18.858	18.7288	18.8779	19.532	21.0004	20.6345	20.1723	20.4184
2717	Syntaxin-8 OS=Rattus norvegicus OX=10116 GN=Stx8 PE=1 SV=1	Stx8	Q9Z2Q7	20.9395	19.8295	20.3043	21.3	17.7164	17.3371	16.9743	16.6763
2718	Syntaxin-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Stxbp1 PE=1 SV=1	Stxbp1	P61765	NaN	14.8924	14.8176	14.9553	17.1479	17.9491	16.6984	17.5883
2719	Syntenin-1 OS=Rattus norvegicus OX=10116 GN=Sdcbp PE=1 SV=1	Sdcbp	Q9JI92	NaN	15.5926	17.9008	15.6468	19.6375	19.4552	19.6601	19.3645
2720	Talin 2 OS=Rattus norvegicus OX=10116 GN=Tln2 PE=1 SV=3	Tln2	D3ZA84	18.1186	17.3982	18.3687	18.7779	22.3782	22.9099	23.0124	23.2266
2721	Tankyrase 1-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Tnks1bp1 PE=1 SV=1	Tnks1bp1	D3ZF26	18.9773	19.6443	18.6172	19.6675	17.8158	19.7823	18.6512	18.6617
2722	Target of myb1 homolog (Chicken) OS=Rattus norvegicus OX=10116 GN=Tom1 PE=1 SV=1	Tom1	Q5XI21	17.3086	17.7651	16.0632	17.4488	22.3678	21.196	21.52	21.3797
2723	Target of myb1-like 2 membrane-trafficking protein OS=Rattus norvegicus OX=10116 GN=Tom1l2 PE=1 SV=1	Tom1l2	A0A0G2K9L2	18.9058	18.3553	17.5568	15.097	21.8471	21.0899	21.4012	21.2951
2724	TATA-box-binding protein-like 1 OS=Rattus norvegicus OX=10116 GN=Tbpl1 PE=4 SV=1	Tbpl1	D4A898	NaN	NaN	NaN	NaN	NaN	16.9453	NaN	NaN
2725	Tax1-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Tax1bp3 PE=1 SV=1	Tax1bp3	A0A1W2Q5Z6	14.6011	14.4486	NaN	NaN	19.1716	18.6178	19.0618	19.2946
2726	Taxilin alpha OS=Rattus norvegicus OX=10116 GN=Txlna PE=1 SV=1	Txlna	B2GV14	16.8253	15.7994	15.7887	13.9844	16.3784	20.3284	19.7927	18.0949
2727	Taxilin beta OS=Rattus norvegicus OX=10116 GN=Txlnb PE=1 SV=1	Txlnb	A0A0G2K2T1	21.8441	21.8681	22.1567	21.6008	22.9446	24.0895	23.9859	23.7343
2728	TBC1 domain family member 1 OS=Rattus norvegicus OX=10116 GN=Tbc1d1 PE=1 SV=1	Tbc1d1	D4AC16	16.6832	16.3089	16.4295	NaN	19.9508	19.7214	20.1012	19.6747
2729	TBC1 domain family member 8B OS=Rattus norvegicus OX=10116 GN=Tbc1d8b PE=1 SV=1	Tbc1d8b	A0A0G2K9M5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2730	TBC1 domain family, member 10b OS=Rattus norvegicus OX=10116 GN=Tbc1d10b PE=1 SV=1	Tbc1d10b	D3ZSY8	NaN	NaN	NaN	15.6269	17.362	NaN	17.6451	17.605
2731	TBC1 domain family, member 13 OS=Rattus norvegicus OX=10116 GN=Tbc1d13 PE=1 SV=3	Tbc1d13	D4AEG7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2732	TBC1 domain family, member 15 OS=Rattus norvegicus OX=10116 GN=Tbc1d15 PE=1 SV=2	Tbc1d15	F7EZ89	17.2715	17.775	17.881	17.0862	20.5518	20.1469	20.2113	20.4571
2733	TBC1 domain family, member 17 OS=Rattus norvegicus OX=10116 GN=Tbc1d17 PE=1 SV=1	Tbc1d17	B1H264	15.3864	15.259	14.7268	15.1242	20.3839	19.966	20.3856	20.4811
2734	TBC1 domain family, member 4 OS=Rattus norvegicus OX=10116 GN=Tbc1d4 PE=1 SV=3	Tbc1d4	D3ZGN0	19.5064	19.4408	19.941	19.127	21.7058	20.8841	21.083	20.5871
2735	T-complex protein 1 subunit alpha OS=Rattus norvegicus OX=10116 GN=Tcp1 PE=1 SV=1	Tcp1	P28480	20.4103	20.4158	19.8214	20.108	24.0825	24.4391	25.0372	25.5258
2736	T-complex protein 1 subunit beta OS=Rattus norvegicus OX=10116 GN=Cct2 PE=1 SV=3	Cct2	Q5XIM9	19.8842	20.1555	20.119	19.5198	24.4415	23.9927	25.1062	25.666
2737	T-complex protein 1 subunit delta OS=Rattus norvegicus OX=10116 GN=Cct4 PE=1 SV=3	Cct4	Q7TPB1	21.4547	20.7718	21.055	21.0003	24.237	23.9853	25.585	25.9203
2738	T-complex protein 1 subunit epsilon OS=Rattus norvegicus OX=10116 GN=Cct5 PE=1 SV=1	Cct5	Q68FQ0	18.0708	19.096	19.4151	19.6219	24.5998	24.1365	25.0178	25.1909
2739	T-complex protein 1 subunit eta OS=Rattus norvegicus OX=10116 GN=Cct7 PE=1 SV=1	Cct7	D4AC23	19.3749	19.7485	19.6286	19.5536	23.7746	23.6463	24.8761	25.5836
2740	T-complex protein 1 subunit gamma OS=Rattus norvegicus OX=10116 GN=Cct3 PE=1 SV=1	Cct3	Q6P502	19.1339	19.7132	19.7761	19.8035	24.1224	24.0612	25.222	25.5827
2741	Tectonin beta-propeller repeat-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Tecpr1 PE=2 SV=1	Tecpr1	Q3ZBA0	NaN	NaN	NaN	NaN	18.2592	18.4965	19.2572	18.7207
2742	Tenascin C OS=Rattus norvegicus OX=10116 GN=Tnc PE=1 SV=1	Tnc	A0A0G2K1L0	20.2278	20.3677	20.6161	20.1238	20.1273	19.7656	19.6921	19.502
2743	Tensin 1 OS=Rattus norvegicus OX=10116 GN=Tns1 PE=1 SV=2	Tns1	F1LN42	17.2744	16.7604	18.5162	16.5293	24.0578	24.3859	24.2597	23.7832
2744	Tensin 3 OS=Rattus norvegicus OX=10116 GN=Tns3 PE=1 SV=2	Tns3	F1LN91	NaN	16.4894	NaN	NaN	19.1496	18.6889	19.4632	18.663
2745	Terminal uridylyl transferase 4 OS=Rattus norvegicus OX=10116 GN=Tut4 PE=1 SV=1	Tut4	A0A0G2JZ04	NaN	NaN	NaN	NaN	NaN	16.182	NaN	14.0297
2746	Tescalcin OS=Rattus norvegicus OX=10116 GN=Tesc PE=4 SV=1	Tesc	D3ZTN1	NaN	16.4412	16.6029	NaN	22.8247	21.9114	22.2481	22.4984
2747	Testin OS=Rattus norvegicus OX=10116 GN=Tes PE=1 SV=1	Tes	Q2LAP6	NaN	NaN	NaN	NaN	16.9087	17.4117	17.9685	18.2893
2748	Tetraspanin OS=Rattus norvegicus OX=10116 GN=Cd81 PE=1 SV=1	Cd81	Q6P9V1	17.8037	17.5023	17.5955	NaN	20.5851	18.9859	20.2251	20.5791
2749	Tetraspanin OS=Rattus norvegicus OX=10116 GN=Tspan18 PE=3 SV=1	Tspan18	D4A3U2	NaN	NaN	NaN	17.6141	19.2309	19.1725	18.9052	18.9666
2750	Tetraspanin OS=Rattus norvegicus OX=10116 GN=Tspan6 PE=1 SV=1	Tspan6	B0BN20	18.6694	18.7172	18.3036	17.732	19.5419	19.7833	18.6798	19.6288
2751	Tetraspanin OS=Rattus norvegicus OX=10116 GN=Tspan8 PE=2 SV=2	Tspan8	O55158	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2752	Tetraspanin OS=Rattus norvegicus OX=10116 GN=Tspan9 PE=1 SV=1	Tspan9	D4AAV9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2753	Tetraspanin-31 OS=Rattus norvegicus OX=10116 GN=Tspan31 PE=2 SV=1	Tspan31	Q5U1V9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2754	Tetratricopeptide repeat domain 1 OS=Rattus norvegicus OX=10116 GN=Ttc1 PE=1 SV=1	Ttc1	Q66H09	16.8776	17.2195	17.4568	15.8112	20.745	18.3229	19.5843	19.8324

2755	Tetratricopeptide repeat domain 38 OS=Rattus norvegicus OX=10116 GN=Ttc38 PE=1 SV=2	Ttc38	D4ACL2	16.4834	16.9638	16.9921	13.5377	16.0045	17.3629	18.1754	16.6056
2756	Tetratricopeptide repeat domain 7B OS=Rattus norvegicus OX=10116 GN=Ttc7b PE=1 SV=3	Ttc7b	F1LUY5	20.4847	20.4243	20.3577	20.6659	NaN	17.2232	16.8563	16.6112
2757	Thioredoxin domain containing 1 OS=Rattus norvegicus OX=10116 GN=Tmx1 PE=1 SV=1	Tmx1	Q52KJ9	NaN	NaN	NaN	NaN	18.2357	18.2976	17.2533	18.1591
2758	Thioredoxin domain containing 13 OS=Rattus norvegicus OX=10116 GN=Tmx4 PE=1 SV=1	Tmx4	G3V912	15.7371	NaN	NaN	16.4841	19.5424	19.5801	19.0406	19.1983
2759	Thioredoxin domain containing 9 OS=Rattus norvegicus OX=10116 GN=Txndc9 PE=1 SV=1	Txndc9	Q5M8C7	14.7921	17.6411	14.5542	16.3372	17.0638	16.5964	16.3355	16.6652
2760	Thioredoxin domain-containing protein 12 OS=Rattus norvegicus OX=10116 GN=Txndc12 PE=2 SV=2	Txndc12	Q498E0	NaN	NaN	NaN	NaN	19.5852	20.1349	19.6251	19.9062
2761	Thioredoxin domain-containing protein 15 OS=Rattus norvegicus OX=10116 GN=Txndc15 PE=2 SV=1	Txndc15	Q5BJT4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2762	Thioredoxin OS=Rattus norvegicus OX=10116 GN=Txn PE=1 SV=2	Txn1	P11232	19.5197	20.8532	20.3215	20.3716	23.0932	22.7398	22.7764	22.9935
2763	Thioredoxin-interacting protein OS=Rattus norvegicus OX=10116 GN=Txnip PE=2 SV=1	Txnip	Q5M7W1	15.951	16.1872	15.7141	NaN	18.4491	15.6973	16.2262	16.5529
2764	Thioredoxin-like protein 1 OS=Rattus norvegicus OX=10116 GN=Txnl1 PE=1 SV=1	Txnl1	A0A0G2K737	19.9421	14.174	19.9065	19.1748	20.8054	21.0978	21.68	21.3078
2765	Thioredoxin-related transmembrane protein 2 OS=Rattus norvegicus OX=10116 GN=Tmx2 PE=2 SV=1	Tmx2	Q5XIK2	15.6662	15.0959	14.9002	15.6658	20.014	20.555	18.7504	20.7041
2766	Thioredoxin-related transmembrane protein 3 OS=Rattus norvegicus OX=10116 GN=Tmx3 PE=1 SV=2	Tmx3	M0R402	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2767	Threonine--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Tars PE=1 SV=1	Tars1	A0A0G2K9V6	NaN	NaN	NaN	NaN	NaN	NaN	16.8093	NaN
2768	Threonyl-tRNA synthetase-like 2 OS=Rattus norvegicus OX=10116 GN=Tarsl2 PE=2 SV=1	Tars3	Q5XI17	14.378	NaN	NaN	NaN	18.6451	17.5526	18.6117	18.5908
2769	Thrombomodulin OS=Rattus norvegicus OX=10116 GN=Thbd PE=1 SV=1	Thbd	O35370	NaN	15.561	NaN	15.2729	16.6295	18.4749	17.6002	17.5499
2770	Thrombospondin 1 OS=Rattus norvegicus OX=10116 GN=Thbs1 PE=1 SV=2	Thbs1	M0R979	25.3524	25.004	25.669	25.0218	20.8869	19.6962	20.502	20.6553
2771	Thrombospondin-4 OS=Rattus norvegicus OX=10116 GN=Thbs4 PE=4 SV=1	Thbs4	A0A0G2K7L8	21.091	20.5093	21.2731	21.4242	18.673	18.7391	18.3705	17.7708
2772	Thy-1 membrane glycoprotein OS=Rattus norvegicus OX=10116 GN=Thy1 PE=1 SV=1	Thy1	P01830	16.4293	16.0328	NaN	16.8596	NaN	NaN	NaN	NaN
2773	Thymidylate synthase OS=Rattus norvegicus OX=10116 GN=Tyms PE=1 SV=1	Tyms	P45352	NaN	NaN	NaN	NaN	17.4445	NaN	17.9019	17.3507
2774	Thymosin beta-10 OS=Rattus norvegicus OX=10116 GN=Tmsb10 PE=1 SV=2	Tmsb10	P63312	NaN	19.5019	17.0842	19.6039	17.2675	20.3535	17.6663	20.2726
2775	Thymosin beta-4 OS=Rattus norvegicus OX=10116 GN=Tmsb4x PE=1 SV=2	Tmsb4x	P62329	20.9751	21.3077	21.4842	20.6608	22.4766	22.3373	22.1749	22.4916
2776	Thyroid hormone receptor interactor 11 OS=Rattus norvegicus OX=10116 GN=Trip11 PE=1 SV=3	Trip11	D4ABD7	15.8348	14.2884	15.1321	16.3247	21.0646	20.5469	20.141	20.8055
2777	Thyroxine-binding globulin OS=Rattus norvegicus OX=10116 GN=Serpina7 PE=3 SV=1	Serpina7	A0A140TAB0	18.9644	19.9332	18.8271	NaN	18.4388	18.1405	17.9195	18.3188
2778	Tia1 cytotoxic granule-associated RNA-binding protein-like 1 OS=Rattus norvegicus OX=10116 GN=Tial1 PE=1 SV=1	Tial1	Q5BJN3	15.6293	15.8282	15.8054	14.7086	19.5671	18.1812	19.0361	17.8225
2779	Tight junction protein 2 OS=Rattus norvegicus OX=10116 GN=Tjp2 PE=1 SV=1	Tjp2	Q3ZB99	NaN	NaN	NaN	NaN	NaN	17.4952	17.2342	16.8562
2780	Tight junction protein ZO-1 OS=Rattus norvegicus OX=10116 GN=Tjp1 PE=1 SV=1	Tjp1	A0A0G2K2P5	21.4645	21.0841	21.6785	21.2468	20.58	21.0122	20.0975	20.4462
2781	Tight junction-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Tjap1 PE=1 SV=1	Tjap1	A0A0G2K0W5	19.6677	19.6521	19.2049	17.2236	18.4038	18.5599	18.2391	18.208
2782	TIP41-like protein OS=Rattus norvegicus OX=10116 GN=Tiprl PE=1 SV=1	Tiprl	A2VCX1	NaN	NaN	NaN	15.3524	20.477	18.8189	20.312	20.0193
2783	Tissue factor pathway inhibitor OS=Rattus norvegicus OX=10116 GN=Tfpi PE=2 SV=1	Tfpi	Q02445	18.3175	18.0461	17.9374	18.5104	NaN	NaN	NaN	NaN
2784	Tissue specific transplantation antigen P35B (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tsta3 PE=1 S	Gfus	G3V762	16.874	NaN	16.6639	16.2867	17.8437	18.16	19.0758	18.2477
2785	Tissue-type transglutaminase OS=Rattus norvegicus OX=10116 GN=Tgm2 PE=1 SV=1	Tgm2	Q9WVJ6	20.3199	19.4358	19.154	18.8928	25.4652	26.7673	27.1562	26.8884
2786	T-kininogen 1 OS=Rattus norvegicus OX=10116 GN=Map1 PE=1 SV=2	Kng2	P01048	26.152	26.2247	26.2993	25.9375	23.7035	23.1606	22.8946	23.3888
2787	T-kininogen 2 OS=Rattus norvegicus OX=10116 PE=1 SV=2	Kng1	P08932	28.3264	28.6085	28.5681	28.3115	25.9687	25.8312	25.2805	25.9956
2788	TMEM9 domain family, member B OS=Rattus norvegicus OX=10116 GN=Tmem9b PE=1 SV=2	Tmem9b	F1LQ83	NaN	NaN	NaN	NaN	NaN	18.1508	17.5465	17.6654
2789	TNFRSF1A-associated via death domain OS=Rattus norvegicus OX=10116 GN=Tradd PE=1 SV=1	Tradd	D3ZZC5	NaN	NaN	NaN	NaN	18.8323	18.547	18.6493	17.8278
2790	Toll-interacting protein OS=Rattus norvegicus OX=10116 GN=Tollip PE=1 SV=1	Tollip	A2RUW1	17.7603	15.4265	16.1512	NaN	19.3921	18.6307	18.5893	18.8872
2791	Trafficking kinesin-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Trak2 PE=1 SV=2	Trak2	Q8R2H7	17.8212	17.4873	16.8829	16.2689	19.9629	20.2143	19.7808	20.0409
2792	Trafficking protein particle complex 12 OS=Rattus norvegicus OX=10116 GN=Trappc12 PE=1 SV=1	Trappc12	D3ZE49	NaN	NaN	NaN	NaN	NaN	14.9447	NaN	15.7739
2793	Trafficking protein particle complex subunit 13 OS=Rattus norvegicus OX=10116 GN=Trappc13 PE=2 SV=2	Trappc13	Q5M887	NaN	NaN	NaN	NaN	16.3173	16.9664	16.7789	16.9146
2794	Trafficking protein particle complex subunit 3 OS=Rattus norvegicus OX=10116 GN=Trappc3 PE=2 SV=1	Trappc3	Q5U1Z2	19.0331	19.408	18.8883	17.7366	19.5829	20.5129	20.4605	20.2824
2795	Transaldolase OS=Rattus norvegicus OX=10116 GN=Taldo1 PE=1 SV=2	Taldo1	Q9EQS0	NaN	NaN	NaN	NaN	17.294	NaN	NaN	16.3705
2796	Transcobalamin 2, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tcn2 PE=4 SV=1	Tcn2	G3V6K1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2797	Transcription elongation factor A protein 1 OS=Rattus norvegicus OX=10116 GN=Tcea1 PE=1 SV=1	Tcea1	Q4KLL0	19.2163	19.8572	19.7641	18.7943	20.0992	NaN	19.161	17.7099
2798	Transcription elongation factor SPT4 OS=Rattus norvegicus OX=10116 GN=Supt4h1 PE=1 SV=1	Supt4h1	B5DEM7	NaN	NaN	NaN	NaN	17.674	NaN	NaN	NaN
2799	Transcription factor BTF3 OS=Rattus norvegicus OX=10116 GN=Btf3 PE=1 SV=1	Btf3	Q5U3Y8	15.4977	NaN	NaN	NaN	21.6671	21.9907	21.477	21.4789
2800	Transcription factor BTF3 OS=Rattus norvegicus OX=10116 GN=Btf3l4 PE=1 SV=1	Btf3l4	D4A3I4	18.4331	18.2649	NaN	NaN	20.4383	20.1541	20.4078	20.4696
2801	Transcription factor EB OS=Rattus norvegicus OX=10116 GN=Tfeb PE=1 SV=1	Tfeb	F7F5J1	NaN	NaN	NaN	NaN	18.7828	19.9943	19.1875	19.262
2802	Transcription factor GATA-4 OS=Rattus norvegicus OX=10116 GN=Gata4 PE=1 SV=1	Gata4	P46152	NaN	NaN	NaN	NaN	NaN	17.4967	NaN	17.5517
2803	Transcription factor Sp1 OS=Rattus norvegicus OX=10116 GN=Sp1 PE=1 SV=2	Sp1	Q01714	NaN	NaN	NaN	NaN	17.4573	16.7771	16.6414	16.5691
2804	Transcription intermediary factor 1-beta OS=Rattus norvegicus OX=10116 GN=Trim28 PE=1 SV=2	Trim28	O08629	18.1234	18.0481	19.3273	19.0043	22.4622	22.5303	22.6892	22.2769
2805	Transcriptional activator protein Pur-alpha OS=Rattus norvegicus OX=10116 GN=Pura PE=1 SV=3	Pura	F1LPS8	NaN	NaN	NaN	NaN	NaN	NaN	16.9672	NaN
2806	Transcriptional activator protein Pur-beta OS=Rattus norvegicus OX=10116 GN=Purb PE=1 SV=1	Purb	A0A0G2JUX5	NaN	NaN	NaN	NaN	20.4008	21.7226	21.1609	21.1963
2807	Transducin (Beta)-like 1 X-linked (Predicted) OS=Rattus norvegicus OX=10116 GN=Tbl1x PE=1 SV=1	Tbl1x	G3V6G5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

2808	Transferrin receptor protein 1 OS=Rattus norvegicus OX=10116 GN=Tfrc PE=1 SV=1	Tfrc	G3V679	25.0914	24.103	24.6622	25.3224	23.6081	24.1319	23.3443	23.201
2809	Transforming growth factor beta-1-induced transcript 1 protein OS=Rattus norvegicus OX=10116 GN=Tgfb1i1 PE=1 SV=2	Tgfb1i1	Q99PD6	14.9899	NaN	NaN	16.4261	23.6582	23.6525	23.6823	23.2326
2810	Transforming growth factor, beta-induced OS=Rattus norvegicus OX=10116 GN=Tgfbi PE=1 SV=2	Tgfbi	D4A8G5	18.7852	18.8989	19.0575	18.4792	16.8279	16.7219	NaN	NaN
2811	Transforming protein RhoA OS=Rattus norvegicus OX=10116 GN=Rhoa PE=1 SV=1	Rhoa	P61589	19.7837	20.9975	20.459	20.0073	23.7552	23.5426	23.4239	23.5871
2812	Transforming, acidic coiled-coil-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Tacc1 PE=1 SV=1	Tacc1	D4A927	NaN	16.9335	17.5732	NaN	15.8044	16.0528	15.1955	15.6129
2813	Transforming, acidic coiled-coil-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Tacc2 PE=1 SV=1	Tacc2	A0A0G2K598	19.1643	19.0762	17.212	18.324	19.5875	20.5032	20.2526	19.9215
2814	Transforming, acidic coiled-coil-containing protein 3 OS=Rattus norvegicus OX=10116 GN=Tacc3 PE=1 SV=3	Tacc3	D3Z962	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2815	Transgelin OS=Rattus norvegicus OX=10116 GN=Tagln PE=1 SV=1	Tagln	A0A0G2JWK7	21.86	21.5516	21.1508	20.7728	23.971	23.0637	23.2924	23.5139
2816	Transgelin-2 OS=Rattus norvegicus OX=10116 GN=Tagln2 PE=1 SV=1	Tagln2	Q5XFX0	20.283	21.4012	20.2644	20.6073	25.1356	24.3035	24.7038	24.7783
2817	Transglutaminase 5 OS=Rattus norvegicus OX=10116 GN=Tgm5 PE=4 SV=1	Tgm5	A0A0G2K142	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2818	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus OX=10116 GN=Vcp PE=1 SV=3	Vcp	P46462	20.0004	20.8295	20.7299	21.0599	24.3781	23.5993	23.8379	24.1513
2819	Transketolase OS=Rattus norvegicus OX=10116 GN=Tkt PE=1 SV=1	Tkt	G3V826	19.8333	19.3828	20.2215	20.5686	20.7717	18.3498	20.004	20.1086
2820	Translation initiation factor eIF-2B subunit alpha OS=Rattus norvegicus OX=10116 GN=Eif2b1 PE=1 SV=1	Eif2b1	A0A0U1RRZ2	NaN	NaN	NaN	NaN	NaN	NaN	17.7337	NaN
2821	Translation initiation factor eIF-2B subunit beta OS=Rattus norvegicus OX=10116 GN=Eif2b2 PE=1 SV=1	Eif2b2	F7EVX2	NaN	NaN	NaN	NaN	17.8438	19.2563	19.1541	17.1837
2822	Translation initiation factor eIF-2B subunit delta OS=Rattus norvegicus OX=10116 GN=Eif2b4 PE=2 SV=1	Eif2b4	Q63186	17.3873	15.9657	16.5331	12.8712	19.9225	21.5986	21.6715	21.3974
2823	Translation initiation factor eIF-2B subunit epsilon OS=Rattus norvegicus OX=10116 GN=Eif2b5 PE=1 SV=2	Eif2b5	Q64350	17.6665	NaN	17.1911	16.5853	19.2037	18.7345	19.3019	19.3487
2824	Translation initiation factor eIF-2B subunit gamma OS=Rattus norvegicus OX=10116 GN=Eif2b3 PE=2 SV=2	Eif2b3	P70541	NaN	NaN	NaN	NaN	17.0811	19.358	19.6649	19.7315
2825	Translationally-controlled tumor protein OS=Rattus norvegicus OX=10116 GN=Tpt1 PE=1 SV=1	Tpt1	P63029	17.001	18.2513	18.0512	18.2543	19.7127	20.4538	19.8915	19.7689
2826	Translin OS=Rattus norvegicus OX=10116 GN=Tsn PE=1 SV=1	Tsn	A0A1B0GWQ7	NaN	NaN	NaN	NaN	18.0064	17.4364	17.7876	17.746
2827	Translocon-associated protein subunit alpha OS=Rattus norvegicus OX=10116 GN=Ssr1 PE=1 SV=1	Ssr1	A0A0G2K075	15.9719	17.9168	16.2639	17.1108	17.9366	18.4274	18.906	19.0321
2828	Translocon-associated protein subunit delta OS=Rattus norvegicus OX=10116 GN=Ssr4 PE=2 SV=1	Ssr4	Q07984	17.5842	18.4171	17.475	17.2653	19.4491	19.2486	19.4577	19.5806
2829	Transmembrane 9 superfamily member 2 OS=Rattus norvegicus OX=10116 GN=Tm9sf2 PE=2 SV=1	Tm9sf2	Q66HG5	NaN	15.1388	NaN	NaN	19.6339	20.3759	19.8397	19.8503
2830	Transmembrane 9 superfamily member OS=Rattus norvegicus OX=10116 GN=Tm9sf3 PE=1 SV=2	Tm9sf3	D3ZUD8	NaN	17.0425	NaN	NaN	NaN	NaN	NaN	NaN
2831	Transmembrane 9 superfamily member OS=Rattus norvegicus OX=10116 GN=Tm9sf4 PE=1 SV=1	Tm9sf4	A0A0G2KA25	NaN	NaN	NaN	NaN	16.4166	15.2983	NaN	16.398
2832	Transmembrane emp24 domain-containing protein 10 OS=Rattus norvegicus OX=10116 GN=Tmed10 PE=1 SV=2	Tmed10	Q63584	20.0718	20.3968	20.1424	19.4588	21.819	22.3646	21.434	21.8423
2833	Transmembrane emp24 domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Tmed2 PE=1 SV=1	Tmed2	Q63524	19.662	19.8618	19.8222	18.4446	21.677	22.1849	21.6159	21.6975
2834	Transmembrane emp24 domain-containing protein 7 OS=Rattus norvegicus OX=10116 GN=Tmed7 PE=1 SV=1	Tmed7	D3ZTX0	18.9384	18.7644	19.3687	18.4083	20.3512	21.2978	19.9308	20.595
2835	Transmembrane emp24 domain-containing protein 9 OS=Rattus norvegicus OX=10116 GN=Tmed9 PE=1 SV=1	Tmed9	Q5I0E7	19.1021	19.7364	19.0985	18.4575	20.6162	21.2889	20.537	20.8346
2836	Transmembrane emp24 protein transport domain containing 4 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116	Tmed4	G3V6N2	16.0264	16.3324	NaN	14.2767	18.6094	18.7377	18.8743	18.6534
2837	Transmembrane protein 206 OS=Rattus norvegicus OX=10116 GN=Tmem206 PE=1 SV=1	Pacc1	Q66H28	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2838	Transmembrane protein 214 OS=Rattus norvegicus OX=10116 GN=Tmem214 PE=2 SV=1	Tmem214	A1L1L2	NaN	NaN	NaN	NaN	NaN	15.9032	NaN	15.7106
2839	Transmembrane protein 33 OS=Rattus norvegicus OX=10116 GN=Tmem33 PE=2 SV=1	Tmem33	Q9Z142	NaN	15.5036	NaN	NaN	17.4986	17.1527	16.8176	17.2606
2840	Transmembrane protein 38a (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Tmem38a PE=4 SV=1	Tmem38a	G3V9T4	NaN	NaN	15.834	NaN	18.845	18.6159	17.9458	18.0188
2841	Transportin 1 OS=Rattus norvegicus OX=10116 GN=Tnpo1 PE=1 SV=3	Tnpo1	F1LQP9	19.7811	NaN	20.9244	19.6824	21.4779	20.9966	20.6599	20.2592
2842	Transportin 2 OS=Rattus norvegicus OX=10116 GN=Tnpo2 PE=1 SV=2	Tnpo2	D3ZER6	NaN	NaN	NaN	NaN	18.6765	18.4043	18.6781	18.2076
2843	Transthyretin OS=Rattus norvegicus OX=10116 GN=Ttr PE=1 SV=1	Ttr	P02767	25.9916	26.3494	26.6006	25.8089	22.1448	21.6163	21.939	21.9704
2844	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hadha PE=1 SV=2	Hadha	Q64428	17.4362	19.1654	16.6924	17.7693	20.3907	22.5709	21.8794	21.8845
2845	Trifunctional enzyme subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hadhb PE=1 SV=1	Hadhb	Q60587	19.5514	18.9454	16.511	20.3111	20.0909	21.7859	21.5011	21.6219
2846	Trifunctional purine biosynthetic protein adenosine-3 OS=Rattus norvegicus OX=10116 GN=Gart PE=1 SV=1	Gart	G3V918	19.1656	19.2662	19.0024	18.6308	21.8047	21.8792	23.5947	23.5803
2847	Triggering receptor-expressed on myeloid cells-like 1 OS=Rattus norvegicus OX=10116 GN=Treml1 PE=1 SV=3	Treml1	D3ZYT6	18.2865	15.3799	18.3961	15.5937	21.7528	21.5637	21.8916	21.9778
2848	Trinucleotide repeat-containing 6B OS=Rattus norvegicus OX=10116 GN=Tnrc6b PE=1 SV=2	Tnrc6b	F1LV37	16.8255	NaN	NaN	NaN	17.5279	18.3496	17.9445	18.0309
2849	TRIO and F-actin-binding protein OS=Rattus norvegicus OX=10116 GN=Triobp PE=1 SV=1	Triobp	A0A0G2K1P8	18.7947	16.3452	16.6278	14.7041	16.0071	17.7222	17.3182	17.0451
2850	Triosephosphate isomerase OS=Rattus norvegicus OX=10116 GN=Tpi1 PE=1 SV=2	Tpi1	P48500	20.9821	21.9001	21.639	21.0514	23.7264	24.162	24.1184	23.8951
2851	Tripartite motif protein 32 OS=Rattus norvegicus OX=10116 GN=Trim32 PE=1 SV=1	Trim32	Q66H79	NaN	15.1097	NaN	14.0974	19.7694	19.6753	18.2469	19.0851
2852	Tripartite motif-containing 25 OS=Rattus norvegicus OX=10116 GN=Trim25 PE=1 SV=3	Trim25	D4A9N5	NaN	NaN	NaN	NaN	18.7704	19.1368	18.4919	18.2524
2853	Tripartite motif-containing 41 OS=Rattus norvegicus OX=10116 GN=Trim41 PE=4 SV=1	Trim41	F1LMK2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2854	Tripartite motif-containing protein 55 OS=Rattus norvegicus OX=10116 GN=Trim55 PE=1 SV=1	Trim55	Q5PQN5	16.7084	16.4296	15.7815	16.4304	21.0332	21.0629	20.6455	20.9054
2855	Tripartite motif-containing protein 72 OS=Rattus norvegicus OX=10116 GN=Trim72 PE=1 SV=1	Trim72	A0JPQ4	15.2036	16.3211	15.1951	16.8568	19.4562	20.1787	19.7964	19.5778
2856	Tripeptidyl-peptidase 2 OS=Rattus norvegicus OX=10116 GN=Tpp2 PE=2 SV=3	Tpp2	Q64560	17.53	17.935	17.5374	17.7439	19.4642	20.7751	20.9735	20.7238
2857	Triple functional domain protein OS=Rattus norvegicus OX=10116 GN=Trio PE=1 SV=4	Trio	F1M0Z1	16.6953	16.5045	16.6824	NaN	16.4762	16.657	16.9963	17.3262
2858	tRNA (guanine(26)-N(2))-dimethyltransferase OS=Rattus norvegicus OX=10116 GN=Trmt1 PE=1 SV=1	Trmt1	A0A140UHW6	18.5682	18.2562	17.9447	18.6171	18.6321	18.5033	18.8639	17.6646
2859	tRNA-splicing endonuclease subunit Sen34 OS=Rattus norvegicus OX=10116 GN=Tsen34 PE=1 SV=1	Tsen34l1	Q5XIB7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2860	tRNA-splicing ligase RtcB homolog OS=Rattus norvegicus OX=10116 GN=Rtcb PE=2 SV=1	Rtcb	Q6AYT3	17.7418	14.4429	16.5849	14.8689	22.7685	22.1725	22.3477	22.1852

2861	Tropomodulin-1 OS=Rattus norvegicus OX=10116 GN=Tmod1 PE=1 SV=1	Tmod1	Q6IMZ5	22.1573	21.2699	21.2701	20.73	22.6653	22.77	21.3284	21.2885
2862	Tropomyosin alpha-1 chain OS=Rattus norvegicus OX=10116 GN=Tpm1 PE=1 SV=3	Tpm1	P04692	16.8952	18.0946	16.5749	17.3471	23.5676	23.5404	21.8815	22.5507
2863	Tropomyosin alpha-3 chain OS=Rattus norvegicus OX=10116 GN=Tpm3 PE=1 SV=2	Tpm3	Q63610	15.5426	NaN	NaN	14.7305	18.8899	19.1417	17.8431	18.2289
2864	Tropomyosin alpha-4 chain OS=Rattus norvegicus OX=10116 GN=Tpm4 PE=1 SV=3	Tpm4	P09495	20.4533	21.0378	20.6968	20.5447	24.1704	24.1451	22.9489	23.2749
2865	Troponin I, cardiac muscle OS=Rattus norvegicus OX=10116 GN=Tnni3 PE=1 SV=2	Tnni3	P23693	NaN	18.1853	15.9613	17.3138	22.6787	21.7281	21.3446	21.0996
2866	Troponin I, slow skeletal muscle OS=Rattus norvegicus OX=10116 GN=Tnni1 PE=1 SV=1	Tnni1	A0A096MIZ5	19.5174	19.4393	18.9956	17.3665	24.1898	23.3628	23.4603	23.746
2867	Troponin T, cardiac muscle OS=Rattus norvegicus OX=10116 GN=Tnnt2 PE=1 SV=2	Tnnt2	P50753	NaN	14.9388	15.6437	15.9618	23.7954	22.6717	22.6468	22.9817
2868	TROVE domain family, member 2 OS=Rattus norvegicus OX=10116 GN=Trove2 PE=1 SV=1	Ro60	D3ZRN5	NaN	NaN	14.9158	NaN	17.6701	17.0723	17.1931	17.5775
2869	Tryptophan--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Wars PE=1 SV=2	Wars1	Q6P7B0	16.1646	17.3437	17.4121	17.7287	22.8222	21.8108	22.9463	23.0902
2870	TSC22 domain family protein 1 OS=Rattus norvegicus OX=10116 GN=Tsc22d1 PE=2 SV=1	Tsc22d1	P62501	NaN	15.8832	NaN	13.8465	20.3987	19.7138	20.1935	20.488
2871	TSC22 domain family protein 4 OS=Rattus norvegicus OX=10116 GN=Tsc22d4 PE=1 SV=1	Tsc22d4	Q3B8N7	19.1359	17.0641	17.8802	19.1112	22.2642	23.413	22.462	22.5049
2872	TSC22 domain family, member 2 OS=Rattus norvegicus OX=10116 GN=Tsc22d2 PE=1 SV=1	Tsc22d2	D3ZDW3	NaN	NaN	NaN	NaN	18.7664	18.8567	19.0315	18.7033
2873	Tuberin OS=Rattus norvegicus OX=10116 GN=Tsc2 PE=1 SV=1	Tsc2	A0A0G2JSL4	17.047	17.8938	18.4785	18.598	20.3716	20.7933	20.5245	20.1249
2874	Tubulin alpha chain OS=Rattus norvegicus OX=10116 GN=Tubal3 PE=1 SV=2	Tubal3	F1LUM5	NaN	NaN	NaN	NaN	18.9056	18.9729	18.6343	18.5509
2875	Tubulin alpha-1A chain OS=Rattus norvegicus OX=10116 GN=Tuba1a PE=1 SV=1	Tuba1a	P68370	25.2491	24.7279	24.6942	25.1429	29.0588	28.9234	28.951	28.9223
2876	Tubulin alpha-1B chain OS=Rattus norvegicus OX=10116 GN=Tuba1b PE=1 SV=1	Tuba1b	Q6P9V9	NaN	14.9266	16.116	16.3725	23.0583	23.415	23.1126	22.5014
2877	Tubulin alpha-1C chain OS=Rattus norvegicus OX=10116 GN=Tuba1c PE=1 SV=1	Tuba1c	Q6AYZ1	19.0737	18.0892	18.0906	18.1118	23.9546	23.9522	23.8143	23.8456
2878	Tubulin alpha-4A chain OS=Rattus norvegicus OX=10116 GN=Tuba4a PE=1 SV=1	Tuba4a	Q5XIF6	19.6295	19.7117	19.3553	19.6727	23.4521	23.6016	23.5216	23.0463
2879	Tubulin beta chain OS=Rattus norvegicus OX=10116 GN=Tubb1 PE=1 SV=1	Tubb1	M0R8B6	17.6197	18.6688	18.5625	18.1217	18.1236	17.572	16.5717	16.375
2880	Tubulin beta chain OS=Rattus norvegicus OX=10116 GN=Tubb4b PE=1 SV=2	Tubb4b	G3V7C6	22.3074	22.2717	21.5879	21.8147	25.9436	25.9264	25.7461	25.8551
2881	Tubulin beta chain OS=Rattus norvegicus OX=10116 GN=Tubb6 PE=1 SV=1	Tubb6	Q4QQV0	23.1668	23.0606	22.3118	23.2096	24.0991	24.131	24.4498	24.0577
2882	Tubulin beta-2A chain OS=Rattus norvegicus OX=10116 GN=Tubb2a PE=1 SV=1	Tubb2a	P85108	22.023	21.4377	21.786	21.3536	24.7072	24.7095	24.891	24.7322
2883	Tubulin beta-2B chain OS=Rattus norvegicus OX=10116 GN=Tubb2b PE=1 SV=1	Tubb2b	Q3KRE8	19.1281	21.3048	19.3832	18.9752	21.1874	21.242	20.8664	20.6152
2884	Tubulin beta-3 chain OS=Rattus norvegicus OX=10116 GN=Tubb3 PE=1 SV=1	Tubb3	Q4QRB4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2885	Tubulin beta-5 chain OS=Rattus norvegicus OX=10116 GN=Tubb5 PE=1 SV=1	Tubb5	P69897	25.7249	25.2874	25.2803	25.4564	29.6238	29.6768	29.5707	29.5182
2886	Tubulin folding cofactor C OS=Rattus norvegicus OX=10116 GN=Tbcc PE=1 SV=1	Tbcc	B2GUZ7	NaN	NaN	NaN	NaN	19.1005	18.087	17.6325	18.8005
2887	Tubulin folding cofactor D OS=Rattus norvegicus OX=10116 GN=Tbcd PE=1 SV=3	Tbcd	F1M1D5	15.9816	16.7229	NaN	14.5477	19.1333	19.3025	20.1484	19.0638
2888	Tubulin gamma-1 chain OS=Rattus norvegicus OX=10116 GN=Tubg1 PE=2 SV=1	Tubg1	P83888	NaN	NaN	NaN	NaN	19.1538	20.0805	19.8808	19.619
2889	Tubulin polymerization-promoting protein family member 3 OS=Rattus norvegicus OX=10116 GN=Tppp3 PE=2 SV=1	Tppp3	Q5PPN5	17.6154	18.4832	18.2264	15.7969	17.6109	17.5531	15.582	16.6221
2890	Tubulin, gamma complex-associated protein 6 OS=Rattus norvegicus OX=10116 GN=Tubgcp6 PE=1 SV=2	Tubgcp6	D4A709	NaN	NaN	NaN	NaN	17.0749	18.1801	17.7084	17.2905
2891	Tubulin-specific chaperone A OS=Rattus norvegicus OX=10116 GN=Tbca PE=1 SV=1	Tbca	Q6PEC1	22.7199	17.6986	16.6418	16.4365	20.7495	18.8766	19.0832	18.8252
2892	Tubulin-specific chaperone cofactor E-like protein OS=Rattus norvegicus OX=10116 GN=Tbcel PE=1 SV=1	Tbcel	Q5PQJ7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2893	Tubulin-specific chaperone E OS=Rattus norvegicus OX=10116 GN=Tbce PE=1 SV=1	Tbce	A0A0G2K191	18.1339	17.2096	18.4135	17.6057	19.9212	20.8119	20.7784	20.4389
2894	Tumor protein D52 OS=Rattus norvegicus OX=10116 GN=Tpd52 PE=1 SV=1	Tpd52	A0A0G2K865	17.2155	17.9751	16.7666	NaN	21.4448	21.1498	21.4058	20.9611
2895	Tumor protein D54 OS=Rattus norvegicus OX=10116 GN=Tpd52l2 PE=1 SV=1	Tpd52l2	Q6PCT3	20.2501	18.6497	19.4618	19.5716	23.187	23.4361	23.4264	23.3222
2896	Tumor susceptibility gene 101 protein OS=Rattus norvegicus OX=10116 GN=Tsg101 PE=1 SV=1	Tsg101	Q6IRE4	16.5665	NaN	14.5084	15.1825	21.686	21.539	21.3621	21.3176
2897	Twinfilin-1 OS=Rattus norvegicus OX=10116 GN=Twf1 PE=1 SV=1	Twf1	Q5RJR2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2898	Type II keratin 23 OS=Rattus norvegicus OX=10116 GN=Kb23 PE=2 SV=1	Kb23	Q6IG08	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2899	Type II keratin Kb15 OS=Rattus norvegicus OX=10116 GN=Kb15 PE=3 SV=1	Kb15	A0A0G2JVA8	23.8509	24.0611	22.9711	24.0274	22.7545	22.1437	22.6459	21.4365
2900	Tyrosine-protein kinase CSK OS=Rattus norvegicus OX=10116 GN=Csk PE=1 SV=1	Csk	P32577	NaN	NaN	NaN	NaN	19.2257	18.218	18.6086	18.4129
2901	Tyrosine-protein kinase Lyn OS=Rattus norvegicus OX=10116 GN=Lyn PE=1 SV=3	Lyn	Q07014	NaN	16.6074	NaN	NaN	16.8281	NaN	NaN	16.6924
2902	Tyrosine-protein kinase receptor OS=Rattus norvegicus OX=10116 GN=Insr PE=1 SV=1	Insr	T2CB11	NaN	NaN	NaN	NaN	14.7651	NaN	15.6271	NaN
2903	Tyrosine-protein kinase Yes OS=Rattus norvegicus OX=10116 GN=Yes1 PE=1 SV=1	Yes1	F1LM93	NaN	NaN	NaN	15.0623	16.7246	NaN	NaN	NaN
2904	Tyrosine-protein phosphatase non-receptor type 11 OS=Rattus norvegicus OX=10116 GN=Ptpn11 PE=1 SV=4	Ptpn11	P41499	15.7507	NaN	13.5968	15.5241	21.9859	22.1292	22.321	21.9195
2905	Tyrosine-protein phosphatase non-receptor type 12 OS=Rattus norvegicus OX=10116 GN=Ptpn12 PE=1 SV=1	Ptpn12	G3V7Q4	NaN	NaN	NaN	NaN	16.9027	18.6092	18.2973	17.1962
2906	Tyrosine-protein phosphatase non-receptor type 23 OS=Rattus norvegicus OX=10116 GN=Ptpn23 PE=1 SV=1	Ptpn23	F1M951	NaN	13.3908	NaN	NaN	20.7061	19.6271	19.9932	19.7851
2907	Tyrosine-protein phosphatase non-receptor type OS=Rattus norvegicus OX=10116 GN=Ptpn21 PE=1 SV=1	Ptpn21	A0A0G2JTB7	18.5313	17.4286	NaN	17.9753	17.9135	17.727	16.6346	16.7876
2908	Tyrosine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Yars PE=1 SV=1	Yars1	A0A0H2UHG0	15.4327	15.0582	16.4354	14.7625	20.1348	19.7417	20.1449	20.0397
2909	U2 snRNP auxiliary factor large subunit OS=Rattus norvegicus OX=10116 GN=U2af2 PE=1 SV=2	U2af2	F2Z3T9	15.7137	14.6607	14.5346	NaN	20.2277	18.8464	17.8481	18.764
2910	U6 snRNA-associated Sm-like protein LSm2 OS=Rattus norvegicus OX=10116 GN=Lsm2 PE=1 SV=1	Lsm2	Q6MG66	NaN	NaN	NaN	NaN	17.4111	17.4539	17.6783	17.7007
2911	U6 snRNA-associated Sm-like protein LSm3 OS=Rattus norvegicus OX=10116 GN=Lsm3 PE=1 SV=1	Lsm3	D4A7U6	NaN	NaN	NaN	NaN	NaN	17.3668	16.9128	NaN
2912	U6 snRNA-associated Sm-like protein LSm5 OS=Rattus norvegicus OX=10116 GN=Lsm5 PE=3 SV=1	Lsm5	D3ZBJ0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2913	Ubiquilin 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ubqln1 PE=1 SV=1	Ubqln1	A0A140TAI1	13.7132	15.3981	NaN	NaN	21.133	19.4778	19.772	20.616

2914	Ubiquilin 2 OS=Rattus norvegicus OX=10116 GN=Ubqln2 PE=1 SV=1	Ubqln2	D4AA63	17.5316	NaN	17.9359	NaN	23.144	21.9141	22.3697	22.5149
2915	Ubiquilin 4 OS=Rattus norvegicus OX=10116 GN=Ubqln4 PE=1 SV=1	Ubqln4	D4A3P1	19.064	18.2178	18.7693	18.3378	21.8174	20.8067	21.1939	21.119
2916	Ubiquinol-cytochrome c reductase, complex III subunit X OS=Rattus norvegicus OX=10116 GN=Uqcr10 PE=1 SV=1	Uqcr10	A0A0G2K8Q8	NaN	NaN	NaN	16.6763	17.9464	19.7865	19.3234	19.6342
2917	Ubiquitin carboxyl-terminal hydrolase 10 OS=Rattus norvegicus OX=10116 GN=Usp10 PE=1 SV=1	Usp10	Q3KR59	NaN	15.75	NaN	14.6205	18.3979	18.936	18.628	18.4071
2918	Ubiquitin carboxyl-terminal hydrolase 15 OS=Rattus norvegicus OX=10116 GN=Usp15 PE=1 SV=1	Usp15	A0A0A0MY07	NaN	NaN	NaN	NaN	16.6127	17.6229	18.3357	18.3658
2919	Ubiquitin carboxyl-terminal hydrolase 19 OS=Rattus norvegicus OX=10116 GN=Usp19 PE=1 SV=1	Usp19	M0RDN9	NaN	NaN	NaN	NaN	17.0968	17.384	17.0534	17.1803
2920	Ubiquitin carboxyl-terminal hydrolase 28 OS=Rattus norvegicus OX=10116 GN=Usp28 PE=1 SV=1	Usp28	A0A140TAA0	15.5079	16.7005	15.3247	NaN	18.1017	18.4313	18.4605	16.7782
2921	Ubiquitin carboxyl-terminal hydrolase 4 OS=Rattus norvegicus OX=10116 GN=Usp4 PE=1 SV=1	Usp4	B2GUZ1	NaN	17.5204	13.9381	NaN	18.1834	18.4079	17.6553	17.5036
2922	Ubiquitin carboxyl-terminal hydrolase 7 OS=Rattus norvegicus OX=10116 GN=Usp7 PE=1 SV=2	Usp7	F1LM09	NaN	NaN	15.1228	NaN	18.4079	17.9097	18.1429	17.5791
2923	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Rattus norvegicus OX=10116 GN=Uchl1 PE=1 SV=2	Uchl1	Q00981	NaN	NaN	NaN	NaN	NaN	17.2726	17.036	17.5995
2924	Ubiquitin carboxyl-terminal hydrolase MINDY-1 OS=Rattus norvegicus OX=10116 GN=Mindy1 PE=2 SV=1	Mindy1	Q5BJQ2	NaN	NaN	NaN	NaN	17.4342	NaN	NaN	18.9482
2925	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus OX=10116 GN=Uchl3 PE=1 SV=2	Uchl3	D4ABI6	NaN	14.7515	NaN	14.5232	20.8224	20.9165	21.1682	20.6912
2926	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus OX=10116 GN=Uchl5 PE=1 SV=1	Uchl5	Q5HZY3	15.7294	16.5785	14.8796	15.4915	19.5025	18.1195	19.2448	18.207
2927	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus OX=10116 GN=Usp13 PE=2 SV=2	Usp13	D3ZDI9	15.1132	15.5616	16.0838	17.5373	20.9583	19.7342	20.5613	20.3772
2928	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus OX=10116 GN=Usp5 PE=1 SV=1	Usp5	D3ZVQ0	20.5567	20.9789	21.3499	20.3219	24.3532	23.2966	23.9972	23.6179
2929	Ubiquitin protein ligase E3 component n-recognin 3 OS=Rattus norvegicus OX=10116 GN=Ubr3 PE=1 SV=3	Ubr3	D4A7F0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2930	Ubiquitin protein ligase E3A OS=Rattus norvegicus OX=10116 GN=Ube3a PE=1 SV=2	Ube3a	F1M7B8	NaN	NaN	14.4674	14.6616	19.6276	19.7026	20.2034	18.8154
2931	Ubiquitin protein ligase E3C (Fragment) OS=Rattus norvegicus OX=10116 GN=Ube3c PE=1 SV=1	Ube3c	A0A1B0GWW0	NaN	NaN	NaN	NaN	17.3232	16.3437	16.6527	16.7802
2932	Ubiquitin protein ligase E3C OS=Rattus norvegicus OX=10116 GN=Ube3c PE=1 SV=3	Ube3c	D3ZHB7	NaN	NaN	NaN	NaN	16.2777	15.3676	NaN	NaN
2933	Ubiquitin recognition factor in ER-associated degradation protein 1 OS=Rattus norvegicus OX=10116 GN=Ufd1 PE=1 SV=1	Ufd1	Q9ES53	17.6338	16.2084	17.7625	17.9908	19.0681	18.8572	19.2163	19.3492
2934	Ubiquitin specific protease 14 OS=Rattus norvegicus OX=10116 GN=Usp14 PE=1 SV=1	Usp14	Q5U2N2	16.6899	17.1066	16.7288	18.8201	21.3957	20.6382	22.1008	21.2277
2935	Ubiquitin thioesterase OTUB1 OS=Rattus norvegicus OX=10116 GN=Otub1 PE=1 SV=1	Otub1	B2RYG6	NaN	16.5152	NaN	NaN	22.2645	21.4591	22.0371	21.8627
2936	Ubiquitin-40S ribosomal protein S27a OS=Rattus norvegicus OX=10116 GN=Rps27a PE=1 SV=2	Rps27a	P62982	21.6064	22.7542	21.9221	22.2822	23.5104	23.4506	23.2296	23.3124
2937	Ubiquitin-60S ribosomal protein L40 OS=Rattus norvegicus OX=10116 GN=Uba52 PE=1 SV=2	Uba52	P62986	NaN	NaN	NaN	NaN	NaN	18.292	17.0756	16.618
2938	Ubiquitin-associated domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Ubac1 PE=1 SV=1	Ubac1	Q5XIR9	NaN	NaN	NaN	NaN	19.2675	17.8658	17.9262	17.7183
2939	Ubiquitin-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Ubap1 PE=2 SV=1	Ubap1	Q5XIS7	NaN	NaN	NaN	NaN	17.3284	16.8094	16.9564	17.0961
2940	Ubiquitin-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Ubap2 PE=1 SV=1	Ubap2	A0A0U1RRQ3	22.1039	22.0156	22.3681	22.6534	23.0643	22.1951	22.2428	22.2592
2941	Ubiquitination factor E4B OS=Rattus norvegicus OX=10116 GN=Ube4b PE=1 SV=3	Ube4b	F1M8V2	NaN	15.886	NaN	NaN	18.8869	18.9684	18.4262	18.5122
2942	Ubiquitin-conjugating enzyme E2 D2 OS=Rattus norvegicus OX=10116 GN=Ube2d2 PE=1 SV=1	Ube2d2	P62839	19.0571	19.6508	19.5218	19.2821	21.8911	21.4346	21.9132	21.4778
2943	Ubiquitin-conjugating enzyme E2 G1 OS=Rattus norvegicus OX=10116 GN=Ube2g1 PE=2 SV=3	Ube2g1	P62255	NaN	15.5653	13.7492	NaN	17.9018	NaN	18.0477	17.154
2944	Ubiquitin-conjugating enzyme E2 N OS=Rattus norvegicus OX=10116 GN=Ube2n PE=1 SV=1	Ube2n	Q9EQX9	19.3663	17.6229	18.8989	19.2067	24.4501	23.3251	23.863	23.8218
2945	Ubiquitin-conjugating enzyme E2 V1 OS=Rattus norvegicus OX=10116 GN=LOC100912618 PE=1 SV=1	Ube2v1	D3ZFY8	20.2318	19.6963	20.115	20.3155	22.9619	22.2027	22.7399	22.5349
2946	Ubiquitin-conjugating enzyme E2 Z OS=Rattus norvegicus OX=10116 GN=Ube2z PE=1 SV=2	Ube2z	Q3B7D1	22.5192	22.8512	22.8254	19.0944	21.0194	21.029	21.2739	21.1829
2947	Ubiquitin-conjugating enzyme E2H OS=Rattus norvegicus OX=10116 GN=Ube2h PE=1 SV=2	Ube2h	M0R4P9	NaN	NaN	16.629	16.8449	20.0367	19.5387	19.9044	19.8602
2948	Ubiquitin-conjugating enzyme E2M OS=Rattus norvegicus OX=10116 GN=Ube2m PE=1 SV=1	Ube2m	D3ZNQ6	18.6176	18.4655	18.8379	17.7497	22.6962	21.2894	21.5832	22.0582
2949	Ubiquitin-conjugating enzyme E2O OS=Rattus norvegicus OX=10116 GN=Ube2o PE=1 SV=2	Ube2o	F1M403	16.6989	18.3906	18.4716	14.0065	22.153	21.5625	21.6062	21.8572
2950	Ubiquitin-fold modifier 1 OS=Rattus norvegicus OX=10116 GN=Ufm1 PE=3 SV=1	Ufm1	Q5BJP3	16.5415	15.3952	16.4062	16.4863	NaN	NaN	NaN	NaN
2951	Ubiquitin-fold modifier-conjugating enzyme 1 OS=Rattus norvegicus OX=10116 GN=Ufc1 PE=2 SV=1	Ufc1	Q6BBI8	NaN	NaN	NaN	NaN	16.9774	17.3076	17.5085	17.2794
2952	Ubiquitin-Like 5 Protein, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ubl5 PE=1 SV=1	Ubl5	A9UMW0	NaN	NaN	NaN	NaN	19.3095	17.915	NaN	17.5952
2953	Ubiquitin-like modifier-activating enzyme 1 OS=Rattus norvegicus OX=10116 GN=Uba1 PE=1 SV=1	Uba1	Q5U300	19.2293	20.1584	20.146	19.992	25.1742	24.1042	24.793	24.8022
2954	Ubiquitin-like modifier-activating enzyme 2 OS=Rattus norvegicus OX=10116 GN=Uba2 PE=1 SV=3	Uba2	F1LS72	NaN	17.4442	NaN	NaN	19.6722	19.5262	20.4795	20.0097
2955	Ubiquitin-like modifier-activating enzyme 5 OS=Rattus norvegicus OX=10116 GN=Uba5 PE=1 SV=1	Uba5	Q5M7A4	17.4762	18.0753	15.5028	17.6	20.558	19.729	20.4698	20.5186
2956	Ubiquitin-like modifier-activating enzyme ATG7 OS=Rattus norvegicus OX=10116 GN=Atg7 PE=2 SV=1	Atg7	Q641Y5	19.289	20.2922	17.1987	17.6228	16.2325	18.4796	16.458	17.9028
2957	Ubiquitin-like protein 4A OS=Rattus norvegicus OX=10116 GN=Ubl4a PE=2 SV=1	Ubl4a	B2GV38	18.4767	18.0679	18.3263	NaN	22.1581	21.3618	21.9304	21.8845
2958	Ubiquitin-like-conjugating enzyme ATG3 OS=Rattus norvegicus OX=10116 GN=Atg3 PE=2 SV=1	Atg3	Q6AZ50	17.0984	15.048	NaN	NaN	19.2093	18.7969	18.514	18.1202
2959	Ubiquitin-specific peptidase 24 OS=Rattus norvegicus OX=10116 GN=Usp24 PE=1 SV=2	Usp24	F1LSM0	NaN	NaN	NaN	NaN	16.4628	16.9159	16.9142	16.9115
2960	Ubiquitin-specific peptidase 47 OS=Rattus norvegicus OX=10116 GN=Usp47 PE=1 SV=1	Usp47	A0A0G2JUX4	17.0159	17.8899	18.3033	17.5759	20.5648	19.8042	20.168	20.406
2961	Ubiquitin-specific peptidase 9, X-linked OS=Rattus norvegicus OX=10116 GN=Usp9x PE=1 SV=1	Usp9x	A0A0G2K2C7	NaN	NaN	14.4124	14.7361	20.6192	21.4325	21.7066	21.3247
2962	UBX domain protein 6 OS=Rattus norvegicus OX=10116 GN=Ubxn6 PE=1 SV=1	Ubxn6	A0A0G2K012	14.951	16.1404	NaN	NaN	20.1497	19.8735	19.5199	20.0913
2963	UBX domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Ubxn1 PE=3 SV=2	Ubxn1	Q499N6	15.3178	NaN	14.8232	NaN	19.3477	18.6668	19.2091	19.3025
2964	UBX domain-containing protein 4 OS=Rattus norvegicus OX=10116 GN=Ubxn4 PE=1 SV=1	Ubxn4	Q5HZY0	NaN	13.4802	NaN	NaN	17.6289	16.9596	16.7071	16.8541
2965	UBX domain-containing protein 7 OS=Rattus norvegicus OX=10116 GN=rCG_52671 PE=1 SV=2	rCG_52671	M0R9B9	NaN	NaN	NaN	NaN	17.9324	NaN	NaN	NaN
2966	UDP-glucose 6-dehydrogenase OS=Rattus norvegicus OX=10116 GN=Ugdh PE=1 SV=1	Ugdh	G3V6C4	18.9456	18.1195	18.4968	18.2857	20.376	19.5976	20.3183	20.4536

2967	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Rattus norvegicus OX=10116 GN=Uggt1 PE=1 SV=2	Uggt1	Q9JLA3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2968	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1 OS=Rattus norvegicus OX=10116 GN=Uap1l1 PE=1 SV=1	Uap1l1	B5DEH4	16.4166	16.3495	17.2144	16.845	19.3579	18.4926	18.8174	19.0146
2969	UHRF1-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Uhrf1bp1 PE=1 SV=3	Uhrf1bp1	D3ZMR2	16.1006	16.3815	NaN	16.3917	18.9054	18.7277	18.4542	16.9696
2970	UMP-CMP kinase OS=Rattus norvegicus OX=10116 GN=Cmpk1 PE=1 SV=1	Cmpk1	A0A0G2JSJ2	20.2164	18.6801	18.7518	19.3363	22.344	22.3941	22.9627	22.5415
2971	Unc-119 lipid-binding chaperone B OS=Rattus norvegicus OX=10116 GN=Mlec PE=1 SV=1	Unc119b	A0A0G2K121	22.7706	22.1531	23.0966	22.9534	20.6681	20.2614	20.1032	20.851
2972	Unc-45 myosin chaperone B OS=Rattus norvegicus OX=10116 GN=Unc45b PE=4 SV=1	Unc45b	A0A096MJB5	22.1444	22.0617	21.971	21.5175	25.9626	25.2086	25.8594	25.647
2973	Uncharacterized protein (Fragment) OS=Rattus norvegicus OX=10116 GN=Gigyf2 PE=1 SV=1	Gigyf2	A0A096MJI4	18.7896	20.2119	17.3016	17.3705	15.3441	13.9639	17.9857	17.1232
2974	Uncharacterized protein (Fragment) OS=Rattus norvegicus OX=10116 PE=4 SV=1	0A096MJL2_RA	A0A096MJL2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2975	Uncharacterized protein (Fragment) OS=Rattus norvegicus OX=10116 PE=4 SV=1	)A0G2K4H3_RA	A0A0G2K4H3	17.7986	17.4093	17.3652	16.8213	18.6376	17.151	17.6451	18.0251
2976	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=Cep170 PE=1 SV=1	Cep170	A0A0G2K315	22.6848	22.6931	23.1925	23.0415	21.2246	20.8393	20.5551	20.9592
2977	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=Cfhr2 PE=1 SV=3	Cfhr2	F1LWS4	21.1106	19.5591	21.023	21.1379	18.4952	19.1837	18.6941	18.5325
2978	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=LOC690813 PE=1 SV=2	LOC690813	F1M1R0	18.6858	17.5571	19.1875	20.0741	16.21	17.4525	18.0394	18.5638
2979	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=R3hcc1 PE=1 SV=3	R3hcc1	F1LZB0	NaN	NaN	NaN	NaN	17.4723	NaN	16.1561	NaN
2980	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=Scgb2b2 PE=4 SV=3	Scgb2b2	F1LSA5	18.679	19.6367	19.4402	18.2208	15.2554	15.6146	15.7602	15.7507
2981	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	)A0G2JW41_RA	A0A0G2JW41	19.2973	19.5187	18.8825	18.7477	NaN	NaN	NaN	NaN
2982	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	)A0G2JXB7_RA	A0A0G2JXB7	NaN	18.4699	18.6964	16.9789	NaN	NaN	NaN	NaN
2983	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	)A0G2JXP0_RA	A0A0G2JXP0	21.1074	20.9764	20.6566	19.3996	16.7655	15.2856	16.7065	16.7847
2984	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	0A0G2JY70_RA	A0A0G2JY70	18.7116	17.9092	18.1337	17.3867	22.7151	23.081	23.1147	23.1734
2985	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	)A0G2JYX2_RA	A0A0G2JYX2	18.3944	18.3118	18.7517	16.6174	17.8466	NaN	NaN	NaN
2986	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	)A0G2JZN1_RA	A0A0G2JZN1	NaN	18.0713	NaN	15.7883	17.0141	16.5622	17.7842	16.5586
2987	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	0A0G2JZS9_RA	A0A0G2JZS9	18.4964	17.6254	17.6719	15.2681	NaN	15.3683	NaN	NaN
2988	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	)A0G2K0N6_RA	A0A0G2K0N6	18.2589	17.0013	16.2539	17.3606	14.8951	15.2974	16.1087	NaN
2989	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	)A0G2K0U9_RA	A0A0G2K0U9	16.4189	13.9457	15.994	NaN	18.821	18.415	18.7827	18.7164
2990	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	0A0G2K332_RA	A0A0G2K332	NaN	NaN	NaN	14.5071	20.0651	20.6962	20.6091	20.3605
2991	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	0A0G2K7I1_RA	A0A0G2K7I1	NaN	14.3522	17.0574	19.4397	14.7763	17.6695	15.119	16.8025
2992	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	)A0G2K7S9_RA	A0A0G2K7S9	17.1872	NaN	NaN	NaN	NaN	15.5991	NaN	NaN
2993	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	)A0G2K980_RA	A0A0G2K980	18.3714	18.676	19.0054	19.6986	NaN	NaN	NaN	15.6814
2994	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	)A0G2KAL1_RA	A0A0G2KAL1	17.8104	16.2099	16.2574	16.2848	NaN	17.0854	NaN	17.1898
2995	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	Copb2	A0A0G2K0P9	NaN	NaN	NaN	NaN	NaN	17.6681	16.2836	18.0898
2996	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	D3Z874_RAT	D3Z874	NaN	NaN	NaN	NaN	16.2442	15.2911	16.2457	15.7578
2997	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	D3ZQR5_RAT	D3ZQR5	18.5792	18.0817	19.3515	17.4921	16.2469	17.1872	16.5464	NaN
2998	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	D4A4L6_RAT	D4A4L6	16.6901	16.9716	17.5113	17.3492	NaN	NaN	NaN	NaN
2999	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	D4A8Y1_RAT	D4A8Y1	NaN	16.144	17.6383	16.9896	19.7049	18.8035	20.0872	18.9752
3000	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	F1LZ11_RAT	F1LZ11	NaN	NaN	NaN	18.1791	NaN	NaN	NaN	NaN
3001	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	M0R4X3_RAT	M0R4X3	NaN	NaN	NaN	15.5211	NaN	NaN	NaN	NaN
3002	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	M0R9U2_RAT	M0R9U2	19.9046	18.9467	20.2651	19.2658	20.0884	20.6075	20.2674	20.3654
3003	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	M0RA79_RAT	M0RA79	19.9988	19.5132	20.7749	21.0008	17.761	18.3194	18.0958	16.695
3004	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	M0RC23_RAT	M0RC23	19.1516	18.885	19.0929	19.6765	NaN	NaN	NaN	NaN
3005	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	M0RCC9_RAT	M0RCC9	16.3833	17.5913	16.3869	NaN	15.9505	15.9715	16.7359	15.8646
3006	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	M0RDF2_RAT	M0RDF2	17.3608	16.8462	16.289	NaN	17.1858	NaN	16.9091	NaN
3007	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	Nemf	A0A0G2K9F2	NaN	NaN	NaN	NaN	NaN	17.8329	NaN	17.6464
3008	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	Crybg3	M0RDY6	18.3154	18.756	19.0366	18.8449	22.6381	22.2055	22.5972	22.5593
3009	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	D3ZZ08_RAT	D3ZZ08	19.5057	19.0086	19.8876	19.3151	NaN	18.8659	15.8379	16.2889
3010	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	D4ACR1_RAT	D4ACR1	17.9912	17.4245	18.626	18.8194	15.5858	NaN	NaN	NaN
3011	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	Dennd5b	M0R5A9	NaN	NaN	NaN	NaN	17.2426	17.1849	17.0638	16.8113
3012	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	F1LTN6_RAT	F1LTN6	24.8696	25.5755	25.2167	24.3729	21.2754	21.278	20.7203	20.739
3013	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	F1LWD0_RAT	F1LWD0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3014	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	F1LXY6_RAT	F1LXY6	19.0395	19.9559	20.1976	15.8372	15.8088	NaN	NaN	15.7473
3015	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	F1LZH0_RAT	F1LZH0	NaN	NaN	17.0872	14.583	NaN	NaN	NaN	NaN
3016	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	F1M2N4_RAT	F1M2N4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3017	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	F1M3U4_RAT	F1M3U4	17.9311	21.4779	17.8462	19.1485	18.988	18.5768	19.7132	19.5272
3018	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	F1M5L5_RAT	F1M5L5	19.1227	18.493	19.0077	18.9629	NaN	NaN	NaN	NaN
3019	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	G3V8Z5_RAT	G3V8Z5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

3020	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	LOC100360848	F1LUS1	16.6731	19.6654	18.4562	NaN	15.1145	NaN	NaN	NaN
3021	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	LOC299458	D3ZC54	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3022	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	M0R4Z4_RAT	M0R4Z4	17.2188	18.9947	17.2224	16.7093	17.6343	17.2295	16.7689	16.8536
3023	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	M0R816_RAT	M0R816	21.0698	21.2929	21.1739	20.1356	NaN	NaN	NaN	NaN
3024	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	M0R8B5_RAT	M0R8B5	18.8787	19.4068	19.1744	19.5199	NaN	15.189	NaN	NaN
3025	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	M0RBK4_RAT	M0RBK4	17.4416	17.4288	17.2395	17.1644	14.7214	NaN	NaN	NaN
3026	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	Srrt	M0R7E6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3027	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	D3ZBB2_RAT	D3ZBB2	14.888	17.6314	15.6065	NaN	NaN	NaN	16.3995	NaN
3028	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	D3ZEP5_RAT	D3ZEP5	17.1327	16.3248	16.2984	18.9098	NaN	NaN	16.8929	NaN
3029	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	D3ZPL2_RAT	D3ZPL2	20.2869	20.9596	21.077	20.0483	15.6219	16.5695	16.316	15.2941
3030	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	F1LTY5_RAT	F1LTY5	15.6847	15.0238	15.003	NaN	14.6578	NaN	NaN	NaN
3031	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	F1LU03_RAT	F1LU03	NaN	NaN	NaN	NaN	NaN	20.658	21.3753	21.2536
3032	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	F1LUV3_RAT	F1LUV3	NaN	NaN	NaN	NaN	17.4251	17.2875	NaN	17.1172
3033	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	F1LX60_RAT	F1LX60	16.8525	17.534	17.5394	16.5824	14.7268	15.4568	14.6867	NaN
3034	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	F1M269_RAT	F1M269	16.8253	16.6255	16.7553	18.034	20.8795	19.9249	21.0678	20.8515
3035	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	Fam114a2	D3ZC89	21.2402	20.86	21.2183	22.3164	23.4086	22.6335	23.2709	23.311
3036	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	Fam98b	D4AE02	18.0784	17.8629	17.8613	17.8421	18.8211	17.4584	17.8751	NaN
3037	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	G3V9J1_RAT	G3V9J1	18.9623	18.3297	19.2419	19.7383	NaN	16.2613	16.7208	17.3669
3038	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	Hspg2	F1LTJ5	17.2063	16.798	16.403	17.1836	20.3393	20.1289	20.1347	20.6993
3039	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	Ighm	F1LM30	17.7502	21.4924	19.7075	16.2176	16.7606	14.8031	NaN	15.2414
3040	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	Palld	F1M265	NaN	15.2351	NaN	NaN	17.3866	16.5974	15.6614	16.3692
3041	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	Pkp2	F1M7L9	17.5259	17.2297	17.4606	16.0711	19.2204	19.5398	18.7176	17.9564
3042	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	)A0G2KA35_RA	A0A0G2KA35	NaN	18.4567	NaN	NaN	21.0715	20.3874	21.0537	22.1422
3043	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	Eno1-ps1	M0R5J4	23.9621	24.151	24.7826	24.7216	24.9604	26.0312	26.3208	25.8834
3044	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	LOC108349792	A0A0G2K3I6	21.1887	20.4193	20.6968	17.8879	23.8381	23.7166	24.5642	24.3588
3045	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	LOC690675	D4A5L9	NaN	NaN	NaN	16.1852	16.0528	20.1668	19.2841	18.9347
3046	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	RGD1561333	D4A6W6	18.8271	17.4832	17.1129	17.7702	22.5855	23.7821	23.557	23.3558
3047	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	RGD1561636	D4AD70	NaN	NaN	NaN	NaN	22.2973	21.4391	21.3505	20.7136
3048	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=2	F1M8P6_RAT	F1M8P6	NaN	NaN	NaN	NaN	18.2536	18.5033	18.9171	18.6593
3049	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=2	Hkdc1	M0R3X7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3050	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=3	LOC100362298	D3ZM33	20.3798	19.7405	19.8808	19.2143	23.6483	25.0834	24.6503	24.6218
3051	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	)A0G2JUY3_RA	A0A0G2JUY3	16.049	NaN	17.2942	17.4846	NaN	NaN	16.1447	16.2853
3052	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	)A0G2K304_RA	A0A0G2K304	16.934	15.9507	17.666	16.1068	NaN	NaN	NaN	NaN
3053	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	)A0G2K3S3_RA	A0A0G2K3S3	21.5114	21.631	21.5452	20.8542	17.2565	16.5539	16.0874	16.479
3054	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	)A0G2K613_RA	A0A0G2K613	19.8006	19.7631	20.4817	18.4466	23.5817	22.6606	22.797	22.721
3055	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	)A0G2K6T8_RA	A0A0G2K6T8	18.3139	18.7143	18.424	15.9599	NaN	NaN	NaN	NaN
3056	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	)A0G2K828_RA	A0A0G2K828	18.5316	18.402	18.4547	20.3539	NaN	NaN	15.666	NaN
3057	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	)A0G2K9A6_RA	A0A0G2K9A6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3058	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	)A0G2K9Z5_RA	A0A0G2K9Z5	16.7253	17.5996	16.0113	NaN	15.4216	15.144	NaN	NaN
3059	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	A140UHW8_R	A0A140UHW8	16.3086	16.435	NaN	NaN	15.1654	15.8466	NaN	16.227
3060	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	D3ZJD3_RAT	D3ZJD3	18.298	17.9207	17.3766	15.2072	22.6943	23.8969	23.5054	23.5391
3061	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	D3ZPN7_RAT	D3ZPN7	20.4693	19.2674	19.9886	19.264	21.6347	23.2259	22.6851	22.678
3062	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	F1LWP8_RAT	F1LWP8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3063	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	F1M4R1_RAT	F1M4R1	18.3173	18.147	17.5356	NaN	NaN	NaN	NaN	NaN
3064	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	Ighm	A0A0G2K477	19.9301	19.0219	19.7267	21.6009	16.2326	NaN	NaN	16.6088
3065	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	Ipo8	A0A0G2K6J6	NaN	NaN	NaN	NaN	NaN	17.6001	17.5004	16.1812
3066	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	LOC102553099	A0A0G2K1A0	NaN	NaN	NaN	NaN	19.0557	18.7993	19.3885	18.8167
3067	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	LOC362382	A0A0G2K3L5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3068	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	M0R5W6_RAT	M0R5W6	16.9225	NaN	18.0949	17.412	15.0081	15.4533	16.8759	NaN
3069	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	M0RBL2_RAT	M0RBL2	21.5359	21.3867	21.6888	21.8673	NaN	NaN	NaN	NaN
3070	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	M0RBP7_RAT	M0RBP7	19.2534	19.2519	19.4494	19.1635	18.8327	19.1746	19.2726	19.077
3071	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	D4A3D1_RAT	D4A3D1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3072	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	F1LVL4_RAT	F1LVL4	21.0703	21.2205	20.5554	20.5374	16.5219	15.0067	14.7586	NaN

3073	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	Ighm	F1LPQ6	21.4113	22.2875	21.2591	21.4749	19.4676	18.8375	19.3083	19.362
3074	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	LOC100363319	M0R3K7	14.7704	16.9995	NaN	NaN	16.8259	17.8831	16.4261	16.4465
3075	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	M0R628_RAT	M0R628	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3076	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	M0RAB8_RAT	M0RAB8	17.9189	NaN	NaN	17.2417	17.6782	NaN	16.9644	NaN
3077	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	M0RAZ1_RAT	M0RAZ1	17.2769	17.2286	18.4864	18.5218	18.5102	17.4153	18.1095	18.2974
3078	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	RGD1561444	D4ABI4	17.7615	17.2144	17.3051	17.304	NaN	18.4697	NaN	NaN
3079	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	RGD1565866	F1M063	NaN	NaN	NaN	NaN	19.716	18.216	18.8761	18.8913
3080	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	Zfp341	F7ETL6	NaN	16.7516	15.4727	16.8266	18.689	17.9203	NaN	18.4678
3081	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=3	F1M1Q7_RAT	F1M1Q7	19.208	16.4059	18.9585	19.7562	NaN	NaN	15.3186	NaN
3082	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=3	F1M861_RAT	F1M861	18.5288	18.6591	18.0508	16.6287	18.1752	17.7438	17.2686	16.8736
3083	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=3	LOC365839	F1M7K9	15.0237	15.8054	15.2823	14.4274	18.0857	17.6266	17.992	18.0148
3084	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=3	Stau2	F1LN29	14.4497	NaN	NaN	14.6668	17.6133	NaN	17.4767	17.4993
3085	Unconventional myosin-Ib OS=Rattus norvegicus OX=10116 GN=Myo1b PE=1 SV=1	Myo1b	Q05096	NaN	NaN	NaN	NaN	16.535	18.3306	NaN	17.5499
3086	Unconventional myosin-Ic OS=Rattus norvegicus OX=10116 GN=Myo1c PE=1 SV=2	Myo1c	Q63355	18.2291	19.3461	18.9401	19.3208	22.1365	22.5598	22.175	22.5329
3087	Unconventional myosin-Ie OS=Rattus norvegicus OX=10116 GN=Myo1e PE=1 SV=1	Myo1e	Q63356	16.5045	NaN	15.7014	14.3679	18.6753	19.2174	18.272	18.2202
3088	Unconventional myosin-IXb OS=Rattus norvegicus OX=10116 GN=Myo9b PE=1 SV=1	Myo9b	A0A0G2JYG5	14.5427	NaN	NaN	NaN	17.0031	16.5989	17.2682	16.8315
3089	UPF0687 protein C20orf27 homolog OS=Rattus norvegicus OX=10116 PE=2 SV=1	RGD1311739	Q4KM45	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3090	UPF0729 protein C18orf32 homolog OS=Rattus norvegicus OX=10116 PE=3 SV=1	RGD1562987	B1WC88	NaN	NaN	NaN	NaN	17.0751	17.6929	16.8514	17.1139
3091	UPF1, RNA helicase and ATPase OS=Rattus norvegicus OX=10116 GN=Upf1 PE=1 SV=1	Upf1	A0A0U1RS25	19.1536	18.7526	14.5051	18.9146	22.7856	22.5117	22.5033	22.1893
3092	Up-regulated during skeletal muscle growth protein 5 OS=Rattus norvegicus OX=10116 GN=Atp5md PE=1 SV=1	Atp5mk	Q9JJW3	18.3368	18.9418	17.7703	17.9077	20.5818	21.6888	21.2915	21.7546
3093	Uracil phosphoribosyltransferase homolog OS=Rattus norvegicus OX=10116 GN=Uprt PE=4 SV=1	Uprt	D4ABC7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3094	Urea transporter OS=Rattus norvegicus OX=10116 GN=Slc14a1 PE=3 SV=1	Slc14a1	M0R8C6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3095	Uridine monophosphate synthetase OS=Rattus norvegicus OX=10116 GN=Umps PE=1 SV=1	Umps	Q4QQS7	NaN	NaN	16.2105	NaN	21.2658	20.207	21.183	21.3172
3096	Uridine-cytidine kinase OS=Rattus norvegicus OX=10116 GN=Uck2 PE=3 SV=1	Uck2	A0A0G2JX05	NaN	NaN	NaN	14.0638	18.8414	18.8048	18.8028	18.6885
3097	Uromodulin OS=Rattus norvegicus OX=10116 GN=Umod PE=4 SV=1	Umod	A0A0G2JSP1	20.603	18.7779	NaN	NaN	NaN	NaN	NaN	NaN
3098	Uroplakin 3B OS=Rattus norvegicus OX=10116 GN=Upk3b PE=2 SV=1	Upk3b	D3ZKW6	NaN	NaN	NaN	NaN	17.8718	17.0636	15.6714	15.9519
3099	Uroporphyrinogen decarboxylase OS=Rattus norvegicus OX=10116 GN=Urod PE=1 SV=1	Urod	B0BN55	NaN	16.2175	16.6408	15.1715	17.0632	16.2494	17.0191	16.4102
3100	Uteroglobin OS=Rattus norvegicus OX=10116 GN=Scgb1a1 PE=1 SV=2	Scgb1a1	P17559	21.2538	21.2751	21.6367	21.1373	16.4253	15.4096	NaN	15.3164
3101	UTP--glucose-1-phosphate uridylyltransferase OS=Rattus norvegicus OX=10116 GN=Ugp2 PE=1 SV=1	Ugp2	Q4V8I9	20.0233	19.8445	19.883	19.287	22.5427	21.7189	22.2192	22.1229
3102	UV excision repair protein RAD23 homolog B OS=Rattus norvegicus OX=10116 GN=Rad23b PE=1 SV=1	Rad23b	Q4KMA2	23.7135	23.009	23.2411	21.9184	22.0355	21.5037	21.6636	21.6868
3103	Vacuolar protein sorting 13 homolog C OS=Rattus norvegicus OX=10116 GN=Vps13c PE=1 SV=2	Vps13c	D4A4K4	21.08	21.456	21.0479	22.2813	22.7397	22.8801	22.579	22.7604
3104	Vacuolar protein sorting 13 homolog D OS=Rattus norvegicus OX=10116 GN=Vps13d PE=1 SV=1	Vps13d	D3ZKC6	12.6304	NaN	NaN	NaN	16.0563	16.2374	NaN	15.1114
3105	Vacuolar protein sorting 4 homolog B OS=Rattus norvegicus OX=10116 GN=Vps4b PE=1 SV=1	Vps4b	Q4KLL7	19.2368	18.713	18.1215	18.5701	21.3912	21.7397	22.2713	21.9979
3106	Vacuolar protein sorting-associated protein 26A OS=Rattus norvegicus OX=10116 GN=Vps26a PE=1 SV=1	Vps26a	Q6AY86	17.0134	NaN	NaN	17.1083	16.7553	17.1639	16.5748	NaN
3107	Vacuolar protein sorting-associated protein 28 homolog OS=Rattus norvegicus OX=10116 GN=Vps28 PE=1 SV=1	Vps28	A0A0H2UHM0	21.026	19.1727	19.6063	21.1238	22.1753	21.8036	21.8345	21.7059
3108	Vacuolar protein sorting-associated protein 29 OS=Rattus norvegicus OX=10116 GN=Vps29 PE=1 SV=1	Vps29	A0A0G2JTS3	17.9039	17.0928	17.6394	14.8561	16.1199	19.2581	19.4863	18.5394
3109	Vacuolar protein sorting-associated protein 33B OS=Rattus norvegicus OX=10116 GN=Vps33b PE=2 SV=1	Vps33b	Q63616	NaN	14.7795	NaN	NaN	17.9425	17.9525	NaN	18.0247
3110	Vacuolar protein sorting-associated protein 35 OS=Rattus norvegicus OX=10116 GN=Vps35 PE=1 SV=1	Vps35	G3V8A5	19.1317	16.4322	14.5541	NaN	19.1378	17.6943	19.3076	19.0354
3111	Vacuolar protein sorting-associated protein 45 OS=Rattus norvegicus OX=10116 GN=Vps45 PE=1 SV=1	Vps45	O08700	19.7448	20.7473	20.371	20.516	19.8368	20.1773	19.9977	19.4083
3112	Vacuolar protein sorting-associated protein 4A OS=Rattus norvegicus OX=10116 GN=Vps4a PE=1 SV=1	Vps4a	F7F1Y3	19.9519	19.6821	20.0973	19.9857	21.1237	21.2404	21.2292	21.0807
3113	Vacuolar-sorting protein SNF8 OS=Rattus norvegicus OX=10116 GN=Snf8 PE=1 SV=1	Snf8	Q5RK19	NaN	15.2011	NaN	NaN	18.8209	18.1803	18.2169	18.5762
3114	Valine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Vars PE=2 SV=2	Vars1	Q04462	16.7374	NaN	17.5554	17.7623	21.5615	20.8662	21.0644	21.2112
3115	Vanin 1 OS=Rattus norvegicus OX=10116 GN=Vnn1 PE=1 SV=1	Vnn1	Q4KLZ0	NaN	15.0669	15.789	16.9609	20.6593	20.765	20.456	20.495
3116	Vascular cell adhesion protein 1 OS=Rattus norvegicus OX=10116 GN=Vcam1 PE=2 SV=1	Vcam1	P29534	16.6012	16.8417	16.3516	15.5371	NaN	16.0269	NaN	16.1743
3117	Vasodilator-stimulated phosphoprotein OS=Rattus norvegicus OX=10116 GN=Vasp PE=1 SV=1	Vasp	A0A0G2K9C0	NaN	14.9525	17.7644	13.9631	22.0459	22.1804	22.0269	21.4263
3118	Versican core protein (Fragments) OS=Rattus norvegicus OX=10116 GN=Vcan PE=2 SV=2	Vcan	Q9ERB4	19.7043	19.5043	18.4347	19.402	20.7133	20.4181	20.9202	20.763
3119	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acadvl PE=1 SV=1	Acadvl	P45953	16.2246	17.2494	15.528	16.1869	18.4899	20.0854	18.9023	19.4394
3120	Very low-density lipoprotein receptor OS=Rattus norvegicus OX=10116 GN=Vldlr PE=4 SV=1	Vldlr	F1LPV2	15.7389	16.0241	16.2788	NaN	NaN	18.191	18.261	17.54
3121	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase OS=Rattus norvegicus OX=10116 GN=Hacd2 PE=1 SV=3	Hacd2	D3ZHG0	NaN	NaN	NaN	NaN	14.4942	15.9879	15.422	14.8604
3122	Very-long-chain 3-oxoacyl-CoA reductase OS=Rattus norvegicus OX=10116 GN=Hsd17b12 PE=2 SV=1	Hsd17b12	Q6P7R8	NaN	NaN	NaN	NaN	18.0908	18.2026	17.9915	17.9268
3123	Very-long-chain enoyl-CoA reductase OS=Rattus norvegicus OX=10116 GN=Tecr PE=1 SV=1	Tecr	Q64232	NaN	NaN	NaN	NaN	NaN	18.015	18.0367	18.0867
3124	Vesicle transport through interaction with t-SNAREs homolog 1B OS=Rattus norvegicus OX=10116 GN=Vti1b PE=1 SV=2	Vti1b	P58200	16.4414	15.7257	17.2063	NaN	20.2296	20.2211	19.7975	20.0938
3125	Vesicle-associated membrane protein 2 OS=Rattus norvegicus OX=10116 GN=Vamp2 PE=1 SV=2	Vamp2	P63045	17.1536	15.8859	16.3598	17.1742	20.4377	20.3467	20.1475	20.0301

3126	Vesicle-associated membrane protein 3 OS=Rattus norvegicus OX=10116 GN=Vamp3 PE=1 SV=1	Vamp3	P63025	20.3425	19.9951	20.1846	20.5674	22.6134	22.5531	22.269	22.293
3127	Vesicle-associated membrane protein 8 OS=Rattus norvegicus OX=10116 GN=Vamp8 PE=1 SV=1	Vamp8	Q9WUF4	17.6735	18.9108	16.4015	18.1239	19.8734	20.5975	19.8541	19.916
3128	Vesicle-associated membrane protein-associated protein A OS=Rattus norvegicus OX=10116 GN=Vapa PE=1 SV=3	Vapa	Q9Z270	18.9466	18.8361	15.1345	NaN	21.2148	22.1193	21.2788	21.7195
3129	Vesicle-associated membrane protein-associated protein B OS=Rattus norvegicus OX=10116 GN=Vapb PE=1 SV=3	Vapb	Q9Z269	18.0335	18.6506	19.1252	NaN	19.3361	20.1269	18.297	19.4734
3130	Vesicle-fusing ATPase OS=Rattus norvegicus OX=10116 GN=Nsf PE=1 SV=1	Nsf	A0A0G2K6U1	18.0553	15.9166	16.5854	16.2846	20.4989	19.447	19.2394	19.7128
3131	Vesicle-trafficking protein SEC22b OS=Rattus norvegicus OX=10116 GN=Sec22b PE=1 SV=3	Sec22b	Q4KM74	19.5492	19.2039	18.834	18.4569	21.0639	21.3726	20.8553	21.1088
3132	Vimentin OS=Rattus norvegicus OX=10116 GN=Vim PE=1 SV=1	Vim	G3V8C3	19.6064	19.8661	19.4322	19.8449	22.9579	23.3843	22.603	22.3667
3133	Vinculin OS=Rattus norvegicus OX=10116 GN=Vcl PE=1 SV=1	Vcl	A0A0G2K8V2	22.7054	22.7514	22.7394	22.5848	25.8798	25.4328	25.7841	25.7738
3134	Vitronectin OS=Rattus norvegicus OX=10116 GN=Vtn PE=1 SV=1	Vtn	Q3KR94	25.1312	25.2539	25.1549	25.3703	22.3482	23.2228	22.208	22.1986
3135	Voltage-dependent anion-selective channel protein 1 OS=Rattus norvegicus OX=10116 GN=Vdac1 PE=1 SV=4	Vdac1	Q9Z2L0	21.5944	22.6261	21.3932	21.616	24.0927	25.066	24.4723	24.7357
3136	Voltage-dependent anion-selective channel protein 2 OS=Rattus norvegicus OX=10116 GN=Vdac2 PE=1 SV=2	Vdac2	P81155	21.8408	21.6169	21.465	21.5746	23.1159	24.067	23.63	23.6654
3137	Voltage-dependent anion-selective channel protein 3 OS=Rattus norvegicus OX=10116 GN=Vdac3 PE=1 SV=1	Vdac3	A0A0G2JSR0	18.5731	19.3572	18.1231	18.1779	21.831	22.2585	21.8624	22.2006
3138	Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Rattus norvegicus OX=10116 GN=Cacna2d1 PE=1 SV=1	Cacna2d1	A0A0G2K7E5	19.0113	19.4692	19.4816	19.638	19.2926	20.1494	18.7992	19.103
3139	Vomeromodulin OS=Rattus norvegicus OX=10116 GN=Bpifb9 PE=1 SV=2	LOC690507	Q63751	18.7057	19.496	19.2402	18.9056	17.2752	14.5772	NaN	NaN
3140	von Willebrand factor A domain-containing protein 5A OS=Rattus norvegicus OX=10116 GN=Vwa5a PE=2 SV=1	Vwa5a	Q75WE7	NaN	14.9462	15.8338	NaN	20.8425	19.6133	20.3966	20.5439
3141	von Willebrand factor OS=Rattus norvegicus OX=10116 GN=Vwf PE=1 SV=3	Vwf	F1M957	24.8367	24.6526	22.4488	22.5685	21.1089	21.3945	21.3562	22.1257
3142	VPS37B, ESCRT-I subunit OS=Rattus norvegicus OX=10116 GN=Vps37b PE=1 SV=1	Vps37b	D3ZU64	NaN	NaN	NaN	NaN	19.0431	18.6827	18.7314	18.7131
3143	VPS37C, ESCRT-I subunit OS=Rattus norvegicus OX=10116 GN=Vps37c PE=1 SV=1	Vps37c	B5DFF4	NaN	NaN	NaN	NaN	18.3102	17.7162	17.3427	17.7481
3144	V-type proton ATPase 116 kDa subunit a isoform 1 OS=Rattus norvegicus OX=10116 GN=Atp6v0a1 PE=2 SV=1	Atp6v0a1	P25286	16.3738	16.3643	17.1428	17.4336	20.0161	20.352	19.7328	19.3349
3145	V-type proton ATPase subunit B, brain isoform OS=Rattus norvegicus OX=10116 GN=Atp6v1b2 PE=1 SV=1	Atp6v1b2	P62815	17.4311	17.4378	16.9629	14.8164	21.533	22.4198	22.7767	22.6586
3146	V-type proton ATPase subunit C 1 OS=Rattus norvegicus OX=10116 GN=Atp6v1c1 PE=2 SV=1	Atp6v1c1	Q5FVI6	NaN	NaN	NaN	NaN	17.8723	16.4115	17.23	17.3871
3147	V-type proton ATPase subunit F OS=Rattus norvegicus OX=10116 GN=Atp6v1f PE=1 SV=1	Atp6v1f	P50408	NaN	13.9141	14.3618	NaN	18.1496	17.0739	18.2568	18.5063
3148	V-type proton ATPase subunit G OS=Rattus norvegicus OX=10116 GN=Atp6v1g1 PE=1 SV=1	Atp6v1g1	B2GUV5	16.4355	16.8024	16.6615	NaN	19.6826	18.9007	19.4664	19.2317
3149	V-type proton ATPase subunit H OS=Rattus norvegicus OX=10116 GN=Atp6v1h PE=1 SV=1	Atp6v1h	A0A0G2K9J2	NaN	NaN	14.9786	NaN	19.5288	19.756	19.996	19.885
3150	V-type proton ATPase subunit OS=Rattus norvegicus OX=10116 GN=Atp6v0d1 PE=1 SV=1	Atp6v0d1	Q5M7T6	18.4941	17.9084	17.8278	16.9347	20.47	20.9245	20.2213	20.0142
3151	WAS protein family, member 2 OS=Rattus norvegicus OX=10116 GN=Wasf2 PE=1 SV=1	Wasf2	A0A0G2K5T9	NaN	NaN	16.0793	NaN	16.3275	19.1018	19.4771	18.6798
3152	WAS/WASL-interacting protein family member 3 OS=Rattus norvegicus OX=10116 GN=Wipf3 PE=1 SV=1	Wipf3	Q9Z0G8	NaN	NaN	NaN	NaN	19.071	18.1903	17.7785	17.8701
3153	WASH complex subunit 1 OS=Rattus norvegicus OX=10116 GN=Washc1 PE=2 SV=1	Washc1	B2RYF7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3154	WD repeat and FYVE domain-containing 3 OS=Rattus norvegicus OX=10116 GN=Wdfy3 PE=1 SV=1	Wdfy3	A0A0G2K9M4	NaN	NaN	NaN	NaN	17.3493	17.6888	18.4091	17.0662
3155	WD repeat domain 37 OS=Rattus norvegicus OX=10116 GN=Wdr37 PE=1 SV=3	Wdr37	D3ZQ02	16.0288	15.8009	16.9474	16.7815	19.8097	18.8762	19.2824	19.5776
3156	WD repeat domain 48 OS=Rattus norvegicus OX=10116 GN=Wdr48 PE=1 SV=1	Wdr48	A0A0G2KAW5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3157	WD repeat domain 62 OS=Rattus norvegicus OX=10116 GN=Wdr62 PE=1 SV=2	Wdr62	F1M5K2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3158	WD repeat domain phosphoinositide-interacting protein 2 OS=Rattus norvegicus OX=10116 GN=Wipi2 PE=1 SV=1	Wipi2	Q6AY57	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3159	WD repeat-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Wdr1 PE=1 SV=3	Wdr1	Q5RKI0	20.8864	21.4551	21.1914	21.0182	21.2199	24.7164	24.8649	24.6907
3160	WD repeat-containing protein 26 OS=Rattus norvegicus OX=10116 GN=Wdr26 PE=3 SV=2	Wdr26	F1LTR1	NaN	NaN	NaN	NaN	18.6222	19.293	18.0451	18.7146
3161	WD repeat-containing protein 6 OS=Rattus norvegicus OX=10116 GN=Wdr6 PE=1 SV=2	Wdr6	Q5XFW6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3162	WD repeat-containing protein 7 OS=Rattus norvegicus OX=10116 GN=Wdr7 PE=1 SV=1	Wdr7	Q9ERH3	NaN	NaN	NaN	NaN	19.5482	18.3948	18.8909	19.0893
3163	WD repeat-containing protein 81 OS=Rattus norvegicus OX=10116 GN=Wdr81 PE=3 SV=1	Wdr81	D4A929	NaN	NaN	NaN	NaN	NaN	17.4758	16.8031	17.7989
3164	WD repeat-containing protein 91 OS=Rattus norvegicus OX=10116 GN=Wdr91 PE=2 SV=1	Wdr91	B2RYI0	17.6747	19.6886	16.9515	16.9752	17.5811	17.6625	17.9694	16.5968
3165	WNK lysine deficient protein kinase 2 OS=Rattus norvegicus OX=10116 GN=Wnk2 PE=1 SV=1	Wnk2	A0A0G2KAS8	NaN	NaN	NaN	NaN	16.3096	17.3541	NaN	16.6687
3166	WNK lysine deficient protein kinase 2 OS=Rattus norvegicus OX=10116 GN=Wnk2 PE=1 SV=2	Wnk2	D3ZMJ7	NaN	NaN	15.167	14.6923	17.0786	18.9077	18.8601	17.8528
3167	WW domain binding protein 2, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Wbp2 PE=1 SV=1	Wbp2	G3V721	16.3898	NaN	NaN	NaN	23.3462	22.6947	23.0874	23.0896
3168	WW domain containing adaptor with coiled-coil OS=Rattus norvegicus OX=10116 GN=Wac PE=1 SV=3	Wac	F1LW69	NaN	NaN	NaN	NaN	17.2998	17.2216	NaN	16.7858
3169	WWC family member 3 OS=Rattus norvegicus OX=10116 GN=Wwc3 PE=1 SV=2	Wwc3	M0R8P6	15.1188	NaN	NaN	NaN	NaN	18.7959	17.3438	16.639
3170	Xaa-Pro dipeptidase OS=Rattus norvegicus OX=10116 GN=Pepd PE=2 SV=1	Pepd	Q5I0D7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3171	Xin actin-binding repeat containing 1 OS=Rattus norvegicus OX=10116 GN=Xirp1 PE=1 SV=2	Xirp1	D4ABA9	16.5701	17.9765	17.9219	17.2583	23.4645	23.5217	23.1972	23.0801
3172	X-prolyl aminopeptidase (Aminopeptidase P) 1, soluble, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Xpnpep1 PE=	Xpnpep1	A0A0G2JV31	16.0702	18.553	17.2491	18.0344	19.3915	20.7028	21.4763	20.2712
3173	Y-box-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Ybx3 PE=1 SV=1	Ybx3	Q62764	14.7062	NaN	NaN	15.5723	19.7081	20.9958	20.7455	20.6917
3174	Yip1 interacting factor homolog (S. cerevisiae) OS=Rattus norvegicus OX=10116 GN=Yif1a PE=1 SV=1	Yif1a	B0BMV4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	16.5434
3175	YTH N(6)-methyladenosine RNA-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ythdf1 PE=1 SV=1	Ythdf1	Q4V8J6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3176	YTH N(6)-methyladenosine RNA-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Ythdf2 PE=1 SV=3	Ythdf2	E9PU11	NaN	NaN	NaN	NaN	21.2924	19.9787	20.2323	19.7599
3177	YTH N(6)-methyladenosine RNA-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Ythdf3 PE=1 SV=1	Ythdf3	D3ZIY3	NaN	14.1767	NaN	NaN	NaN	18.0383	16.793	NaN
3178	YY1-associated factor 2 OS=Rattus norvegicus OX=10116 GN=Yaf2 PE=1 SV=3	Yaf2	D3ZII7	NaN	NaN	NaN	NaN	15.8826	NaN	16.0141	NaN

3179	Zinc finger CCCH-type-containing 7B OS=Rattus norvegicus OX=10116 GN=Zc3h7b PE=1 SV=1	Zc3h7b	A0A0G2K214	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3180	Zinc finger FYVE-type-containing 1 OS=Rattus norvegicus OX=10116 GN=Zfyve1 PE=1 SV=1	Zfyve1	D4A3T4	17.1047	17.2133	15.3122	17.4488	21.3794	20.2438	20.3984	20.4497
3181	Zinc finger FYVE-type-containing 16 OS=Rattus norvegicus OX=10116 GN=Zfyve16 PE=1 SV=2	Zfyve16	D4ADF6	17.1771	16.3017	NaN	18.4821	19.0132	18.9906	19.0945	18.7787
3182	Zinc finger protein 275 OS=Rattus norvegicus OX=10116 GN=Zfp275 PE=4 SV=1	Zfp275	D3ZRH5	NaN	NaN	NaN	NaN	15.8467	NaN	16.6632	16.2568
3183	Zinc finger protein 330 OS=Rattus norvegicus OX=10116 GN=Zfp330 PE=1 SV=1	Zfp330	D3ZSN4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3184	Zinc finger protein 36, C3H type-like 2 OS=Rattus norvegicus OX=10116 GN=Zfp36l2 PE=1 SV=1	Zfp36l2	D3ZHK9	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3185	Zinc finger, C2HC-type-containing 1A OS=Rattus norvegicus OX=10116 GN=Zc2hc1a PE=1 SV=1	Zc2hc1a	A0A0G2K782	15.3177	15.1247	15.6996	NaN	17.4351	19.2287	19.2491	18.939
3186	ZW10 interactor OS=Rattus norvegicus OX=10116 GN=Zwint PE=1 SV=1	Zwint	Q8VIL3	20.1496	19.62	19.2957	19.192	21.2385	20.1109	20.3054	20.1356
3187	Zyxin OS=Rattus norvegicus OX=10116 GN=Zyx PE=1 SV=1	Zyx	D4A7U1	21.86	21.6636	21.8989	21.3178	24.2799	23.5618	23.7935	23.7574

Table S2. Comparison of Log2 abundances of proteins detected in at least 3 out of 4 samples of heart and plasma EVs.

#	Description	Gene name	Accession	-log *P*	Difference	P3	P5	P7	P9	H3-H4	H5-H6	H7-H8	H9-H10
1	[F-actin]-monooxygenase MICAL1 OS=Rattus norvegicus OX=10116 GN=Mical1 PE=1 SV=1	Mical1	D3ZBP4	0.851675	-0.755851746	21.5769844	23.1447926	21.321804	22.4698372	21.4478436	21.7627449	21.2147961	21.0646267
2	[Protein ADP-ribosylarginine] hydrolase-like protein 1 OS=Rattus norvegicus OX=10116 GN=Adprhl1 PE=2 SV=1	Adprhl1	Q5XIB3	2.89761682	6.698092461	17.8803387	17.5435429	17.2001667	12.9120255	22.8115654	22.8729172	23.4990311	23.1449299
3	10 kDa heat shock protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hspe1 PE=1 SV=3	Hspe1	P26772	1.57865983	2.789615631	18.0012913	18.8925457	17.3560371	16.3786793	18.1018181	21.554327	20.9277573	21.2031136
4	14-3-3 protein beta/alpha OS=Rattus norvegicus OX=10116 GN=Ywhab PE=1 SV=3	Ywhab	P35213	4.9632497	3.802592278	17.8842106	17.9879513	18.1101036	16.9028053	21.5685406	21.5334053	21.3389015	21.6545925
5	14-3-3 protein epsilon OS=Rattus norvegicus OX=10116 GN=Ywhae PE=1 SV=1	Ywhae	P62260	6.16320429	2.853987694	22.1360416	22.549654	22.4637909	22.3539848	25.3768082	24.9575081	25.2068996	25.3782063
6	14-3-3 protein eta OS=Rattus norvegicus OX=10116 GN=Ywhah PE=1 SV=2	Ywhah	P68511	3.83072047	4.654275894	18.3934059	20.3948917	18.3259983	18.007452	23.6170654	23.2964649	23.3550739	23.4702473
7	14-3-3 protein gamma OS=Rattus norvegicus OX=10116 GN=Ywhag PE=1 SV=2	Ywhag	P61983	4.29682985	4.112957478	19.9414539	19.2559013	20.1160984	18.3496647	23.5691643	23.5153465	23.4735279	23.5569096
8	14-3-3 protein theta OS=Rattus norvegicus OX=10116 GN=Ywhaq PE=1 SV=1	Ywhaq	P68255	6.112528	3.381102562	20.4311943	20.8216209	20.9612732	20.2767754	23.9692669	24.0115223	24.03438	24.0001049
9	14-3-3 protein zeta/delta OS=Rattus norvegicus OX=10116 GN=Ywhaz PE=1 SV=1	Ywhaz	A0A0G2JV65	5.70811274	2.271435261	21.4316959	21.4574394	21.4793549	21.7197933	23.8874931	23.5161095	23.748291	24.022131
10	26S proteasome non-ATPase regulatory subunit 1 OS=Rattus norvegicus OX=10116 GN=Psmd1 PE=1 SV=1	Psmd1	G3V8B6	4.26909748	3.096107483	21.5596218	20.3509254	21.2404709	21.0239887	24.3745098	23.6441193	24.2489109	24.2918968
11	26S proteasome non-ATPase regulatory subunit 11 OS=Rattus norvegicus OX=10116 GN=Psmd11 PE=1 SV=2	Psmd11	F1LMZ8	2.00591777	2.283674717	22.5353584	20.41576	20.2730808	19.9596996	23.4367142	22.5855885	23.1720638	23.1242313
12	26S proteasome non-ATPase regulatory subunit 13 OS=Rattus norvegicus OX=10116 GN=Psmd13 PE=1 SV=1	Psmd13	B0BN93	3.29299628	2.625152111	21.7536087	20.6128063	20.5688438	20.3440857	23.9265938	22.84655	23.4490337	23.5577755
13	26S proteasome non-ATPase regulatory subunit 2 OS=Rattus norvegicus OX=10116 GN=Psmd2 PE=1 SV=1	Psmd2	Q4FZT9	5.37635704	4.342190742	19.4834557	19.4415264	20.2629166	19.7520123	24.4673615	23.5272198	24.2571182	24.0569744
14	26S proteasome non-ATPase regulatory subunit 9 OS=Rattus norvegicus OX=10116 GN=Psmd9 PE=1 SV=1	Psmd9	G3V9P0	1.70683602	4.202494144	16.5006123	15.625618	16.1362076	21.3140106	21.7041702	21.0608616	21.7914047	21.8299885
15	26S proteasome regulatory subunit 4 OS=Rattus norvegicus OX=10116 GN=Psmc1 PE=1 SV=1	Psmc1	P62193	4.92195039	4.72711277	18.6063328	18.2352943	18.1664295	19.5827408	23.5747356	22.9311275	23.5595646	23.4338207
16	26S proteasome regulatory subunit 6A OS=Rattus norvegicus OX=10116 GN=Psmc3 PE=1 SV=1	Psmc3	Q6P6U2	6.25400185	4.36192894	19.0370445	19.0903015	19.2941093	19.1639481	23.8108902	22.9556885	23.655241	23.6112995
17	26S proteasome regulatory subunit 6B OS=Rattus norvegicus OX=10116 GN=Psmc4 PE=1 SV=1	Psmc4	Q63570	6.10164806	5.637299538	17.4584484	16.6329422	17.6373062	17.8100224	22.8856506	22.9384232	23.2085018	23.0553417
18	26S proteasome regulatory subunit 7 OS=Rattus norvegicus OX=10116 GN=Psmc2 PE=1 SV=1	Psmc2	G3V7L6	5.96291193	3.796947479	20.4998055	20.6201839	20.2401295	20.1006031	24.4981556	23.7689438	24.2412357	24.1401768
19	26S proteasome regulatory subunit 8 OS=Rattus norvegicus OX=10116 GN=Psmc5 PE=1 SV=1	Psmc5	P62198	3.94168823	3.608829498	20.6506081	20.0084515	19.8684464	21.6280136	24.3257408	24.0002193	24.1749992	24.0898781
20	2-oxoglutarate dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ogdh PE=1 SV=1	Ogdh	Q5XI78	0.60211892	0.502664089	21.5646629	20.625618	20.4188862	20.5155106	20.4345665	21.7392082	21.3721008	21.5894585
21	3'(2'),5'-bisphosphate nucleotidase 1 OS=Rattus norvegicus OX=10116 GN=Bpnt1 PE=1 SV=1	Bpnt1	A0A0G2K0V3	4.98770084	4.609997034	15.5126019	14.9825907	14.5001774	15.4964142	20.3571033	19.176033	19.6816845	19.7169514
22	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Rattus norvegicus OX=10116 GN=Hsd17b10 PE=1 SV=1	Hsd17b10	B0BMW2	2.6598745	3.425238132	14.9601965	15.7691269	14.750371	15.8320446	16.9649391	19.5376358	18.9848309	19.5252857
23	3-ketoacyl-CoA thiolase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acaa2 PE=1 SV=3	Acaa2	G3V9U2	1.62020673	2.189178944	19.7137947	18.9962311	18.3693771	17.1577492	19.5139065	21.9018955	20.8320065	20.7460594
24	3-mercaptopyruvate sulfurtransferase OS=Rattus norvegicus OX=10116 GN=Mpst PE=1 SV=3	Mpst	P97532	2.26292471	1.958003521	17.8855495	19.4691715	19.4668941	18.3100414	21.3229752	20.282692	20.8181572	20.5398464
25	3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Rattus norvegicus OX=10116 GN=Papss1 PE=1 SV=1	Papss1	A0A0G2K0L0	1.22447576	-0.952898026	19.2341461	18.7365398	19.1047363	20.3371983	18.7156582	18.6687088	17.7463589	18.4703026
26	40S ribosomal protein S10 OS=Rattus norvegicus OX=10116 GN=Rps10 PE=2 SV=1	Rps10	P63326	6.17835	5.359024048	18.5035801	18.7371826	18.6846046	19.1975784	23.5772038	24.4832764	24.3640594	24.1345024
27	40S ribosomal protein S11 OS=Rattus norvegicus OX=10116 GN=Rps11 PE=1 SV=3	Rps11	P62282	6.3916046	6.860810757	17.3725662	16.8912296	17.8735104	17.1157913	23.6916351	24.664938	24.2898903	24.0498772
28	40S ribosomal protein S12 OS=Rattus norvegicus OX=10116 GN=Rps12 PE=1 SV=1	Rps12	Q6PDW1	4.02892387	2.749999523	20.5544567	20.7114105	19.9386272	20.129509	23.7345257	22.5868549	23.0445137	22.9681072
29	40S ribosomal protein S13 OS=Rattus norvegicus OX=10116 GN=Rps13 PE=1 SV=2	Rps13	P62278	4.48366059	2.755561829	20.603199	20.3255939	20.4124756	20.8478127	22.6816883	23.7179146	23.4662075	23.3455181
30	40S ribosomal protein S14 OS=Rattus norvegicus OX=10116 GN=Rps14 PE=2 SV=3	Rps14	P13471	6.96967563	5.54079628	19.0459824	18.3513355	18.7352886	18.4340611	24.2062511	24.3707294	24.2692986	23.8835735
31	40S ribosomal protein S15a OS=Rattus norvegicus OX=10116 GN=Rps15a PE=1 SV=2	Rps15a	P62246	3.91868718	4.923208237	19.6241016	19.2059155	18.6305351	17.1626492	23.1724072	23.9099598	23.7175961	23.5160713
32	40S ribosomal protein S16 OS=Rattus norvegicus OX=10116 GN=Rps16 PE=1 SV=2	Rps16	P62250	2.23987529	2.006196976	22.8412609	22.5535583	22.2536278	20.8268814	23.6125088	24.2836952	24.3455715	24.2583408
33	40S ribosomal protein S17-like OS=Rattus norvegicus OX=10116 GN=LOC100362366 PE=3 SV=1	LOC100362366	D3ZFA8	0.34888247	0.214255333	23.2879314	23.6830997	23.5029449	22.5433731	23.368372	23.7179623	23.3963261	23.3917103
34	40S ribosomal protein S2 OS=Rattus norvegicus OX=10116 GN=Rps2 PE=1 SV=1	Rps2	P27952	3.78053996	2.77696991	22.1752377	21.4202633	21.7113304	21.646822	23.6882324	25.0789394	24.6997623	24.5945988
35	40S ribosomal protein S23 OS=Rattus norvegicus OX=10116 GN=Rps23 PE=1 SV=3	Rps23	P62268	5.04188632	6.459777832	17.1797943	16.9663906	16.0387287	15.3214951	22.3867302	23.2917213	22.8913403	22.7757282
36	40S ribosomal protein S24 OS=Rattus norvegicus OX=10116 GN=LOC100363469 PE=3 SV=1	LOC100363469	D4ACJ1	4.69397871	6.398174286	15.842083	14.8106833	16.3646965	14.32969	21.1037331	22.3133183	21.9480305	21.5747681
37	40S ribosomal protein S25 OS=Rattus norvegicus OX=10116 GN=Rps25 PE=2 SV=1	Rps25	P62853	4.67569255	4.488971233	19.4533768	18.7510052	19.0025597	19.4666672	22.7526054	24.3401699	23.869072	23.6676464
38	40S ribosomal protein S26 OS=Rattus norvegicus OX=10116 GN=Rps26 PE=3 SV=3	Rps26	P62856	5.0800741	5.118424892	18.2330551	17.5268974	17.0661316	17.7636623	22.1456146	23.446146	22.8908062	22.5808792
39	40S ribosomal protein S27-like OS=Rattus norvegicus OX=10116 GN=Rps27l PE=1 SV=3	Rps27l	P24051	4.45971091	6.913618088	14.517704	17.3074512	16.7399368	16.2955093	23.6686382	23.1227188	22.9146767	22.8090401
40	40S ribosomal protein S28 OS=Rattus norvegicus OX=10116 GN=Rps28 PE=1 SV=1	Rps28	P62859	3.70955178	4.016800165	18.0210629	15.9825716	17.4519558	16.4707088	21.5546494	20.7860661	20.7722454	20.8805389
41	40S ribosomal protein S29 OS=Rattus norvegicus OX=10116 GN=Rps29 PE=1 SV=2	Rps29	P62275	1.96592481	1.880814075	17.6027431	17.341856	17.954874	18.0660038	21.0594254	19.3886795	19.1361008	18.9045277
42	40S ribosomal protein S3 OS=Rattus norvegicus OX=10116 GN=Rps3 PE=1 SV=1	Rps3	P62909	6.66383386	5.094806671	19.7694378	19.4875031	19.2377567	20.1238708	24.6542683	24.8690758	24.7843781	24.690073
43	40S ribosomal protein S30 OS=Rattus norvegicus OX=10116 GN=LOC100360647 PE=1 SV=1	Fau	Q5BJN7	2.5809209	1.789279938	18.0543175	18.9200096	19.473156	19.6319122	20.7544212	20.9875145	20.6619949	20.8325844
44	40S ribosomal protein S3a OS=Rattus norvegicus OX=10116 GN=LOC100365839 PE=3 SV=1	LOC100365839	M0R6L4	4.26258035	4.276986599	20.6250153	19.650362	20.1198444	20.0664768	23.3065052	25.0063362	24.6768456	24.579958
45	40S ribosomal protein S4 OS=Rattus norvegicus OX=10116 GN=Rps4x PE=3 SV=1	Rps4x-ps9	A0A0H2UHX3	5.01781676	3.032104969	22.160677	21.3412018	21.8945618	22.1005669	24.5880527	25.0854073	25.1007729	24.8511944
46	40S ribosomal protein S5 OS=Rattus norvegicus OX=10116 GN=Rps5 PE=1 SV=1	Rps5	B0BN81	4.67877212	4.867607594	18.8413277	18.5911255	18.6007729	19.8602886	23.0880318	24.4085102	23.9151554	23.9522476
47	40S ribosomal protein S6 OS=Rattus norvegicus OX=10116 GN=Rps6 PE=1 SV=1	Rps6	P62755	4.87093706	4.829005241	19.2429619	18.8957138	18.5831585	19.9070721	23.3563385	24.5011883	24.2024345	23.8849659
48	40S ribosomal protein S7 OS=Rattus norvegicus OX=10116 GN=Rps7 PE=1 SV=1	Rps7	P62083	5.07967269	4.234348774	18.5361786	17.9787655	17.4241753	17.3557224	21.8278084	22.3186207	21.8585625	22.2272453
49	40S ribosomal protein S8 OS=Rattus norvegicus OX=10116 GN=Rps8 PE=1 SV=2	Rps8	P62243	3.34824795	2.767733097	21.6735992	21.0522366	20.9839039	20.1414833	23.1269207	24.3296089	23.7810287	23.684597
50	40S ribosomal protein S9 OS=Rattus norvegicus OX=10116 GN=Rps9 PE=1 SV=4	Rps9	P29314	5.06426523	5.13807869	19.5874367	18.9906635	18.8433857	18.2578487	23.3501282	24.4917812	24.2881012	24.1016388
51	40S ribosomal protein SA OS=Rattus norvegicus OX=10116 GN=Rpsa PE=1 SV=3	Rpsa	P38983	4.2989236	3.324766636	19.8536549	18.6630344	19.4231434	18.4923172	22.5598488	22.3882656	22.4553185	22.3277836
52	4F2 cell-surface antigen heavy chain OS=Rattus norvegicus OX=10116 GN=Slc3a2 PE=1 SV=1	Slc3a2	A0A0H2UHQ0	0.44709781	0.290477276	20.213707	19.6762142	19.0974884	20.3292503	20.1490288	20.2944565	20.0859165	19.9491673
53	4-trimethylaminobutyraldehyde dehydrogenase OS=Rattus norvegicus OX=10116 GN=Aldh9a1 PE=1 SV=1	Aldh9a1	A0A0G2JSI1	3.31530792	3.374424458	19.8296413	19.281023	19.5441933	19.5361996	21.5357838	23.0075455	23.5355129	23.6099129
54	5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Rattus norvegicus OX=10116 GN=Prkaa1 PE=1 SV=2	Prkaa1	P54645	5.38550552	2.874105453	17.3890781	17.4151077	17.1832027	16.8550739	20.4614792	19.9502888	20.0275211	19.8995953
55	5'-AMP-activated protein kinase subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Prkab1 PE=1 SV=4	Prkab1	P80386	2.81150538	5.1327281	14.9936781	17.121748	13.8799753	17.8971653	21.1532001	21.1100044	21.3647156	20.7955589
56	5'-AMP-activated protein kinase subunit gamma-1 OS=Rattus norvegicus OX=10116 GN=Prkag1 PE=1 SV=3	Prkag1	P80385	3.32402464	2.202239513	19.0321293	19.7930393	19.6226692	19.4859028	22.3194923	21.0236206	21.500988	21.8985977
57	5'-nucleotidase OS=Rattus norvegicus OX=10116 GN=Nt5e PE=1 SV=1	Nt5e	P21588	3.88139436	3.37264061	15.4981909	17.1177502	15.8524141	15.8830223	19.7549343	19.7249546	19.1320992	19.2299519
58	5-oxoprolinase OS=Rattus norvegicus OX=10116 GN=Oplah PE=1 SV=2	Oplah	P97608	3.88388486	4.105236769	14.7094231	15.2543011	16.0215721	14.2772493	18.6018429	19.5075436	19.8038139	18.7702923
59	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hspd1 PE=1 SV=1	Hspd1	P63039	2.35663318	1.527311802	22.4426746	21.9312286	21.440527	22.5139828	22.9161663	23.8700638	23.7030544	23.9483757

60	60S acidic ribosomal protein P0 OS=Rattus norvegicus OX=10116 GN=Rplp0 PE=1 SV=2	Rplp0	P19945	5.02783998	3.241580963	20.9476261	20.6664257	20.9897614	21.0685863	23.5859051	24.6528912	24.1574574	24.2424698
61	60S acidic ribosomal protein P1 OS=Rattus norvegicus OX=10116 GN=Rplp1 PE=3 SV=1	Rplp1	P19944	2.6369936	2.680538177	18.0157604	18.3783646	18.6781921	20.1340485	20.7568398	21.8720932	21.5019855	21.7975998
62	60S acidic ribosomal protein P2 OS=Rattus norvegicus OX=10116 GN=Rplp2 PE=1 SV=2	Rplp2	P02401	4.04654185	3.738778591	20.6609859	20.4489384	20.0625896	21.6685257	23.8610668	24.8853569	24.5544491	24.4952812
63	60S ribosomal protein L10 OS=Rattus norvegicus OX=10116 GN=Rpl10 PE=1 SV=3	Rpl10	Q6PDV7	4.87838241	5.981395245	17.6492901	17.529089	16.4100075	17.8646717	22.4319515	24.0013237	23.5267067	23.4186573
64	60S ribosomal protein L10a OS=Rattus norvegicus OX=10116 GN=Rpl10a PE=1 SV=2	Rpl10a	P62907	4.06035802	5.168228626	17.4412994	19.681675	18.4217319	18.6544266	22.8309269	24.2856579	23.907568	23.8478947
65	60S ribosomal protein L11 OS=Rattus norvegicus OX=10116 GN=Rpl11 PE=1 SV=2	Rpl11	P62914	5.98827034	4.427837849	19.3606033	18.4076099	19.2622585	18.9940395	23.3585033	23.597393	23.4391441	23.3408222
66	60S ribosomal protein L12 OS=Rattus norvegicus OX=10116 GN=Rpl12 PE=2 SV=1	Rpl12	P23358	5.63879066	3.77340126	21.0334854	20.4812527	20.2363434	20.7702637	24.0275097	24.6289959	24.4833622	24.4750824
67	60S ribosomal protein L13 OS=Rattus norvegicus OX=10116 GN=LOC100360491 PE=3 SV=1	LOC100360491	D3ZRM9	6.49335492	4.228730202	20.9968128	20.3917503	20.8559227	20.634428	24.6549263	25.2059727	24.9462795	24.9866562
68	60S ribosomal protein L13a OS=Rattus norvegicus OX=10116 GN=Rpl13a PE=1 SV=1	Rpl13a	Q5RK10	5.6374592	5.696574211	17.8098335	17.1713219	17.33811	17.2248592	22.2464581	23.6121235	23.2838097	23.1880302
69	60S ribosomal protein L14 OS=Rattus norvegicus OX=10116 GN=Rpl14 PE=1 SV=1	Rpl14	B5DEM5	4.5277395	4.181750774	18.9926662	18.6631756	18.8996487	18.4425545	22.0262756	23.7390022	23.012331	22.9474392
70	60S ribosomal protein L15 OS=Rattus norvegicus OX=10116 GN=Rpl15 PE=1 SV=2	Rpl15	P61314	5.24031834	4.336912155	19.4248943	18.9351158	18.6195927	18.9168701	22.63941	23.7560997	23.4877987	23.3608131
71	60S ribosomal protein L17 OS=Rattus norvegicus OX=10116 GN=Rpl17 PE=1 SV=1	Rpl17	A0A0H2UHQ1	4.19691704	5.00898838	18.8436012	18.2374592	18.0564861	17.0483017	22.0971928	23.7078457	23.0481033	23.36866
72	60S ribosomal protein L18 OS=Rattus norvegicus OX=10116 GN=Rpl18 PE=1 SV=1	Rpl18	A0A0H2UHS7	4.48470018	3.542685032	20.0315552	19.6388493	19.7368183	18.6901684	22.6898422	23.3313274	23.1707191	23.0762424
73	60S ribosomal protein L18a OS=Rattus norvegicus OX=10116 GN=Rpl18a PE=2 SV=1	Rpl18a	P62718	5.4110983	4.613975525	18.1539536	18.3919506	18.2695732	18.4436073	22.139082	23.4757481	23.0928249	23.0073318
74	60S ribosomal protein L19 OS=Rattus norvegicus OX=10116 GN=Rpl19 PE=1 SV=1	Rpl19	P84100	4.477609	5.301180363	18.1450443	16.9722786	17.7085609	16.4401035	21.8464451	23.2868671	22.7186184	22.6187782
75	60S ribosomal protein L23 OS=Rattus norvegicus OX=10116 GN=Rpl23 PE=2 SV=1	Rpl23	P62832	4.58948759	5.307657242	18.5613785	19.444849	19.0388374	17.7090645	24.7752457	23.9360638	23.7031307	23.5703182
76	60S ribosomal protein L24 OS=Rattus norvegicus OX=10116 GN=Rpl24 PE=2 SV=1	Rpl24	P83732	5.31229629	3.474711418	19.8938961	19.4832993	19.5671844	19.8591671	22.5940933	23.5024967	23.3795433	23.2262592
77	60S ribosomal protein L26 OS=Rattus norvegicus OX=10116 GN=Rpl26 PE=1 SV=1	Rpl26	G3V6I9	2.09191471	3.358102798	16.8634224	19.0884514	20.5041504	20.1059628	21.6568127	22.8692417	22.8181114	22.6502323
78	60S ribosomal protein L27 OS=Rattus norvegicus OX=10116 GN=Rpl27 PE=2 SV=2	Rpl27	P61354	2.99703995	4.542895317	17.9592628	14.955204	17.7185974	18.0522766	21.2540188	22.0900955	21.8760891	21.6367188
79	60S ribosomal protein L29 OS=Rattus norvegicus OX=10116 GN=Rpl29 PE=1 SV=3	Rpl29	P25886	7.69923704	6.056071997	14.3557167	14.2463312	14.3496561	14.4388933	20.210392	20.6636391	20.6607437	20.0801105
80	60S ribosomal protein L3 OS=Rattus norvegicus OX=10116 GN=Rpl3 PE=1 SV=3	Rpl3	P21531	4.19118472	5.369089127	19.3502731	17.3889236	19.2139282	17.9182396	23.1324654	24.3579159	23.9749374	23.8824024
81	60S ribosomal protein L31 OS=Rattus norvegicus OX=10116 GN=Rpl31 PE=2 SV=1	Rpl31	P62902	4.88599111	6.003234386	17.5239048	17.5368805	16.4285526	16.0189838	22.1605835	23.3625221	23.0518341	22.9463196
82	60S ribosomal protein L32 OS=Rattus norvegicus OX=10116 GN=Rpl32 PE=1 SV=2	Rpl32	P62912	5.16266149	4.057021141	18.3467941	18.5239277	18.0237141	19.1346207	22.1243668	22.6187134	22.860424	22.6536369
83	60S ribosomal protein L34 OS=Rattus norvegicus OX=10116 GN=Rpl34 PE=1 SV=1	Rpl34	B2RZD4	4.97062008	5.536725044	17.058073	16.0317898	17.3853474	16.0885639	21.5482426	22.6553955	22.1872826	22.3197536
84	60S ribosomal protein L35a OS=Rattus norvegicus OX=10116 GN=Rpl35a PE=3 SV=1	Rpl35al1	P04646	3.76482415	3.720359325	17.1119461	18.355442	18.8960171	17.5707512	21.1937618	22.2211151	21.7827129	21.6180038
85	60S ribosomal protein L36 OS=Rattus norvegicus OX=10116 PE=3 SV=1	LOC100361060	D3ZZ95	3.45711752	4.4834795	17.379612	15.6369839	15.7666941	15.1929197	19.3503418	21.1430149	20.8191395	20.5976315
86	60S ribosomal protein L37a OS=Rattus norvegicus OX=10116 GN=Rpl37a PE=3 SV=1	Rpl37a	A0A0H2UHU1	3.65392177	4.86419487	17.3670158	16.2432861	14.5486507	16.5871487	20.6058292	21.4198723	21.09519	21.0819893
87	60S ribosomal protein L4 OS=Rattus norvegicus OX=10116 GN=Rpl4 PE=1 SV=1	Rpl4	Q6P3V9	4.76271748	4.177391529	20.1075897	19.8637638	20.2875214	20.1171017	23.3692036	24.9360771	24.3888798	24.3913822
88	60S ribosomal protein L5 OS=Rattus norvegicus OX=10116 GN=Rpl5 PE=1 SV=3	Rpl5	P09895	1.54213498	2.218400002	19.4904671	16.3203526	19.1027565	18.7256527	20.9738827	21.2954388	20.035635	20.2078724
89	60S ribosomal protein L6 OS=Rattus norvegicus OX=10116 PE=3 SV=1	Rpl6-ps1	F1LQS3	3.79959156	4.125136852	20.2902336	18.9810524	20.4885178	19.9033604	23.1298504	24.9035969	24.0754166	24.0548477
90	60S ribosomal protein L7 OS=Rattus norvegicus OX=10116 GN=Rpl7 PE=1 SV=1	Rpl7	B0K031	4.93641004	5.09707737	18.8410645	19.1014633	18.7443237	18.4405651	22.8716812	24.5841656	24.068964	23.9909153
91	60S ribosomal protein L7a-like OS=Rattus norvegicus OX=10116 GN=LOC108349606 PE=4 SV=1	LOC108349606	D3ZU22	5.26465771	4.364089012	18.8358307	18.9593754	19.6351261	18.9665222	22.8420944	23.9025555	23.6560879	23.4524727
92	60S ribosomal protein L9 OS=Rattus norvegicus OX=10116 GN=Rpl9 PE=1 SV=1	Rpl9	P17077	4.29066419	5.05586338	17.2452965	19.0366154	17.4381256	18.5936432	22.476717	23.5145779	23.4047031	23.1411362
93	6-phosphogluconate dehydrogenase, decarboxylating OS=Rattus norvegicus OX=10116 GN=Kif1b PE=1 SV=1	Pgd	A0A0G2K7Q8	0.26293904	-0.272348881	16.9229355	18.3910141	18.6753178	18.2822456	17.478754	18.2635975	17.6420918	17.7976742
94	6-phosphogluconolactonase OS=Rattus norvegicus OX=10116 GN=Pgls PE=1 SV=1	Pgls	G3V8D5	3.70854592	3.479958773	15.6834879	16.7589626	17.3502159	17.4346962	19.8466015	20.3031597	20.5237579	20.4736786
95	72 kDa type IV collagenase OS=Rattus norvegicus OX=10116 GN=Mmp2 PE=1 SV=3	Mmp2	E9PSM5	2.23222317	-1.345143795	18.5240669	18.9787731	19.3630276	18.9650307	16.8429413	18.1196861	17.8146687	17.673027
96	A kinase (PRKA) anchor protein 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Akap1 PE=1 SV=2	Akap1	D4A9M6	1.25798641	0.55227232	19.8813934	19.2851639	20.0689125	20.0564594	20.4046574	20.7338772	20.3171577	20.0453262
97	Ab1-205 OS=Rattus norvegicus OX=10116 GN=Surf4 PE=1 SV=1	Surf4	Q7TP91	1.30636763	1.634782791	17.6559372	19.4080353	16.2064877	17.9126072	19.5789928	19.6743736	19.2298393	19.2389927
98	ABR, RhoGEF and GTPase-activating protein OS=Rattus norvegicus OX=10116 GN=Abr PE=1 SV=1	Abr	A0A0G2JTR4	1.84929186	2.383639574	17.1711826	17.5288239	14.7710485	17.3591175	19.3703194	18.3496323	19.4476604	19.1971188
99	Abraxas 2, BRISC complex subunit OS=Rattus norvegicus OX=10116 GN=Abraxas2 PE=1 SV=3	Abraxas2	D4A415	3.67906052	2.783890247	16.4185638	16.5894585	15.5801105	16.0384426	18.2179356	19.0663776	19.5126781	18.9651451
100	Ac1002 OS=Rattus norvegicus OX=10116 GN=Adh4 PE=1 SV=1	Adh4	Q7TQ90	0.49687135	0.369889259	19.61063	18.3773441	19.5056038	19.7834816	19.7748432	19.88591	19.7475395	19.3483238
101	Ac1873 OS=Rattus norvegicus OX=10116 GN=Fga PE=1 SV=1	Fga	Q7TQ70	3.41165713	-1.537103653	29.5044651	29.1484222	29.259985	29.5205097	27.9967155	27.8289776	27.2763042	28.18297
102	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acat1 PE=1 SV=1	Acat1	P17764	1.8919691	2.950646639	19.0068951	18.6775684	18.2142696	15.9191809	19.5608463	21.6977901	20.9572544	21.4046097
103	Acetyl-CoA carboxylase 1 OS=Rattus norvegicus OX=10116 GN=Acaca PE=1 SV=1	Acaca	P11497	1.39191789	0.869095802	19.7562103	19.175539	19.7245159	18.53862	19.8911877	19.8548164	20.5218201	20.4034443
104	Acetyl-CoA carboxylase beta OS=Rattus norvegicus OX=10116 GN=Acacb PE=1 SV=1	Acacb	A0A0G2K1F2	4.13800768	2.952414513	20.6421623	20.3177414	20.8144112	20.9863014	22.8809147	24.0242233	24.0462208	23.6189156
105	Acetyl-Coenzyme A dehydrogenase, medium chain OS=Rattus norvegicus OX=10116 GN=Acadm PE=1 SV=1	Acadm	G3V796	1.38383068	-1.544788837	19.1055813	19.8782806	18.1863194	19.8660221	17.9091949	18.1316738	16.420784	18.3953953
106	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Rattus norvegicus OX=10116 GN=Anp32a PE=1 SV=2	Anp32a	F7EL36	3.34708801	5.239652872	16.5832424	14.5424843	15.6076927	13.0663919	20.1739693	19.9959316	20.282053	20.306469
107	Aconitate hydratase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Aco2 PE=1 SV=2	Aco2	Q9ER34	1.88307794	3.897431374	19.6918926	20.692009	20.3624115	16.5098801	21.5409698	24.1961288	23.4459305	23.6628895
108	Actin, alpha cardiac muscle 1 OS=Rattus norvegicus OX=10116 GN=Actc1 PE=2 SV=1	Actc1	P68035	6.23611853	5.550210476	22.6518078	21.6767502	21.9585762	22.5052929	28.0246067	27.5072803	27.7063961	27.7549858
109	Actin, alpha skeletal muscle OS=Rattus norvegicus OX=10116 GN=Acta1 PE=1 SV=1	Acta1	P68136	1.10274289	1.667303562	20.1543884	20.8751678	21.5136204	23.6400242	23.643589	22.549736	23.469656	23.1894341
110	Actin, cytoplasmic 1 OS=Rattus norvegicus OX=10116 GN=Actb PE=1 SV=1	Actb	P60711	5.00431646	1.747694969	20.1317921	20.0745792	20.0533199	20.55373	21.9361591	21.8979454	21.8700104	22.1000862
111	Actin, cytoplasmic 2 OS=Rattus norvegicus OX=10116 GN=Actg1 PE=1 SV=1	Actg1	P63259	6.51576221	3.155191422	25.9182549	26.3255329	26.0477886	26.0909023	29.5021362	29.0325241	29.2094936	29.2590904
112	Actin-related protein 2 OS=Rattus norvegicus OX=10116 GN=Actr2 PE=2 SV=1	Actr2	Q5M7U6	4.77920026	2.528561592	19.0402851	18.1867752	18.5961685	18.5932579	21.2118893	20.8300419	21.3145866	21.1742153
113	Actin-related protein 2/3 complex subunit 3 OS=Rattus norvegicus OX=10116 GN=Arpc3 PE=1 SV=1	Arpc3	B2GV73	4.29165753	2.839666843	17.6063709	18.662962	18.2515945	18.8222771	21.2365112	21.023428	21.1428661	21.2990665
114	Actin-related protein 2/3 complex subunit 4 OS=Rattus norvegicus OX=10116 GN=Arpc4 PE=1 SV=1	Arpc4	B2RZ72	2.45269718	2.387173653	17.3649235	18.1628246	16.9430428	19.2266407	20.158514	20.0996456	20.4335823	20.5543842
115	Actin-related protein 3 OS=Rattus norvegicus OX=10116 GN=Actr3 PE=1 SV=1	Actr3	A0A0G2K1C0	3.32839534	2.338544846	18.4048996	17.8568211	19.3168316	18.5639153	20.4454727	20.8373814	21.1734447	21.0403481
116	Activator of Hsp90 ATPase activity 1 OS=Rattus norvegicus OX=10116 GN=Ahsa1 PE=1 SV=1	Ahsa1	B0BN63	3.27554235	5.816232681	17.8925095	15.0277386	16.8042068	19.0874386	23.15938	22.779623	23.1132679	23.0245533
117	Acyl-CoA thioesterase 11 OS=Rattus norvegicus OX=10116 GN=Acot11 PE=4 SV=3	Acot11	F1LX28	3.14394777	4.879666328	18.3422661	16.1683159	16.9713421	19.4390717	23.22896	22.7514744	22.4470978	22.0121288
118	Acyl-CoA-binding protein OS=Rattus norvegicus OX=10116 GN=Dbi PE=1 SV=1	Dbi	Q6TXF3	0.71571822	-0.986970901	21.1772118	23.2301846	20.1888123	20.854126	20.2436352	20.8094044	20.3058758	20.1435356
119	Acyl-coenzyme A thioesterase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acot2 PE=1 SV=1	Acot2	O55171	2.67299827	2.557208538	16.3345737	15.6835938	14.8185225	14.1911364	18.2291584	17.4743042	17.8001633	17.7530346
120	Adaptor-related protein complex 3 subunit delta 1 OS=Rattus norvegicus OX=10116 GN=Ap3d1 PE=1 SV=1	Ap3d1	B5DFK6	2.81291239	3.531721115	15.7806177	15.3366785	18.0449047	17.3815727	20.1023712	20.2314281	20.1021385	20.2347202

121	Adducin 1 (Alpha), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Add1 PE=1 SV=1	Add1	A0A0G2JSM7	3.3802444	4.130834341	16.5993404	17.1594982	14.650363	16.7643375	20.928091	20.4027176	20.2781315	20.0879364
122	Adenine phosphoribosyltransferase OS=Rattus norvegicus OX=10116 GN=Aprt PE=1 SV=1	Aprt	P36972	5.20775635	3.752734184	16.9975643	17.7029209	18.0748005	17.3248539	21.5019722	21.0028992	21.2748604	21.3313446
123	Adenosylhomocysteinase OS=Rattus norvegicus OX=10116 GN=Ahcy PE=1 SV=3	Ahcy	P10760	4.54762823	5.415673971	16.3714199	16.6136112	15.9510374	17.2252674	20.8099461	22.206665	22.6440105	22.1634102
124	Adenylate kinase isoenzyme 1 OS=Rattus norvegicus OX=10116 GN=Ak1 PE=1 SV=3	Ak1	P39069	6.29509883	4.893598557	19.8534813	19.6574001	19.0466957	19.6208515	24.7479343	24.1197758	24.5109482	24.3741646
125	Adenylosuccinate lyase OS=Rattus norvegicus OX=10116 GN=Adsl PE=1 SV=1	Adsl	D3ZW08	5.83660854	5.040775299	18.4071999	17.6288662	17.6795902	17.2636089	22.4311581	22.8474827	22.9067993	22.9569263
126	Adenylosuccinate synthetase isozyme 2 OS=Rattus norvegicus OX=10116 GN=Adss PE=1 SV=1	Adss	D4AEP0	2.83589537	2.349585056	16.7056007	16.4953594	16.0301571	17.0662518	18.191288	18.5641327	19.8786373	19.0616512
127	Adenylyl cyclase-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Cap1 PE=1 SV=3	Cap1	Q08163	3.35396713	2.884573936	19.7215233	19.7138538	20.3117752	18.5851479	22.795826	21.9302483	22.7840614	22.3604603
128	Adenylyl cyclase-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Cap2 PE=1 SV=1	Cap2	P52481	4.07257197	4.506958485	18.9965611	19.5508709	17.9405899	18.0872326	23.8329391	22.4218311	23.3084011	23.039917
129	Adenylyltransferase and sulfurtransferase MOCS3 OS=Rattus norvegicus OX=10116 GN=Mocs3 PE=1 SV=1	Mocs3	D4A8L5	2.8302522	-1.2208848	17.3691177	16.9905586	17.0172939	17.3127308	15.9255943	16.0301723	16.4057827	15.4446125
130	Adhesion G protein-coupled receptor E5 OS=Rattus norvegicus OX=10116 GN=Adgre5 PE=1 SV=1	Adgre5	A0A0G2JSI4	1.17900952	-2.216847897	18.1661396	21.5566311	17.3124256	20.1740704	17.2057495	17.6879349	16.7855892	16.6626015
131	Adhesion G protein-coupled receptor F5 OS=Rattus norvegicus OX=10116 GN=Adgrf5 PE=1 SV=1	Adgrf5	A0A0G2JZZ0	2.21379753	-1.740045071	19.9791832	18.4759216	19.0573883	18.7897396	17.386385	17.6083984	16.5664654	17.7808037
132	Adipocyte plasma membrane-associated protein OS=Rattus norvegicus OX=10116 GN=Apmap PE=1 SV=1	Apmap	A0A0G2K6G2	0.38970082	-0.844136953	18.4084263	15.6844883	16.8731365	18.2349644	17.4588871	14.3793955	17.0228748	16.9633102
133	Adiponectin a OS=Rattus norvegicus OX=10116 GN=C1qb PE=1 SV=1	C1qb	G3V7N9	1.44597927	-1.323915482	21.9715157	21.6979027	21.8534508	20.7416897	19.0864697	20.9220352	20.3375797	20.6228123
134	ADP/ATP translocase 1 OS=Rattus norvegicus OX=10116 GN=Slc25a4 PE=1 SV=3	Slc25a4	Q05962	0.92267464	0.851633549	24.0905647	25.8177471	23.8945503	24.9933128	25.1610794	25.9177246	25.5468426	25.5770626
135	ADP/ATP translocase 2 OS=Rattus norvegicus OX=10116 GN=Slc25a5 PE=1 SV=3	Slc25a5	Q09073	1.84484085	0.733502865	21.4161606	21.078886	20.645977	21.2575264	21.4445095	22.0165215	22.0298424	21.8416882
136	ADP-ribosylation factor 1 OS=Rattus norvegicus OX=10116 GN=Arf1 PE=1 SV=2	Arf1	P84079	4.43655696	3.467596531	21.4866009	20.9229088	22.0752945	22.1787167	25.4390316	24.7921143	25.1946964	25.1080647
137	ADP-ribosylation factor 4 OS=Rattus norvegicus OX=10116 GN=Arf4 PE=2 SV=2	Arf4	P61751	5.16254029	4.361056328	19.9377708	18.8944054	18.710537	19.2187672	23.9383926	23.3259411	23.5012302	23.4401417
138	ADP-ribosylation factor 5 OS=Rattus norvegicus OX=10116 GN=Arf5 PE=1 SV=2	Arf5	P84083	2.72521395	4.119957447	20.4303551	18.1339092	19.9623756	17.1670418	23.4746437	22.782589	23.0143108	22.901968
139	ADP-ribosylation factor 6 OS=Rattus norvegicus OX=10116 GN=Arf6 PE=1 SV=2	Arf6	P62332	3.86223045	3.824665308	16.3328133	15.3027878	16.1214275	14.7599936	20.0882359	18.8629856	19.3093376	19.5551243
140	ADP-ribosylation factor GTPase-activating protein 1 OS=Rattus norvegicus OX=10116 GN=Arfgap1 PE=1 SV=1	Arfgap1	Q62848	6.73312562	3.625519753	19.24473	18.9077263	19.1917725	19.3531399	22.6356392	23.0732117	22.6888809	22.8017159
141	ADP-ribosylation factor GTPase-activating protein 2 OS=Rattus norvegicus OX=10116 GN=Arfgap2 PE=1 SV=1	Arfgap2	Q3MID3	3.84884249	4.988516569	14.4303923	15.6471281	17.0037441	14.7071772	20.5233479	20.5090446	20.4711037	20.2390118
142	Afamin OS=Rattus norvegicus OX=10116 GN=Afm PE=1 SV=1	Afm	G3V9R9	4.84380893	-3.768096447	22.4488697	22.4241676	22.9074078	21.8164787	18.1134167	18.7882671	19.0241604	18.5986938
143	AHNAK nucleoprotein OS=Rattus norvegicus OX=10116 GN=Ahnak PE=1 SV=1	Ahnak	A0A0G2JUA5	6.02534039	4.162374496	23.4998264	23.4210777	23.3810387	24.1640053	27.7126408	27.7434444	28.0410805	27.6182804
144	A-kinase anchor protein 12 OS=Rattus norvegicus OX=10116 GN=Akap12 PE=1 SV=1	Akap12	Q5QD51	3.95435702	2.177556992	21.4741249	22.2921696	22.3732395	21.6342297	24.2049904	24.3213158	24.0345306	23.9231548
145	A-kinase anchor protein 13 OS=Rattus norvegicus OX=10116 GN=Akap13 PE=1 SV=2	Akap13	F1M3G7	5.16124095	3.020462513	19.2723866	19.287138	19.6642342	19.3311214	22.2353535	22.9224911	22.4269428	22.0519428
146	A-kinase anchor protein 2 OS=Rattus norvegicus OX=10116 GN=Akap2 PE=1 SV=2	Akap2	F1LPQ9	0.58799198	-0.667150497	24.1627636	25.68433	24.1540318	26.1714916	24.3071327	24.7332802	24.213726	24.249876
147	A-kinase anchor protein SPHKAP OS=Rattus norvegicus OX=10116 GN=Sphkap PE=1 SV=1	Sphkap	A0A0G2K3J4	3.80262414	3.546099663	18.1693687	19.5566807	18.5686893	17.5418339	22.0479221	22.0202065	22.0265255	21.9263172
148	AKT1 substrate 1 OS=Rattus norvegicus OX=10116 GN=Akt1s1 PE=1 SV=1	Akt1s1	D3ZH75	1.41399428	-1.155407906	23.8167515	22.4216862	22.3942509	23.86236	22.3733521	21.9523792	21.8369236	21.710762
149	Alanine--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Aars PE=1 SV=3	Aars1	P50475	2.92540251	2.697052002	19.5076828	18.8871632	20.1045589	19.4109116	21.6742554	21.708765	23.3449268	21.9705772
150	Alcohol dehydrogenase [NADP(+)] OS=Rattus norvegicus OX=10116 GN=Akr1a1 PE=1 SV=2	Akr1a1	P51635	0.77973434	0.368130207	18.568327	17.8698444	18.3483429	18.3113155	18.7108192	19.1127853	18.489624	18.257122
151	Alcohol dehydrogenase 1 OS=Rattus norvegicus OX=10116 GN=Adh1 PE=1 SV=3	Adh1	P06757	3.42614351	1.628954411	18.6173859	18.1245956	18.8228493	19.0949364	20.5703163	20.1408424	20.162178	20.302248
152	Aldehyde dehydrogenase family 16 member A1 OS=Rattus norvegicus OX=10116 GN=Aldh16a1 PE=2 SV=1	Aldh16a1	Q3T1L0	2.76817746	2.910913944	17.3030396	18.3230896	18.64501	18.601593	20.0401745	20.7794876	21.8647442	21.8319817
153	Aldehyde dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Aldh2 PE=1 SV=2	Aldh2	F1LN88	4.97813994	3.853239059	18.163435	17.2503967	17.9097385	18.2061749	21.4766598	22.2506714	21.4708099	21.7445602
154	Aldose reductase OS=Rattus norvegicus OX=10116 GN=Akr1b1 PE=1 SV=3	Akr1b1	P07943	6.85346562	4.460393429	18.6484413	18.1003952	18.6992264	18.6982517	23.1018028	23.0280304	23.05163	22.8064251
155	Alpha globin OS=Rattus norvegicus OX=10116 GN=Hba-a3 PE=1 SV=2	Hba-a3	Q63910	3.3659842	-4.28101635	21.6480217	20.7815399	21.2721214	20.063633	17.8487129	17.0803223	15.5178795	16.1943359
156	Alpha glucosidase 2 alpha neutral subunit (Predicted) OS=Rattus norvegicus OX=10116 GN=Ganab PE=1 SV=1	Ganab	D3ZAN3	4.39447357	3.802333832	18.5040779	17.3243961	16.9135056	17.7281551	21.3304577	21.5224667	21.1581745	21.6683712
157	Alpha-1,4 glucan phosphorylase OS=Rattus norvegicus OX=10116 GN=Pygb PE=1 SV=2	Pygb	G3V6Y6	5.21689959	6.128995419	19.5888748	18.1711292	18.7776566	19.2162647	24.2440739	25.4092331	25.4537907	25.1628094
158	Alpha-1,4 glucan phosphorylase OS=Rattus norvegicus OX=10116 GN=Pygm PE=1 SV=1	Pygm	G3V8V3	5.68341235	5.179522991	22.6621857	21.963974	21.7982655	21.7050304	26.6585579	27.3777428	27.5683002	27.2429466
159	Alpha-1-acid glycoprotein OS=Rattus norvegicus OX=10116 GN=Orm1 PE=1 SV=1	Orm1	A0A0H2UHF8	0.85974886	-1.173523426	18.0817795	19.9362259	20.199049	17.5131989	17.864769	17.7203789	17.3467541	18.1042576
160	Alpha-1-antiproteinase OS=Rattus norvegicus OX=10116 GN=Serpina1 PE=1 SV=1	Serpina1	A0A0G2JZ73	5.366509	-5.167212486	28.0029354	28.0758171	28.3712292	29.2919388	23.6133995	23.1490364	22.9384441	23.3721905
161	Alpha-1-inhibitor 3 OS=Rattus norvegicus OX=10116 GN=A1i3 PE=1 SV=1	LOC297568	P14046	4.30015219	-4.553541183	23.0721855	23.246212	23.6873646	23.6744938	19.3989849	18.4500141	17.9102745	19.7068176
162	Alpha-1-macroglobulin OS=Rattus norvegicus OX=10116 GN=A1m PE=1 SV=1	Pzp	Q63041	7.17782463	-4.964723587	27.7726536	28.198637	28.290966	28.1326103	23.4543571	22.9736481	23.0451813	23.0627861
163	Alpha-2 antiplasmin OS=Rattus norvegicus OX=10116 GN=Serpinf1 PE=1 SV=1	Serpinf1	Q80ZA3	2.493198	-1.691861629	20.5704994	19.7686253	20.8799515	20.1608753	18.3400974	19.037632	19.1565342	18.0782413
164	Alpha-2-glycoprotein 1, zinc OS=Rattus norvegicus OX=10116 GN=Azgp1 PE=1 SV=1	Azgp1	Q3B8R6	1.99178595	-3.191096544	19.4238701	19.4040813	19.8595352	20.6695061	18.1465378	16.1499691	17.7168255	14.5792742
165	Alpha-2-HS-glycoprotein OS=Rattus norvegicus OX=10116 GN=Ahsg PE=1 SV=2	Ahsg	P24090	3.84081	-1.87383461	28.4023056	28.1415482	28.2215824	27.8859272	26.7114887	26.064888	25.8770676	26.5025806
166	Alpha-2-macroglobulin OS=Rattus norvegicus OX=10116 GN=A2m PE=2 SV=2	A2m	P06238	7.93184321	-5.052050114	29.6014061	29.7060356	29.9158058	29.9260426	24.9137974	24.7663193	24.4898663	24.7711067
167	Alpha-actinin-4 OS=Rattus norvegicus OX=10116 GN=Actn4 PE=1 SV=1	Actn4	A0A0G2K5U9	3.14746758	2.739783287	17.402132	18.0360794	16.5060616	17.7812691	20.4395256	19.3796787	20.2743874	20.5910835
168	Alpha-aminoadipic semialdehyde dehydrogenase OS=Rattus norvegicus OX=10116 GN=Aldh7a1 PE=1 SV=2	Aldh7a1	Q64057	5.06689803	4.934051514	15.452569	14.6846008	14.4674168	15.4783373	19.2907162	19.9258347	20.2264919	20.3760872
169	Alpha-centractin OS=Rattus norvegicus OX=10116 GN=Actr1a PE=1 SV=1	Actr1a	P85515	6.6610226	5.274066448	18.0791721	17.6692352	18.4742603	18.4086494	23.2621746	23.4082546	23.6725178	23.3846359
170	Alpha-crystallin B chain OS=Rattus norvegicus OX=10116 GN=Cryab PE=1 SV=1	Cryab	P23928	5.86618624	5.392559528	23.674511	22.7175255	22.8418064	22.4836483	28.0346146	28.2887173	28.5871487	28.3772488
171	Alpha-fetoprotein OS=Rattus norvegicus OX=10116 GN=Afp PE=2 SV=1	Afp	P02773	6.0122452	-4.292910099	30.0508347	29.6958523	30.2382927	30.0178833	26.1854191	25.4955921	25.3696022	25.7806091
172	Alpha-fetoprotein OS=Rattus norvegicus OX=10116 GN=Afp PE=4 SV=1	Afp	G3V6D0	6.51470437	-4.698898315	25.1521263	25.1562996	25.1956825	25.5825138	20.9119282	20.3875027	20.2210217	20.7705765
173	Alpha-kinase 2 OS=Rattus norvegicus OX=10116 GN=Alpk2 PE=4 SV=3	Alpk2	F1LTG2	1.84023523	2.408890724	17.8497353	17.1432343	16.2030602	18.7193089	20.3398075	20.9675465	19.2853107	18.9582367
174	Alpha-kinase 3 OS=Rattus norvegicus OX=10116 GN=Alpk3 PE=1 SV=2	Alpk3	D3ZH28	0.89418799	0.835600138	15.7401247	15.3815327	16.0690651	16.6916599	15.9229698	17.5139179	16.4162884	17.3716068
175	Alpha-parvin OS=Rattus norvegicus OX=10116 GN=Parva PE=1 SV=1	Parva	G3V818	3.39862425	4.374073029	15.3549919	17.1654587	17.7819023	15.5465469	20.4834976	20.7587357	21.2273159	20.8756428
176	Alpha-soluble NSF attachment protein OS=Rattus norvegicus OX=10116 GN=Napa PE=1 SV=2	Napa	P54921	5.91477542	1.967607498	20.7622604	20.5814114	20.9098587	20.6420155	22.7719345	22.8476295	22.5447464	22.6016655
177	Alpha-synuclein OS=Rattus norvegicus OX=10116 GN=Snca PE=1 SV=1	Snca	P37377	2.82608926	-2.331745625	20.2383327	18.8464813	20.1318989	19.6380844	17.554018	18.0950832	16.9963665	16.8823471
178	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Rattus norvegicus OX=10116 GN=Aimp2 PE=2	Aimp2	Q32PX2	5.70104642	3.896998882	19.0984001	18.1679935	18.5531082	18.5325584	22.4753933	22.1937943	22.657074	22.6137943
179	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 OS=Rattus norvegicus OX=10116 GN=Aimp1 PE=	Aimp1	Q4G079	6.99126165	5.397559643	18.5394573	18.3146935	18.1684666	17.7101936	23.6724262	23.4253426	23.6339016	23.5913792
180	Aminopeptidase B OS=Rattus norvegicus OX=10116 GN=Rnpep PE=1 SV=1	Rnpep	G3V6V1	2.96504967	5.407137632	14.8074379	15.7228193	16.1924267	14.9907341	18.2563744	21.5983772	21.9154625	21.5717545
181	Aminopeptidase N OS=Rattus norvegicus OX=10116 GN=Anpep PE=1 SV=2	Anpep	P15684	0.01772552	0.016758442	18.492609	18.3778419	18.6953487	19.103693	19.2300816	19.0957718	18.1754265	18.2352467

182	Aminopeptidase OS=Rattus norvegicus OX=10116 GN=Npepps PE=1 SV=1	Npepps	F1M9V7	1.43133404	2.864198208	17.6474495	18.4641171	17.7500858	18.8787575	17.964325	21.8544941	22.2612095	22.1171741
183	Aminopeptidase-like 1 OS=Rattus norvegicus OX=10116 GN=Npepl1 PE=1 SV=2	Npepl1	D4A3E2	1.28707878	1.429778099	16.0515652	16.5058136	16.6718254	16.0463371	17.7979946	16.1836529	18.8751965	18.1378098
184	AMP deaminase 1 OS=Rattus norvegicus OX=10116 GN=Ampd1 PE=1 SV=1	Ampd1	P10759	2.77029777	-1.742944241	19.5986023	19.2737522	18.7386761	18.8062763	17.6964779	17.256155	16.6921272	17.8007698
185	Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (Glycogen debranching enzyme, glycogen storage disease type III) (Predicte	Agl	D4AEH9	3.62728513	5.016164064	16.6182137	15.9136124	15.1524382	18.1401844	21.2882309	21.6775169	21.6103706	21.3129864
186	Anamorsin OS=Rattus norvegicus OX=10116 GN=Ciapin1 PE=1 SV=1	Ciapin1	Q5XID1	4.20818116	3.172866344	19.447464	18.3238564	18.5971375	18.2426033	22.2998161	21.6028614	21.7987881	21.6010609
187	Anaphase promoting complex subunit 1 (Predicted) OS=Rattus norvegicus OX=10116 GN=Anapc1 PE=1 SV=2	Anapc1	F1M801	0.0195401	-0.016474724	19.1668587	19.3329391	18.5496216	18.1241302	18.9528236	18.6617794	18.7652645	18.7277832
188	Angiopoietin-like 6 OS=Rattus norvegicus OX=10116 GN=Angptl6 PE=1 SV=1	Angptl6	B2RYM1	0.76248072	-0.764499426	17.8445263	17.0394421	16.9799271	16.1264648	16.6131763	15.2254286	16.3289146	16.764843
189	Angiotensinogen OS=Rattus norvegicus OX=10116 GN=Agt PE=1 SV=1	Agt	P01015	4.62332045	-3.852445602	23.7918968	24.2447357	24.4333134	23.3429527	20.7069988	20.1575203	19.8028069	19.7357903
190	Anion exchange protein OS=Rattus norvegicus OX=10116 GN=Slc4a1 PE=1 SV=1	Slc4a1	F8WFT7	5.52992004	-5.613713264	25.2598705	25.3068676	24.6384888	25.3509769	20.3907185	19.2688522	19.123127	19.3186531
191	Ankycorbin OS=Rattus norvegicus OX=10116 GN=Rai14 PE=1 SV=2	Rai14	Q5U312	6.30087278	3.500942707	16.8376904	16.7047634	17.2080936	16.5464935	20.507122	20.298151	20.2974968	20.1980419
192	Ankyrin 1 OS=Rattus norvegicus OX=10116 GN=Ank1 PE=1 SV=1	Ank1	D3Z9Z0	3.55150124	-2.4802742	22.1838417	22.2367859	21.0639324	22.3525505	19.217104	19.5382996	19.8251324	19.3354778
193	Ankyrin repeat and LEM domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Ankle1 PE=4 SV=2	Ankle1	D4A332	0.17334943	0.245141983	19.7897396	19.3549213	19.2560539	17.4827271	19.6133003	18.6432343	19.2744312	19.3330441
194	Annexin A1 OS=Rattus norvegicus OX=10116 GN=Anxa1 PE=1 SV=2	Anxa1	P07150	0.69555549	-0.201836109	22.3051758	22.3983231	22.2301388	22.5598049	22.0696793	22.534914	22.0238495	22.0576553
195	Annexin A2 OS=Rattus norvegicus OX=10116 GN=Anxa2 PE=1 SV=2	Anxa2	Q07936	3.47004352	2.274138451	22.3561153	23.543787	22.6001682	22.1788445	25.1499825	25.2214565	24.8634834	24.9121094
196	Annexin A3 OS=Rattus norvegicus OX=10116 GN=Anxa3 PE=1 SV=4	Anxa3	P14669	1.48464233	1.965241671	13.8240957	16.8835907	16.4675922	15.7377071	17.227932	18.2469063	17.5073605	17.7917538
197	Annexin A5 OS=Rattus norvegicus OX=10116 GN=Anxa5 PE=1 SV=3	Anxa5	P14668	2.70481373	1.975598335	19.6750946	21.1855125	21.0105858	21.1376877	22.9453201	22.8926697	22.5957222	22.477562
198	Annexin OS=Rattus norvegicus OX=10116 GN=Anxa11 PE=1 SV=1	Anxa11	Q5XI77	5.05416098	5.622727394	17.4609509	18.1067047	17.9489822	16.4499149	23.2877426	22.6398792	23.3107529	23.2190876
199	Annexin OS=Rattus norvegicus OX=10116 GN=Anxa6 PE=1 SV=1	Anxa6	Q6IMZ3	4.62825879	3.94606781	21.104744	21.949316	21.7949543	20.4945107	25.3037186	25.2214565	25.2229462	25.3796749
200	Annexin OS=Rattus norvegicus OX=10116 GN=Anxa7 PE=1 SV=1	Anxa7	Q6IRJ7	3.42552202	2.794138432	18.9754944	19.5281181	19.6437092	18.3660412	22.4018402	21.2006474	21.9464645	22.1409645
201	Antisecretory factor OS=Rattus norvegicus OX=10116 GN=Psmd4 PE=1 SV=1	Psmd4	O88321	7.54351011	4.845593929	18.6568089	18.6495762	18.817112	18.7633419	23.6485558	23.2152042	23.5909786	23.814476
202	AP complex subunit beta OS=Rattus norvegicus OX=10116 GN=Ap1b1 PE=1 SV=3	Ap1b1	G3V9N8	4.9992134	4.418035984	16.2483158	17.3605824	16.3193665	16.84231	21.6802731	20.8302631	20.8535271	21.0786552
203	AP-2 complex subunit alpha OS=Rattus norvegicus OX=10116 GN=Ap2a1 PE=1 SV=1	Ap2a1	D3ZUY8	2.92149494	2.309831619	18.9640121	19.4251499	18.8428841	20.5094929	22.1117706	21.7548351	21.545435	21.5688248
204	AP-2 complex subunit alpha OS=Rattus norvegicus OX=10116 GN=Ap2a2 PE=1 SV=1	Ap2a2	Q66HM2	0.38392444	0.432617664	23.1810265	23.1166363	22.8078175	21.1562138	23.3248711	23.0094566	22.745451	22.9123859
205	AP-2 complex subunit beta OS=Rattus norvegicus OX=10116 GN=Ap2b1 PE=1 SV=1	Ap2b1	P62944	5.84841326	4.39625597	19.8583412	19.9123096	19.3030262	19.1927414	24.3070965	24.0721169	23.7689705	23.7032585
206	AP-2 complex subunit mu OS=Rattus norvegicus OX=10116 GN=Ap2m1 PE=1 SV=1	Ap2m1	P84092	2.43256467	4.522201777	19.588026	19.1845932	18.5020714	15.277442	22.8760891	22.7120647	22.5035591	22.5492268
207	AP2-associated protein kinase 1 OS=Rattus norvegicus OX=10116 GN=Aak1 PE=1 SV=2	Aak1	F1LRI7	0.79775551	0.659554958	23.7463455	23.7929783	22.0584831	23.0578747	23.8120327	23.9989948	23.6694984	23.8133755
208	AP-3 complex subunit beta OS=Rattus norvegicus OX=10116 GN=Ap3b1 PE=1 SV=1	Ap3b1	A0A0G2JWD6	4.34447803	2.105255127	19.7461739	19.4131584	19.1638222	19.8626919	22.0173855	21.5235672	21.5848122	21.481102
209	AP-3 complex subunit mu-1 OS=Rattus norvegicus OX=10116 GN=Ap3m1 PE=1 SV=1	Ap3m1	P53676	3.4665711	3.463459492	16.0585709	17.700264	15.6613817	15.8134851	19.9509449	19.6406002	19.727459	19.7685356
210	Apolipoprotein A-I OS=Rattus norvegicus OX=10116 GN=Apoa1 PE=1 SV=2	Apoa1	P04639	4.5805196	-2.654272556	29.2851563	29.1060047	29.2430191	28.7279053	26.9186897	26.0347404	26.2350044	26.5565605
211	Apolipoprotein A-II OS=Rattus norvegicus OX=10116 GN=Apoa2 PE=2 SV=1	Apoa2	P04638	2.81169433	-2.529486179	27.0078888	25.3791351	27.0052567	26.9811039	23.9020767	23.6380444	24.0336113	24.6817074
212	Apolipoprotein A-IV OS=Rattus norvegicus OX=10116 GN=Apoa4 PE=1 SV=2	Apoa4	P02651	5.17442309	-3.774950504	30.3190956	30.406044	30.1092911	30.0766716	27.1654129	26.3805618	26.0428314	26.2224941
213	Apolipoprotein A-V OS=Rattus norvegicus OX=10116 GN=Apoa5 PE=1 SV=1	Apoa5	A0A0H2UHP7	3.66245178	3.115683556	18.6784496	17.2434483	18.501688	17.7889004	21.6730843	20.6366367	21.2502174	21.1152821
214	Apolipoprotein B editing complex 2 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Apobec2 PE=1 SV=1	Apobec2	B4F789	7.13212457	7.07120347	15.3558321	15.6009045	15.9891253	15.1932497	22.8256989	22.1724472	22.6750889	22.7506905
215	Apolipoprotein B-100 OS=Rattus norvegicus OX=10116 GN=Apob PE=1 SV=1	Apob	F1M6Z1	5.26164506	-4.059268951	29.2602978	28.597578	28.7577839	28.8450813	25.4773998	24.7092361	24.4454346	24.5915947
216	Apolipoprotein C-I OS=Rattus norvegicus OX=10116 GN=Apoc1 PE=3 SV=1	Apoc1	P19939	6.29399862	-3.494932652	27.7958412	27.4484711	27.3401852	27.6868153	23.9834709	24.4258334	23.7908287	24.2314491
217	Apolipoprotein C-II (Predicted) OS=Rattus norvegicus OX=10116 GN=Apoc2 PE=1 SV=1	Apoc2	G3V8D4	4.94720916	-2.1884408	27.7452602	27.6529388	27.4950199	27.4644318	25.7764778	25.1591969	25.1540565	25.5141563
218	Apolipoprotein C-III OS=Rattus norvegicus OX=10116 GN=Apoc3 PE=1 SV=1	Apoc3	A0A0G2K8Q1	5.4101127	-3.022148132	25.5644779	25.5685539	25.6731167	26.2592144	22.9290276	22.6483898	22.5364475	22.8629055
219	Apolipoprotein C-IV OS=Rattus norvegicus OX=10116 GN=Apoc4 PE=2 SV=2	Apoc4	P55797	5.35896204	-4.237127304	25.7679939	25.8970966	26.0416737	26.4632053	22.4725475	21.4909	21.5823994	21.6756134
220	Apolipoprotein D OS=Rattus norvegicus OX=10116 GN=Apod PE=3 SV=1	Apod	M0R4S2	3.75303627	-4.325610876	20.2209225	20.6093559	20.147089	19.6447697	15.5426331	17.2386951	15.5579386	14.9804268
221	Apolipoprotein E OS=Rattus norvegicus OX=10116 GN=Apoe PE=1 SV=1	Apoe	A0A0G2K151	5.76488711	-2.475481033	28.4553204	28.0658035	28.0938702	27.9883671	25.875597	25.7250671	25.4600296	25.6407433
222	Apolipoprotein F OS=Rattus norvegicus OX=10116 GN=Apof PE=2 SV=1	Apof	Q5M889	0.87395846	-0.895357132	18.7408657	19.6791248	19.7951832	17.8586807	17.6376953	18.5542393	18.5475616	17.7529297
223	Apolipoprotein H OS=Rattus norvegicus OX=10116 GN=Apoh PE=1 SV=1	Apoh	Q5I0M1	4.74628874	-2.802184582	26.3871384	25.9976559	26.5660324	26.567173	23.6990967	23.7524014	23.0279694	23.8297939
224	Apolipoprotein M OS=Rattus norvegicus OX=10116 GN=Apom PE=1 SV=2	Apom	P14630	4.68393211	-2.362660408	24.9349098	24.5554428	25.1204433	25.2071247	22.5232639	22.2887688	22.6167946	22.9384518
225	Apolipoprotein N OS=Rattus norvegicus OX=10116 GN=Apon PE=1 SV=1	Apon	Q5M890	2.46450602	-4.57960701	23.1990395	22.0803185	22.7655163	22.8055344	19.4244595	15.3050404	18.7484303	19.0540504
226	Apoptosis regulator BAX OS=Rattus norvegicus OX=10116 GN=Bax PE=1 SV=1	Bax	G3V8T9	6.30066009	6.069629431	14.8345327	14.1822643	15.106452	14.6571913	21.2271786	20.3134518	20.7475681	20.7707596
227	Apoptosis-inducing factor 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Aifm1 PE=1 SV=1	Aifm1	Q9JM53	0.29561267	-0.642468691	18.8767738	18.3750458	17.9304218	15.1997766	17.9354935	17.0249634	16.8075809	16.0441055
228	Aquaporin-1 OS=Rattus norvegicus OX=10116 GN=Aqp1 PE=1 SV=4	Aqp1	P29975	5.16931397	2.200730801	18.7635574	19.1650238	19.0344219	18.8437881	21.4689026	21.0582256	20.8935318	21.1890545
229	ARF GTPase-activating protein GIT1 OS=Rattus norvegicus OX=10116 GN=Git1 PE=1 SV=1	Git1	Q9Z272	0.78536069	0.519165039	22.4538116	23.3048992	21.9655056	22.807291	22.7916107	23.4846096	23.3734493	22.958498
230	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2 OS=Rattus norvegicus OX=10116 GN=Asap2 PE=1 SV=1	Asap2	A0A0G2K808	0.47388086	-0.562699795	25.130394	26.4433708	24.9988174	23.8409729	24.502058	24.7685623	24.4510002	24.4411354
231	Arginase-1 OS=Rattus norvegicus OX=10116 GN=Arg1 PE=1 SV=2	Arg1	P07824	1.31205369	-1.485359192	18.6521931	20.940134	18.3926983	19.3435497	17.5027084	17.739296	17.7623177	18.3828163
232	Arginine--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Rars PE=1 SV=2	Rars1	P40329	4.38284028	5.631339073	17.5194054	16.8578224	19.0051613	18.8833408	23.8004189	23.4713917	23.8154964	23.7037792
233	Armadillo repeat containing 6 OS=Rattus norvegicus OX=10116 GN=Armc6 PE=1 SV=1	Armc6	B2RYL4	3.38718548	3.099286556	16.8003616	16.7347927	16.4368935	17.6449261	19.2222137	19.6302681	20.3552818	20.8063564
234	Arp2/3 complex 34 kDa subunit OS=Rattus norvegicus OX=10116 GN=Arpc2 PE=1 SV=1	Arpc2	A0A0G2K9A2	3.56093128	3.780568838	16.2191067	16.4099045	15.247694	14.4669485	19.2757587	18.8019943	19.7004471	19.6877289
235	Asparaginyl-tRNA synthetase OS=Rattus norvegicus OX=10116 GN=Nars PE=1 SV=2	Nars1	F1LPV0	3.21723931	2.624372959	20.1837196	19.9877129	19.9933281	18.6461411	21.8236656	22.271204	22.6248779	22.5886459
236	Aspartate aminotransferase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Got1 PE=1 SV=3	Got1	P13221	4.51267647	4.472132683	16.5599384	16.5252609	18.041647	16.4310894	21.2343864	21.5653133	21.5282688	21.1184978
237	Aspartate aminotransferase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Got2 PE=1 SV=2	Got2	P00507	2.36934401	3.795943499	17.7415295	19.1569328	17.0038414	15.8685427	19.8394051	22.1911564	21.3618965	21.5621624
238	Aspartate-beta-hydroxylase OS=Rattus norvegicus OX=10116 GN=Asph PE=1 SV=1	Asph	A0A096MKE0	3.70907735	2.883774519	14.346138	15.1109324	13.7415981	13.7598248	16.973978	17.4580097	16.7695313	17.2920723
239	Aspartate--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Dars PE=1 SV=1	Dars1	P15178	4.96082412	5.262636185	19.0435219	18.4486618	18.20965	19.8900146	24.1183796	23.8312435	24.295145	24.397625
240	Aspartyl aminopeptidase OS=Rattus norvegicus OX=10116 GN=Dnpep PE=1 SV=1	Dnpep	Q4V8H5	3.347355	2.849995136	19.0880775	19.0433884	19.0160294	20.3406277	21.5232754	22.5679359	22.6325111	22.164381
241	Asporin OS=Rattus norvegicus OX=10116 GN=Aspn PE=1 SV=1	Aspn	Q5XIH1	0.68851061	-0.606516361	18.1962833	17.5913391	18.2714882	19.3743095	17.1637726	17.8345852	18.1603146	17.8486824
242	Ataxin 2 OS=Rattus norvegicus OX=10116 GN=Atxn2 PE=1 SV=3	Atxn2	F1M049	5.74411551	4.157369137	16.8427181	16.8061066	16.4648151	17.2206383	20.9350262	21.4080486	21.0348721	20.5858078

243	Ataxin 2-like OS=Rattus norvegicus OX=10116 GN=Atxn2l PE=1 SV=1	Atxn2l	B3DMA1	3.67066275	3.80216217	18.5173531	17.161602	19.1491146	18.8785744	21.9268169	22.7640133	22.2079735	22.016489
244	Ataxin-10 OS=Rattus norvegicus OX=10116 GN=Atxn10 PE=1 SV=1	Atxn10	Q9ER24	3.61246264	3.851540565	19.2927742	18.73703	18.5871944	20.5618	23.2242031	22.5601139	23.5935555	23.2070885
245	ATP synthase F(0) complex subunit B1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5pb PE=1 SV=1	Atp5pb	P19511	2.98573406	3.842823505	17.8626804	18.7088566	18.0097466	16.1000595	20.5772629	22.1378174	21.5226231	21.8149338
246	ATP synthase protein 8 OS=Rattus norvegicus OX=10116 GN=Mt-atp8 PE=1 SV=2	mt-Atp8	P11608	0.41255767	0.767435074	19.4558544	21.9187641	19.0859585	19.8100586	19.3024483	21.6500511	21.2802544	21.1076221
247	ATP synthase subunit alpha OS=Rattus norvegicus OX=10116 GN=Atp5f1a PE=1 SV=1	Atp5f1a	F1LP05	3.45660968	2.862136364	22.8562946	22.7344856	22.2467365	22.0450764	24.3177605	25.84342	25.556612	25.6133461
248	ATP synthase subunit beta OS=Rattus norvegicus OX=10116 GN=Atp5f1b PE=1 SV=1	Atp5f1b	G3V6D3	3.28456766	3.079927921	22.609827	22.7216911	21.6595821	21.8349667	24.1854935	25.6797752	25.5334988	25.7470112
249	ATP synthase subunit d, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5pd PE=1 SV=3	Atp5pd	P31399	3.43263513	3.151310921	20.0747147	20.3933697	19.0766315	19.4432774	22.008606	23.3872242	22.8390675	23.3583393
250	ATP synthase subunit delta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5f1d PE=1 SV=1	Atp5f1d	G3V7Y3	4.11123366	4.34980154	18.3756008	18.7515335	18.1557522	16.8490715	21.9088974	22.8549709	22.2934208	22.473875
251	ATP synthase subunit e, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5me PE=1 SV=3	Atp5me	P29419	3.57672341	3.050570965	17.9960098	18.8843536	17.7006626	18.0250072	20.2925282	21.6070404	21.3522644	21.5564842
252	ATP synthase subunit epsilon, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5f1e PE=1 SV=2	Atp5f1e	P29418	2.85728654	4.585897923	16.1813354	16.9990883	15.9303703	13.5991135	19.1673508	20.8591747	20.5272465	20.4997272
253	ATP synthase subunit f, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5mf PE=1 SV=1	Atp5mf	D3ZAF6	0.85521329	1.742049217	16.6537724	17.1586857	15.9678478	20.2087498	18.0263977	19.8533974	19.4389629	19.6384945
254	ATP synthase subunit g, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5mg PE=1 SV=2	Atp5mg	Q6PDU7	2.53986588	5.043769836	17.566637	17.5918999	16.2588501	13.785759	19.7511463	21.954277	21.6810226	21.9917793
255	ATP synthase subunit O, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5po PE=1 SV=1	Atp5po	Q06647	3.82078854	3.740625381	19.1757698	20.2249794	19.287529	18.7308865	22.1934605	23.5571461	23.1559277	23.475132
256	ATP synthase-coupling factor 6, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5pf PE=1 SV=1	Atp5pf	P21571	3.56491573	3.623016357	17.8408051	17.4465294	16.1976242	17.7069664	20.0678444	21.4019299	21.0303936	21.1838226
257	ATPase H+-transporting V1 subunit A OS=Rattus norvegicus OX=10116 GN=Atp6v1a PE=1 SV=1	Atp6v1a	D4A133	2.32900253	3.277493954	16.7598953	16.779068	16.5041409	19.3947029	19.7858505	20.5723915	21.012888	21.1766529
258	ATPase H+-transporting V1 subunit D OS=Rattus norvegicus OX=10116 GN=Atp6v1d PE=1 SV=1	Atp6v1d	Q6P503	2.03124339	2.354545116	15.3023911	16.0086861	16.3117428	16.9388866	16.9820099	19.323616	18.6271057	19.0471554
259	ATPase, H+ transporting, V1 subunit E isoform 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Atp6v1e1 PE=1 SV=	Atp6v1e1	G3V7L8	4.60239589	3.303590775	17.3722095	17.6335239	17.5130901	17.4416637	20.2466145	20.4362068	21.4733849	21.0186443
260	ATP-binding cassette sub-family D member 3 OS=Rattus norvegicus OX=10116 GN=Abcd3 PE=1 SV=3	Abcd3	P16970	1.2667851	2.172859907	15.3046827	14.8613825	14.4609976	15.1102457	15.5060177	18.5295811	15.6270647	18.7660847
261	ATP-binding cassette subfamily E member 1 OS=Rattus norvegicus OX=10116 GN=Abce1 PE=1 SV=1	Abce1	D3ZD23	3.73705053	2.192143917	17.3268509	17.7916012	17.646204	17.4682808	20.128149	19.0399342	20.0599842	19.7734451
262	ATP-binding cassette sub-family F member 1 OS=Rattus norvegicus OX=10116 GN=Abcf1 PE=1 SV=1	Abcf1	Q6MG08	4.32417512	7.117428303	13.2405653	14.3143692	14.2036505	16.4286861	21.2508011	21.7047234	21.9031811	21.7982788
263	ATP-binding cassette subfamily F member 2 OS=Rattus norvegicus OX=10116 GN=Abcf2 PE=1 SV=1	Abcf2	A2VD14	0.25398404	0.909225464	14.2796059	20.5772228	20.3126888	17.9276314	19.150013	19.5072803	19.1039524	18.972805
264	ATP-binding cassette sub-family F member 3 OS=Rattus norvegicus OX=10116 GN=Abcf3 PE=2 SV=1	Abcf3	Q66H39	4.16046887	4.929853439	15.3703022	17.6070614	15.8545914	16.0080051	21.542511	21.1993198	20.8512077	20.9663353
265	ATP-citrate synthase OS=Rattus norvegicus OX=10116 GN=Acly PE=1 SV=1	Acly	G3V9G4	4.06221522	3.177240849	15.5134678	16.6184597	15.2476091	15.946887	18.9286594	18.6307774	19.4208527	19.0550976
266	ATP-dependent 6-phosphofructokinase OS=Rattus norvegicus OX=10116 GN=Pfkm PE=1 SV=1	Pfkm	A0A0G2KBC7	6.37435297	4.534533978	21.7060699	21.7307072	21.2378483	21.2355099	26.2804394	25.6736755	26.1845055	25.9096508
267	ATP-dependent 6-phosphofructokinase, liver type OS=Rattus norvegicus OX=10116 GN=Pfkl PE=1 SV=3	Pfkl	P30835	4.65410603	6.25074935	16.9092121	16.0061779	15.5016165	15.4144745	21.2806473	21.9413185	23.1928082	22.4197044
268	ATP-dependent 6-phosphofructokinase, platelet type OS=Rattus norvegicus OX=10116 GN=Pfkp PE=1 SV=2	Pfkp	P47860	4.82787923	6.379730701	19.6434288	19.8246422	19.7175312	17.801096	25.6941414	25.2179527	25.8785915	25.7149353
269	ATP-dependent RNA helicase DDX1 OS=Rattus norvegicus OX=10116 GN=Ddx1 PE=1 SV=1	Ddx1	Q641Y8	1.98184294	4.05074501	18.2634277	18.1603127	14.0031929	18.4915047	21.9833183	21.1058903	21.0251255	21.0070839
270	Attractin OS=Rattus norvegicus OX=10116 GN=Atrn PE=2 SV=1	Atrn	Q99J86	0.05514882	0.051472664	17.9052353	18.1417942	18.1813812	17.4106102	18.7871017	17.7188911	17.739109	17.5998096
271	Baculoviral IAP repeat-containing 6 OS=Rattus norvegicus OX=10116 GN=Birc6 PE=1 SV=1	Birc6	A0A0G2JZ53	2.57465171	3.333280802	17.5577888	15.1758356	16.6575356	18.2025833	19.9031334	20.5606441	20.4923038	19.9707851
272	Band 4.1-like protein 1-like OS=Rattus norvegicus OX=10116 GN=Epb41l1 PE=1 SV=1	Epb41l1	A0A0G2K0F3	0.33773468	-0.461449385	16.9782715	15.3044615	16.5972786	17.805809	16.8855286	16.0538139	15.617733	16.2829475
273	Barrier-to-autointegration factor OS=Rattus norvegicus OX=10116 GN=Banf1 PE=1 SV=1	Banf1	Q9R1T1	1.19153245	1.03605175	22.3010616	21.6736679	21.3000698	21.2716084	21.8598042	23.6547928	22.8942776	22.2817402
274	Basal cell adhesion molecule OS=Rattus norvegicus OX=10116 GN=Bcam PE=2 SV=1	Bcam	Q9ESS6	4.48991281	1.790186405	20.0683613	19.8239269	19.5285149	19.4088707	21.6103153	21.6029854	21.4139442	21.3631744
275	Basic leucine zipper and W2 domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Bzw1 PE=1 SV=1	Bzw1	Q6P7P5	3.03978444	4.591794968	14.6391964	16.3813362	17.3609047	18.0785046	21.1342411	21.262455	21.5439587	20.886467
276	Basic leucine zipper and W2 domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Bzw2 PE=1 SV=1	Bzw2	Q9WTT7	4.62126199	4.84080267	17.0009956	17.4721031	16.5665455	18.2426987	22.5549507	21.7423534	22.483736	21.8645134
277	Basigin OS=Rattus norvegicus OX=10116 GN=Bsg PE=1 SV=2	Bsg	P26453	6.52293245	3.985621452	18.5675507	19.2113419	18.7904587	18.6931648	22.910944	22.9735107	22.6389866	22.6815605
278	B-cell receptor-associated protein 31 OS=Rattus norvegicus OX=10116 GN=Bcap31 PE=1 SV=1	Bcap31	Q6AY58	1.19146901	2.276015282	19.5315514	17.9273872	16.0330791	20.6254978	20.5811825	21.0970936	20.6803188	20.8629818
279	Bcl2-associated athanogene 3 OS=Rattus norvegicus OX=10116 GN=Bag3 PE=1 SV=1	Bag3	Q5U2U8	7.14027581	6.26304388	18.38484	18.4180927	17.8711472	17.8123703	24.5346107	24.5996838	24.3316822	24.072649
280	Beta-1,4-galactosyltransferase 1 OS=Rattus norvegicus OX=10116 GN=B4galt1 PE=1 SV=1	B4galt1	G3V722	0.46910445	-0.708581924	18.694521	15.7855129	16.9769878	17.4012165	16.1837769	16.1281223	16.2302074	17.4818039
281	Beta-2-microglobulin OS=Rattus norvegicus OX=10116 GN=B2m PE=1 SV=1	B2m	P07151	1.7808614	-1.329960346	21.1032753	20.9950123	21.086668	19.5725479	19.3753452	19.4240685	18.9446411	19.6936073
282	Beta-casein OS=Rattus norvegicus OX=10116 GN=Csn2 PE=3 SV=1	Csn2	G3V9R5	0.61840139	-1.662749052	21.2826138	19.966589	20.7965221	15.6996679	17.8756294	17.7943516	17.884964	17.5394516
283	Beta-enolase OS=Rattus norvegicus OX=10116 GN=Eno3 PE=1 SV=3	Eno3	P15429	1.87421832	-0.582631111	25.3011971	25.6704445	25.8986816	25.9767418	25.0498695	24.9652557	25.2301178	25.2712975
284	Bifunctional purine biosynthesis protein PURH OS=Rattus norvegicus OX=10116 GN=Atic PE=1 SV=2	Atic	O35567	4.00473823	2.867269039	18.5340023	17.7125072	17.6256351	18.2769489	20.4595356	20.5858173	21.3888702	21.1839466
285	Biliverdin reductase A OS=Rattus norvegicus OX=10116 GN=Blvra PE=1 SV=1	Blvra	P46844	3.55786096	4.023553848	16.423769	16.6313057	16.0360241	14.5545635	20.5106812	19.8035507	20.1054955	19.3201504
286	Biliverdin reductase B OS=Rattus norvegicus OX=10116 GN=Blvrb PE=1 SV=1	Blvrb	B5DF65	3.17855595	1.445004463	17.5678768	18.1959229	18.3274765	17.8925571	19.3848152	19.1286144	19.8391991	19.4112225
287	Biotinidase OS=Rattus norvegicus OX=10116 GN=Btd PE=1 SV=1	Btd	A0A140TAI2	2.54425404	-1.251027584	17.2377701	17.5574589	17.4279747	16.7910767	15.9884987	16.0158195	15.522501	16.4833508
288	Bleomycin hydrolase OS=Rattus norvegicus OX=10116 GN=Blmh PE=1 SV=1	Blmh	A1A5L1	0.92218883	-1.550782204	20.0368633	21.2413902	19.8629131	23.5313282	19.3742046	19.9795666	19.5602856	19.5553093
289	Blood vessel epicardial substance OS=Rattus norvegicus OX=10116 GN=Bves PE=1 SV=2	Bves	Q3BCU4	4.3406414	2.63682127	18.0631962	17.9601955	18.7135048	18.5598927	21.2039661	21.2878056	20.8021278	20.5501747
290	BPI fold-containing family A, member 2F OS=Rattus norvegicus OX=10116 GN=Bpifa2f PE=2 SV=1	Bpifa2f	Q63550	2.11705836	-4.58335042	19.9586887	18.474184	20.6277599	23.9529457	16.1024418	16.4808769	15.9056826	16.1911755
291	BPI fold-containing family B member 1 OS=Rattus norvegicus OX=10116 GN=Bpifb1 PE=4 SV=1	Bpifb1	A0A140TAH2	4.06588581	-4.013603687	21.6797371	21.4232101	21.0443211	21.8855534	18.3984623	17.0930557	17.8444309	16.642458
292	Brain acid soluble protein 1 OS=Rattus norvegicus OX=10116 GN=Basp1 PE=1 SV=1	Basp1	A0A0G2K1L8	3.35459978	1.953979969	19.7920437	20.33251	20.7977142	19.823307	22.4076786	22.1532764	21.7204418	22.280098
293	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Rattus norvegicus OX=10116 GN=Arfgef1 PE=1 SV=1	Arfgef1	D4A631	0.25054908	-0.324959278	19.3675461	18.9616718	18.1735592	19.3806171	19.3432827	17.3337784	18.9302597	18.9762363
294	BRISC and BRCA1-A complex member 1 OS=Rattus norvegicus OX=10116 GN=Babam1 PE=1 SV=1	Babam1	Q5XIJ6	6.07035334	6.065241337	14.3107395	14.1440964	14.5169897	15.381896	20.4868832	20.9328213	20.6939564	20.5010262
295	BTB (POZ) domain containing 1 OS=Rattus norvegicus OX=10116 GN=Btbd1 PE=2 SV=1	Btbd1	Q5RKI2	1.62248037	-1.729826212	19.4011955	19.1798782	18.262434	19.1965542	15.8355379	18.2000351	17.2877483	17.7974358
296	BUB3 mitotic checkpoint protein OS=Rattus norvegicus OX=10116 GN=Bub3 PE=1 SV=1	Bub3	Q4FZS2	1.31446456	2.052121878	16.4272213	16.3985004	16.8790894	13.6842413	17.7306442	19.0594578	17.2696953	17.5377426
297	BWK4 OS=Rattus norvegicus OX=10116 GN=Erp44 PE=1 SV=1	Erp44	Q5VLR5	2.69223142	2.218755245	19.930624	18.0976162	18.8518658	19.1110096	21.066576	21.7735043	20.837492	21.1885643
298	C1r protein OS=Rattus norvegicus OX=10116 GN=C1r PE=1 SV=1	C1r	B5DEH7	7.01456689	-3.310061932	23.3059502	23.220871	23.0206928	22.9395847	20.0043964	19.8174419	19.7630215	19.6619911
299	C-1-tetrahydrofolate synthase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Mthfd1 PE=1 SV=1	Mthfd1	G3V6S5	7.14096127	3.526497841	21.732605	21.6099548	21.9158173	21.5362053	25.1313152	25.0996494	25.4404697	25.2291393
300	C4b-binding protein alpha chain OS=Rattus norvegicus OX=10116 GN=C4bpa PE=1 SV=1	C4bpa	Q5M891	4.37850434	-2.462138653	20.8562336	21.562685	21.3722324	20.7671471	18.6665192	18.862463	18.3187733	18.8619881
301	Cadherin 11 OS=Rattus norvegicus OX=10116 GN=Cdh11 PE=1 SV=1	Cdh11	F1MAH6	0.34974632	-0.439682961	19.4118481	17.2082386	18.9017029	18.9901924	17.6930771	17.907732	18.7234173	18.4290237
302	Cadherin 15 OS=Rattus norvegicus OX=10116 GN=Cdh15 PE=2 SV=1	Cdh15	Q75NI5	2.45559371	-3.221853971	19.8696976	18.9420357	19.6826286	20.2185307	17.5163841	17.5791988	15.1171312	15.6127625
303	Cadherin 5 OS=Rattus norvegicus OX=10116 GN=Cdh5 PE=1 SV=2	Cdh5	F1M7E5	4.43754475	-2.889458656	24.2731476	23.6645851	23.7811928	23.8732586	21.5069046	20.825531	20.4561691	21.2457447

304	Cadherin-1 OS=Rattus norvegicus OX=10116 GN=Cdh1 PE=1 SV=1	Cdh1	Q9R0T4	0.15810949	0.38145256	17.7176285	17.2863865	15.5589428	16.5188751	17.6252213	15.3896961	16.4837093	19.1090164
305	Calcium/calmodulin-dependent protein kinase kinase 2 OS=Rattus norvegicus OX=10116 GN=Camkk2 PE=1 SV=3	Camkk2	F1LPT4	0.16752502	-0.540009737	18.500082	20.017231	16.6940002	15.7768812	15.5766544	19.4398994	17.132206	16.6793957
306	Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Rattus norvegicus OX=10116 GN=Camk2d PE=1 SV=	Camk2d	P15791	2.84035998	6.310583115	16.6002216	17.8405914	18.8764706	13.6780415	22.5947189	23.3849297	23.1759415	23.0820675
307	Calcyclin-binding protein OS=Rattus norvegicus OX=10116 GN=Cacybp PE=1 SV=1	Cacybp	Q6AYK6	2.91907022	4.037220001	14.7231293	17.0917645	16.5725536	15.7029171	21.1902676	18.8891144	19.9556675	20.204195
308	Caldesmon 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Cald1 PE=1 SV=1	Cald1	G3V9E3	1.67097963	4.127654552	18.1667786	13.2711067	16.4082108	18.8728485	22.2046776	20.5181808	20.3547764	20.1519279
309	Calmodulin-3 OS=Rattus norvegicus OX=10116 GN=Calm3 PE=1 SV=1	Calm3	P0DP31	4.98631885	2.534409046	21.1406631	21.6211147	21.5144367	22.0054932	24.2730732	24.1077976	23.9928856	24.0455875
310	Calnexin OS=Rattus norvegicus OX=10116 GN=Canx PE=1 SV=1	Canx	P35565	3.71861788	2.627073288	21.6804295	22.5700169	21.4283886	21.2081451	24.3325615	24.6689892	24.046526	24.3471966
311	Calpain small subunit 1 OS=Rattus norvegicus OX=10116 GN=Capns1 PE=1 SV=3	Capns1	Q64537	4.74458918	3.766479969	19.9086971	20.6021614	20.8343067	19.9127197	23.5219269	24.1133842	24.3820076	24.3064861
312	Calpain-1 catalytic subunit OS=Rattus norvegicus OX=10116 GN=Capn1 PE=1 SV=1	Capn1	F1LS29	1.78762461	1.630154133	17.0649014	19.2570763	17.7513199	18.4759846	19.9483032	19.9159546	19.8701363	19.3355045
313	Calpain-2 catalytic subunit OS=Rattus norvegicus OX=10116 GN=Capn2 PE=1 SV=3	Capn2	Q07009	6.0460857	4.050305367	20.3845596	20.5989323	20.7990131	20.2532997	24.1225433	24.5387573	24.8316917	24.7440338
314	Calpastatin OS=Rattus norvegicus OX=10116 GN=Cast PE=1 SV=1	Cast	F1LPH1	3.47784469	5.425360441	15.8006468	18.2527103	14.7254715	16.4174137	21.7307529	21.6484604	21.6280804	21.8903904
315	Calponin (Fragment) OS=Rattus norvegicus OX=10116 GN=Cnn2 PE=1 SV=3	Cnn2	D3ZRX9	4.09682649	6.500550032	14.8733931	15.7196922	15.4071865	12.7071991	21.4814053	21.104311	21.1564102	20.9675446
316	Calponin-1 OS=Rattus norvegicus OX=10116 GN=Cnn1 PE=1 SV=1	Cnn1	Q08290	3.9466342	4.335773945	18.2751522	17.7560635	17.7442799	16.1894379	22.3297348	21.4607468	21.8511868	21.6663609
317	Calponin-3 OS=Rattus norvegicus OX=10116 GN=Cnn3 PE=1 SV=1	Cnn3	P37397	4.31051769	4.292850971	18.6580791	18.935894	17.7672062	17.1538563	22.6011314	22.4513016	22.4081726	22.2258339
318	Calreticulin OS=Rattus norvegicus OX=10116 GN=Calr PE=1 SV=1	Calr	P18418	4.61092297	2.861429214	21.0809917	21.2391644	20.7985382	20.4117928	23.354269	24.0917206	23.5931969	23.9370174
319	Calsequestrin OS=Rattus norvegicus OX=10116 GN=Casq2 PE=1 SV=2	Casq2	F1M944	4.34410083	3.430755138	20.3838806	20.1106701	20.7394028	19.4906769	23.3944874	24.1898327	23.3448257	23.5185051
320	Calsequestrin-1 OS=Rattus norvegicus OX=10116 GN=Casq1 PE=1 SV=2	Casq1	P19633	0.72849038	0.568475723	16.9044971	17.1491089	17.1640072	15.6728649	17.6621647	16.9865475	17.2950916	17.2205772
321	Calumenin OS=Rattus norvegicus OX=10116 GN=Calu PE=1 SV=1	Calu	G3V6S3	4.01604456	3.188750267	18.8966789	18.4048958	18.8919296	19.7537632	21.9533062	22.7664948	21.8340015	22.1484661
322	cAMP-dependent protein kinase catalytic subunit beta OS=Rattus norvegicus OX=10116 GN=Prkacb PE=1 SV=2	Prkacb	P68182	4.75455711	5.232105494	14.901803	15.8894854	16.4770012	15.1134901	20.475193	20.5315666	21.4451866	20.8582554
323	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Rattus norvegicus OX=10116 GN=Prkar1a PE=1 SV=2	Prkar1a	P09456	6.49841092	5.225550175	19.1292934	18.3439808	19.0406418	18.8412056	24.3773594	23.7729836	24.0727863	24.034193
324	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus OX=10116 GN=Prkar2b PE=1 SV=3	Prkar2b	P12369	3.61124076	4.533947706	16.7157402	16.429575	16.6225586	14.2796965	20.6707726	20.3138561	20.6322231	20.5665092
325	cAMP-specific 3',5'-cyclic phosphodiesterase 4D OS=Rattus norvegicus OX=10116 GN=Pde4d PE=1 SV=4	Pde4d	P14270	3.01005546	4.341351509	15.6697807	16.254097	17.8444595	18.7410641	21.8520927	21.0686016	21.4988251	21.4552879
326	Caprin-1 OS=Rattus norvegicus OX=10116 GN=Caprin1 PE=1 SV=1	Caprin1	A0A0G2K8H0	4.82221691	5.399426937	17.191658	18.1310768	17.2034969	16.378479	22.6005363	23.2892208	22.2454472	22.3672142
327	Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase OS=Rattus norvegicus OX=10116 GN=Ca	Cad	D4A8A0	4.85099634	4.433192253	20.2177143	19.1497478	19.6848679	20.070055	23.4846935	24.5865974	24.51017	24.2736931
328	Carbonic anhydrase 1 OS=Rattus norvegicus OX=10116 GN=Ca1 PE=1 SV=1	Car1	B0BNN3	1.39635374	-0.577796459	20.8010998	20.8943157	20.8589439	20.0971699	20.4153118	20.0566864	19.9639568	19.9043884
329	Carbonic anhydrase 2 OS=Rattus norvegicus OX=10116 GN=Ca2 PE=1 SV=2	Car2	P27139	1.12256631	-2.184442759	19.5839882	18.9039803	20.0678959	19.861969	14.4760275	18.1639194	18.4545269	18.5855885
330	Carbonyl reductase [NADPH] 1-like OS=Rattus norvegicus OX=10116 GN=LOC102556347 PE=1 SV=1	Cbr1	M0R3X6	4.35968878	6.644534588	17.0264072	19.227335	18.0701256	16.6705933	24.0531864	24.8698921	24.811636	23.8378849
331	Carboxypeptidase A4 OS=Rattus norvegicus OX=10116 GN=Cpa4 PE=4 SV=1	Cpa4	D3ZHS5	0.44283488	-0.228166103	18.2953434	17.6838932	17.9620647	18.4831467	18.1513824	17.8340664	17.4818554	18.0444794
332	Carboxypeptidase B2 OS=Rattus norvegicus OX=10116 GN=Cpb2 PE=2 SV=1	Cpb2	Q9EQV9	5.84658705	-4.04151535	21.1245422	20.8600082	20.9118195	20.6834965	17.3484612	16.8986473	16.7530479	16.4136486
333	Carboxypeptidase N catalytic chain OS=Rattus norvegicus OX=10116 GN=Cpn1 PE=2 SV=1	Cpn1	Q9EQV8	4.2222986	-1.428810596	21.0099621	20.6166515	20.5830536	20.5723362	19.2647591	19.4716206	19.0032959	19.3270855
334	Carboxypeptidase N subunit 2 OS=Rattus norvegicus OX=10116 GN=Cpn2 PE=1 SV=1	Cpn2	F1LQT4	4.95777781	-4.700203419	20.4243851	21.4835377	20.6921577	20.4937725	15.4729977	16.2899036	16.652338	15.8778
335	Carboxypeptidase OS=Rattus norvegicus OX=10116 GN=Ctsa PE=1 SV=1	Ctsa	Q6AYS3	0.63143233	-1.029007196	18.3555946	18.8040962	17.1701202	17.2410469	15.2680502	18.5084	16.8042965	16.8740826
336	Carboxypeptidase Q OS=Rattus norvegicus OX=10116 GN=Cpq PE=1 SV=1	Cpq	Q6IRK9	1.90622648	-2.21551466	18.7598209	16.5356884	18.237093	18.0372543	16.4681702	15.1929007	14.7837286	16.2629986
337	Cardiac phospholamban OS=Rattus norvegicus OX=10116 GN=Pln PE=1 SV=1	Pln	P61016	6.29965038	10.07215047	14.0292387	14.9160652	15.315484	13.5048819	24.3754787	25.0345497	24.3145981	24.3296452
338	Cardiac troponin C OS=Rattus norvegicus OX=10116 GN=Tnnc1 PE=2 SV=1	Tnnc1	Q4PP99	1.85557392	6.444845915	14.2182713	13.7762709	20.6890316	20.1039486	24.4753532	23.0677662	23.351059	23.6727276
339	CArG-binding factor A OS=Rattus norvegicus OX=10116 GN=Hnrnpab PE=1 SV=1	Hnrnpab	Q9QX80	4.95107968	5.951749802	14.0973721	15.6512604	15.8631048	15.8962278	21.4889507	21.5810184	21.1986275	21.0463676
340	Carnitine O-palmitoyltransferase 1, liver isoform OS=Rattus norvegicus OX=10116 GN=Cpt1a PE=1 SV=2	Cpt1a	P32198	0.51596935	-0.538609505	21.2014694	21.1508293	20.2875748	19.2781506	20.1259289	19.4575176	20.1194057	20.0607338
341	Carnitine O-palmitoyltransferase 1, muscle isoform OS=Rattus norvegicus OX=10116 GN=Cpt1b PE=1 SV=1	Cpt1b	Q63704	4.18945527	5.788074255	14.1769981	16.4775887	15.3262749	15.9640303	20.9135571	22.2117825	20.8243237	21.1475258
342	Cask-interacting protein 2 OS=Rattus norvegicus OX=10116 GN=Caskin2 PE=1 SV=1	Caskin2	D4A9T0	1.97713742	1.439043522	18.7620296	18.5178852	17.7340946	17.9102783	19.2158756	20.4738064	19.8304882	19.1602917
343	Caspase 14 OS=Rattus norvegicus OX=10116 GN=Casp14 PE=3 SV=1	Casp14	D3ZZ65	0.4224144	-1.411468744	17.3346443	20.5517502	17.5981045	20.1773014	13.8412066	18.6673317	18.6892109	18.8181763
344	Caspase-3 OS=Rattus norvegicus OX=10116 GN=Casp3 PE=2 SV=2	Casp3	P55213	3.2390396	3.947895527	15.3854046	13.1804581	15.4146414	15.0960913	18.4369469	18.1042442	19.1681137	19.1588726
345	Catalase OS=Rattus norvegicus OX=10116 GN=Cat PE=1 SV=3	Cat	P04762	3.38717866	3.120453358	19.8894825	21.0883045	19.7901707	19.1337547	22.9564972	23.6162434	22.955658	22.8551273
346	Catenin (Cadherin associated protein), alpha 1 OS=Rattus norvegicus OX=10116 GN=Ctnna1 PE=1 SV=1	Ctnna1	Q5U302	5.01454849	4.763266087	18.536768	19.1998978	17.5669842	18.2596512	23.404459	23.1479874	23.0169621	23.046957
347	Catenin (Cadherin associated protein), beta 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ctnnb1 PE=1 SV=1	Ctnnb1	A0A0G2JT93	4.15994145	3.535908699	17.3215733	16.39505	18.0525894	17.3937778	21.2124939	20.6683941	20.7514381	20.6742992
348	Cathelicidin antimicrobial peptide OS=Rattus norvegicus OX=10116 GN=Camp PE=1 SV=1	Camp	G3V8S9	5.99991891	-5.77277565	22.0981159	22.0530052	21.9723911	22.6557903	17.1282272	16.0360889	16.2135124	16.3103714
349	Cathepsin B OS=Rattus norvegicus OX=10116 GN=Ctsb PE=1 SV=1	Ctsb	Q6IN22	1.12396415	-0.887425423	19.1468258	18.2995739	19.3715267	18.9038639	18.5963421	17.9358158	17.1170044	18.5229263
350	Cathepsin D OS=Rattus norvegicus OX=10116 GN=Ctsd PE=1 SV=1	Ctsd	P24268	0.15992768	-0.196715832	19.5963688	21.0721474	19.9200172	19.8717403	19.2751312	20.8018894	20.097374	19.4990158
351	Cation-dependent mannose-6-phosphate receptor OS=Rattus norvegicus OX=10116 GN=M6pr PE=1 SV=1	M6pr	Q6AY20	3.54755207	3.480929375	19.0089226	19.6079884	19.1195068	17.5357037	22.375843	22.5954037	22.0773125	22.1472797
352	Caveolae-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Cavin1 PE=1 SV=1	Cavin1	G3V8L9	6.9440377	4.438109875	19.4373207	19.5118923	19.9675217	19.5558109	23.8313637	23.9576302	24.2335262	24.2024651
353	Caveolae-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Cavin2 PE=1 SV=3	Cavin2	Q66H98	5.50337149	4.30056715	18.7559967	17.679636	18.3112717	17.8963718	22.6546345	22.169384	22.5720711	22.4494553
354	Caveolae-associated protein 4 OS=Rattus norvegicus OX=10116 GN=Cavin4 PE=1 SV=1	Cavin4	B1PRL5	6.09654396	4.379220963	16.0511036	15.2444468	15.9812565	15.9942427	19.9819527	20.4062271	20.1914558	20.2082977
355	Caveolin-1 OS=Rattus norvegicus OX=10116 GN=Cav1 PE=1 SV=3	Cav1	P41350	4.00825807	4.472476721	18.0001907	15.8413076	16.9225998	16.1336288	21.1617603	21.4370823	21.0087872	21.1800041
356	CCR4-NOT transcription complex, subunit 3 OS=Rattus norvegicus OX=10116 GN=Cnot3 PE=1 SV=2	Cnot3	D3ZUV9	0.03930073	0.048666	19.8982544	19.6274395	19.6757793	18.2742329	19.9756336	19.0699425	19.067831	19.556963
357	CD163 antigen (Predicted) OS=Rattus norvegicus OX=10116 GN=Cd163 PE=1 SV=1	Cd163	D3Z9U2	1.34137387	-0.696840286	19.5808735	19.7898083	19.0741158	18.941061	18.5696278	18.8987865	18.1478672	18.9822159
358	CD248 antigen, endosialin (Predicted) OS=Rattus norvegicus OX=10116 GN=Cd248 PE=4 SV=1	Cd248	D3ZN06	0.01265234	-0.015516758	16.8611469	17.2710476	16.7164116	15.7799034	16.7164078	15.8726692	17.095871	16.8814945
359	CD34 antigen (Predicted) OS=Rattus norvegicus OX=10116 GN=Cd34 PE=1 SV=1	Cd34	B1PLB1	2.53936151	3.29213953	18.1254406	17.6460361	17.2298489	15.0643005	20.4807549	20.4007759	20.1444283	20.2082253
360	CD48 antigen OS=Rattus norvegicus OX=10116 GN=Cd48 PE=1 SV=1	Cd48	P10252	2.92119704	2.149749756	17.4775658	17.2663956	17.406826	16.953907	18.4523544	20.0918293	19.7723999	19.3871098
361	CD59 glycoprotein OS=Rattus norvegicus OX=10116 GN=Cd59 PE=1 SV=2	Cd59	P27274	0.18376112	-0.164356232	20.4379044	20.6671791	21.2260418	19.7471657	20.775032	20.4699326	20.0124168	20.1634846
362	CD9 antigen OS=Rattus norvegicus OX=10116 GN=Cd9 PE=1 SV=2	Cd9	P40241	0.60578291	0.326025486	20.1848354	19.8483963	19.7619839	19.0787964	20.1326809	20.1732864	19.7294216	20.142725
363	Cdc42 effector protein 2 OS=Rattus norvegicus OX=10116 GN=Cdc42ep2 PE=1 SV=1	Cdc42ep2	Q5PQP4	0.30992713	0.603016138	16.5450878	13.8490705	16.9399853	17.3768177	17.3196621	16.8668423	16.4680691	16.4684525
364	CDGSH iron sulfur domain 2 OS=Rattus norvegicus OX=10116 GN=Cisd2 PE=1 SV=1	Cisd2	D4AAE9	2.21015784	-1.268661976	19.5097294	19.5379486	20.0827332	19.6942768	18.2352428	19.2611904	18.0480843	18.2055225

365	CDGSH iron-sulfur domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Cisd1 PE=3 SV=1	Cisd1	B0K020	4.12192497	5.215202332	16.8140488	15.8440847	15.7965136	14.3449707	20.4227905	21.3903561	20.9839668	20.8633137
366	CDW92 antigen, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Slc44a1 PE=1 SV=1	Slc44a1	A0A0G2K0P8	0.35798617	0.246358395	19.16646	19.1343002	18.6801739	18.1145821	19.4266701	19.150486	18.7033405	18.8004532
367	Cell cycle and apoptosis regulator 2 OS=Rattus norvegicus OX=10116 GN=Ccar2 PE=1 SV=1	Ccar2	F1LM55	0.89801165	1.800192118	18.3348789	17.1539021	18.7621517	14.2954931	18.7150955	19.0608597	19.2511368	18.7201023
368	Cell division control protein 42 homolog OS=Rattus norvegicus OX=10116 GN=Cdc42 PE=1 SV=2	Cdc42	Q8CFN2	3.44584212	2.24246645	20.1839638	20.5081577	20.6461296	19.4682503	22.7722244	22.1128807	22.2100849	22.6811771
369	Cell growth regulator with EF hand domain 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Cgref1 PE=1 SV=1	Cgref1	A0A0A0MXV3	2.83062203	-1.789737701	18.5317173	18.8212776	18.8754253	19.0665436	16.1522675	17.1388626	17.5250683	17.3198147
370	Cell surface glycoprotein MUC18 OS=Rattus norvegicus OX=10116 GN=Mcam PE=1 SV=2	Mcam	Q9EPF2	3.59377111	5.370392561	13.9534483	14.6398754	15.8045235	17.085392	21.0935097	20.7187691	20.6657391	20.4867916
371	Centromere/kinetochore protein zw10 homolog OS=Rattus norvegicus OX=10116 GN=Zw10 PE=2 SV=3	Zw10	Q4V8C2	3.73106443	2.102314472	17.2469749	16.7689724	17.5019569	16.8777332	18.8628654	19.6414223	18.8797722	19.4208355
372	Centrosomal protein 350 OS=Rattus norvegicus OX=10116 GN=Cep350 PE=1 SV=3	Cep350	F1LPD3	2.42901983	-1.337844849	19.0111122	18.7234917	19.4700565	18.8290501	17.8467045	17.5876637	17.0539303	18.1940327
373	Ceruloplasmin OS=Rattus norvegicus OX=10116 GN=Cp PE=1 SV=1	Cp	A0A0G2K9I6	6.14412434	-3.998950481	25.1178684	25.5832939	25.664381	25.1246777	21.6507339	21.4949112	21.1671638	21.1816101
374	cGMP-inhibited 3',5'-cyclic phosphodiesterase A OS=Rattus norvegicus OX=10116 GN=Pde3a PE=1 SV=1	Pde3a	Q62865	0.74545612	-0.313418388	22.1760273	21.5413876	21.8173962	22.2247639	21.8452263	21.2623558	21.6301975	21.7681217
375	Chaperonin containing Tcp1, subunit 6A (Zeta 1) OS=Rattus norvegicus OX=10116 GN=Cct6a PE=1 SV=1	Cct6a	Q3MHS9	3.69241432	3.804864883	20.4235134	21.1793079	20.0188675	20.5601768	23.8820534	23.4814186	24.7451382	25.2927151
376	Chaperonin subunit 8 (Theta) (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Cct8 PE=1 SV=1	Cct8	D4ACB8	4.83567367	4.538599491	20.582634	19.9446526	20.3595066	21.0546055	24.6812153	24.4708633	25.2907047	25.6530132
377	Charged multivesicular body protein 2A OS=Rattus norvegicus OX=10116 GN=Chmp2a PE=1 SV=1	Chmp2a	B2RZB5	2.98971342	3.296485424	16.4816685	18.7599659	17.5314636	16.456974	20.9279442	20.4734058	20.5088406	20.5058231
378	Charged multivesicular body protein 6 OS=Rattus norvegicus OX=10116 GN=Chmp6 PE=1 SV=1	Chmp6	D3ZDR2	0.74836312	0.332977772	18.8762188	18.607542	18.6753159	18.7301712	19.5903397	19.0564404	18.5589771	19.0154018
379	Chloride intracellular channel protein 1 OS=Rattus norvegicus OX=10116 GN=Clic1 PE=1 SV=1	Clic1	Q6MG61	1.5394012	1.865684032	21.1433659	21.4729881	21.5706177	21.3519669	21.470211	23.765377	24.5065498	23.2595367
380	Chloride intracellular channel protein OS=Rattus norvegicus OX=10116 GN=Clic4 PE=1 SV=1	Clic4	G3V8C4	4.38165038	3.608950615	19.0355301	19.4335423	19.776886	19.99683	22.6832924	23.1912117	23.9106331	22.8934536
381	CHMP family, member 7 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Chmp7 PE=1 SV=1	Chmp7	D4A7H9	3.15419775	1.568153858	20.2102413	19.249052	19.5209236	19.3176765	21.4527569	20.9262371	21.0859241	21.1055908
382	Choline-phosphate cytidylyltransferase A OS=Rattus norvegicus OX=10116 GN=Pcyt1a PE=1 SV=2	Pcyt1a	P19836	3.72592843	4.367328167	17.5053673	18.7389088	16.7530079	18.925272	22.4992218	21.9066887	22.5817585	22.4041996
383	Chromosome segregation 1-like OS=Rattus norvegicus OX=10116 GN=Cse1l PE=1 SV=1	Cse1l	D3ZPR0	5.98286517	4.812426567	17.9610138	17.8657475	18.620348	17.9181042	22.5264606	22.7444153	23.2473011	23.0967426
384	Ciliary rootlet coiled-coil, rootletin OS=Rattus norvegicus OX=10116 GN=Crocc PE=1 SV=2	Crocc	F1M6Q2	1.19772044	-1.371150494	19.9379311	21.1909943	19.449337	21.2428837	18.8461552	20.2742672	18.6165733	18.5995483
385	Citrate synthase OS=Rattus norvegicus OX=10116 GN=Cs PE=1 SV=1	Cs	G3V936	0.70439893	2.022062778	17.0166779	18.2756786	16.2922649	21.7721767	18.4529572	21.7195301	20.5965137	20.6760483
386	Clathrin coat assembly protein AP180 OS=Rattus norvegicus OX=10116 GN=Snap91 PE=1 SV=3	Snap91	F1LRK0	2.76735816	2.997151852	17.4956074	17.9826794	17.5500507	15.9355068	21.2097855	19.7313576	19.9295177	20.0817909
387	Clathrin heavy chain OS=Rattus norvegicus OX=10116 GN=Cltc PE=1 SV=1	Cltc	F1M779	3.49976953	2.365359306	22.7374249	22.9048634	22.437603	22.5054989	25.8924828	24.9136276	24.5980453	24.6426716
388	Clathrin interactor 1 OS=Rattus norvegicus OX=10116 GN=Clint1 PE=1 SV=1	Clint1	Q6DGF2	4.97585689	3.350426674	19.1012402	18.537302	19.0228977	18.9418697	22.8960495	22.0428524	21.9889336	22.0771809
389	Clathrin light chain A OS=Rattus norvegicus OX=10116 GN=Clta PE=1 SV=1	Clta	P08081	1.74650614	1.752706528	19.9563484	19.6473732	18.7088909	18.4799767	22.164484	20.5051785	20.7024269	20.4313259
390	Clathrin light chain B OS=Rattus norvegicus OX=10116 GN=Cltb PE=1 SV=1	Cltb	P08082	2.28854501	4.222003937	19.5075207	15.9275303	16.1199646	17.6292782	22.9358177	21.7108269	20.8078556	20.6178093
391	Cleavage and polyadenylation specific factor 6, 68kDa (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Cpsf	Cpsf6	D3ZPL1	0.79942609	-0.919038773	20.1732521	20.0232983	19.8869209	20.0718765	20.4296036	19.4478893	18.895422	17.7062778
392	Cleavage and polyadenylation-specific factor 1 OS=Rattus norvegicus OX=10116 GN=Cpsf1 PE=1 SV=1	Cpsf1	B5DEL2	0.0880603	-0.128102303	20.5145683	19.8504276	20.1890697	18.9051647	20.5413303	19.3792877	20.229002	18.7972012
393	CLIP-associating protein 2 OS=Rattus norvegicus OX=10116 GN=Clasp2 PE=1 SV=1	Clasp2	A0A0G2JZM8	1.9446052	2.674545288	14.4122868	16.4981995	17.0227108	17.4422112	18.6821556	19.6418667	19.4477825	18.3017845
394	Clustered mitochondria protein homolog OS=Rattus norvegicus OX=10116 GN=Cluh PE=1 SV=1	Cluh	A0A0U1RRV5	4.53647175	2.422269821	20.7446671	20.1949081	19.9615631	20.6831455	22.5938931	23.0376244	22.9257393	22.7161064
395	Clusterin OS=Rattus norvegicus OX=10116 GN=Clu PE=1 SV=1	Clu	G3V836	4.68214052	-3.373759747	25.5290108	25.334959	25.1047668	25.2868023	22.5161171	22.1476002	21.2456188	21.8511639
396	Coactosin-like protein OS=Rattus norvegicus OX=10116 GN=Cotl1 PE=1 SV=1	Cotl1	B0BNA5	1.32384673	1.790971041	16.4216003	17.543045	18.3085461	15.1843271	18.6860085	18.2360039	18.3954353	19.3039551
397	Coagulation factor IX OS=Rattus norvegicus OX=10116 GN=F9 PE=2 SV=2	F9	P16296	0.81458844	-0.872579098	18.8906918	18.1678391	18.2565689	17.4808788	18.2336617	16.6698627	16.4475422	17.9545956
398	Coagulation factor V OS=Rattus norvegicus OX=10116 GN=F5 PE=1 SV=1	F5	A0A0G2K3W2	6.41221914	-2.937338829	24.3580513	24.346899	24.6565399	24.2177887	21.5804653	21.3953838	21.2499027	21.6041718
399	Coagulation factor X OS=Rattus norvegicus OX=10116 GN=F10 PE=1 SV=1	F10	A0A0H2UHR6	4.0675342	-3.340430737	21.3196907	21.3510761	21.4079189	20.4972153	17.6373825	18.1617565	18.3400803	17.0749588
400	Coagulation factor XI OS=Rattus norvegicus OX=10116 GN=F11 PE=1 SV=1	F11	A0A0G2K4I9	4.34003957	-2.930455446	19.3227043	18.9141922	19.6948814	18.5923996	15.7705564	16.3976078	16.2631721	16.3710194
401	Coagulation factor XII OS=Rattus norvegicus OX=10116 GN=F12 PE=1 SV=1	F12	A0A0H2UI19	3.73835978	-3.290117741	21.0689831	21.4402103	21.9951878	21.062685	18.9065876	17.34445	17.8029976	18.35256
402	Coagulation factor XIII A chain OS=Rattus norvegicus OX=10116 GN=F13a1 PE=1 SV=1	F13a1	G3V811	1.48235528	-1.460007191	19.7307796	19.6808681	19.8653984	19.0809917	19.1892147	16.7831497	18.3792953	18.1663494
403	Coagulation factor XIII B chain OS=Rattus norvegicus OX=10116 GN=F13b PE=1 SV=1	F13b	B1H260	1.73769952	-1.242341518	20.329586	19.6860981	20.1485043	19.5298882	17.843792	19.4842987	18.5976772	18.7989426
404	Coatomer protein complex, subunit zeta 1 OS=Rattus norvegicus OX=10116 GN=Copz1 PE=1 SV=1	Copz1	D4A8T3	3.23601833	3.384054184	16.8610802	17.6201305	15.6457567	15.7804136	20.4391212	19.4568787	19.843277	19.7043209
405	Coatomer protein complex, subunit zeta 2 OS=Rattus norvegicus OX=10116 GN=Copz2 PE=1 SV=2	Copz2	D4ADP9	1.29840595	3.526739359	13.3003855	14.0704603	14.6023855	19.6417446	19.1416626	18.6610279	18.7409744	19.1782684
406	Coatomer subunit alpha OS=Rattus norvegicus OX=10116 GN=Copa PE=1 SV=1	Copa	G3V6T1	5.10156801	4.673772812	19.3311596	18.4850712	18.5890789	19.710289	23.3728237	23.7694054	23.5851612	24.0832996
407	Coatomer subunit beta OS=Rattus norvegicus OX=10116 GN=Copb1 PE=1 SV=1	Copb1	P23514	4.79776221	5.543254375	17.718792	17.2380943	17.4791374	15.9051151	22.178297	22.8413696	22.5168419	22.9776478
408	Coatomer subunit beta' OS=Rattus norvegicus OX=10116 GN=Copb2 PE=1 SV=3	Copb2	O35142	6.36801122	-2.586344242	26.6522312	26.6973038	26.5352402	26.6736069	24.3302975	24.0249901	23.8147221	24.0429955
409	Coatomer subunit delta OS=Rattus norvegicus OX=10116 GN=Arcn1 PE=2 SV=1	Arcn1	Q66H80	3.27565266	2.371080399	18.884491	20.3828545	19.4047909	19.1415691	21.5502052	21.9277897	21.6771564	22.1428757
410	Coatomer subunit epsilon OS=Rattus norvegicus OX=10116 GN=Cope PE=1 SV=3	Cope	G3V8Q1	4.99502696	5.295457125	15.9051228	15.6292372	17.1111355	16.8070812	21.3898563	21.8078747	21.3778038	22.0588703
411	Coatomer subunit gamma OS=Rattus norvegicus OX=10116 GN=Copg1 PE=1 SV=1	Hmces	A0A0G2K1F3	4.4396983	3.610589981	18.9943619	17.9099483	17.8917122	18.873209	21.9843578	21.7653027	21.9192924	22.4426384
412	Coatomer subunit gamma OS=Rattus norvegicus OX=10116 GN=Copg2 PE=1 SV=1	Copg2	A0A0H2UHV9	3.18783849	5.101811409	15.759346	12.9841146	15.6856966	13.0131111	19.4657784	19.5216007	19.2876415	19.5744934
413	Cofilin 2 OS=Rattus norvegicus OX=10116 GN=Cfl2 PE=1 SV=1	Cfl2	M0RC65	5.52015715	4.457715034	17.4597378	17.7016582	18.0974789	17.7220078	22.614439	21.5904903	22.091465	22.5153484
414	Cofilin-1 OS=Rattus norvegicus OX=10116 GN=Cfl1 PE=1 SV=3	Cfl1	P45592	4.01443063	2.881783485	21.7959633	21.9526062	22.2760887	21.8381405	24.8583851	24.1431103	24.7969341	25.5915031
415	Coiled coil domain-containing 88A OS=Rattus norvegicus OX=10116 GN=Ccdc88a PE=1 SV=3	Ccdc88a	D3ZYD7	0.98946833	-0.744811058	18.9370213	19.1572399	18.9760532	17.5896778	17.6459045	17.8155041	18.2937698	17.9255695
416	Coiled-coil domain-containing 141 OS=Rattus norvegicus OX=10116 GN=Ccdc141 PE=1 SV=2	Ccdc141	D3ZEY0	3.06642916	1.838891029	19.9005432	19.7095852	19.7758541	19.5519276	20.9124146	22.3068504	21.6740017	21.4002075
417	Coiled-coil domain-containing 6 OS=Rattus norvegicus OX=10116 GN=Ccdc6 PE=1 SV=3	Ccdc6	D4AEK9	3.12772017	3.980378389	16.1286144	15.9739618	13.5274343	15.233283	19.4777908	19.3229599	18.5727139	19.4113426
418	Coiled-coil domain-containing protein 91 OS=Rattus norvegicus OX=10116 GN=Ccdc91 PE=1 SV=1	Ccdc91	Q6AY97	3.09672787	2.616830349	14.7179165	14.8924751	16.3044548	15.8983593	18.2983818	17.5855465	18.0781059	18.3184929
419	Cold shock domain-containing protein E1 OS=Rattus norvegicus OX=10116 GN=Csde1 PE=2 SV=1	Csde1	P18395	2.98660693	4.263445377	18.101923	17.1258354	15.3265266	18.4894753	21.245945	21.4245453	21.9135761	21.5134754
420	Collagen alpha-1(I) chain OS=Rattus norvegicus OX=10116 GN=Col1a1 PE=1 SV=5	Col1a1	P02454	3.6179351	-2.528013229	21.4029713	21.6620026	22.0258846	21.2533531	18.3698902	19.5977364	18.8541965	19.4103355
421	Collagen alpha-1(XI) chain OS=Rattus norvegicus OX=10116 GN=Col11a1 PE=1 SV=2	Col11a1	P20909	4.07175961	1.405001163	19.1719666	18.5301228	18.9002705	18.8100109	20.422657	20.0800228	20.2339458	20.2957497
422	Collagen alpha-1(XII) chain OS=Rattus norvegicus OX=10116 GN=Col12a1 PE=1 SV=1	Col12a1	A0A0G2KAJ7	0.74940023	0.396619797	19.0860062	19.6875591	19.8542213	19.044775	19.7088833	20.2845745	19.6111374	19.6544456
423	Collagen alpha-2(I) chain OS=Rattus norvegicus OX=10116 GN=Col1a2 PE=1 SV=3	Col1a2	P02466	0.26997335	0.522306442	17.2037811	17.5479202	17.8875217	16.8484097	15.6873646	18.9634628	18.9004784	18.0255527
424	Collagen type IV alpha 2 chain OS=Rattus norvegicus OX=10116 GN=Col4a2 PE=1 SV=3	Col4a2	F1M6Q3	1.84676373	1.37384367	16.4840546	16.0824623	16.6705551	15.9335022	18.6400871	17.3987026	16.9130707	17.7140884
425	Collagen type VI alpha 1 chain OS=Rattus norvegicus OX=10116 GN=Col6a1 PE=1 SV=1	Col6a1	D3ZUL3	0.74849127	-0.367815495	19.209404	18.7362289	19.443964	19.6137676	19.0425339	18.5599556	18.7192211	19.210392

426	Collectin sub-family member 11 OS=Rattus norvegicus OX=10116 GN=Colec11 PE=1 SV=2	Colec11	F1LSS7	3.81572121	-3.638984203	20.9283104	19.9491291	20.3045578	19.1073418	16.3428173	17.0236568	16.0694141	16.297514
427	COMM domain-containing protein 3 OS=Rattus norvegicus OX=10116 GN=Commd3 PE=1 SV=1	Commd3	Q6P9U3	1.41036631	1.240028143	16.5183945	15.3561945	15.9962482	16.7494812	16.4798431	17.8340912	17.2044201	18.0620766
428	Common salivary protein 1 OS=Rattus norvegicus OX=10116 GN=Csap1 PE=4 SV=1	Csap1	M0R7K9	0.86247821	1.736608744	15.2781096	16.6482582	16.8593369	18.6699028	16.4023094	19.1612091	19.4367294	19.4017944
429	Complement C1q subcomponent subunit A OS=Rattus norvegicus OX=10116 GN=C1qa PE=1 SV=2	C1qa	P31720	3.19715656	-1.225876808	20.7881927	21.0222931	20.8107719	21.0427265	19.629591	20.1333065	19.2754688	19.7221107
430	Complement C1q subcomponent subunit C OS=Rattus norvegicus OX=10116 GN=C1qc PE=1 SV=1	C1qc	A0A0H2UHK1	1.78849993	-1.242211342	20.9421635	21.1122246	21.4292336	19.9086037	19.3109589	20.0187778	19.2916641	19.8019791
431	Complement C1s subcomponent OS=Rattus norvegicus OX=10116 GN=C1s PE=1 SV=1	C1s	G3V7L3	2.87065042	-4.336370945	22.2741261	22.2429466	25.3216457	22.5270157	19.122448	18.6917534	18.2418995	18.9641495
432	Complement C2 OS=Rattus norvegicus OX=10116 GN=C2 PE=1 SV=1	C2	Q6MG73	0.14993721	-0.149729252	18.2778378	19.4677525	19.3749771	18.0713711	18.6710491	18.8172836	18.7933521	18.3113365
433	Complement C3 OS=Rattus norvegicus OX=10116 GN=C3 PE=1 SV=1	C3	M0RBF1	6.1006012	-3.367703915	28.4524364	28.5210056	28.7190609	28.9930267	25.2862148	25.2691383	25.0708122	25.5885487
434	Complement C4 OS=Rattus norvegicus OX=10116 GN=C4 PE=1 SV=3	C4a	P08649	7.02512672	-3.723816395	24.8179874	25.2104015	25.1984806	24.8520622	21.3001671	21.3721905	21.3987846	21.112524
435	Complement C5 OS=Rattus norvegicus OX=10116 GN=C5 PE=1 SV=2	C5	A0A096P6L9	4.28299048	-3.06538105	23.1610584	22.8195305	23.1079712	22.7357254	20.6972313	19.4526272	19.854908	19.5579948
436	Complement C7 OS=Rattus norvegicus OX=10116 GN=C7 PE=1 SV=1	C7	A0A0G2K7X7	0.58365485	-0.446006775	21.074173	20.7626286	21.0047741	21.4566994	20.3152733	20.4266758	21.6035786	20.1687202
437	Complement C8 alpha chain OS=Rattus norvegicus OX=10116 GN=C8a PE=1 SV=1	C8a	D3ZWD6	4.42264422	-2.162259102	21.3739929	21.572443	21.7867737	21.4607239	19.3909206	19.8604164	18.9915371	19.3020229
438	Complement C8 gamma chain OS=Rattus norvegicus OX=10116 GN=C8g PE=1 SV=1	C8g	D3ZPI8	1.14281253	-1.586037874	18.7385921	17.943449	18.9449062	15.8819647	16.2279091	16.0326214	16.8744717	16.0297585
439	Complement component C1q receptor OS=Rattus norvegicus OX=10116 GN=Cd93 PE=1 SV=1	Cd93	Q9ET61	1.80457412	1.532107115	16.1071548	15.9282904	16.5832367	16.9687233	17.6828365	19.1013222	17.4397945	17.4918804
440	Complement component C6 OS=Rattus norvegicus OX=10116 GN=C6 PE=2 SV=1	C6	Q811M5	2.17308121	-1.372537613	19.4668789	19.8373108	19.8424644	18.6404018	18.1505527	17.6761112	17.9179249	18.5523167
441	Complement component C8 beta chain OS=Rattus norvegicus OX=10116 GN=C8b PE=2 SV=2	C8b	P55314	4.46405089	-2.334664822	21.3771896	21.2888985	21.9004784	21.4832535	18.9478397	19.6016865	18.888546	19.2730885
442	Complement component C9 OS=Rattus norvegicus OX=10116 GN=C9 PE=1 SV=1	C9	F7F389	3.40720659	-3.124817371	22.1200142	22.9087181	22.0344086	21.5369148	19.8230247	18.9175777	18.1947098	19.1654739
443	Complement component receptor 1-like protein OS=Rattus norvegicus OX=10116 GN=Cr1l PE=1 SV=1	Cd46	A0A0G2K7Y0	3.9630952	1.293581963	19.478714	19.3384132	19.4121094	19.8166733	20.9212017	20.9898281	20.5452118	20.7639961
444	Complement factor B OS=Rattus norvegicus OX=10116 GN=Cfb PE=1 SV=1	Cfb	Q7TP05	6.27368712	-3.714957237	24.2378769	24.3751011	24.4513893	24.2138805	21.0564098	20.4727478	20.3393745	20.5498867
445	Complement factor H OS=Rattus norvegicus OX=10116 GN=Cfh PE=1 SV=1	Cfh	G3V9R2	8.00131834	-4.015572071	24.4831753	24.4522572	24.7385578	24.4453526	20.6615486	20.4685593	20.3776588	20.5492878
446	Complement factor H-related protein B OS=Rattus norvegicus OX=10116 GN=LOC100361907 PE=1 SV=1	LOC100361907	A0A0G2JYC4	0.97135312	-0.974767208	19.1922646	17.7293758	18.9094162	19.1266251	17.2540855	18.6858501	18.0957375	17.0229397
447	Complement factor I OS=Rattus norvegicus OX=10116 GN=Cfi PE=1 SV=1	Cfi	A0A0G2K135	5.51639987	-4.458183765	23.1764412	23.4510479	23.6442108	22.939846	18.7416077	18.9277496	18.3249969	19.3844566
448	Complement factor properdin OS=Rattus norvegicus OX=10116 GN=Cfp PE=1 SV=1	Cfp	B0BNN4	3.19447785	-1.909965515	20.2610397	20.787714	20.8624191	20.3403397	18.1479034	19.2023544	18.9485588	18.3128338
449	Condensin complex subunit 2 OS=Rattus norvegicus OX=10116 GN=Ncaph PE=1 SV=3	Ncaph	D4A8M7	4.04956274	3.485730171	19.0014133	18.0452213	18.7301083	17.4471016	21.9709187	21.3810673	21.9284458	21.8863335
450	COP9 (Constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana) (Predicted), isoform CRA_a OS=Rattus no	Cops6	D3ZI16	6.56105738	4.460565805	16.4389362	16.1566505	15.8562737	15.8596144	20.7639942	20.4084473	20.2921753	20.6891212
451	COP9 signalosome complex subunit 1 OS=Rattus norvegicus OX=10116 GN=Gps1 PE=1 SV=1	Gps1	A0A0G2JT06	1.20079736	-0.963968277	24.2773857	25.6267586	24.0134373	25.2141857	23.9360161	24.2797413	23.6019115	23.4582253
452	COP9 signalosome complex subunit 2 OS=Rattus norvegicus OX=10116 GN=Cops2 PE=1 SV=1	Cops2	P61203	2.95426646	4.815215588	17.4302425	17.3245716	17.1423149	14.0231228	21.4063454	21.0807304	21.3057785	21.3882599
453	COP9 signalosome complex subunit 3 OS=Rattus norvegicus OX=10116 GN=Cops3 PE=1 SV=1	Cops3	Q68FW9	5.42021919	3.537277222	18.3359032	18.4747772	17.8792801	17.7289085	21.9897308	21.3990726	21.6880455	21.4911289
454	COP9 signalosome complex subunit 4 OS=Rattus norvegicus OX=10116 GN=Cops4 PE=1 SV=1	Cops4	Q68FS2	1.98786517	2.386744499	19.7852497	21.3006859	20.3552799	18.2774391	22.6599369	21.9894314	22.2916412	22.3246231
455	COP9 signalosome complex subunit 8 OS=Rattus norvegicus OX=10116 GN=Cops8 PE=2 SV=1	Cops8	Q6P4Z9	3.82152763	5.711998701	15.9493074	15.1005745	15.6345034	13.1401548	21.3684139	20.6097565	20.4677448	20.2266197
456	COP9 signalosome subunit 5 OS=Rattus norvegicus OX=10116 GN=Cops5 PE=1 SV=1	Cops5	F7EUU4	1.94972095	3.210579872	15.398037	18.4424057	14.6330357	16.7186737	20.3957577	19.0493889	19.4415417	19.1477833
457	COP9 signalosome subunit 7A OS=Rattus norvegicus OX=10116 GN=Cops7a PE=1 SV=1	Cops7a	F1MAA2	2.5731353	1.683301449	18.2917328	18.1177292	17.9022751	18.7888203	20.786665	19.5323009	19.6316719	19.8831253
458	Copper chaperone for superoxide dismutase OS=Rattus norvegicus OX=10116 GN=Ccs PE=1 SV=1	Ccs	A0A0G2JSZ9	3.18290554	2.651052475	18.7051926	16.976532	18.3317623	18.542593	21.0114422	20.4949322	20.7412949	20.9126205
459	Copper transport protein ATOX1 OS=Rattus norvegicus OX=10116 GN=Atox1 PE=1 SV=1	Atox1	Q9WUC4	1.83518608	3.688049078	15.3374424	16.5292816	17.0601883	12.7805262	18.1222973	18.8092155	18.9396591	20.5884628
460	Cortactin, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Cttn PE=1 SV=3	Cttn	D3ZGE6	3.98840362	4.267441273	18.9487038	17.0352974	18.2914677	17.0761852	22.0243645	22.1155434	22.1659603	22.115551
461	Corticosteroid-binding globulin OS=Rattus norvegicus OX=10116 GN=Serpina6 PE=1 SV=2	Serpina6	P31211	4.59020911	-4.832542419	22.8137245	21.9447861	22.7187805	22.7547455	18.4596958	17.190237	18.2422962	17.0096378
462	C-reactive protein OS=Rattus norvegicus OX=10116 GN=Crp PE=1 SV=1	Crp	P48199	1.90506903	-2.405958652	20.3117008	21.0330009	21.216013	20.7872715	16.504467	19.3741379	19.0731297	18.7724171
463	Creatine kinase B-type OS=Rattus norvegicus OX=10116 GN=Ckb PE=1 SV=2	Ckb	P07335	5.04904047	3.423948288	19.4565067	19.8213596	20.0603085	19.6791573	22.930233	22.738121	23.6836586	23.3611126
464	Creatine kinase M-type OS=Rattus norvegicus OX=10116 GN=Ckm PE=1 SV=1	Ckm	A0A0G2JSP8	1.90860424	2.930726528	24.5225563	24.593792	24.8458366	23.9220238	25.0060959	27.9215698	28.4718781	28.207571
465	CREB-regulated transcription coactivator 2 OS=Rattus norvegicus OX=10116 GN=Crtc2 PE=1 SV=1	Crtc2	Q3LRZ1	0.86729967	-0.571321964	19.2709808	18.5675049	19.0417824	19.0380268	19.045002	17.858284	17.9487305	18.7809906
466	CREB-regulated transcription coactivator 3 OS=Rattus norvegicus OX=10116 GN=Crtc3 PE=1 SV=2	Crtc3	F1LVL6	0.3516769	-0.258099079	19.1948681	19.1080742	19.3759689	20.1384201	19.7155991	18.7446041	18.9902859	19.334446
467	Crystallin beta-gamma domain-containing 3 OS=Rattus norvegicus OX=10116 GN=Crybg3 PE=1 SV=2	Crybg3	F1M8T4	1.98425205	3.002740383	15.487958	16.7597294	17.2381477	13.8626947	17.956356	19.0487804	18.9352913	19.4190636
468	C-terminal-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ctbp1 PE=1 SV=3	Ctbp1	Q9Z2F5	3.79326887	3.634056568	18.7031078	16.8487988	18.0924587	17.2255783	21.6165276	21.0439987	21.403656	21.3419876
469	CTP synthase OS=Rattus norvegicus OX=10116 GN=Ctps1 PE=1 SV=1	Ctps1	B1WC02	2.48346952	4.415441513	19.7053909	18.9396229	18.2197361	15.5282383	22.3970413	21.9254131	22.7706699	22.9616299
470	C-type lectin domain family 11 member A OS=Rattus norvegicus OX=10116 GN=Clec11a PE=2 SV=1	Clec11a	O88201	3.24736432	-4.593341827	21.4256115	21.0322647	21.6807079	21.4710464	18.6958237	16.4782524	15.459671	16.6025162
471	C-type lectin domain family 3, member B OS=Rattus norvegicus OX=10116 GN=Clec3b PE=1 SV=1	Clec3b	D3ZUU6	2.67573271	-2.073031425	18.3514767	19.8145752	19.1703777	19.4827023	16.5182934	17.3718395	16.9576454	17.6792278
472	C-type mannose receptor 2 OS=Rattus norvegicus OX=10116 GN=Mrc2 PE=1 SV=2	Mrc2	F1LMA7	0.21677684	0.256941319	17.9164734	18.221138	18.2215519	16.4641838	17.9209156	18.5749569	17.5442905	17.8109493
473	Cullin 2 OS=Rattus norvegicus OX=10116 GN=Cul2 PE=1 SV=1	Cul2	A0A0G2K761	2.81151395	4.563261032	16.9045925	16.0074711	13.3649311	14.0285091	19.830986	19.4768028	19.5228634	19.7278957
474	Cullin 4A OS=Rattus norvegicus OX=10116 GN=Cul4a PE=1 SV=1	Cul4a	B2RYJ3	2.45224511	-0.566033363	20.2780952	19.8383884	20.1919537	20.2625942	19.6182537	19.3834324	19.6554794	19.6497326
475	Cullin-5 OS=Rattus norvegicus OX=10116 GN=Cul5 PE=1 SV=1	Cul5	A0A0H2UHG3	0.76592198	2.070773602	21.1169262	19.8633919	18.6867256	15.0704308	21.3955898	20.1227531	21.0330811	20.4691448
476	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus OX=10116 GN=Cand1 PE=1 SV=1	Cand1	P97536	5.66300672	4.351043701	18.5441818	19.478857	19.377491	19.3550873	23.5005665	23.3571358	23.8880463	23.4140434
477	Cullin-associated NEDD8-dissociated protein 2 OS=Rattus norvegicus OX=10116 GN=Cand2 PE=4 SV=1	Cand2	A0A0G2K139	4.46414824	5.677466393	18.5355072	18.3799572	17.8002834	17.5368538	22.4032898	24.1606655	24.4886971	23.9098148
478	Cyclin-dependent kinase 1 OS=Rattus norvegicus OX=10116 GN=Cdk1 PE=1 SV=1	Cdk1	P39951	2.0423622	2.749114037	19.2547817	21.3767872	18.2890911	20.8890915	22.8407974	22.363842	22.789978	22.8115902
479	Cyclin-dependent-like kinase 5 OS=Rattus norvegicus OX=10116 GN=Cdk5 PE=1 SV=1	Cdk5	Q03114	1.49359464	2.285571098	15.8922491	16.6610909	15.679925	12.9338017	17.8035526	17.3548012	17.7721367	17.3788605
480	Cystatin-C OS=Rattus norvegicus OX=10116 GN=Cst3 PE=1 SV=2	Cst3	P14841	0.51836528	-0.590508461	21.180687	20.3104134	21.0850506	19.9347363	18.7677078	20.6495686	20.3404026	20.3911743
481	Cysteine and glycine-rich protein 1 OS=Rattus norvegicus OX=10116 GN=Csrp1 PE=1 SV=2	Csrp1	P47875	4.90597468	3.696391582	17.2849979	16.249424	17.406826	16.9682407	20.6403275	20.8746719	20.8097744	20.3702812
482	Cysteine and glycine-rich protein 3 OS=Rattus norvegicus OX=10116 GN=Csrp3 PE=1 SV=1	Csrp3	G3V7U0	6.14089825	4.884485722	20.5040684	19.849474	20.2804031	20.1254692	25.1552238	25.3488998	25.2616062	24.5316277
483	Cysteine and histidine-rich domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Chordc1 PE=3 SV=1	Chordc1	D4A4T9	2.57977197	2.720818996	16.4547787	17.9656601	16.646656	18.3870926	20.4155674	19.265173	20.3830471	20.2736759
484	Cysteine-rich protein 1 OS=Rattus norvegicus OX=10116 GN=Crip1 PE=1 SV=2	Crip1	P63255	1.06184704	2.121186733	19.2806416	19.6775055	19.1544914	15.5829887	19.3881836	21.2658482	20.8966827	20.6296597
485	Cysteine-rich protein 2 OS=Rattus norvegicus OX=10116 GN=Crip2 PE=2 SV=1	Crip2	P36201	5.59106748	3.521332741	22.293766	22.6305599	21.951498	22.078661	26.0717545	25.4865265	25.9301987	25.5513363
486	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Uqcrc1 PE=1 SV=1	Uqcrc1	Q68FY0	3.50527274	3.668149471	18.9553967	19.8207321	18.3328342	18.67243	21.4950657	23.1496429	22.7964611	23.0128212

487	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Uqcrc2 PE=1 SV=2	Uqcrc2	P32551	1.9575561	1.390589714	21.3820553	21.9245911	22.4447441	21.601408	22.3227978	23.6759987	23.455286	23.4610748
488	Cytochrome b-c1 complex subunit 7 OS=Rattus norvegicus OX=10116 GN=Uqcrb PE=1 SV=1	Uqcrb	B2RYS2	2.74960649	3.7190485	19.2765026	19.2855892	17.7604618	16.7820835	21.0168228	22.5010986	22.1996498	22.2632599
489	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Rattus norvegicus OX=10116 GN=Uqcrfs1 PE=1 SV=2	Uqcrfs1	P20788	3.00835089	2.867899895	18.6955853	19.4115238	18.3437042	17.8561764	20.4329243	21.9230404	21.5111237	21.9115009
490	Cytochrome c oxidase subunit 2 OS=Rattus norvegicus OX=10116 GN=Mtco2 PE=1 SV=3	mt-Co2	P00406	3.27682861	3.535441875	19.4746571	19.914053	17.9984226	18.6311646	21.6605587	22.9115543	22.5907764	22.9971752
491	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox4i1 PE=1 SV=1	Cox4i1	P10888	3.32054851	3.742684841	19.9735317	20.4596424	18.938179	18.5412331	22.3050919	23.7473564	23.3210773	23.5098
492	Cytochrome c oxidase subunit 5A, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox5a PE=1 SV=1	Cox5a	P11240	3.43732909	4.434260845	18.9913654	18.7973042	16.8299141	17.4571095	21.5118465	22.9952927	22.5524387	22.7531586
493	Cytochrome c oxidase subunit 6C-2 OS=Rattus norvegicus OX=10116 GN=Cox6c2 PE=1 SV=3	Cox6c	P11951	3.25090301	5.42001009	16.6145725	18.2526588	15.1324415	15.2147036	20.696661	22.2733898	21.7866917	22.1376743
494	Cytochrome c oxidase subunit 7A2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox7a2 PE=1 SV=1	Cox7a2	P35171	4.26173457	5.052636623	16.2069893	16.2131062	15.9259138	15.293292	19.6616879	21.7486401	21.2299004	21.2096195
495	Cytochrome c oxidase subunit 7C, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox7c PE=1 SV=2	Cox7c	P80432	3.16273101	3.416976452	17.557024	18.3842564	16.5354328	16.9549656	19.7867756	21.363781	20.7631912	21.1858368
496	Cytochrome c-1 OS=Rattus norvegicus OX=10116 GN=Cyc1 PE=1 SV=3	Cyc1	D3ZFQ8	2.60879329	3.748665333	17.6592236	17.7038193	14.9167557	17.477108	19.7110939	21.0155849	21.0276184	20.9972706
497	Cytoplasmic aconitate hydratase OS=Rattus norvegicus OX=10116 GN=Aco1 PE=1 SV=1	Aco1	G3V6S2	3.9606422	3.633609295	17.9131432	16.7223949	17.002943	17.8211136	20.2694454	20.8566704	21.4290409	21.4388752
498	Cytoplasmic dynein 1 heavy chain 1 OS=Rattus norvegicus OX=10116 GN=Dync1h1 PE=1 SV=2	Dync1h1	M0R9X8	5.17476725	3.12110424	24.8613052	24.5271645	24.3266258	23.878933	27.4083481	27.4937439	27.7022495	27.4741039
499	Cytoplasmic dynein 1 intermediate chain 2 OS=Rattus norvegicus OX=10116 GN=Dync1i2 PE=1 SV=1	Dync1i2	Q6AZ35	1.35210556	1.067415237	22.2414265	21.9181252	23.5369453	22.4565983	23.2498684	23.1872082	23.8324738	24.1532059
500	Cytoplasmic dynein 1 light intermediate chain 1 OS=Rattus norvegicus OX=10116 GN=Dync1li1 PE=1 SV=1	Dync1li1	G3V7G0	4.05175271	4.518994331	17.8028564	18.1453724	18.4285202	19.9239578	22.7198296	23.1948338	23.3696175	23.0924034
501	Cytoplasmic dynein 1 light intermediate chain 2 OS=Rattus norvegicus OX=10116 GN=Dync1li2 PE=1 SV=1	Dync1li2	Q5D023	6.44892763	7.744068384	14.8901253	15.3315277	14.2099228	15.6517286	22.7055416	22.6917763	23.027317	22.634943
502	Cytoplasmic FMR1-interacting protein OS=Rattus norvegicus OX=10116 GN=Cyfip1 PE=1 SV=1	Cyfip1	D4A8H8	4.14282627	4.175592422	16.9077682	17.1765728	16.0084476	18.0654793	21.4507675	20.9898071	21.2152653	21.2047977
503	Cytoplasmic linker-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Clasp1 PE=1 SV=3	Clasp1	F1LNR0	3.18170136	1.82223177	19.9603729	20.1537533	20.2619305	19.3262844	21.7117653	22.2214737	21.764595	21.2934341
504	Cytoskeleton-associated protein 4 OS=Rattus norvegicus OX=10116 GN=Ckap4 PE=1 SV=2	Ckap4	D3ZH41	6.1306072	3.638558865	19.6546898	20.1933956	19.9489231	19.5971375	23.3862457	23.6396313	23.2461071	23.6763973
505	Cytoskeleton-associated protein 5 OS=Rattus norvegicus OX=10116 GN=Ckap5 PE=1 SV=3	Ckap5	F1M949	2.49350421	3.17245245	19.4319267	21.6503334	18.7707367	20.6851597	23.1501808	23.8687954	23.1804047	23.0285854
506	Cytosol aminopeptidase OS=Rattus norvegicus OX=10116 GN=Lap3 PE=1 SV=1	Lap3	Q68FS4	3.27521193	3.097071648	16.4497032	18.0515385	16.3904953	16.1770782	19.6324062	19.98242	20.2667274	19.5755482
507	Cytosolic Fe-S cluster assembly factor NUBP2 OS=Rattus norvegicus OX=10116 GN=Nubp2 PE=1 SV=1	Nubp2	Q68FS1	1.20957463	0.853509903	20.6774826	21.1451168	20.6924992	19.6725731	22.0062599	21.2650318	21.2224197	21.1079998
508	Cytosolic iron-sulfur assembly component 2B OS=Rattus norvegicus OX=10116 GN=Ciao2b PE=1 SV=1	Ciao2b	D3Z8Q7	1.54610192	2.453129053	15.8958464	15.9844112	15.3858509	16.2532806	15.9084511	18.5455875	19.3917904	19.4860764
509	Cytosolic non-specific dipeptidase OS=Rattus norvegicus OX=10116 GN=Cndp2 PE=1 SV=1	Cndp2	Q6Q0N1	0.46858511	0.750757217	18.6489334	20.7580738	19.7402954	19.5403347	18.6928577	20.9028568	21.1967525	20.8981991
510	D-3-phosphoglycerate dehydrogenase OS=Rattus norvegicus OX=10116 GN=Phgdh PE=1 SV=3	Phgdh	O08651	4.73603432	1.738637924	21.3331928	21.3484516	21.5405006	21.6518593	23.0268974	22.9806213	23.3592415	23.4617958
511	D-dopachrome decarboxylase OS=Rattus norvegicus OX=10116 GN=Ddt PE=1 SV=3	Ddt	P80254	2.88562781	2.103660822	16.8814526	16.6624527	15.7050104	16.4186134	18.8468056	17.8275204	18.3737698	19.0340767
512	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ddx17 PE=1 SV=1	Ddx17	A0A096MIX2	0.4912646	1.678203106	17.6298771	17.0519905	11.9298916	18.3638172	19.3961277	17.7851868	16.8384895	17.6685848
513	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a OS=Rattus norvegicus OX=10116 GN=Ddx19a PE=1 SV=1	Ddx19a	Q68FX3	6.09027578	4.59000206	19.0152111	18.8174133	19.2542591	18.5440617	23.7136269	23.0157204	23.631216	23.6303902
514	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 OS=Rattus norvegicus OX=10116 GN=Ddx5 PE=1 SV=1	Ddx5	Q6AYI1	2.61469577	4.943585873	18.5765209	17.9702358	18.5190125	14.5078526	22.8295155	22.2074223	22.2845459	22.0264816
515	Dead end homolog 1 (Zebrafish) OS=Rattus norvegicus OX=10116 GN=Hars PE=1 SV=1	Hars1	Q4QQV4	4.07510531	1.961954117	17.4772282	17.6348076	17.5630951	17.4393749	20.0224056	19.08675	19.2691708	19.5839958
516	DEAD-box helicase 3, X-linked OS=Rattus norvegicus OX=10116 GN=Ddx3x PE=1 SV=1	Ddx3x	A0A0G2K719	5.69379169	3.370968819	20.5746212	20.0252342	20.2766819	20.7583656	24.0706749	23.7277355	23.6751385	23.6452293
517	Decapping mRNA 1A OS=Rattus norvegicus OX=10116 GN=Dcp1a PE=1 SV=1	Dcp1a	D4AE80	2.11959624	2.78409934	14.222477	17.3917904	15.0012703	15.8240805	18.4153728	18.9425049	18.090498	18.1276398
518	Dedicator of cytokinesis 7 OS=Rattus norvegicus OX=10116 GN=Dock7 PE=1 SV=1	Dock7	A0A0G2K3H2	3.87284523	3.060472965	17.4477139	17.5599575	17.2964973	18.3845596	20.0108795	21.2353096	20.8798237	20.8046074
519	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ech1 PE=1 SV=2	Ech1	Q62651	0.52402124	0.912845612	17.0201359	16.4222927	17.6024017	17.2992706	16.2209301	19.9403725	18.0671597	17.7670212
520	Deoxythymidylate kinase OS=Rattus norvegicus OX=10116 GN=Dtymk PE=1 SV=1	Dtymk	D3ZUJ5	1.66260673	1.02162981	17.2694721	17.6052074	17.1817703	17.5393658	19.0465832	18.442461	18.6418304	17.5514603
521	Desmin OS=Rattus norvegicus OX=10116 GN=Des PE=1 SV=1	Des	Q6P725	4.88999585	4.134170055	17.3610859	17.8031311	18.0728474	16.6890545	21.4387798	21.656702	21.4839668	21.8833504
522	Desmocollin 1 OS=Rattus norvegicus OX=10116 GN=Dsc1 PE=4 SV=1	Dsc1	A0A0G2KA90	0.81807706	-1.249321461	18.5159531	20.8328495	18.1688671	18.1836834	17.9247818	18.5201645	17.7040005	16.5551205
523	Desmoglein 1 OS=Rattus norvegicus OX=10116 GN=Dsg1 PE=4 SV=1	Dsg1	D3ZM39	1.07420345	-1.391749382	20.2492847	21.6618309	19.3181019	20.9705429	19.616415	20.1467648	18.7413902	18.1281929
524	Desmoplakin OS=Rattus norvegicus OX=10116 GN=Dsp PE=1 SV=1	Dsp	F1LMV6	0.27836496	-0.327793121	22.8625278	24.1065159	22.5236549	24.1576786	23.089632	23.7771358	22.7914543	22.6809826
525	Destrin OS=Rattus norvegicus OX=10116 GN=Dstn PE=1 SV=3	Dstn	Q7M0E3	4.89968708	3.678190708	19.693821	20.118021	20.3103161	19.2627277	23.8176422	23.0834045	23.6760902	23.5205116
526	Deubiquitinating protein VCIP135 OS=Rattus norvegicus OX=10116 GN=Vcpip1 PE=1 SV=2	Vcpip1	Q8CF97	1.44273931	2.364302158	16.738287	17.2881298	17.2477551	16.440134	20.589016	20.0751877	19.7226734	16.7846375
527	Developmentally-regulated GTP-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Drg1 PE=1 SV=1	Drg1	Q5I0F0	3.89243843	5.136393785	15.921134	13.9805899	16.5768108	14.7342443	20.6673489	20.1931114	20.4745979	20.423296
528	Developmentally-regulated GTP-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Drg2 PE=1 SV=1	Drg2	A0A0G2KAI8	0.55216537	1.006521225	21.6933594	21.1116867	18.5823555	18.7718048	21.7050705	20.3659592	21.3119946	20.8022671
529	Diacylglycerol kinase zeta OS=Rattus norvegicus OX=10116 GN=Dgkz PE=1 SV=1	Dgkz	O08560	2.59416084	4.644901752	18.1642151	16.1430531	14.1792469	14.4735966	20.1060104	20.0086403	20.7210464	20.7040215
530	Dickkopf WNT-signaling pathway inhibitor 3 OS=Rattus norvegicus OX=10116 GN=Dkk3 PE=2 SV=1	Dkk3	B1H219	0.94153255	1.701622725	15.9460373	13.3488913	16.2565041	16.6655788	18.2518826	15.7352028	17.58181	17.454607
531	Dihydrofolate reductase OS=Rattus norvegicus OX=10116 GN=Dhfr PE=1 SV=3	Dhfr	Q920D2	0.29593814	0.43103838	18.7703094	17.1608906	19.0606613	18.8644638	19.6519909	17.7544212	18.7705402	19.4035263
532	Dihydrolipoyl dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Dld PE=1 SV=1	Dld	Q6P6R2	0.72105637	2.459467888	17.8052998	12.6500072	18.5816345	18.4088802	16.7542572	20.6061535	19.6282158	20.2950668
533	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Rattus norve	Dlat	P08461	2.97722848	3.199235916	17.6077271	19.0058727	17.2438869	17.6695862	19.9486485	21.5557537	21.3243675	21.4952469
534	Dihydropyrimidinase-related protein 2 OS=Rattus norvegicus OX=10116 GN=Dpysl2 PE=1 SV=1	Dpysl2	P47942	6.66717602	5.383496284	18.3355751	19.1968689	18.9756508	18.8223343	24.3047428	24.4314499	24.151041	23.9771805
535	Dihydropyrimidinase-related protein 3 OS=Rattus norvegicus OX=10116 GN=Dpysl3 PE=1 SV=2	Dpysl3	Q62952	6.56510954	5.26138258	18.6833038	19.3629799	18.945549	18.4364929	24.3244514	24.0967731	24.0613708	23.9912605
536	Dipeptidyl peptidase 4 OS=Rattus norvegicus OX=10116 GN=Dpp4 PE=1 SV=1	Dpp4	A0A0G2K238	2.8050096	2.588086843	15.2194452	17.0148335	16.4091053	16.3666306	19.4421158	19.0747471	18.0759563	18.7695427
537	Diphosphoinositol polyphosphate phosphohydrolase 2 OS=Rattus norvegicus OX=10116 GN=Nudt4 PE=2 SV=1	Nudt4	Q99MY2	2.13189735	3.680190325	16.6863251	13.1525297	16.5514278	17.1436806	19.8986168	19.3148403	19.4670105	19.5742569
538	Disabled homolog 2 OS=Rattus norvegicus OX=10116 GN=Dab2 PE=1 SV=1	Dab2	O88797	3.14312146	2.463873863	16.6279259	17.3666821	16.5829735	16.3112011	20.0828342	18.6059322	18.9671555	19.088356
539	DNA damage-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ddb1 PE=1 SV=1	Ddb1	G3V8T4	4.56689602	2.861625195	19.9309921	19.5214634	19.2572231	19.2599411	22.7691994	21.8330154	22.3739948	22.4399109
540	DNA damage-inducible 1 homolog 2 OS=Rattus norvegicus OX=10116 GN=Ddi2 PE=1 SV=1	Ddi2	A0A096MJP9	2.91329122	2.682531357	16.4724197	14.5375929	15.8031664	16.3945198	18.8289108	18.4910698	18.4605179	18.1573257
541	DNA helicase OS=Rattus norvegicus OX=10116 GN=Mcm2 PE=1 SV=2	Mcm2	D3ZP96	1.02557629	-0.58043766	21.6598511	21.6760597	22.4836235	22.2178135	21.0079269	21.1345558	21.8315697	21.7415447
542	DNA helicase OS=Rattus norvegicus OX=10116 GN=Mcm3 PE=1 SV=3	Mcm3	D3ZFP4	3.05215877	2.416116714	19.4193707	18.6585369	18.6575928	20.0127869	22.1729031	21.190073	21.7270222	21.3227558
543	DNA helicase OS=Rattus norvegicus OX=10116 GN=Mcm4 PE=1 SV=1	Mcm4	G3V681	6.31556523	5.339408398	16.8678799	17.3750553	17.1787643	16.5752449	22.044529	22.3526726	22.7700768	22.1872997
544	DNA helicase OS=Rattus norvegicus OX=10116 GN=Mcm5 PE=1 SV=1	Mcm5	A0A0G2JY07	5.42104172	5.497093678	15.6217976	16.7218704	16.1753063	15.3051529	21.6726379	21.059391	21.6606846	21.4197884
545	DNA helicase OS=Rattus norvegicus OX=10116 GN=Mcm6 PE=1 SV=1	Mcm6	A9CMB8	3.69142675	6.008789539	15.0767756	16.9592075	14.7692156	17.7308674	21.7304268	21.8213711	22.6000862	22.4193401
546	DNA replication licensing factor MCM7 OS=Rattus norvegicus OX=10116 GN=Mcm7 PE=1 SV=1	Mcm7	Q6AYN8	5.89747363	5.669831514	15.8440161	15.5380001	16.1485233	15.7105961	20.8728428	21.20401	21.8733845	21.9702244
547	DNA-directed RNA polymerase II subunit GRINL1A OS=Rattus norvegicus OX=10116 GN=Polr2m PE=2 SV=1	Myzap	H8Y6S5	4.70700585	4.674213171	14.410593	15.8966303	15.6614342	16.0648994	20.3943958	20.1774082	20.2282104	19.9303951

548	DnaJ (Hsp40) homolog, subfamily A, member 2 OS=Rattus norvegicus OX=10116 GN=Dnaja2 PE=1 SV=1	Dnaja2	Q5M9H7	5.48407363	4.186609268	19.2541885	18.1977348	18.9261646	18.664629	23.239296	22.640667	23.0097198	22.8994713
549	DnaJ (Hsp40) homolog, subfamily B, member 1 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Dnajb1 PE	Dnajb1	B0K030	3.47834756	3.24119997	16.1104374	16.3912716	15.6021423	17.3960648	20.0844898	19.1222134	19.3289375	19.9290752
550	DnaJ (Hsp40) homolog, subfamily B, member 4 OS=Rattus norvegicus OX=10116 GN=Dnajb4 PE=1 SV=1	Dnajb4	Q5XIP0	5.22660308	6.495090008	15.4893265	13.8622904	15.7687931	14.621232	21.4942646	21.5065956	21.2311726	21.4899693
551	DnaJ heat shock protein family (Hsp40) member C13 OS=Rattus norvegicus OX=10116 GN=Dnajc13 PE=1 SV=2	Dnajc13	D3ZN27	5.74283887	2.87489748	18.3511219	19.0023556	18.487709	18.6391678	21.5035801	21.6943016	21.3480225	21.4340401
552	DnaJ heat shock protein family (Hsp40) member C7 OS=Rattus norvegicus OX=10116 GN=Dnajc7 PE=1 SV=1	Dnajc7	A0A0G2K435	4.69982644	3.967916965	17.0852737	17.4989662	17.2764759	18.3686047	21.61553	21.0266876	21.7081604	21.7506104
553	DnaJ homolog subfamily B member 11 OS=Rattus norvegicus OX=10116 GN=Dnajb11 PE=2 SV=1	Dnajb11	Q6TUG0	4.67739693	2.86622715	16.0273342	16.493866	16.1347599	15.3695068	18.9773178	18.732954	18.9178791	18.8622246
554	DnaJ homolog subfamily C member 5 OS=Rattus norvegicus OX=10116 GN=Dnajc5 PE=1 SV=1	Dnajc5	P60905	3.9352335	2.715830803	16.0742302	16.9338894	15.6611786	15.692255	18.7671432	18.7893467	18.6425648	19.0258217
555	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Rattus norvegicus OX=10116 GN=Ddost	Ddost	Q641Y0	2.73080135	2.779419661	16.4710236	15.6982889	16.8446121	16.6923389	20.1068478	18.436367	18.3885784	19.892149
556	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Rattus norvegicus OX=10116 GN=Rpn1 PE=1 S	Rpn1	Q6P7A7	5.53411477	2.686439991	20.1152573	19.891346	20.1144962	19.8040752	22.4701729	22.8697281	22.3872986	22.9437351
557	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Rattus norvegicus OX=10116 GN=Rpn2 PE=2 S	Rpn2	P25235	3.42381989	1.641740322	19.1421852	19.1396351	19.3584442	19.7393208	20.6557713	21.3528519	20.6958656	21.2420578
558	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Rattus norvegicus OX=10116 GN=Dad1 P	Dad1	P61805	0.73482651	0.385284424	18.9947205	19.1532402	19.9746685	18.8841763	19.730978	19.7793255	19.5008755	19.5367641
559	Drebrin OS=Rattus norvegicus OX=10116 GN=Dbn1 PE=1 SV=3	Dbn1	Q07266	4.16919381	2.920150757	16.8689938	16.1394997	16.1580791	16.6003475	18.7811394	19.1644058	19.8571033	19.6448746
560	Drebrin-like protein OS=Rattus norvegicus OX=10116 GN=Dbnl PE=1 SV=1	Dbnl	Q9JHL4	4.25904279	6.752481461	17.6369076	14.9989185	17.1198864	15.2581844	22.8493195	23.1357708	23.2484474	22.7902851
561	Dual specificity mitogen-activated protein kinase kinase 1 OS=Rattus norvegicus OX=10116 GN=Map2k1 PE=1 SV=2	Map2k1	Q01986	4.86575377	8.7757833	14.9085703	13.0641069	15.4428215	12.6834822	22.829031	22.5664597	22.9360027	22.8706207
562	Dynactin subunit 1 OS=Rattus norvegicus OX=10116 GN=Dctn1 PE=1 SV=1	Dctn1	A0A0G2K428	4.79287631	4.59249258	19.9876556	18.8334942	20.0919094	19.1693878	23.6388836	24.4239902	24.4666328	23.9229107
563	Dynactin subunit 2 OS=Rattus norvegicus OX=10116 GN=Dctn2 PE=1 SV=1	Dctn2	A0A0G2JUC7	4.71446399	7.13208437	16.3071823	17.3040981	14.7337646	15.2163868	23.0975552	22.7585526	23.3487129	22.8849487
564	Dynactin subunit 3 OS=Rattus norvegicus OX=10116 GN=Dctn3 PE=1 SV=1	Dctn3	D4A1B8	2.12466924	4.994630337	19.9477901	14.3318624	15.1676226	15.4931984	21.0823135	21.287096	21.3841343	21.165451
565	Dynactin subunit 4 OS=Rattus norvegicus OX=10116 GN=Dctn4 PE=1 SV=1	Dctn4	Q9QUR2	5.13544805	4.854222298	14.8768311	15.3604307	14.8933039	14.1492558	19.0501308	20.0116444	20.0273285	19.6076069
566	Dynamin-1-like protein OS=Rattus norvegicus OX=10116 GN=Dnm1l PE=1 SV=1	Dnm1l	O35303	6.63364007	4.61228466	20.2182961	19.618866	20.1362724	19.8195972	24.8044453	24.2706337	24.6565857	24.5105057
567	Dynamin-2 OS=Rattus norvegicus OX=10116 GN=Dnm2 PE=1 SV=1	Dnm2	P39052	1.94122744	1.399733543	20.3850594	19.7607403	20.4967098	21.3849926	22.3897228	21.4880409	22.0570736	21.6915989
568	Dynein assembly factor 4, axonemal OS=Rattus norvegicus OX=10116 GN=Dnaaf4 PE=1 SV=1	Dnaaf4	Q5VJS5	1.77308093	-1.060765266	21.7618523	22.5456123	21.6563473	22.5043755	20.4834785	21.5444603	21.0136547	21.1835327
569	Dynein light chain 1, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Dynll1 PE=1 SV=1	Dynll1	P63170	6.3095488	4.040082455	19.5180511	19.3673038	19.3144951	18.98633	23.048214	23.7001038	23.3841743	23.2140179
570	Dystonin OS=Rattus norvegicus OX=10116 GN=Dst PE=1 SV=3	Dst	D3ZC56	5.70911026	4.361953735	19.3886108	19.4155464	19.845171	19.2729626	23.2183666	24.0033722	24.0966778	24.0516891
571	E3 ubiquitin-protein ligase HUWE1 OS=Rattus norvegicus OX=10116 GN=Huwe1 PE=1 SV=1	Huwe1	A0A0G2JVW5	2.49309477	3.149404526	15.9388752	18.4973183	18.3351765	18.3269386	21.5886936	20.6576614	20.4018536	21.047718
572	E3 ubiquitin-protein ligase OS=Rattus norvegicus OX=10116 GN=Nedd4 PE=1 SV=1	Nedd4	A0A0G2K8P3	3.65410027	2.311405659	21.3513412	21.8178139	22.4068432	22.052042	23.6968765	24.4673443	24.5479126	24.1615295
573	E3 ubiquitin-protein ligase RNF114 OS=Rattus norvegicus OX=10116 GN=Rnf114 PE=2 SV=1	Rnf114	Q6J2U6	3.46084448	5.036322594	16.8913288	16.0908089	16.0548267	13.9806042	21.634201	20.1677113	20.7068901	20.6540565
574	E3 ubiquitin-protein ligase TRIP12 OS=Rattus norvegicus OX=10116 GN=Trip12 PE=1 SV=1	Trip12	A0A1W2Q676	3.67141318	2.758179426	14.8862686	14.5250349	15.2604284	15.7085218	18.1431389	18.2088928	17.8905582	17.1703815
575	E3 ubiquitin-protein ligase UBR4 OS=Rattus norvegicus OX=10116 GN=Ubr4 PE=1 SV=1	Ubr4	F1LQI5	3.94170459	5.327994347	14.9962444	17.9089832	16.4557114	16.544796	22.0433178	21.6762733	21.7893829	21.7087383
576	Early endosome antigen 1 OS=Rattus norvegicus OX=10116 GN=Eea1 PE=1 SV=1	Eea1	A0A0G2K051	2.4026566	2.528789997	15.7280226	15.3825817	14.7958088	13.7340097	18.3141537	17.6131344	17.1339531	16.6943417
577	Eefsec protein OS=Rattus norvegicus OX=10116 GN=Eefsec PE=1 SV=1	Eefsec	B5DEJ5	0.11749326	0.356751442	17.3822842	17.5958748	14.2193089	19.008234	18.5133171	17.4883022	16.0593071	17.5717812
578	EH domain-binding protein 1-like 1 OS=Rattus norvegicus OX=10116 GN=Ehbp1l1 PE=1 SV=1	Ehbp1l1	A0A0G2K6R8	3.87585863	4.06052494	18.9030266	18.8239727	17.4590645	17.1647091	22.3222847	22.2496109	22.25811	21.762867
579	EH domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Ehd1 PE=1 SV=1	Ehd1	Q641Z6	5.89614934	2.59354496	20.9006042	20.53965	20.6240692	20.7614098	23.5787544	23.0479965	23.3070221	23.26614
580	EH domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Ehd2 PE=1 SV=1	Ehd2	Q4V8H8	5.05149772	3.080451012	17.5039577	17.2355938	18.1731148	17.4646053	20.9055023	20.5717888	20.7419586	20.479826
581	EH domain-containing protein 3 OS=Rattus norvegicus OX=10116 GN=Ehd3 PE=1 SV=2	Ehd3	Q8R491	0.34894931	-0.451378822	15.957509	15.2308941	16.2062874	17.5723991	16.5106621	15.695075	15.7122669	15.2435703
582	EH-domain-containing 4 OS=Rattus norvegicus OX=10116 GN=Ehd4 PE=1 SV=1	Ehd4	Q8R3Z7	3.99153067	1.465875149	22.3995247	22.3430309	22.8551674	22.3372707	24.2208176	23.8164597	23.9981956	23.7630215
583	Elastin microfibril interfacer 1 OS=Rattus norvegicus OX=10116 GN=Emilin1 PE=1 SV=1	Emilin1	D3Z9E1	0.53067388	-0.753543377	17.6458588	16.8998718	18.447216	17.8843231	18.5068054	17.1673603	16.1288967	16.0600338
584	Elastin OS=Rattus norvegicus OX=10116 GN=Eln PE=1 SV=2	Eln	D4A9U4	0.51473971	0.430155754	19.4962158	19.8840008	19.5387783	19.0635147	20.3434277	19.4787235	19.2134781	20.6675034
585	ELAV-like protein 1 OS=Rattus norvegicus OX=10116 GN=Elavl1 PE=1 SV=1	Elavl1	B5DF91	3.70115101	4.962042809	16.4718552	14.4682598	15.5551233	13.8866339	20.5272255	20.2282104	20.0241795	19.450428
586	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Rattus norvegicus OX=10116 GN=Etfa PE=1 SV=4	Etfa	P13803	5.73364534	2.048162937	19.8923988	19.9439316	19.9362068	19.9470501	22.1684055	22.1775398	21.792429	21.7738647
587	Electron transfer flavoprotein subunit beta OS=Rattus norvegicus OX=10116 GN=Etfb PE=1 SV=3	Etfb	Q68FU3	2.73111291	3.008188248	19.0093422	19.6377621	17.7662888	17.2936192	21.1363297	21.8906822	21.1932068	21.5195465
588	ELKS/Rab6-interacting/CAST family member 1 OS=Rattus norvegicus OX=10116 GN=Erc1 PE=1 SV=1	Erc1	A0A0G2JYT1	1.94458652	3.059919357	17.4127789	16.2934933	17.434576	14.3164692	18.681015	20.5204411	19.6993351	18.7962036
589	Elongation factor 1-alpha 1 OS=Rattus norvegicus OX=10116 GN=Eef1a1 PE=2 SV=1	Eef1a1	P62630	6.25090826	3.606715679	25.9293575	25.3474083	25.7994213	25.7606087	29.5629482	29.067276	29.3743038	29.2591305
590	Elongation factor 1-alpha 2 OS=Rattus norvegicus OX=10116 GN=Eef1a2 PE=1 SV=1	Eef1a2	P62632	6.0672321	6.493279457	17.0921497	18.3352375	18.0392284	17.307579	24.2622299	23.8534126	24.279068	24.352602
591	Elongation factor 1-delta OS=Rattus norvegicus OX=10116 GN=Eef1d PE=1 SV=2	Eef1d	Q68FR9	4.74970979	4.663640976	20.0347691	18.7471294	19.4051838	19.9397793	24.7441196	23.5811939	24.2233086	24.2328033
592	Elongation factor 1-gamma OS=Rattus norvegicus OX=10116 GN=Eef1g PE=2 SV=3	Eef1g	Q68FR6	4.10870493	3.138952255	20.1987972	20.1322765	20.2354221	19.6854954	24.062191	22.6210766	23.0572376	23.0672951
593	Elongation factor 2 OS=Rattus norvegicus OX=10116 GN=Eef2 PE=1 SV=4	Eef2	P05197	6.74422138	4.574028492	22.5169487	22.573843	22.819931	22.8904819	27.6273994	26.9198151	27.2893944	27.2607098
594	Elongation factor Tu, mitochondrial OS=Rattus norvegicus OX=10116 GN=Tufm PE=1 SV=1	Tufm	P85834	3.01065911	3.348417282	17.3152676	18.0255718	15.7228489	17.0054321	19.6278915	20.2143574	20.7391262	20.8814144
595	Elongator complex protein 1 OS=Rattus norvegicus OX=10116 GN=Elp1 PE=1 SV=2	Elp1	F1LP76	4.64059134	2.347053051	20.6504803	20.9392033	21.2174473	20.749136	22.84342	23.1576366	23.5720348	23.3713875
596	Elongator complex protein 2 OS=Rattus norvegicus OX=10116 GN=Elp2 PE=2 SV=1	Elp2	Q496Z0	4.57285213	3.23522377	17.2021351	17.551033	16.6717987	16.6233139	19.7526436	20.4917221	20.4950733	20.2497368
597	Elongator complex protein 3 OS=Rattus norvegicus OX=10116 GN=Elp3 PE=1 SV=2	Elp3	D4ACM1	5.54620064	3.583220005	17.2202473	17.035017	16.912878	17.6218128	20.7740154	20.6996021	21.1764565	20.4727612
598	Elongin-B OS=Rattus norvegicus OX=10116 GN=Elob PE=1 SV=1	Elob	P62870	4.46262704	5.867390156	16.4423599	14.9703541	17.4391003	16.859972	22.5076828	22.0386162	22.329464	22.305584
599	Elongin-C OS=Rattus norvegicus OX=10116 GN=Eloc PE=1 SV=1	Eloc	P83941	5.5849093	6.924026489	14.0929852	15.2133083	15.3469973	15.8712645	22.5258884	21.8603764	21.9459038	21.8884926
600	Embigin OS=Rattus norvegicus OX=10116 GN=Emb PE=1 SV=1	Emb	O88775	2.34809015	-2.061337948	19.8500214	20.1286716	19.1956005	20.1720219	16.6674137	18.3970318	17.6488724	18.3876457
601	ENAH, actin regulator OS=Rattus norvegicus OX=10116 GN=Enah PE=1 SV=1	Enah	A0A0G2K6I4	5.36302876	2.736401558	20.418541	20.4092503	20.3502541	19.9753799	22.7872868	23.1733093	23.3447037	22.7937317
602	Endophilin-A2 OS=Rattus norvegicus OX=10116 GN=Sh3gl1 PE=1 SV=1	Sh3gl1	O35964	2.00442276	1.310640335	19.9626999	19.3922138	20.5362682	20.8900547	21.5066662	21.7394333	21.6263599	21.1513386
603	Endophilin-B1 OS=Rattus norvegicus OX=10116 GN=Sh3glb1 PE=2 SV=1	Sh3glb1	Q6AYE2	4.29979511	4.312061787	19.8480225	19.4237442	18.1433544	18.7341194	23.6678524	22.9217949	23.6622715	23.1455688
604	Endophilin-B2 OS=Rattus norvegicus OX=10116 GN=Sh3glb2 PE=1 SV=1	Sh3glb2	A0A0G2K9P4	4.32565597	4.381378174	18.3384285	18.0577736	16.5608044	17.6934299	22.4522247	21.8107948	22.1574726	21.7554569
605	Endoplasmic reticulum chaperone BiP OS=Rattus norvegicus OX=10116 GN=Hspa5 PE=1 SV=1	Hspa5	P06761	5.59950237	2.667967796	22.868145	23.1521168	23.0946312	23.3803864	25.8480835	25.9738789	25.4572124	25.8879757
606	Endoplasmic reticulum metallopeptidase 1 OS=Rattus norvegicus OX=10116 GN=Ermp1 PE=1 SV=1	Ermp1	F1M6W2	1.16653759	0.914622545	15.7951488	15.3288593	16.2374954	16.0929089	15.7006731	17.1449909	17.085434	17.1818047
607	Endoplasmic reticulum resident protein 29 OS=Rattus norvegicus OX=10116 GN=Erp29 PE=1 SV=2	Erp29	P52555	1.80975998	2.644443512	17.2115135	19.932209	18.0127811	16.5016174	19.9968987	21.2517529	20.2486973	20.7385464
608	Endoplasmic reticulum-golgi intermediate compartment 1 OS=Rattus norvegicus OX=10116 GN=Ergic1 PE=1 SV=2	Ergic1	F1LU48	3.37583248	4.849386692	17.9383411	17.446867	15.9442825	14.9794865	21.3974609	21.7352886	21.442852	21.1309223

609	Endoplasmin OS=Rattus norvegicus OX=10116 GN=Hsp90b1 PE=1 SV=1	Hsp90b1	A0A0A0MY09	5.2225372	3.212435246	21.3420982	22.0727329	21.4521751	21.305666	24.6406937	24.9025249	24.4705734	25.0086212
610	Enhancer of mRNA-decapping protein 4 OS=Rattus norvegicus OX=10116 GN=Edc4 PE=1 SV=1	Edc4	Q3ZAV8	2.51377754	1.597707272	19.8705635	19.3262043	19.2793446	18.3969383	20.9184074	20.4409618	20.816124	21.0883865
611	Enoyl-CoA delta isomerase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Eci2 PE=1 SV=1	Eci2	Q5XIC0	1.87038339	3.223119736	15.8394804	17.5450668	14.0563231	17.8045864	19.1051922	20.4586105	18.9735298	19.6006031
612	Epidermal growth factor receptor pathway substrate 15 OS=Rattus norvegicus OX=10116 GN=Eps15 PE=1 SV=2	Eps15	E9PSY8	2.39062502	3.080630541	14.6563511	12.8331413	15.0693684	15.5038157	18.0193424	17.7236347	18.0704098	16.5718117
613	Epidermal growth factor receptor pathway substrate 15-like 1 OS=Rattus norvegicus OX=10116 GN=Eps15l1 PE=1 SV=3	Eps15l1	D3ZJR1	3.83070591	5.733082056	14.843977	13.9204016	16.118351	16.707159	21.8267174	20.8359833	20.6868782	21.1726379
614	Epsilon 1 globin OS=Rattus norvegicus OX=10116 GN=Hbe1 PE=1 SV=1	Hbe1	O88752	3.21529385	-2.948206902	21.0316467	21.2956676	21.4445019	20.9182186	18.3246365	17.2091637	18.0479164	19.3154907
615	Epsilon 3 globin OS=Rattus norvegicus OX=10116 GN=Hbg1 PE=2 SV=1	Hbg1	O88754	2.33677869	-1.204014778	21.5071831	20.328907	20.8945904	21.3760376	19.8812733	19.846756	19.9170742	19.6455555
616	ER lumen protein-retaining receptor 2 OS=Rattus norvegicus OX=10116 GN=Kdelr2 PE=2 SV=1	Kdelr2	Q5U305	0.49240198	0.826057434	17.1232071	19.3736134	18.8435192	18.154707	18.9012241	20.8087597	19.1179314	17.9713612
617	ER membrane protein complex subunit 1 OS=Rattus norvegicus OX=10116 GN=Emc1 PE=1 SV=1	Emc1	D4A994	3.42706404	-1.668380737	19.7271461	19.2312622	19.0584373	19.8588943	18.0563526	17.9962349	17.5442085	17.6054211
618	ERCC excision repair 6-like, spindle assembly checkpoint helicase OS=Rattus norvegicus OX=10116 GN=Ercc6l PE=1 SV=1	Ercc6l	D4A0G9	0.14225475	0.56492734	20.4238529	21.0048313	19.5672798	14.4398546	19.224762	19.7588654	19.2706718	19.4412289
619	Erlin-2 OS=Rattus norvegicus OX=10116 GN=Erlin2 PE=1 SV=1	Erlin2	B5DEH2	3.2823992	3.336783648	15.5356445	15.917717	15.547286	13.9220009	18.000906	18.8462143	18.4583931	18.9642696
620	ERO1-like protein alpha OS=Rattus norvegicus OX=10116 GN=Ero1a PE=1 SV=1	Ero1a	Q8R4A1	4.70065585	2.326336384	17.413662	17.2975559	17.5258713	16.7727528	19.6879654	19.684351	19.2856789	19.6571922
621	Erythrocyte membrane protein band 4.1 OS=Rattus norvegicus OX=10116 GN=Epb41 PE=1 SV=1	Epb41	A0A0G2K161	2.93584662	-3.33351469	20.6422215	20.8108768	19.5174294	19.4938908	17.577322	17.5440655	15.851532	16.1574402
622	Erythrocyte membrane protein band 4.1-like 2 OS=Rattus norvegicus OX=10116 GN=Epb41l2 PE=1 SV=3	Epb41l2	D3ZDT1	4.64873752	-2.441403389	22.0923786	21.9954891	22.7305679	22.5962181	19.9627895	20.167635	19.7258472	19.7927685
623	Erythrocyte membrane protein band 4.2 OS=Rattus norvegicus OX=10116 GN=Epb42 PE=1 SV=1	Epb42	B5DF57	5.85305604	-2.706419468	22.3351936	22.1293945	21.9481163	22.423378	19.2351933	19.498188	19.6532593	19.623764
624	Ethanolamine-phosphate cytidylyltransferase OS=Rattus norvegicus OX=10116 GN=Pcyt2 PE=1 SV=1	Pcyt2	O88637	0.88446333	1.910730124	16.9471016	14.5163956	17.4999943	15.6291618	19.3416862	15.5199556	18.6245327	18.7493992
625	Eukaryotic peptide chain release factor GTP-binding subunit ERF3B-like OS=Rattus norvegicus OX=10116 GN=Gspt1 PE=1 S	Gspt1	Q6AYD5	2.69750117	6.106497526	19.666523	13.9493933	16.9789925	16.7296257	23.0497589	22.6129475	23.0968914	22.9909267
626	Eukaryotic peptide chain release factor subunit 1 OS=Rattus norvegicus OX=10116 GN=Etf1 PE=2 SV=3	Etf1	Q5U2Q7	5.70998688	3.674010754	17.8577118	17.8414459	18.3578892	18.4765167	22.0381279	21.4717121	21.9064846	21.813282
627	Eukaryotic translation elongation factor 1 beta 2 OS=Rattus norvegicus OX=10116 GN=Eef1b2 PE=1 SV=1	Eef1b2	B5DEN5	4.19516016	3.052337646	17.4474335	17.5601788	18.1035824	18.12043	21.5325108	20.2984428	20.7477436	20.862278
628	Eukaryotic translation elongation factor 1 epsilon 1 OS=Rattus norvegicus OX=10116 GN=Eef1e1 PE=1 SV=1	Eef1e1	B2RYN3	2.56991233	0.770503998	20.4075451	20.7402859	20.8857746	20.3190041	21.4651718	21.1421585	21.4997635	21.3275318
629	Eukaryotic translation initiation factor 1 OS=Rattus norvegicus OX=10116 GN=Eif1 PE=1 SV=1	Eif1	B0K008	6.27389762	3.281918049	17.1161041	16.8992329	17.4102116	17.0638428	20.4589939	20.1072693	20.4846783	20.5661221
630	Eukaryotic translation initiation factor 2 subunit 1 OS=Rattus norvegicus OX=10116 GN=Eif2s1 PE=1 SV=2	Eif2s1	P68101	4.57224214	4.996449947	18.5222378	18.2873993	17.2366924	16.7071152	22.8995571	22.6688709	22.6179333	22.5528831
631	Eukaryotic translation initiation factor 2 subunit 3, X-linked OS=Rattus norvegicus OX=10116 GN=Eif2s3 PE=1 SV=2	Eif2s3	P81795	3.87557028	3.903048992	17.0301991	18.887188	18.1214275	18.9258385	22.2305126	22.1751614	22.2747383	21.8964367
632	Eukaryotic translation initiation factor 2 subunit beta OS=Rattus norvegicus OX=10116 GN=Eif2s2 PE=1 SV=1	Eif2s2	Q6P685	6.47285499	3.981330872	18.1449089	18.1800213	17.5212936	18.0116711	22.1183357	21.9410057	21.9185295	21.8053474
633	Eukaryotic translation initiation factor 3 subunit B OS=Rattus norvegicus OX=10116 GN=Eif3b PE=1 SV=1	Eif3b	Q4G061	1.58517989	1.800752163	19.8575954	17.7200623	17.6119919	17.9485397	20.7355442	19.2485771	20.1187763	20.2383003
634	Eukaryotic translation initiation factor 3 subunit C OS=Rattus norvegicus OX=10116 GN=Eif3c PE=1 SV=1	Eif3c	B5DFC8	2.47855052	2.684801102	17.8363552	17.0691166	17.3889008	19.5657215	20.8815384	20.5452976	20.8390293	20.3334332
635	Eukaryotic translation initiation factor 3 subunit F OS=Rattus norvegicus OX=10116 GN=Eif3f PE=1 SV=3	Eif3f	D4AC36	3.48749442	4.899335861	14.8589897	16.5317974	15.7501621	17.9387283	21.5056973	20.8690395	21.2478428	21.0544415
636	Eukaryotic translation initiation factor 3 subunit G OS=Rattus norvegicus OX=10116 GN=Eif3g PE=1 SV=1	Eif3g	Q5RK09	3.03246018	3.417411804	17.8330898	18.6756916	16.0499573	17.6197186	21.3497105	20.7340813	20.9792023	20.7851105
637	Eukaryotic translation initiation factor 3 subunit M OS=Rattus norvegicus OX=10116 GN=Eif3m PE=1 SV=1	Eif3m	D3ZAZ0	3.11981283	2.934243917	17.1138058	15.8339281	16.9322643	17.173336	20.4283657	19.465723	20.0502052	18.8460159
638	Eukaryotic translation initiation factor 4 gamma, 1 OS=Rattus norvegicus OX=10116 GN=Eif4g1 PE=1 SV=1	Eif4g1	D3ZU13	6.41913988	4.47628212	19.9140797	20.2958641	20.0442924	19.4904709	24.5871525	24.4545975	24.4384289	24.1696568
639	Eukaryotic translation initiation factor 4 gamma, 3 OS=Rattus norvegicus OX=10116 GN=Eif4g3 PE=1 SV=2	Eif4g3	D4A554	2.25769528	3.65590477	15.2928772	19.2212467	17.1162128	17.9895191	20.7058125	21.7061501	21.2408714	20.590641
640	Eukaryotic translation initiation factor 4, gamma 2 OS=Rattus norvegicus OX=10116 GN=Eif4g2 PE=1 SV=2	Eif4g2	F1LN59	4.46810091	5.013940573	17.2534695	16.6140842	17.7130547	15.7750826	22.3894234	21.6853046	21.7083035	21.6284218
641	Eukaryotic translation initiation factor 4A1 OS=Rattus norvegicus OX=10116 GN=Eif4a1 PE=1 SV=1	Eif4a1	Q6P3V8	5.13413958	3.837965012	20.5380135	21.01828	20.7910347	20.1219044	24.733675	23.9244671	24.7072964	24.4556541
642	Eukaryotic translation initiation factor 4B OS=Rattus norvegicus OX=10116 GN=Eif4b PE=1 SV=1	Eif4b	Q5RKG9	1.47168767	2.47294569	18.3062687	18.8934841	18.9381504	15.30266	21.0468483	19.9423523	19.9551849	20.3879604
643	Eukaryotic translation initiation factor 4E OS=Rattus norvegicus OX=10116 GN=Eif4e PE=1 SV=1	Eif4e	A0A1W2Q627	0.61150108	1.513930798	17.8575211	21.3810368	18.4306183	16.28302	20.1387272	21.3072109	19.5458813	19.0160999
644	Eukaryotic translation initiation factor 4H OS=Rattus norvegicus OX=10116 GN=Eif4h PE=1 SV=1	Eif4h	Q5XI72	2.29470885	3.98122263	18.6090012	17.2947979	15.3248386	18.7022495	22.9054317	20.8070393	21.1229153	21.0203915
645	Eukaryotic translation initiation factor 5A-1 OS=Rattus norvegicus OX=10116 GN=Eif5a PE=1 SV=3	Eif5a	Q3T1J1	5.34047519	4.172179222	17.9876518	18.9335079	18.9696808	18.8244724	23.0982933	22.7062073	22.5410004	23.0585289
646	Exocyst complex component 1 OS=Rattus norvegicus OX=10116 GN=Exoc1 PE=1 SV=1	Exoc1	A0A0G2JYT4	1.6508438	3.083898544	17.731842	18.4811707	17.6682796	14.107914	19.4253674	20.5129986	20.3337402	20.0526943
647	Exopolyphosphatase PRUNE1 OS=Rattus norvegicus OX=10116 GN=Prune1 PE=1 SV=1	Prune1	Q6AYG3	3.21971602	2.916487694	16.3583355	16.2143898	17.7818661	17.7658539	19.9812107	19.6578827	20.2056904	19.9416122
648	Exportin 7 OS=Rattus norvegicus OX=10116 GN=Xpo7 PE=1 SV=1	Xpo7	A0A0G2JWA3	0.48395047	-0.678451538	19.4515839	18.946476	19.4498882	19.6488285	16.9162464	19.6771145	19.3757896	18.8138199
649	Exportin-1 OS=Rattus norvegicus OX=10116 GN=Xpo1 PE=1 SV=1	Xpo1	Q80U96	4.77902044	3.90075779	18.4315052	19.267313	18.9521236	17.85783	22.496603	22.4231339	22.6877689	22.5042973
650	Extracellular superoxide dismutase [Cu-Zn] OS=Rattus norvegicus OX=10116 GN=Sod3 PE=1 SV=2	Sod3	Q08420	2.25270554	-2.144530773	18.5478745	18.8790169	19.9928455	19.8449345	17.4616241	16.6183777	16.541111	18.0654354
651	Ezrin OS=Rattus norvegicus OX=10116 GN=Ezr PE=1 SV=3	Ezr	P31977	3.06274351	2.63651371	20.1879044	20.0655403	21.0743542	19.099659	23.0496235	22.6511097	22.3722153	22.9005642
652	F-actin-capping protein subunit alpha-1 OS=Rattus norvegicus OX=10116 GN=Capza1 PE=1 SV=1	Capza1	B2GUZ5	4.58021804	3.169685364	18.700676	19.162714	19.0303288	19.5281296	22.9100266	21.9755764	22.0208282	22.1941586
653	F-actin-capping protein subunit alpha-2 OS=Rattus norvegicus OX=10116 GN=Capza2 PE=1 SV=1	Capza2	Q3T1K5	3.04798138	4.788499355	14.8508778	17.7882824	17.4995556	18.1312428	22.5652294	21.551302	21.6299706	21.677454
654	F-actin-capping protein subunit beta OS=Rattus norvegicus OX=10116 GN=Capzb PE=1 SV=1	Capzb	Q5XI32	2.87500719	2.958444118	19.3491669	19.3193474	20.0082912	21.5069485	23.3393517	22.8467922	22.9468594	22.8845272
655	Fam49b protein OS=Rattus norvegicus OX=10116 GN=Fam49b PE=1 SV=1	Cyrib	B2GUZ9	3.91371928	3.065855503	17.4649372	18.4101887	16.8766556	17.9085369	20.9281616	20.3651676	20.8617134	20.7686977
656	Family with sequence similarity 114, member A1 OS=Rattus norvegicus OX=10116 GN=Fam114a1 PE=1 SV=2	Fam114a1	D4A777	0.25132891	0.169904709	22.3919449	21.8141727	21.7805233	21.4440804	22.5974045	21.7936077	21.9409676	21.7783604
657	Family with sequence similarity 120A OS=Rattus norvegicus OX=10116 GN=Fam120a PE=1 SV=2	Fam120a	D4AB03	4.16389318	2.802659988	18.5072021	19.3610134	18.9756279	19.3857937	21.6449833	22.4331207	21.8423233	21.5198498
658	Family with sequence similarity 49, member A OS=Rattus norvegicus OX=10116 GN=Fam49a PE=1 SV=1	Cyria	B0BN65	3.93755936	4.004545212	18.6316357	18.5056057	17.1752357	17.5467796	21.2344627	21.9408112	22.5601387	22.142025
659	Far upstream element-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Fubp1 PE=1 SV=1	Fubp1	A0A140TAJ3	4.15740258	2.701839447	18.5543613	19.0549393	18.8360844	18.8788471	22.3026886	21.2490807	21.3740864	21.2057343
660	Far upstream element-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Khsrp PE=1 SV=1	Khsrp	A0A0G2K2B3	4.28270168	6.359889984	17.3749714	17.5256271	17.4743538	15.0223026	23.6086292	23.1015015	23.0998154	23.0268688
661	FAS-associated death domain protein OS=Rattus norvegicus OX=10116 GN=Fadd PE=1 SV=1	Fadd	Q8R2E7	3.77830299	4.347248316	15.0875607	14.7684155	15.7170448	13.8739767	19.8518867	18.187067	19.4252682	19.371769
662	FAS-associated factor 1 OS=Rattus norvegicus OX=10116 GN=Faf1 PE=1 SV=1	Faf1	Q924K2	3.25164534	2.570471287	17.0361195	17.575531	17.6290798	16.1563644	20.0312672	19.1671486	19.7629967	19.7175674
663	Fascin OS=Rattus norvegicus OX=10116 GN=Fscn1 PE=1 SV=2	Fscn1	P85845	2.28679224	3.262238741	14.2282801	16.5217361	17.4058895	14.6836491	18.6587601	18.9774876	19.2253742	19.0268679
664	Fatty acid synthase OS=Rattus norvegicus OX=10116 GN=Fasn PE=1 SV=3	Fasn	P12785	4.12004106	3.439361572	19.7499752	19.8061848	19.9326439	19.6204605	22.2021313	23.258461	23.7587261	23.6473923
665	Fatty acid-binding protein 5 OS=Rattus norvegicus OX=10116 GN=Fabp5 PE=1 SV=3	Fabp5	P55053	1.11553478	0.508089542	22.1740532	22.4460659	23.0942078	22.3513584	23.2974319	22.727644	22.9075451	23.1654224
666	Fatty acid-binding protein, adipocyte OS=Rattus norvegicus OX=10116 GN=Fabp4 PE=1 SV=1	Fabp4	A0A0G2K586	1.5002974	1.254421711	19.7858906	20.5546398	21.7827816	20.6277809	22.0159931	21.9380569	22.3462067	21.468523
667	Fatty acid-binding protein, heart OS=Rattus norvegicus OX=10116 GN=Fabp3 PE=1 SV=2	Fabp3	P07483	5.68615362	8.452045918	14.6278391	16.3519897	16.3531952	14.8407488	24.2234325	24.0040169	23.9086304	23.8458767
668	F-BAR domain only protein 2 OS=Rattus norvegicus OX=10116 GN=Fcho2 PE=1 SV=1	Fcho2	D3ZYR1	2.50190705	1.270509958	15.0263643	15.373682	15.4581537	15.6615419	16.2527065	16.8982944	17.1814842	16.2692966
669	F-box only protein 30 OS=Rattus norvegicus OX=10116 GN=Fbxo30 PE=1 SV=1	Fbxo30	Q5XI67	3.83338498	2.578626633	17.2543545	16.5705757	16.7952995	16.0356731	19.5773888	18.7759151	19.3304024	19.2867031

670	Fc fragment of IgG-binding protein OS=Rattus norvegicus OX=10116 GN=Fcgbp PE=1 SV=3	Fcgbp	D3ZJF8	0.3882675	-0.410682678	24.1002464	25.0036068	23.450592	22.9208088	23.4402428	23.7702904	23.2274418	23.3945484
671	Fermitin family member 2 OS=Rattus norvegicus OX=10116 GN=Fermt2 PE=1 SV=1	Fermt2	A0A0G2JWC7	2.28173878	3.675489902	20.5517864	21.4838696	19.4959087	17.5681267	23.9603291	23.2149715	23.4550018	23.1713486
672	Fermitin family member 3 OS=Rattus norvegicus OX=10116 GN=Fermt3 PE=1 SV=1	Fermt3	B2GVB9	2.39249405	-3.662310362	20.3735085	19.6977367	20.5898438	20.7383099	16.7465649	16.6166668	18.5989704	14.7879553
673	Ferritin heavy chain OS=Rattus norvegicus OX=10116 GN=Fth1 PE=1 SV=3	Fth1	P19132	2.07066047	0.749409199	20.0369587	19.5443134	19.8402328	20.312254	20.3887157	20.7250443	20.7057629	20.9118729
674	Fetub protein OS=Rattus norvegicus OX=10116 GN=Fetub PE=1 SV=1	Fetub	Q6IRS6	5.38075539	-3.474511147	25.0309849	25.4529514	25.7298107	25.1956635	22.1241837	21.7941952	21.4625359	22.1304512
675	Fibrillin 1 OS=Rattus norvegicus OX=10116 GN=Fbn1 PE=1 SV=1	Fbn1	G3V9M6	3.06177566	2.705379963	18.741415	17.301506	18.7929688	19.2280045	20.9987831	21.5794792	21.0006866	21.3064651
676	Fibrillin 2 OS=Rattus norvegicus OX=10116 GN=Fbn2 PE=4 SV=3	Fbn2	F1M5Q4	2.7064084	-3.147100449	20.1718521	19.6569767	19.9118404	20.440794	17.5498886	16.1523571	15.7152882	18.1755276
677	Fibrinogen beta chain OS=Rattus norvegicus OX=10116 GN=Fgb PE=1 SV=4	Fgb	P14480	2.92300415	-1.341965675	29.180521	28.9243965	29.0046253	29.304121	28.0246773	27.7964287	27.1388378	28.0858574
678	Fibrinogen gamma chain OS=Rattus norvegicus OX=10116 GN=Fgg PE=1 SV=3	Fgg	P02680	2.94290764	-1.335134506	28.7807751	28.4815159	28.4564133	28.7026577	27.5003281	27.2335758	26.6821499	27.6647701
679	Fibrinogen-like 2 OS=Rattus norvegicus OX=10116 GN=Fgl2 PE=1 SV=1	Fgl2	G3V7P2	0.73597383	-0.792994976	21.2398071	20.3063087	21.1354923	20.1900005	19.9078922	18.6541557	20.6120129	20.525568
680	Fibronectin OS=Rattus norvegicus OX=10116 GN=Fn1 PE=1 SV=2	Fn1	A0A096P6L8	3.62231569	-2.410810471	19.9360638	19.413269	20.2819042	19.6094627	17.5203209	17.8680611	16.7108631	17.4982128
681	Fibronectin OS=Rattus norvegicus OX=10116 GN=Fn1 PE=1 SV=3	Fn1	F1LST1	4.10607148	-2.976550102	28.679451	28.4130611	28.91675	29.125843	25.8699722	25.882	25.0750389	26.4018936
682	Fibulin 2 OS=Rattus norvegicus OX=10116 GN=Fbln2 PE=1 SV=1	Fbln2	G3V6X1	2.75294211	3.251508236	16.3586712	16.709013	18.0747604	15.1258793	19.6718369	19.9003124	19.7805786	19.921629
683	Fibulin-1 OS=Rattus norvegicus OX=10116 GN=Fbln1 PE=1 SV=1	Fbln1	B1WC21	3.86145801	2.474902153	18.9925137	18.8867474	19.6831131	19.6564693	22.0274487	22.1981907	21.4591694	21.4336433
684	Fibulin-1 OS=Rattus norvegicus OX=10116 GN=Fbln1 PE=1 SV=1	Fbln1	D3ZQ25	0.72636154	0.348716736	21.6098118	20.923048	21.9922771	21.2595406	21.6796608	21.7594318	21.8953438	21.845108
685	Fibulin-5 OS=Rattus norvegicus OX=10116 GN=Fbln5 PE=2 SV=1	Fbln5	Q9WVH8	3.06857855	2.573985577	17.5471687	17.031498	17.8374825	16.2113132	19.5544548	20.334444	19.2975864	19.7369194
686	Ficolin (Collagen/fibrinogen domain containing) 1 OS=Rattus norvegicus OX=10116 GN=Fcna PE=1 SV=1	Fcna	Q5M8B4	2.5936962	-2.385068417	20.6378441	20.8686733	20.5436459	19.4682617	16.9269619	18.2987347	18.5837955	18.1686592
687	Filamin A OS=Rattus norvegicus OX=10116 GN=Flna PE=1 SV=1	Flna	C0JPT7	2.75508186	1.498627663	22.6911469	23.1247311	22.8961315	22.0575676	23.8102665	24.5986538	24.2041187	24.1510487
688	Filamin-A-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Filip1 PE=1 SV=2	Filip1	F1LM79	2.48639466	1.417377949	18.0949173	18.7672997	18.2707119	18.8138142	19.4552956	20.5878887	19.7977238	19.7753468
689	Filamin-C OS=Rattus norvegicus OX=10116 GN=Flnc PE=1 SV=1	Flnc	D3ZHA0	5.97547723	3.775335789	22.585207	22.7627335	22.9997406	23.3199539	26.5880833	26.8787479	26.8530922	26.4490547
690	FLII, actin-remodeling protein OS=Rattus norvegicus OX=10116 GN=Flii PE=1 SV=1	Flii	Q5RKI5	3.02785018	4.979403019	16.7058773	15.0741978	14.1176262	17.6666317	20.2343006	21.1502914	21.0773067	21.0200462
691	Focal adhesion kinase 1 OS=Rattus norvegicus OX=10116 GN=Ptk2 PE=1 SV=1	Ptk2	A0A0G2KAT5	2.44473173	2.829419136	14.9638739	15.0493803	15.545249	13.8504877	18.473875	17.8870392	16.2378769	18.1278763
692	Four and a half LIM domains 1 OS=Rattus norvegicus OX=10116 GN=Fhl1 PE=1 SV=1	Fhl1	Q6P792	3.42145274	2.969621181	20.1477737	20.2524166	20.826849	19.7062893	22.4786873	23.7283268	23.8569374	22.7478619
693	Fragile X mental retardation syndrome-related protein 1 OS=Rattus norvegicus OX=10116 GN=Fxr1 PE=1 SV=1	Fxr1	Q5XI81	4.40379261	5.70779109	14.2174492	16.2435226	16.0526066	15.9411917	21.1118546	22.0799408	21.0847073	21.0094318
694	Fructose-bisphosphate aldolase A OS=Rattus norvegicus OX=10116 GN=Aldoa PE=1 SV=2	Aldoa	P05065	5.22232752	2.72089529	22.7817345	23.467392	23.4398384	22.9670467	25.9830933	25.8840733	25.974762	25.6976643
695	FRY microtubule-binding protein OS=Rattus norvegicus OX=10116 GN=Fry PE=1 SV=3	Fry	E9PTY6	1.69824625	1.139375687	21.3701706	21.4600449	20.9473267	20.6177254	21.4527531	22.8283958	22.5963879	22.0752335
696	Fumarate hydratase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Fh PE=1 SV=1	Fh	P14408	2.91838551	6.138948917	17.2618504	17.4933968	13.9345837	14.6711788	20.4402161	22.1216793	22.1424599	23.21245
697	FXYD domain-containing ion transport regulator OS=Rattus norvegicus OX=10116 GN=Fxyd1 PE=1 SV=1	Fxyd1	A0A0H2UHS8	4.57883488	4.872947693	15.3052273	17.1151085	15.7834959	15.7924757	20.715847	21.3819027	20.6560688	20.7342796
698	FYVE and coiled-coil domain containing 1 (Predicted) OS=Rattus norvegicus OX=10116 GN=Fyco1 PE=1 SV=1	Fyco1	D3Z9D2	0.57376095	1.023883581	15.0256767	16.5425568	14.0010624	17.0878887	15.3449469	17.2262497	17.1495171	17.0320053
699	G protein beta subunit-like, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Mlst8 PE=1 SV=1	Mlst8	G3V7F1	2.26189475	2.150799513	13.4276819	14.7863827	14.6457987	15.5987062	16.3344135	16.5987301	17.4487228	16.6799011
700	G protein-coupled receptor 21 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Rabgap1 PE=1 SV=1	Rabgap1	D3ZX42	1.94762995	3.470750809	16.8537617	17.0164852	18.3779297	13.8762875	20.3920307	19.9907074	20.0274124	19.5973167
701	G protein-coupled receptor kinase interacting ArfGAP 2 OS=Rattus norvegicus OX=10116 GN=Git2 PE=1 SV=1	Git2	Q66H91	3.02016444	2.518330097	18.9168205	19.7526169	20.1134434	18.3811741	21.4398365	22.0836811	21.9835682	21.7302895
702	G3BP stress granule assembly factor 1 OS=Rattus norvegicus OX=10116 GN=G3bp1 PE=1 SV=1	G3bp1	D3ZYS7	4.33612201	5.131647348	17.7148933	16.6164894	15.898984	17.3659134	21.7545605	22.8634548	21.8742256	21.6306286
703	Galactokinase 1 OS=Rattus norvegicus OX=10116 GN=Galk1 PE=1 SV=1	Galk1	Q5RKH2	1.99292542	3.997947931	19.4248562	15.2956324	19.6763363	19.5726395	22.1443233	22.2126617	22.8718967	22.7323742
704	Galectin-1 OS=Rattus norvegicus OX=10116 GN=Lgals1 PE=1 SV=2	Lgals1	P11762	4.73260877	2.389514923	20.6851425	21.1017857	21.0689449	21.472744	23.1949558	23.562006	23.719759	23.409956
705	Gamma-enolase OS=Rattus norvegicus OX=10116 GN=Eno2 PE=1 SV=2	Eno2	P07323	2.07505594	3.043707371	14.8936806	16.8176212	15.2230968	15.6401882	16.7564392	19.1683197	19.8323917	18.9922657
706	Gamma-tubulin complex component OS=Rattus norvegicus OX=10116 GN=Tubgcp2 PE=1 SV=1	Tubgcp2	B2RYP8	1.79683651	1.881886721	16.3006248	15.3361931	15.6845617	16.9049416	17.651123	18.7368774	18.5671654	16.7987022
707	GCN1 eIF2 alpha kinase activator-like 1 OS=Rattus norvegicus OX=10116 GN=Gcn1 PE=1 SV=3	Gcn1	F1LRI5	7.64570401	4.266504765	18.5031376	18.8388081	18.3134918	18.6484241	22.811882	22.8562107	22.8859463	22.8158417
708	Gelsolin OS=Rattus norvegicus OX=10116 GN=Gsn PE=1 SV=1	Gsn	Q68FP1	0.61933628	0.359502792	25.1015224	24.2163658	25.2171745	25.2519398	25.6690407	25.1947174	25.2635822	25.0976734
709	General vesicular transport factor p115 OS=Rattus norvegicus OX=10116 GN=Uso1 PE=1 SV=1	Uso1	P41542	2.75757286	4.406356573	16.5179539	17.45611	15.6058245	13.7110863	20.2413387	19.7215195	20.7088375	20.2447052
710	Gephyrin OS=Rattus norvegicus OX=10116 GN=Gphn PE=1 SV=3	Gphn	Q03555	2.22812268	1.923843861	18.1021519	18.4209175	18.4154358	16.7552605	19.2788696	20.3960629	20.0155506	19.698658
711	Geranylgeranyl transferase type-2 subunit alpha OS=Rattus norvegicus OX=10116 GN=Rabggta PE=1 SV=1	Rabggta	Q08602	1.7829127	2.285051346	20.2906418	19.5811787	19.5987663	19.4617443	20.0344105	22.4395981	22.8627872	22.7357407
712	GLI pathogenesis-related 2 OS=Rattus norvegicus OX=10116 GN=Glipr2 PE=1 SV=3	Glipr2	F1M5V2	4.70122684	2.344279289	19.3956108	20.1525211	19.7650299	19.5177708	21.8981228	22.2540684	21.8629246	22.192934
713	Globin a1 OS=Rattus norvegicus OX=10116 GN=LOC103694855 PE=1 SV=1	Hbb-b1	Q62669	5.48775462	-2.728354931	25.7117844	25.4655609	25.9393177	25.9364185	23.308239	22.7260475	23.117466	22.9879093
714	Globin a4 OS=Rattus norvegicus OX=10116 GN=Hbb PE=1 SV=1	Hbb	A0A0G2JSW3	1.34070247	-3.566362381	24.5058384	24.0538235	24.3587532	21.1964626	21.2107162	21.588501	20.5805454	16.4696655
715	Globin c2 OS=Rattus norvegicus OX=10116 GN=Hba-a2 PE=1 SV=1	Hba-a2	A0A0G2JSV6	6.79559784	-2.361998558	28.7458649	28.4252739	28.6163368	28.5708389	26.3692989	26.2419968	26.0997963	26.1992283
716	Globin e1 OS=Rattus norvegicus OX=10116 GN=Hbz PE=3 SV=1	Hbz	G3V8R3	3.03325877	1.388727427	15.0619202	16.0277977	15.7259321	16.02808	17.0305328	17.0696907	17.1471996	17.1512165
717	Glucose-6-phosphate isomerase OS=Rattus norvegicus OX=10116 GN=Gpi PE=1 SV=1	Gpi	Q6P6V0	4.71684428	2.851229668	18.4776955	19.1221542	19.2825089	18.4472389	21.4923611	21.8970108	21.7757969	21.5693474
718	Glutamate dehydrogenase 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Glud1 PE=1 SV=2	Glud1	P10860	1.29819396	-1.75138998	18.1804104	18.0187454	18.7639675	18.79702	15.3540735	18.2260456	17.4616985	15.7127657
719	Glutamate--cysteine ligase regulatory subunit OS=Rattus norvegicus OX=10116 GN=Gclm PE=1 SV=1	Gclm	P48508	2.31449183	3.163116455	18.2463799	18.1968632	16.4128246	19.6205978	22.1776314	21.235445	20.9166412	20.7994137
720	Glutamine fructose-6-phosphate transaminase 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Gfpt1 PE=1 SV=1	Gfpt1	A0A0G2KB56	2.60103148	2.981742382	18.8394699	16.5755615	19.0731125	18.8984547	21.531332	21.101841	21.3308334	21.3495617
721	Glutamine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Qars PE=1 SV=1	Qars1	Q66H61	5.25076294	4.203379631	19.3964386	19.69314	18.5328617	19.0967102	23.6913624	23.0461273	23.4311543	23.3640251
722	Glutamyl aminopeptidase OS=Rattus norvegicus OX=10116 GN=Enpep PE=1 SV=2	Enpep	P50123	3.0322066	2.338080406	18.9331665	17.9842052	17.8702927	17.3484058	20.902914	19.9524918	20.2065964	20.4263897
723	Glutamyl-prolyl-tRNA synthetase OS=Rattus norvegicus OX=10116 GN=Eprs PE=1 SV=1	Eprs	A0A0G2JZI2	6.32597316	5.157186031	20.744091	20.6073189	20.7011471	19.8596306	25.8303928	25.3949623	25.6586952	25.6568813
724	Glutaredoxin-3 OS=Rattus norvegicus OX=10116 GN=Glrx3 PE=1 SV=2	Glrx3	Q9JLZ1	4.20981993	5.26671505	17.694912	17.627203	18.6359615	16.1548843	22.4691143	22.9418507	23.1173382	22.6515179
725	Glutathione peroxidase 1 OS=Rattus norvegicus OX=10116 GN=Gpx1 PE=1 SV=4	Gpx1	P04041	1.34984032	0.48621273	19.1285725	19.1832256	19.2173023	19.8308296	19.9302616	19.859808	19.9770565	19.5376549
726	Glutathione peroxidase 3 OS=Rattus norvegicus OX=10116 GN=Gpx3 PE=2 SV=2	Gpx3	P23764	4.03164892	-5.759598732	22.9719391	22.5710716	23.2484398	24.9103374	18.3260155	17.0180416	18.2408085	17.0785275
727	Glutathione peroxidase OS=Rattus norvegicus OX=10116 GN=Gpx4 PE=1 SV=2	Gpx4	F8WFK6	1.23318831	-0.810119152	22.073307	21.9397793	22.6758881	23.0218105	22.3166828	21.3606567	21.4887218	21.3042469
728	Glutathione S-transferase Mu 5 OS=Rattus norvegicus OX=10116 GN=Gstm5 PE=1 SV=3	Gstm5	Q9ZLB2	1.38068856	1.277646542	20.5851078	20.6043072	20.1144905	19.4422531	20.6163692	20.9095783	22.2966595	22.0341377
729	Glutathione S-transferase P OS=Rattus norvegicus OX=10116 GN=Gstp1 PE=1 SV=2	Gstp1	P04906	1.57863713	1.611071587	18.449297	19.1813393	18.2978153	20.6367035	20.9059753	20.836998	20.9051476	20.3613205
730	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus OX=10116 GN=Gapdh PE=1 SV=3	Gapdh	P04797	5.83696638	3.090543747	27.5709457	27.0421181	27.4043026	27.4226551	30.2582474	30.2317791	30.6174297	30.6947403

731	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus OX=10116 PE=1 SV=1	A0A0G2K7M1_RAT	A0A0G2K7M1	0.61803661	-1.246510983	16.8372097	20.0766926	16.6343727	19.5360088	17.1273861	17.9575462	16.5424786	16.470829
732	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus OX=10116 PE=1 SV=1	M0R660_RAT	M0R660	3.99210464	4.562384129	20.0728798	19.5199852	19.8757305	21.368103	24.0443439	24.6854649	24.8370247	25.5194016
733	Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Rattus norvegicus OX=10116 GN=Gpd1l PE=1 SV=1	Gpd1l	D3ZAP9	3.98050353	5.974321842	16.0443382	15.7068596	14.8634605	15.7117996	19.756279	21.9900074	22.5158119	21.961647
734	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Rattus norvegicus OX=10116 GN=Gpd1 PE=1 SV=4	Gpd1	O35077	2.24264299	1.741509438	19.3984318	18.6500759	19.9666061	19.6628017	20.3569298	21.589838	21.6776943	21.0194912
735	Glycine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Gars PE=1 SV=1	Gars1	G3V7G8	5.6499245	5.486327171	17.9388218	18.3834095	17.5719357	18.6874065	23.9674854	23.0725918	23.6794033	23.8074017
736	Glycogen [starch] synthase, muscle OS=Rattus norvegicus OX=10116 GN=Gys1 PE=1 SV=1	Gys1	A2RRU1	5.08409407	5.56992054	17.3023415	16.3218708	17.6265488	17.2249203	22.9830551	21.9200001	22.636404	23.2159042
737	Glycogenin-1 OS=Rattus norvegicus OX=10116 GN=Gyg1 PE=2 SV=4	Gyg1	O08730	4.34462237	9.236914873	17.9577656	15.5303068	15.6219473	14.1684866	25.5904503	23.8934441	25.1135502	25.6287212
738	Glycophorin-C OS=Rattus norvegicus OX=10116 GN=Gypc PE=1 SV=1	Gypc	Q6XFR6	0.36136525	-0.699561119	18.6411839	18.2612591	17.7608585	18.5526352	17.9534168	17.6059551	19.3971462	15.461174
739	Glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Gpld1 PE=1 S	Gpld1	G3V8B1	4.50403685	-2.720227718	24.3105488	23.5568008	23.2860661	23.3629036	20.7774029	20.8035545	20.9952583	21.0591927
740	GMP reductase OS=Rattus norvegicus OX=10116 GN=Gmpr PE=3 SV=1	Gmpr	F1LRV6	3.29614892	2.344604492	16.8272343	18.3772736	18.026125	17.6098633	20.1939468	20.0067749	19.8126926	20.2054996
741	GMP synthase [glutamine-hydrolyzing] OS=Rattus norvegicus OX=10116 GN=Gmps PE=1 SV=1	Gmps	Q4V7C6	3.5471644	4.875346899	17.3921394	17.857975	18.24786	15.5485544	21.8111019	21.6861591	22.2648697	22.7857857
742	Golgi apparatus protein 1 OS=Rattus norvegicus OX=10116 GN=Glg1 PE=1 SV=1	Glg1	G3V8G5	4.11013326	4.907639027	15.4254761	17.6727047	16.7704144	15.9203358	20.9505768	21.6854362	21.387495	21.3959789
743	Golgi brefeldin A-resistant guanine nucleotide exchange factor 1 OS=Rattus norvegicus OX=10116 GN=Gbf1 PE=1 SV=2	Gbf1	F1M8X9	2.82387335	2.203836441	19.2214508	19.1319313	18.9490643	17.6298046	20.5016193	21.1401405	21.0633011	21.0425358
744	Golgi reassembly-stacking protein 2 OS=Rattus norvegicus OX=10116 GN=Gorasp2 PE=1 SV=1	Gorasp2	Q68G33	2.1871492	4.759460926	17.1294155	20.7255917	17.7387447	15.0933247	22.4860878	22.232542	22.4849644	22.5213261
745	Golgi to ER traffic protein 4 OS=Rattus norvegicus OX=10116 GN=Get4 PE=1 SV=2	Get4	F1LXF5	2.29622138	4.043132067	16.662056	18.0083961	18.3697834	14.2846003	21.2551804	20.6263103	21.0247498	20.5911236
746	Golgi-associated, gamma adaptin ear-containing, ARF-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Gga1 PE=1 SV	Gga1	Q5FVF3	3.37051632	5.421607018	16.4222679	15.6657953	13.5812864	17.130825	21.3620758	21.2703114	20.922842	20.9313736
747	Group specific component OS=Rattus norvegicus OX=10116 GN=Gc PE=1 SV=1	Gc	Q68FY4	6.94679366	-3.920918465	25.2027969	24.9436836	25.5012703	25.2872639	21.4548931	21.3256283	21.1158543	21.3549652
748	Growth factor receptor-bound protein 10 OS=Rattus norvegicus OX=10116 GN=Grb10 PE=4 SV=1	Grb10	A0A0G2JYJ1	4.87583715	4.328381062	15.7901802	16.6411552	17.0380611	16.1530914	20.8194771	21.1997814	20.652689	20.2640648
749	GTPase KRas OS=Rattus norvegicus OX=10116 GN=Kras PE=1 SV=3	Kras	P08644	1.03997609	1.43872571	15.7422533	18.0296154	16.4740982	17.6285877	18.8313293	19.1739559	16.9860287	18.6381435
750	GTPase-activating protein and VPS9 domains 1 OS=Rattus norvegicus OX=10116 GN=Gapvd1 PE=1 SV=3	Gapvd1	D4A022	4.17545254	2.0406003	17.7689533	17.41646	18.0342312	17.699379	20.0209274	19.6348476	19.3634186	20.0622311
751	GTP-binding nuclear protein Ran OS=Rattus norvegicus OX=10116 GN=Ran PE=1 SV=3	Ran	P62828	3.79454027	1.99313879	21.2188892	20.591465	21.4180622	21.2865219	23.4090118	22.7055035	23.2714729	23.1015053
752	GTP-binding protein OS=Rattus norvegicus OX=10116 GN=Rrad PE=3 SV=1	Rrad	G3V7K9	3.51881778	6.512559414	15.0268755	13.8497763	16.4036903	17.8000774	22.7502956	22.3828125	22.1276684	21.8698807
753	GTP-binding protein Rheb OS=Rattus norvegicus OX=10116 GN=Rheb PE=1 SV=1	Rheb	Q62639	5.35581926	6.095351458	15.2935352	15.1539907	15.6996841	16.6933002	22.3021488	21.636198	21.8084049	21.4751644
754	GTP-binding protein SAR1b OS=Rattus norvegicus OX=10116 GN=Sar1b PE=2 SV=1	Sar1b	Q5HZY2	3.19869321	5.12966013	15.126915	18.7145844	18.0376453	16.9365253	22.4135265	22.0423336	22.3908939	22.4875565
755	Guanine nucleotide binding protein, alpha 11 OS=Rattus norvegicus OX=10116 GN=Gna11 PE=1 SV=1	Gna11	G3V6Q6	2.40973197	1.99883604	17.8296947	16.7796078	16.6487427	18.3800812	19.8053684	19.2660294	19.2045174	19.3575554
756	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Rattus norvegicus OX=10116 GN=Gnai2 PE=1 SV=3	Gnai2	P04897	6.46139551	1.894584179	22.0991459	22.1354961	22.0999184	22.1620159	24.2404213	23.967392	23.8794689	23.9876308
757	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Rattus norvegicus OX=10116 GN=Gng5 PE=3 SV=	Gng5	P63219	4.24191634	2.344085217	19.4184799	19.7589245	20.0897789	19.1101608	22.1397228	22.071804	21.7229996	21.8191586
758	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Gnb1 PE=1 SV=4	Gnb1	P54311	5.06980744	2.304589748	21.6234798	21.888649	21.8363495	21.2201042	24.0598793	24.0161114	23.7631302	23.9478207
759	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Rattus norvegicus OX=10116 GN=Gnb2 PE=1 SV=4	Gnb2	P54313	4.17676762	1.649751663	21.0510025	20.9541855	20.7780819	20.5382576	22.1749516	22.7687569	22.4038544	22.5729713
760	Guanine nucleotide-binding protein G(k) subunit alpha OS=Rattus norvegicus OX=10116 GN=Gnai3 PE=1 SV=3	Gnai3	P08753	2.30781143	1.946504593	17.8621273	18.5112591	18.5112076	16.6086941	19.8549805	19.8550777	19.7321129	19.8371353
761	Guanine nucleotide-binding protein G(o) subunit alpha OS=Rattus norvegicus OX=10116 GN=Gnao1 PE=1 SV=2	Gnao1	P59215	5.13134066	4.877745628	16.7976284	17.7784138	16.1886845	16.6881771	21.9506931	21.7704659	21.6230755	21.6196518
762	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Rattus norvegicus OX=10116 GN=Gnas PE=1 SV=	Gnas	Q63803	3.39559462	1.249747753	18.6373405	18.7860966	19.288414	19.0082722	20.109251	19.9208069	20.2811985	20.4078579
763	Guanine nucleotide-binding protein subunit beta-4 OS=Rattus norvegicus OX=10116 GN=Gnb4 PE=2 SV=4	Gnb4	O35353	2.85503582	1.540694237	16.3477097	15.7478218	16.5972672	16.4129333	18.1141968	18.1919861	17.6418552	17.3204708
764	Guanine nucleotide-binding protein subunit gamma OS=Rattus norvegicus OX=10116 GN=Gng10 PE=1 SV=1	Gng10	Q3KRE3	2.52761687	2.251318455	18.2668171	18.9575844	18.727644	16.9216614	20.5507431	20.7348614	20.3240509	20.2693253
765	Guanine nucleotide-binding protein subunit gamma OS=Rattus norvegicus OX=10116 GN=Gng12 PE=1 SV=1	Gng12	G3V6P8	4.11084579	1.907104969	19.9138145	19.6291561	19.3748074	19.2442379	21.6499271	21.5897312	21.0511665	21.4996109
766	Guanine nucleotide-binding protein subunit gamma OS=Rattus norvegicus OX=10116 GN=Gng2 PE=1 SV=2	Gng2	M0RBJ0	4.56417894	2.056997538	15.6721163	16.3673248	16.3377323	16.2625008	18.3002663	18.2411003	17.9986877	18.32761
767	Guanylate kinase 1 OS=Rattus norvegicus OX=10116 GN=Guk1 PE=1 SV=2	Guk1	E9PTV0	0.01529483	0.017704725	16.2826805	16.1782627	16.5818062	16.8998661	15.7166319	16.0876141	17.0421429	17.1670456
768	H2-K region expressed gene 2, rat orthologue OS=Rattus norvegicus OX=10116 GN=Pfdn6 PE=1 SV=1	Pfdn6	Q6MGC4	2.28161	3.848748922	15.2565632	15.431673	15.8901272	12.886672	19.7394829	17.1206093	18.4858131	19.5141258
769	Haloacid dehalogenase-like hydrolase domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Hdhd2 PE=1 SV=1	Hdhd2	Q6QI86	1.05071071	1.487580061	16.5208721	15.6692762	15.8554735	15.7398987	18.2253685	18.6309586	15.4481688	17.431345
770	Haptoglobin OS=Rattus norvegicus OX=10116 GN=Hp PE=1 SV=3	Hp	P06866	4.15868749	-4.476942062	24.3552113	23.795845	24.8452282	25.3942776	20.8572273	20.4157047	19.6478806	19.5619812
771	HAUS augmin-like complex, subunit 7 OS=Rattus norvegicus OX=10116 GN=Haus7 PE=1 SV=1	Haus7	B0BN53	0.89484372	1.135496378	15.8581905	16.2517414	17.3592224	15.9092169	18.2545795	17.6867981	15.9034214	18.0755577
772	HBS1-like protein OS=Rattus norvegicus OX=10116 GN=Hbs1l PE=1 SV=1	Hbs1l	A0A0G2K2P6	4.17614424	4.964224815	14.5426846	16.132555	15.8568192	16.829771	20.5531483	21.0035877	21.1874027	20.4745903
773	Heat shock 27kD protein family, member 7 (Cardiovascular) OS=Rattus norvegicus OX=10116 GN=Hspb7 PE=2 SV=1	Hspb7	B5DFG4	5.08298575	5.653995991	17.8906536	16.3936253	17.8519974	17.6256332	23.5855961	22.6392021	23.0309849	23.1221104
774	Heat shock 27kDa protein 1 OS=Rattus norvegicus OX=10116 GN=Hspb1 PE=1 SV=1	Hspb1	G3V913	6.09209187	4.74984026	23.1484871	22.4421043	22.792799	22.9454269	27.7431202	27.0628376	27.7816048	27.7406158
775	Heat shock 70 kDa protein 14 OS=Rattus norvegicus OX=10116 GN=Hspa14 PE=2 SV=1	Hspa14	Q6AYB4	1.41744678	2.298930645	17.5268555	18.7994041	15.5307608	15.5282984	18.2056217	19.1565533	19.5960407	19.6228256
776	Heat shock 70 kDa protein 4 OS=Rattus norvegicus OX=10116 GN=Hspa4 PE=1 SV=1	Hspa4	F1LRV4	0.16443738	-0.073987007	21.5340176	21.3562717	22.0268097	21.3522987	21.4037628	21.3451824	21.6242065	21.6002979
777	Heat shock cognate 71 kDa protein OS=Rattus norvegicus OX=10116 GN=Hspa8 PE=1 SV=1	Hspa8	P63018	5.56128408	3.175550461	23.1811085	22.4606953	23.0618801	23.2134686	26.3300419	26.1727943	26.0206585	26.0958195
778	Heat shock protein beta-6 OS=Rattus norvegicus OX=10116 GN=Hspb6 PE=1 SV=1	Hspb6	P97541	2.53818182	4.348184586	20.4188557	20.479578	20.6107426	16.9488029	24.1502762	23.5709648	24.1023312	24.0271454
779	Heat shock protein HSP 90-alpha OS=Rattus norvegicus OX=10116 GN=Hsp90aa1 PE=1 SV=3	Hsp90aa1	P82995	6.44262665	4.482356548	20.6272507	20.7272301	20.8500423	20.7811432	25.5882816	24.7206707	25.2869396	25.3192005
780	Heat shock protein HSP 90-beta OS=Rattus norvegicus OX=10116 GN=Hsp90ab1 PE=1 SV=4	Hsp90ab1	P34058	6.31663136	4.005932331	24.2205505	24.0377293	24.1148701	23.943182	28.4387035	27.634016	28.133173	28.1341686
781	HECT domain E3 ubiquitin protein ligase 1 OS=Rattus norvegicus OX=10116 GN=Hectd1 PE=1 SV=3	Hectd1	D3ZLS5	2.25639498	1.045249462	21.3336258	21.3663101	20.7093887	20.5803604	22.3432446	21.681284	22.0171604	22.128994
782	Hemoglobin subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Hbb PE=1 SV=3	Hbb	P02091	5.60052625	-2.602909565	29.0192184	28.58951	28.9110737	28.572361	26.4323463	26.2210369	26.0465508	25.9805908
783	Hemoglobin subunit beta-2 OS=Rattus norvegicus OX=10116 PE=1 SV=2	Hbb-bs	P11517	5.22871631	-3.038994789	26.6304226	25.9918957	26.560154	26.2464428	23.4957218	23.4262791	23.4567432	22.8941917
784	Hemopexin OS=Rattus norvegicus OX=10116 GN=Hpx PE=1 SV=3	Hpx	P20059	4.04175569	-4.750597954	23.2918339	24.6554241	23.8012085	22.832077	19.0551071	19.7592926	18.2351608	18.5285912
785	Heparin cofactor 2 OS=Rattus norvegicus OX=10116 GN=Serpind1 PE=1 SV=1	Serpind1	A0A0G2K8K3	3.18517924	-1.970355034	23.4581585	22.9539242	23.3824234	23.4406853	21.5448532	20.5457001	21.4050369	21.858181
786	Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Rattus norvegicus OX=10116 GN=Hgs PE=1 SV=1	Hgs	A0A140TAH1	4.57832863	2.727894306	19.5375938	19.291853	19.3668251	18.8439579	22.5264282	21.9493942	21.7452602	21.7307243
787	Hepatoma-derived growth factor-related protein 2 OS=Rattus norvegicus OX=10116 GN=Hdgfl2 PE=1 SV=2	Hdgfl2	Q925G1	4.02095247	-2.723105431	25.6199856	25.0765686	25.6573372	26.2302647	23.44487	22.6091518	22.7915459	22.8461666
788	Hermansky-Pudlak syndrome 5 protein homolog OS=Rattus norvegicus OX=10116 GN=Saa4 PE=1 SV=1	Hps5	Q7TMC3	5.82822188	-3.074973583	23.6317234	23.5171242	23.5406017	23.1812496	20.2531071	20.0941887	20.5851936	20.6383152
789	Heterogeneous nuclear ribonucleoprotein D0 OS=Rattus norvegicus OX=10116 GN=Hnrnpd PE=1 SV=2	Hnrnpd	Q9JJ54	1.35570841	1.280644417	18.813755	19.425951	18.8354816	18.8474388	21.6708984	19.8925953	19.9868889	19.4948215
790	Heterogeneous nuclear ribonucleoprotein F OS=Rattus norvegicus OX=10116 GN=Hnrnpf PE=1 SV=3	Hnrnpf	Q794E4	3.29728002	5.729264498	18.1910076	18.1451778	14.8673773	16.0790195	23.1887302	22.1891384	22.4298763	22.3918953
791	Heterogeneous nuclear ribonucleoprotein H OS=Rattus norvegicus OX=10116 GN=Hnrnph1 PE=1 SV=1	Hnrnph1	A0A0G2JTG7	5.43133712	3.765314102	17.8549919	18.1936855	17.4962902	18.186121	22.1901493	21.6041679	21.4815044	21.5165234

792	Heterogeneous nuclear ribonucleoprotein K OS=Rattus norvegicus OX=10116 GN=Hnrnpk PE=1 SV=1	Hnrnpk	Q5D059	7.05018365	5.726299286	18.5456486	18.6330528	18.7391605	19.2979259	24.7173023	24.3010635	24.5794201	24.5231991
793	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus OX=10116 GN=Hnrnpm PE=1 SV=1	Hnrnpm	F1M3D3	4.93357947	2.500575066	22.7078133	22.2210922	22.4954414	22.0448761	25.1900787	24.8908653	24.7613907	24.6291885
794	Heterogeneous nuclear ribonucleoprotein Q OS=Rattus norvegicus OX=10116 GN=Syncrip PE=1 SV=2	Syncrip	M0R735	4.9801296	3.064375401	19.3777332	19.16996	19.0390739	19.6695309	21.9084473	22.7657795	22.3153381	22.5242348
795	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus OX=10116 GN=Hnrnpu PE=1 SV=1	Hnrnpu	Q6IMY8	1.48066575	3.002109051	18.3368645	18.4884624	18.2621212	22.6879025	22.1048527	22.6655273	22.41605	22.5973568
796	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus OX=10116 GN=Hnrnpa2b1 PE=1 SV=1	Hnrnpa2b1	A7VJC2	2.18036661	1.873064518	16.4976864	17.8229866	16.7945213	17.6128597	20.0529747	18.6826038	18.7223797	18.7623539
797	Hexokinase-1 OS=Rattus norvegicus OX=10116 GN=Hk1 PE=1 SV=4	Hk1	P05708	4.27671089	2.369251728	20.9748154	20.6188831	20.7093391	20.5566311	22.4832363	23.1038017	23.4751549	23.2744827
798	Hexokinase-2 OS=Rattus norvegicus OX=10116 GN=Hk2 PE=1 SV=1	Hk2	P27881	3.0129453	3.376776218	16.5604019	16.8087807	17.4900894	17.9441986	19.3493252	20.3557301	21.2906036	21.3149166
799	HGF activator OS=Rattus norvegicus OX=10116 GN=Hgfac PE=1 SV=1	Hgfac	Q5EBA7	2.43903358	-2.74254632	18.847271	18.4883938	20.3498917	19.7735748	17.2590084	16.2520294	17.3516655	15.6262426
800	High density lipoprotein binding protein (Vigilin) OS=Rattus norvegicus OX=10116 GN=Hdlbp PE=1 SV=1	Hdlbp	Q3KRF2	4.31677475	5.202543259	17.8512287	17.7912312	16.027338	16.1353016	22.2034187	22.2095451	22.1045341	22.0977745
801	Histidine-rich glycoprotein OS=Rattus norvegicus OX=10116 GN=Hrg PE=1 SV=1	Hrg	A0A0G2K3G0	4.08289749	-4.080293179	24.0429153	23.950573	23.9676723	22.9644337	20.4290428	19.7958546	18.7299309	19.6495934
802	Histone H2A OS=Rattus norvegicus OX=10116 GN=Hist1h2ak PE=3 SV=1	H2ac4	D3ZVK7	1.57959437	1.81546402	20.7660656	19.9355793	18.7557373	19.8718491	20.2998352	22.4080067	21.9433308	21.9399147
803	Histone H2B OS=Rattus norvegicus OX=10116 GN=Hist1h2bd PE=3 SV=2	Hist1h2bd	D3ZWM5	2.14582029	1.45241785	20.7661839	20.5883255	19.9445324	20.801136	21.1159401	22.547123	22.1119881	22.134798
804	Histone H3 OS=Rattus norvegicus OX=10116 GN=Hist2h3c2 PE=1 SV=1	LOC102549173	D3ZJ08	2.09668625	1.532615185	19.8220997	20.0563126	18.8693657	18.9891491	20.2754364	21.5088215	21.1356678	20.9474621
805	Histone H4 OS=Rattus norvegicus OX=10116 GN=Hist1h4b PE=1 SV=2	Hist1h4m	P62804	1.60091	1.126235962	20.625433	20.2948017	19.0995598	20.4914513	21.2805004	21.6265278	21.2052345	20.9039268
806	Homer protein homolog 3 OS=Rattus norvegicus OX=10116 GN=Homer3 PE=1 SV=2	Homer3	Q9Z2X5	1.42275251	-1.989412785	22.157238	20.267992	23.5721169	21.6470032	20.6948242	19.3530064	20.1409321	19.4979362
807	Hormone-sensitive lipase OS=Rattus norvegicus OX=10116 GN=Lipe PE=1 SV=3	Lipe	P15304	1.17407998	0.726164341	19.6979637	19.7097168	20.9192944	19.5910416	20.6780262	20.4829388	20.8084602	20.8532486
808	Hsc70-interacting protein OS=Rattus norvegicus OX=10116 GN=St13 PE=1 SV=1	St13	P50503	4.46095412	4.233496189	18.4829559	17.9385719	19.436903	18.6280613	23.4859962	22.3678493	22.7728844	22.7937469
809	Hsd17b4 protein OS=Rattus norvegicus OX=10116 GN=Hsd17b4 PE=1 SV=1	Hsd17b4	Q6IN39	3.21586548	3.270052671	15.883502	17.5500317	15.6069393	17.3298111	19.937149	19.9673386	19.6539021	19.8921051
810	Hsp90 co-chaperone Cdc37 OS=Rattus norvegicus OX=10116 GN=Cdc37 PE=1 SV=2	Cdc37	Q63692	3.9153933	1.982272625	21.0819855	20.3222523	20.9316006	20.930315	23.1206779	22.3932266	22.838707	22.8426323
811	Huntingtin interacting protein 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Hip1 PE=1 SV=1	Hip1	G3V8Y8	2.0950573	-1.075434685	20.6152954	20.897728	21.2230606	20.2593155	20.1331654	19.8128014	19.3842793	19.3634148
812	Huntingtin interacting protein 2 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ube2k PE=1 SV=1	Ube2k	D3ZXS8	2.76959693	5.000130415	14.777544	18.1348896	15.1505899	17.733551	21.8752174	20.448885	21.5690136	21.9039803
813	Huntingtin-interacting protein K OS=Rattus norvegicus OX=10116 GN=Hypk PE=1 SV=1	Hypk	F1M8A5	0.43278138	0.546966791	17.0347824	17.4627151	17.636404	15.2671499	17.1616707	17.778532	17.1443901	17.5043259
814	Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Hmgcs1 PE=1 SV=1	Hmgcs1	P17425	0.44331562	1.61724782	20.9642315	19.3369598	20.0124454	13.7430716	19.7883282	20.0140018	20.5681362	20.1552334
815	Hypoxanthine-guanine phosphoribosyltransferase OS=Rattus norvegicus OX=10116 GN=Hprt1 PE=1 SV=1	Hprt1	P27605	4.97974519	3.732831001	17.479414	17.6119308	17.874033	18.6539364	21.3794079	21.7878056	21.7104931	21.6729317
816	Hypoxia up-regulated protein 1 OS=Rattus norvegicus OX=10116 GN=Hyou1 PE=1 SV=1	Hyou1	Q63617	3.11398423	4.571518421	16.6033306	15.2786579	16.9174175	13.8903885	20.0738697	20.6839294	19.6691093	20.5489597
817	Ig gamma-2A chain C region OS=Rattus norvegicus OX=10116 GN=Igg-2a PE=1 SV=1	LOC679045	P20760	4.34048848	-5.127706528	26.6567974	26.4947872	26.4024353	25.3314877	22.0694504	21.3445129	20.6331902	20.327528
818	Ig gamma-2B chain C region OS=Rattus norvegicus OX=10116 GN=Igh-1a PE=1 SV=1	Igh-6	P20761	6.02465666	-4.753943443	24.2551918	24.2362328	24.3894672	24.6324139	20.037138	19.016613	19.6821976	19.7615833
819	Ig gamma-2C chain C region OS=Rattus norvegicus OX=10116 PE=2 SV=1	IGG2C_RAT	P20762	3.08284244	-4.51382637	20.801096	20.5098286	21.635891	22.8403587	18.3082714	16.4813099	15.9190998	17.0231876
820	Ig kappa chain C region, A allele OS=Rattus norvegicus OX=10116 PE=1 SV=1	Igkc	P01836	1.44428923	-3.323076248	21.160881	16.8134155	21.2800999	22.2835369	17.5428295	17.274189	16.7474918	16.681118
821	Ig lambda-2 chain C region OS=Rattus norvegicus OX=10116 PE=4 SV=1	LAC2_RAT	P20767	4.31991605	-5.309170246	23.0009403	23.0089626	21.8370132	21.4451332	17.3214436	17.6553745	16.9070969	16.1714535
822	Immunoglobulin-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Igbp1 PE=2 SV=2	Igbp1	O08836	5.55593404	4.822583437	14.8033266	15.144516	15.1656561	14.1448145	20.1014481	19.4061756	19.5686798	19.4723434
823	Importin 4 OS=Rattus norvegicus OX=10116 GN=Ipo4 PE=1 SV=2	Ipo4	D4A2D7	3.67815471	2.711763382	19.6912804	18.4176617	18.2735405	19.0130367	21.7063389	21.3405247	21.4132099	21.7824993
824	Importin 5 OS=Rattus norvegicus OX=10116 GN=Ipo5 PE=1 SV=1	Ipo5	D4A781	4.27582998	5.083508015	18.6616383	16.8968487	17.1063271	16.4358025	22.0709476	22.424551	22.6882191	22.2509308
825	Importin 9 OS=Rattus norvegicus OX=10116 GN=Ipo9 PE=1 SV=2	Ipo9	D4A857	5.10819794	4.672202587	18.0865803	17.8732758	16.9253407	16.8876266	22.2922382	21.8949203	22.299202	21.9752731
826	Importin subunit alpha OS=Rattus norvegicus OX=10116 GN=Kpna6 PE=1 SV=3	Kpna6	F1LT58	0.01610961	0.00920105	20.7183399	20.6513271	20.7143116	21.1573029	21.1984329	20.455246	20.7459087	20.8784981
827	Importin subunit alpha OS=Rattus norvegicus OX=10116 GN=LOC100359600 PE=3 SV=1	LOC100359600	M0R7I0	3.04144773	4.103234291	19.6448288	18.1762218	16.4614773	18.4049511	22.773428	22.0534115	22.1074009	22.1661758
828	Importin subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Kpnb1 PE=1 SV=1	Kpnb1	F2Z3Q8	0.68323911	-0.344216347	24.6466694	24.5408344	25.0337048	23.9863796	24.4443016	23.9374371	24.3282089	24.1207752
829	Inducible T-cell co-stimulator ligand OS=Rattus norvegicus OX=10116 GN=Icoslg PE=1 SV=3	Icoslg	F1LVL2	1.09756336	1.962312698	17.6507854	17.7629128	15.2447023	14.0183001	18.0467052	18.4209023	18.248745	17.8095989
830	Inosine triphosphate pyrophosphatase OS=Rattus norvegicus OX=10116 GN=Itpa PE=3 SV=1	Itpa	D3ZW55	3.9417556	4.481125832	14.6897888	16.3335876	16.607233	16.9093971	20.5857716	20.3866482	20.8589211	20.6331692
831	Inosine-5'-monophosphate dehydrogenase 2 OS=Rattus norvegicus OX=10116 GN=Impdh2 PE=1 SV=1	Impdh2	E9PU28	1.97871008	2.609859943	18.5763397	20.1409473	17.851963	20.3523655	22.910511	21.1999683	21.7193813	21.5311947
832	Inositol-1-monophosphatase OS=Rattus norvegicus OX=10116 GN=Impa1 PE=1 SV=1	Impa1	F1M978	2.9679994	3.881957054	13.5444975	15.5255222	15.045722	16.4659748	19.7357616	18.5252056	18.8928547	18.9557228
833	Insulin-degrading enzyme OS=Rattus norvegicus OX=10116 GN=Ide PE=1 SV=1	Ide	P35559	0.59662325	1.662010908	14.6510153	16.4033585	15.0138531	20.3281212	17.8968258	18.8137569	18.0211372	18.3126717
834	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Igf2bp3 PE=1 SV=1	Igf2bp3	A0A0G2K0Y2	3.24168027	2.593960285	17.6434841	19.0020084	18.4960308	18.934866	20.7080345	21.7809696	20.8686752	21.0945511
835	Insulin-like growth factor 2 receptor OS=Rattus norvegicus OX=10116 GN=Igf2r PE=1 SV=1	Igf2r	G3V824	6.54748835	3.355079651	23.5497456	23.650095	24.0007515	23.4781494	27.0369911	27.2058296	26.8684578	26.9877815
836	Insulin-like growth factor 2, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Igf2 PE=3 SV=1	Igf2	A0A0G2JTA6	1.54677671	-1.243042946	19.8741055	19.2369804	20.497673	19.4597492	18.5934105	19.2709827	18.5813828	17.6505604
837	Insulin-like growth factor-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Igfbp1 PE=1 SV=2	Igfbp1	P21743	0.69847966	-1.197981596	14.589221	17.0915585	18.0726547	17.2847118	16.4361172	14.876689	15.1165066	15.8169069
838	Insulin-like growth factor-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Igfbp2 PE=1 SV=3	Igfbp2	P12843	2.97257919	-3.950483084	21.0554867	20.1078625	21.3022251	20.9500046	17.5019398	18.2675056	16.3968544	15.4473467
839	Integrin alpha 5 (Mapped) OS=Rattus norvegicus OX=10116 GN=Itga5 PE=1 SV=1	Itga5	A0A0G2K1E2	3.43525481	5.043540955	15.1975765	15.0821657	15.0519629	17.9132805	20.8521481	20.8851204	20.7862625	20.8956184
840	Integrin beta 1 binding protein 2 (Predicted) OS=Rattus norvegicus OX=10116 GN=Itgb1bp2 PE=4 SV=1	Itgb1bp2	D3ZW59	1.97543903	3.087016821	16.6313801	13.8089466	14.2661829	17.0036736	18.5326958	17.900259	19.01301	18.6122856
841	Integrin beta OS=Rattus norvegicus OX=10116 GN=Itgb1 PE=1 SV=1	Itgb1	A0A0G2JSK5	6.42303113	2.376171112	21.4848881	21.5735912	21.2335739	21.2972717	23.7783165	23.8555527	23.5971966	23.8629436
842	Integrin beta OS=Rattus norvegicus OX=10116 GN=Itgb3 PE=1 SV=2	Itgb3	M0RCF3	4.69628125	-2.538958549	23.0458755	22.5635529	23.1137218	22.6355057	20.6973305	20.1326904	19.9762897	20.3965111
843	Integrin subunit alpha 2b OS=Rattus norvegicus OX=10116 GN=Itga2b PE=1 SV=2	Itga2b	D3ZAC0	4.77811462	-2.772860527	22.884779	22.5418892	22.9969788	22.8641644	19.9054089	19.5786743	20.1930065	20.5192795
844	Integrin subunit alpha 6 OS=Rattus norvegicus OX=10116 GN=Itga6 PE=1 SV=1	Itga6	G3V667	1.80852229	1.222206831	15.6779356	15.9189482	15.8723564	15.4235678	16.9128132	16.7942181	17.8769855	16.1976185
845	Integrin subunit alpha V OS=Rattus norvegicus OX=10116 GN=Itgav PE=1 SV=1	Itgav	A0A0G2JVZ6	3.01000982	2.182146072	17.6221428	17.7917309	18.6746292	18.9896069	20.6387272	20.2145748	20.1828403	20.7705517
846	Integrin-linked protein kinase OS=Rattus norvegicus OX=10116 GN=Ilk PE=2 SV=1	Ilk	Q99J82	3.8798925	3.73571825	20.9609375	19.2673664	19.7196121	19.1045895	23.335371	23.5070896	23.7825603	23.3703575
847	Inter alpha-trypsin inhibitor, heavy chain 4 OS=Rattus norvegicus OX=10116 GN=Itih4 PE=1 SV=1	Itih4	Q5EBC0	4.39147592	-3.338396549	25.1294098	25.5854149	25.1921825	24.6811295	22.4205875	22.0022392	21.2771854	21.5345383
848	Inter-alpha trypsin inhibitor, heavy chain 1 OS=Rattus norvegicus OX=10116 GN=Itih1 PE=1 SV=1	Itih1	B2RYM3	4.49158444	-3.223860264	23.4319897	23.4575367	23.9087353	23.8350086	20.9035206	19.7778683	20.2432957	20.8131447
849	Inter-alpha-trypsin inhibitor heavy chain 2 OS=Rattus norvegicus OX=10116 GN=Itih2 PE=1 SV=3	Itih2	D3ZFH5	6.34937808	-3.244517326	25.29146	25.1489658	25.4958534	25.6234379	22.3912907	22.0727005	21.9461441	22.1715126
850	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Rattus norvegicus OX=10116 GN=Itih3 PE=1 SV=3	Itih3	D3ZBS2	5.27834027	-2.835810184	25.4578915	24.964838	25.6577511	25.6621037	22.8122082	22.6080189	22.3679142	22.6112022
851	Interferon regulatory factor 2-binding protein-like OS=Rattus norvegicus OX=10116 GN=Irf2bpl PE=1 SV=1	Irf2bpl	Q5EIC4	3.41103891	3.896526814	14.0460958	16.3727398	15.6384535	16.0596104	19.8962059	19.4833584	19.0346222	19.2888203
852	Interferon-induced transmembrane protein 2 OS=Rattus norvegicus OX=10116 GN=Ifitm2 PE=1 SV=1	Ifitm2	Q9R175	0.64343124	0.916317701	16.3758068	16.9561405	17.1472263	17.1139355	15.9509268	18.0900745	18.1751556	19.042223

853	Interferon-induced transmembrane protein 3 OS=Rattus norvegicus OX=10116 GN=ifitm3 PE=2 SV=1	Ifitm3	P26376	3.1188394	4.027327061	16.8902054	15.4389534	16.4382496	14.068531	19.5413113	20.1655827	19.6234207	19.614933
854	Interleukin 1 receptor accessory protein b OS=Rattus norvegicus OX=10116 GN=Il1rap PE=1 SV=1	Il1rap	D1M8S3	0.28179956	0.35940361	18.7680111	17.7079639	19.1792412	19.3809509	18.2391319	19.9934349	18.8393841	19.4018307
855	IQ motif containing GTPase activating protein 1 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Iqgap1 PE	Iqgap1	G3V7Q7	2.97499097	1.889616966	21.5818634	20.2975578	20.6098709	21.150507	23.2262821	22.5620403	22.6676731	22.7422714
856	IQ motif-containing GTPase-activating protein 3 OS=Rattus norvegicus OX=10116 GN=Iqgap3 PE=1 SV=1	Iqgap3	D3ZCS4	2.75844789	1.325643063	19.5474911	18.6212444	19.0879745	18.6541176	20.3338985	20.4852886	20.4331837	19.9610291
857	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Rattus norvegicus OX=10116 GN=Iah1 PE=2 SV=2	Iah1	Q711G3	1.26403769	1.136968851	15.658452	15.1024342	15.5415287	17.2625103	16.9344864	16.9271145	17.2016773	17.0495224
858	Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Idh3a PE=1 SV=2	Idh3a	F1LNF7	5.36178874	4.588240147	18.5090084	17.8285122	17.7004452	17.6510391	21.9540672	23.0075092	22.5481796	22.5322094
859	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus OX=10116 GN=Idh2 PE=1 SV=2	Idh2	P56574	2.29417558	2.711684704	20.3905983	20.9575787	21.4495182	19.9360943	21.8306141	24.1245632	23.5555954	24.0697556
860	Isoleucine-tRNA synthetase (Predicted) OS=Rattus norvegicus OX=10116 GN=Iars PE=1 SV=2	Iars1	F1LS86	4.05133844	3.838015079	18.5568352	20.1397972	18.401228	18.8336887	23.0777187	22.5423546	22.9557457	22.7077904
861	Junction plakoglobin OS=Rattus norvegicus OX=10116 GN=Jup PE=1 SV=1	Jup	Q6P0K8	0.0987746	-0.127298355	23.1086922	24.4392624	22.4427032	23.6683083	23.3979874	23.8197556	23.0725021	22.8595276
862	Junctophilin-2 OS=Rattus norvegicus OX=10116 GN=Jph2 PE=1 SV=1	Jph2	Q2PS20	1.18145572	1.562756062	18.7945328	17.5476036	17.7410564	15.5153656	18.8113022	19.3026123	18.7651634	18.9705048
863	Jupiter microtubule associated homolog 1 OS=Rattus norvegicus OX=10116 GN=JPT1 PE=1 SV=3	Jpt1	Q6AXU6	0.43795049	1.037215233	16.6674595	17.3540421	16.6535263	13.4805508	16.3692417	18.7880611	16.0988655	17.0482712
864	Kelch-like family member 31 OS=Rattus norvegicus OX=10116 GN=Klhl31 PE=4 SV=1	Klhl31	D3ZLT6	3.54048921	4.173177242	18.1373253	17.3282337	15.6413746	17.6167984	20.9779873	21.423111	21.5903835	21.4249592
865	Keratin 16 OS=Rattus norvegicus OX=10116 GN=Krt16 PE=1 SV=1	Krt16	Q6IFU9	0.49845438	1.48428297	22.2491207	23.0920277	17.3708363	21.3982029	23.4236526	23.2079926	22.1325569	21.2831173
866	Keratin 76 OS=Rattus norvegicus OX=10116 GN=Krt76 PE=2 SV=1	Krt76	Q6IFZ5	0.07691802	-0.068006992	26.7116489	26.5420933	25.9580765	25.7137375	26.6058693	25.5972233	26.1280975	26.3223381
867	Keratin 78 OS=Rattus norvegicus OX=10116 GN=Krt78 PE=3 SV=1	Krt78	A0A0G2K4H7	1.06713203	-1.102473259	18.8645706	21.1203461	19.3393669	19.557909	18.0108299	18.5749092	18.8775902	19.0089703
868	Keratin 84 OS=Rattus norvegicus OX=10116 GN=Krt84 PE=3 SV=1	Krt84	A0A0G2K0I4	0.41143262	0.873404503	15.9202194	17.5061684	16.0938187	16.2897186	17.902338	18.6605873	17.9627533	14.7778645
869	Keratin, type I cytoskeletal 10 OS=Rattus norvegicus OX=10116 GN=Krt10 PE=1 SV=1	Krt10	A0A0G2K2V6	1.25349735	-1.01575613	27.1269608	28.6306572	26.7763233	27.393795	26.3744659	26.8646469	26.4631939	26.162405
870	Keratin, type I cytoskeletal 13 OS=Rattus norvegicus OX=10116 GN=Krt13 PE=3 SV=1	Krt13	Q6IFV4	0.06403255	0.268560171	20.195509	21.5845947	15.4625731	20.8977718	20.6067467	18.1920414	20.2092209	20.2066803
871	Keratin, type I cytoskeletal 14 OS=Rattus norvegicus OX=10116 GN=Krt14 PE=2 SV=1	Krt14	Q6IFV1	0.72206266	-0.651686668	26.7304249	28.0948563	26.2826214	26.9486618	26.6018772	26.8140812	26.1620674	25.8717918
872	Keratin, type I cytoskeletal 15 OS=Rattus norvegicus OX=10116 GN=Krt15 PE=1 SV=1	Krt15	Q6IFV3	0.21302316	-0.371869087	20.6354618	20.940794	18.4132118	19.5253639	20.4466476	18.5532703	19.6657162	19.361721
873	Keratin, type I cytoskeletal 17 OS=Rattus norvegicus OX=10116 GN=Krt17 PE=1 SV=1	Krt17	A0A0G2K9Q9	0.64263403	-0.58516407	24.8032799	26.3268528	24.3714943	25.1222935	24.700798	24.8241539	24.4504032	24.307909
874	Keratin, type I cytoskeletal 17 OS=Rattus norvegicus OX=10116 GN=Krt17 PE=1 SV=1	Krt17	Q6IFU8	0.45925111	1.381455183	12.9613714	18.92346	16.0039787	16.4873276	18.9760303	16.637867	16.4800034	17.8080578
875	Keratin, type I cytoskeletal 42 OS=Rattus norvegicus OX=10116 GN=Krt42 PE=3 SV=1	Krt42	Q6IFU7	0.67992266	-0.561215878	23.6754265	24.2953796	23.0902157	23.4233837	23.4463768	23.7072678	22.6588631	22.4270344
876	Keratin, type II cytoskeletal 1 OS=Rattus norvegicus OX=10116 GN=Krt1 PE=1 SV=1	Krt1	A0A0G2JST3	0.57157248	-0.633043766	26.226284	27.8568497	25.769659	26.0347576	25.8657436	26.3818588	25.7878189	25.3199539
877	Keratin, type II cytoskeletal 1b OS=Rattus norvegicus OX=10116 GN=Krt77 PE=3 SV=1	Krt77	A0A0G2JZQ9	0.07070241	-0.21724081	19.0455437	23.3937626	19.5862656	18.7507248	20.2858467	19.565836	20.3449802	19.7106705
878	Keratin, type II cytoskeletal 2 epidermal OS=Rattus norvegicus OX=10116 GN=Krt2 PE=3 SV=1	Krt2	Q6IG02	1.7077232	-1.103127003	26.1304188	26.545702	25.095005	25.6075649	24.3705902	25.0854988	24.6652641	24.8448296
879	Keratin, type II cytoskeletal 5 OS=Rattus norvegicus OX=10116 GN=Krt5 PE=1 SV=1	Krt5	A0A0G2K509	1.46592179	-1.089164734	27.9164009	29.0711308	27.3966923	28.1541214	27.2536144	27.473053	26.8070774	26.6479416
880	Keratin, type II cytoskeletal 5 OS=Rattus norvegicus OX=10116 GN=Krt5 PE=1 SV=1	Krt5	Q6P6Q2	0.52070175	-0.667500496	23.8846073	25.585125	23.5956669	25.1433525	24.3262939	24.5627689	23.5763226	23.0733643
881	Keratin, type II cytoskeletal 6A OS=Rattus norvegicus OX=10116 GN=Krt6a PE=1 SV=1	LOC683313	Q4FZU2	0.0112355	0.020213127	25.0195313	26.2468739	25.0323811	23.4570675	25.2817688	25.3211327	24.6921616	24.5416431
882	Keratin, type II cytoskeletal 73 OS=Rattus norvegicus OX=10116 GN=Krt73 PE=1 SV=1	Krt73	Q6IG03	1.31885284	-0.942483902	26.0656776	27.2735767	25.813715	26.8807354	25.8049297	25.8935184	25.3513832	25.2139378
883	Keratin, type II cytoskeletal 75 OS=Rattus norvegicus OX=10116 GN=Krt75 PE=1 SV=1	Krt75	A0A0H2UHH5	0.41022466	0.665245056	20.6698151	21.9725285	19.6356373	20.1929607	22.0678635	22.1572323	20.9097729	19.9970531
884	Keratin, type II cytoskeletal 8 OS=Rattus norvegicus OX=10116 GN=Krt8 PE=1 SV=3	Krt8	Q10758	1.08340179	-1.031517982	22.1509724	23.5906239	21.5433006	22.2325497	21.4135399	22.0082397	21.0180359	20.9515591
885	Keratinocyte differentiation-associated protein OS=Rattus norvegicus OX=10116 GN=Krtdap PE=2 SV=1	Krtdap	P85411	7.21796749	-4.894563675	23.3831215	22.8986931	23.1750717	23.3660851	18.4760609	18.4010658	18.0127163	18.3548737
886	Kinesin family member 11 OS=Rattus norvegicus OX=10116 GN=Kif11 PE=1 SV=1	Kif11	F1MAB8	2.43592382	3.289528131	17.9362869	15.2410669	17.2024288	15.2839088	19.551054	20.3248749	19.5456448	19.4002304
887	Kinesin family member 13A OS=Rattus norvegicus OX=10116 GN=Kif13a PE=1 SV=1	Kif13a	D3ZM20	2.84461428	1.88516283	18.2081318	17.6166077	17.9001904	16.6491127	19.5421371	19.4942856	19.4979362	19.3803349
888	Kinesin family member 4A OS=Rattus norvegicus OX=10116 GN=Kif4a PE=1 SV=1	Kif4a	E9PSJ3	1.15295625	-0.74110508	18.7989922	18.040926	18.3009243	17.3656216	16.9950333	17.4997292	17.3093319	17.7379494
889	Kinesin light chain 1 OS=Rattus norvegicus OX=10116 GN=Klc1 PE=1 SV=2	Klc1	P37285	3.6556666	4.731595039	19.7970314	18.3617592	19.1938992	17.1236629	23.1030273	23.6282883	23.6232185	23.0481987
890	Kinesin light chain 2 OS=Rattus norvegicus OX=10116 GN=Klc2 PE=1 SV=1	Klc2	B2GV74	3.74933989	3.628234863	20.3446751	20.5241776	20.1250305	18.6258526	23.5417309	23.7009201	23.5994797	23.2905445
891	Kinesin light chain 4 OS=Rattus norvegicus OX=10116 GN=Klc4 PE=1 SV=1	Klc4	Q5PQM2	3.62729012	3.232749462	19.914114	20.5954132	19.5281773	18.6729317	23.0211334	23.0932045	22.9189491	22.6083469
892	Kinesin-1 heavy chain OS=Rattus norvegicus OX=10116 GN=Kif5b PE=1 SV=1	Kif5b	Q2PQA9	4.231329	2.051698685	23.7412357	23.423811	24.1788597	23.9081554	25.6314869	26.118639	26.0652122	25.6435184
893	Kinesin-like protein KIF15 OS=Rattus norvegicus OX=10116 GN=Kif15 PE=2 SV=1	Kif15	Q7TSP2	1.64575257	2.199151039	19.2320976	18.381834	18.987009	16.4882069	19.4734135	21.1804104	20.8217239	20.4102039
894	Kinesin-like protein KIF1B OS=Rattus norvegicus OX=10116 GN=Kif1b PE=1 SV=2	Kif1b	O88658	3.50584525	4.144779682	16.3791809	18.239996	16.371109	15.7083626	20.807785	21.1793079	20.7065735	20.5841007
895	Kinesin-like protein KIF1C OS=Rattus norvegicus OX=10116 GN=Kif1c PE=1 SV=1	Kif1c	F1M9C8	1.50344811	-1.076218605	19.8585434	20.5115147	20.1214943	20.1324272	18.0795383	19.7114944	19.4822025	19.0458698
896	Kinetochore associated 1 (Predicted) OS=Rattus norvegicus OX=10116 GN=Kntc1 PE=4 SV=2	Kntc1	D3ZVJ3	4.6646126	4.116539478	15.6026707	14.7672958	15.2003183	14.388669	18.5250359	19.6290798	19.1352577	19.1357384
897	Kinetochore protein Nuf2 OS=Rattus norvegicus OX=10116 GN=Nuf2 PE=2 SV=1	Nuf2	Q6AYL9	6.76202366	-4.223616123	21.2318821	21.1815166	21.8083858	21.362236	17.3349247	17.0869198	17.0495243	17.2181873
898	Kinetochore protein Spc25 OS=Rattus norvegicus OX=10116 GN=Spc25 PE=2 SV=1	Spc25	Q5M856	0.10022739	-0.227869034	19.4218559	21.361475	18.5742321	19.8307743	20.7297592	19.9867687	19.6466331	17.9137001
899	Kininogen-1 OS=Rattus norvegicus OX=10116 GN=Kng1 PE=2 SV=1	Kng2l1	P08934	4.41919794	-2.619925022	25.0532722	24.7673912	25.1376686	24.8660564	22.7691784	21.8839149	22.0044079	22.6871872
900	KN motif and ankyrin repeat domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Kank2 PE=1 SV=2	Kank2	D3ZD05	2.61142867	3.715356588	16.7226543	17.0687809	16.4412632	14.0906591	19.5939808	20.6619701	19.7197456	19.2090874
901	Lactadherin OS=Rattus norvegicus OX=10116 GN=Mfge8 PE=1 SV=1	Mfge8	Q1PBJ1	3.40699575	-1.888374329	22.9151001	22.5574455	22.3971519	22.490118	20.2097473	21.3235207	20.8061085	20.4669418
902	Lamin A, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Lmna PE=1 SV=1	Lmna	G3V8L3	0.9877011	1.729584694	16.3785381	17.4605217	16.8078747	19.9994469	20.5260754	18.9301739	18.8291607	19.2793102
903	Lamina-associated polypeptide 2, isoform beta OS=Rattus norvegicus OX=10116 GN=Tmpo PE=1 SV=3	Tmpo	Q62733	0.5080642	0.679230452	17.0451946	14.6988211	16.8807659	17.3461285	17.2842999	17.2263603	17.2890224	16.8881493
904	Laminin subunit beta 1 OS=Rattus norvegicus OX=10116 GN=Lamb1 PE=1 SV=3	Lamb1	D3ZQN7	0.60712576	0.605699062	19.2040997	20.4400826	18.7988167	18.243433	19.8771915	19.8356171	19.5539608	19.8424587
905	Laminin subunit gamma 1 OS=Rattus norvegicus OX=10116 GN=Lamc1 PE=1 SV=1	Lamc1	F1MAA7	2.02211788	2.40294075	16.3939266	19.0990143	18.41185	17.7022305	21.086586	19.9328537	19.8933926	20.3059521
906	Large neutral amino acids transporter small subunit 1 OS=Rattus norvegicus OX=10116 GN=Slc7a5 PE=1 SV=2	Slc7a5	Q63016	0.52731567	-0.222878456	18.2286663	18.121706	18.3530769	17.6071548	17.994379	17.8019028	17.57794	18.0448685
907	Large proline-rich protein BAG6 OS=Rattus norvegicus OX=10116 GN=Bag6 PE=1 SV=2	Bag6	Q6MG49	1.28732714	3.467480421	21.0262508	17.7616959	15.2167807	21.0620193	22.7823906	21.98559	22.3742332	21.7944546
908	Late endosomal/lysosomal adaptor, MAPK and MTOR activator 2 OS=Rattus norvegicus OX=10116 GN=Lamtor2 PE=1 SV=1	Lamtor2	D4A465	4.20834273	3.426247835	15.3165283	15.699811	16.8552437	16.0625629	19.6168938	19.1064262	19.3843136	19.5315037
909	Latent-transforming growth factor beta-binding protein 4 OS=Rattus norvegicus OX=10116 GN=Ltbp4 PE=1 SV=2	Ltbp4	D4A917	2.32711285	3.178632498	17.2992516	16.7903519	15.9866762	14.6851025	19.0598221	20.6804733	18.6147366	19.1208801
910	LDL receptor-related protein 1 OS=Rattus norvegicus OX=10116 GN=Lrp1 PE=1 SV=1	Lrp1	G3V928	1.09550141	-1.928260803	21.7151642	23.6262474	21.9945393	22.5712166	18.1195126	21.5593414	21.3766499	21.1386204
911	Lecithin cholesterol acyltransferase OS=Rattus norvegicus OX=10116 GN=Lcat PE=1 SV=1	Lcat	O35849	3.94577627	-2.769679546	19.8938332	18.7494869	19.7925034	19.3699455	16.7802124	16.414278	17.1265316	16.4060287
912	Lectin, mannose-binding 2 OS=Rattus norvegicus OX=10116 GN=Lman2 PE=1 SV=1	Lman2	B0BNG3	3.14734087	2.294770718	19.8226757	19.3240051	18.7616272	19.5989609	20.9086475	22.251379	21.7456036	21.7807217
913	Leucine-rich repeat flightless-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Lrrfip1 PE=1 SV=1	Lrrfip1	Q66HF9	5.81319669	6.91753006	14.1999664	14.1801414	15.5905352	14.9416666	21.2952061	21.958786	21.8405113	21.4879265

914	Leucine-rich repeat-containing 40 OS=Rattus norvegicus OX=10116 GN=Lrrc40 PE=1 SV=3	Lrrc40	G3V7I7	4.03545168	5.510371447	16.7516422	15.8601828	16.076498	14.0152073	21.1632462	20.8465023	21.3713551	21.3639126
915	Leucine-rich repeats and calponin homology domain-containing 3 OS=Rattus norvegicus OX=10116 GN=Lrch3 PE=1 SV=2	Lrch3	D4A8M4	2.53637242	3.351747036	15.2529507	13.4017782	13.8238096	16.1272049	17.2949238	18.5897865	18.3262959	17.8017254
916	Leucyl-cystinyl aminopeptidase OS=Rattus norvegicus OX=10116 GN=Lnpep PE=1 SV=1	Lnpep	P97629	5.86621706	4.604869366	18.3215618	17.5172043	17.5113525	17.4402599	21.9996815	22.5976944	22.3276463	22.2848339
917	Leucyl-tRNA synthetase OS=Rattus norvegicus OX=10116 GN=Lars PE=1 SV=1	Lars1	Q5PPJ6	3.74565996	5.560592651	15.7565212	18.7292976	16.9208374	16.095705	22.6764927	22.098196	22.6688843	22.3011589
918	Leukocyte surface antigen CD47 OS=Rattus norvegicus OX=10116 GN=Cd47 PE=1 SV=1	Cd47	A0A0G2JTH4	0.38941515	-0.280790329	19.4891891	18.9929142	18.4870911	19.521986	19.1685715	18.8169804	18.2861481	19.0963192
919	Leukosialin OS=Rattus norvegicus OX=10116 GN=Spn PE=1 SV=2	Spn	R9PXZ7	0.12344408	-0.184762716	16.0312176	16.4683247	16.5011349	16.3943043	16.4159546	15.2705088	17.6144924	15.3549747
920	Leukotriene A(4) hydrolase OS=Rattus norvegicus OX=10116 GN=Lta4h PE=1 SV=1	Lta4h	Q499P2	0.77991297	1.667706966	19.5109081	18.0810108	18.3379192	18.3417473	17.2226563	21.4042702	21.3230762	20.9924107
921	LIM and cysteine-rich domains 1 OS=Rattus norvegicus OX=10116 GN=Lmcd1 PE=1 SV=1	Lmcd1	Q6AYF2	5.25486145	5.394693375	18.1878967	18.3775768	17.1658745	17.2372513	22.7025242	23.1209126	23.5560608	23.1678753
922	LIM and senescent cell antigen-like-containing domain protein OS=Rattus norvegicus OX=10116 GN=Lims1 PE=1 SV=1	Lims1	C0KUC6	3.97746248	4.869935513	19.0272579	18.9781761	17.4958916	16.9397812	22.7467327	23.3133945	22.9623508	22.8983707
923	LIM and SH3 domain protein 1 OS=Rattus norvegicus OX=10116 GN=Lasp1 PE=1 SV=1	Lasp1	Q99MZ8	0.06436788	-0.167135954	17.4213505	18.0654831	14.4736719	17.8549786	17.0671329	17.7322025	16.3721542	15.9754505
924	LIM domain 7 OS=Rattus norvegicus OX=10116 GN=Lmo7 PE=1 SV=1	Lmo7	A0A0G2K174	6.08511389	6.500150204	16.4389648	16.5382156	16.3919182	17.4385548	22.7976265	23.72019	23.2068615	23.0835762
925	LIM domain-binding 3 OS=Rattus norvegicus OX=10116 GN=Ldb3 PE=1 SV=1	Ldb3	A0A096MJ01	8.47609437	7.300004482	19.6040516	19.3918476	19.4835186	19.7563248	27.0838699	26.6992283	27.0293331	26.6233292
926	LIM domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Limd1 PE=1 SV=1	Limd1	B5DEH0	4.9258613	3.320354939	18.6992474	18.4278774	18.9371529	18.3879375	21.5971184	22.5329857	21.9731541	21.6303768
927	Lipoma-preferred partner homolog OS=Rattus norvegicus OX=10116 GN=Lpp PE=1 SV=1	Lpp	Q5XI07	5.7426877	5.320625782	17.8671131	18.5153179	18.1149635	17.501339	23.2169304	23.8678551	23.2963257	22.9001255
928	Lipopolysaccharide-binding protein OS=Rattus norvegicus OX=10116 GN=Lbp PE=1 SV=1	Lbp	Q3MID7	3.28104212	-2.68356514	21.4795952	21.0634804	20.5402317	20.7402592	19.2310448	18.0448895	18.1932831	17.6200886
929	Lipoprotein lipase OS=Rattus norvegicus OX=10116 GN=Lpl PE=1 SV=1	Lpl	Q06000	3.94665756	1.095590115	18.822485	18.584444	18.7145348	19.1336117	19.9771271	19.9719944	19.8273792	19.8609352
930	L-lactate dehydrogenase A chain OS=Rattus norvegicus OX=10116 GN=Ldha PE=1 SV=1	Ldha	P04642	4.87635334	3.599805355	21.5170021	22.0247936	22.1293831	21.0769196	24.8993378	25.3607178	25.5371685	25.3500957
931	L-lactate dehydrogenase B chain OS=Rattus norvegicus OX=10116 GN=Ldhb PE=1 SV=2	Ldhb	P42123	4.65789779	5.711364269	21.0518856	21.1591892	20.9178581	20.1252384	25.2909241	26.7268562	27.1767292	26.9051189
932	LOC683667 protein OS=Rattus norvegicus OX=10116 GN=Sri PE=1 SV=1	Sri	B0BNJ1	5.37398716	4.815526009	18.004612	17.8628902	17.9902382	16.7789192	22.6459312	22.2612839	22.4345837	22.5569649
933	LOC685144 protein OS=Rattus norvegicus OX=10116 GN=Sec24c PE=1 SV=1	Sec24c	B5DEG8	4.56365814	4.633368492	14.7491608	15.1752415	16.3393116	16.1230621	20.4721909	20.1471195	19.8508472	20.4500923
934	Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acadl PE=1 SV=1	Acadl	P15650	1.5738087	1.76177597	19.6370945	19.3757572	18.0399971	20.6563396	20.5117664	21.8110905	21.0691051	21.3643303
935	Long-chain-fatty-acid--CoA ligase 1 OS=Rattus norvegicus OX=10116 GN=Acsl1 PE=1 SV=1	Acsl1	P18163	2.5326953	-0.943071842	23.2689075	23.0261803	23.3483696	22.7920685	22.3221149	22.4994202	21.8401585	22.001545
936	Low molecular weight phosphotyrosine protein phosphatase OS=Rattus norvegicus OX=10116 GN=Acp1 PE=1 SV=2	Acp1	Z4YNF4	0.03349718	-0.041991949	17.4950523	15.745492	17.4494457	17.2917614	17.1716309	17.073576	16.875597	16.6929798
937	LPS-responsive beige-like anchor protein OS=Rattus norvegicus OX=10116 GN=Lrba PE=1 SV=1	Lrba	A0A0G2JYI0	0.91974733	0.753128529	17.271307	18.6173801	17.6542149	17.0725803	19.0132847	18.2328625	18.4858913	17.8959579
938	LRP chaperone MESD OS=Rattus norvegicus OX=10116 GN=Mesd PE=2 SV=1	Mesd	Q5U2R7	0.10821467	-0.112875938	20.6806107	20.7019215	21.1763496	19.4554806	20.0450268	20.4879761	20.5248871	20.5049686
939	LRP16 protein OS=Rattus norvegicus OX=10116 GN=Macrod1 PE=1 SV=1	Macrod1	A0A0G2K5F1	3.74822966	4.519114017	15.8520937	15.7741165	15.6274586	13.7266397	19.1830082	19.8442898	20.2190304	19.8104362
940	LRRGT00199 OS=Rattus norvegicus OX=10116 GN=Taf3 PE=1 SV=1	Atp5f1c	Q6QI09	3.47035042	4.335137367	18.3118076	18.8863201	16.8165588	17.3758831	21.0802135	22.7058983	22.4393749	22.5056324
941	LUC7-like 2 (S. cerevisiae) OS=Rattus norvegicus OX=10116 GN=Luc7l2 PE=1 SV=1	Luc7l2	B2RYP6	2.58337019	6.20838356	17.480484	17.8858509	14.3021441	12.8307276	22.5889149	21.8357162	21.4615669	21.4465427
942	Lumican OS=Rattus norvegicus OX=10116 GN=Lum PE=1 SV=1	Lum	P51886	1.89871611	-1.060220242	22.8892307	21.9718113	22.3226357	22.6969471	21.9332924	21.0748444	21.0059948	21.6256123
943	Lupus La protein homolog OS=Rattus norvegicus OX=10116 GN=Ssb PE=1 SV=1	Ssb	Q66HM7	0.87162199	0.845157146	21.0881062	20.8670444	21.1681843	19.4099903	20.9874115	22.1627274	21.1667805	21.5970345
944	Lymphocyte cytosolic protein 1 OS=Rattus norvegicus OX=10116 GN=Lcp1 PE=1 SV=1	Lcp1	A0A0G2K014	0.0916076	-0.085950136	16.0439854	16.715971	15.7184658	16.9032726	16.4068203	15.8464804	16.7398796	16.044714
945	Lys-63-specific deubiquitinase BRCC36 OS=Rattus norvegicus OX=10116 GN=Brcc3 PE=2 SV=1	Brcc3	B2RYM5	1.51655834	-1.415052414	21.8942451	23.2077942	21.4343357	23.3592319	21.3939762	21.2330761	20.8897324	20.7186127
946	Lysine demethylase 3B OS=Rattus norvegicus OX=10116 GN=Kdm3b PE=1 SV=2	Kdm3b	M0RDF1	2.76507756	2.44929719	15.5692577	15.4035797	15.4587336	15.8474236	19.017046	16.8913555	18.3147488	17.8530331
947	Lysine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Kars PE=1 SV=1	Kars1	Q5XIM7	4.26741528	3.231784821	20.4284363	20.2942772	20.3375092	19.1988239	23.4772263	22.9649582	23.5451355	23.1988659
948	Lysophospholipid acyltransferase 5 OS=Rattus norvegicus OX=10116 GN=Lpcat3 PE=2 SV=1	Lpcat3	Q5FVN0	4.18865124	1.685720444	19.3725033	19.0090179	18.9708328	18.9507084	20.4906921	21.0725403	20.5616531	20.9210587
949	Lysosome membrane protein 2 OS=Rattus norvegicus OX=10116 GN=Scarb2 PE=1 SV=2	Scarb2	P27615	2.51251697	3.309928894	15.0910931	16.3215752	17.1567688	14.3170815	18.6388168	19.7544174	18.5200119	19.2129879
950	Lysosome-associated membrane glycoprotein 1 OS=Rattus norvegicus OX=10116 GN=Lamp1 PE=1 SV=1	Lamp1	P14562	4.70917667	3.08288765	20.0658188	20.4757576	20.0974884	19.2726421	23.1576214	23.0345249	23.0543251	22.9967861
951	Lysosome-associated membrane glycoprotein 2 OS=Rattus norvegicus OX=10116 GN=Lamp2 PE=1 SV=3	Lamp2	P17046	3.5320634	1.829008579	18.3159599	17.675808	18.2065315	17.7104149	19.3054981	20.0932465	19.7881069	20.0378971
952	Lysozyme OS=Rattus norvegicus OX=10116 GN=Lyz2 PE=1 SV=1	Lyz2	F1M8E9	2.34882055	-2.845679283	17.650959	18.5457077	19.7754326	18.8475151	15.1608219	16.789608	16.547905	14.9385624
953	Lysyl oxidase-like 1 OS=Rattus norvegicus OX=10116 GN=Loxl1 PE=2 SV=1	Loxl1	Q5FWS5	3.83893584	-1.980906963	20.6344872	19.9622784	19.8356915	20.2887287	17.9196625	18.5765877	18.006155	18.2951527
954	Macrophage colony-stimulating factor 1 receptor OS=Rattus norvegicus OX=10116 GN=Csf1r PE=1 SV=2	Csf1r	D4ACA7	0.22599432	0.203542233	17.3958473	17.0437202	17.9165802	17.8202686	18.0188923	18.4620972	17.3424282	17.1671677
955	Macrophage migration inhibitory factor OS=Rattus norvegicus OX=10116 GN=Mif PE=1 SV=4	Mif	P30904	3.03870565	2.157704353	19.4618664	18.0014114	18.9538708	19.2193508	21.1149864	20.6122513	21.2985973	21.2414818
956	MAGE family member D2 OS=Rattus norvegicus OX=10116 GN=Maged2 PE=1 SV=1	Maged2	Q3B7U1	5.00895727	3.41323185	19.1677589	18.5964069	18.3933945	18.647728	22.6725407	21.97085	21.9829197	21.8319054
957	Major vault protein OS=Rattus norvegicus OX=10116 GN=Mvp PE=1 SV=1	Mvp	A0A140TAE0	2.22257296	3.275340557	18.8596478	20.5404549	18.5296326	18.5568523	21.4858894	21.9727993	21.8791389	24.2501221
958	Malate dehydrogenase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Mdh1 PE=1 SV=3	Mdh1	O88989	7.27257739	4.520179749	19.6823521	20.01614	19.9984264	20.3118572	24.4255257	24.5451336	24.6510887	24.4677467
959	Malate dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mdh2 PE=1 SV=2	Mdh2	P04636	2.09737908	2.733588219	20.8358593	21.5440941	19.3226643	20.7189465	21.868063	24.3354168	23.4415302	23.710907
960	Mannan-binding lectin serine peptidase 2 OS=Rattus norvegicus OX=10116 GN=Masp2 PE=1 SV=1	Masp2	A2VCV7	4.49783239	-5.473973274	22.1213264	21.2896042	21.7342873	22.0870018	16.8429222	17.0276184	16.441124	15.024662
961	Mannan-binding lectin serine protease 1 OS=Rattus norvegicus OX=10116 GN=Masp1 PE=1 SV=1	Masp1	A0A0H2UHA1	2.58762785	-2.203467369	21.1749592	20.9093056	21.1628342	20.7685852	19.6777573	17.6272602	18.7591743	19.1376228
962	Mannose receptor, C type 1 OS=Rattus norvegicus OX=10116 GN=Mrc1 PE=1 SV=3	Mrc1	D3ZD31	4.44502772	-0.825083733	21.8901291	21.912487	21.7793884	21.7273846	21.0110874	21.1512527	20.8495255	20.9971886
963	Mannose-6-phosphate isomerase OS=Rattus norvegicus OX=10116 GN=Mpi PE=2 SV=1	Mpi	Q68FX1	2.11994202	2.412303209	14.4893684	16.5781059	16.0576992	15.9457121	17.5563068	18.4653225	19.2307396	17.4677296
964	Mannose-binding protein A OS=Rattus norvegicus OX=10116 GN=Mbl1 PE=1 SV=1	Mbl1	P19999	4.94246436	-2.699516296	20.223875	20.2596817	20.3629112	20.092886	16.9642582	17.8158646	17.5977039	17.7634621
965	MAP7 domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Map7d1 PE=1 SV=1	Map7d1	D4A644	2.07427458	4.802488804	19.724596	19.7475491	19.1523094	14.6722755	22.726963	23.7647114	23.1414871	22.8735237
966	Matrin-3 OS=Rattus norvegicus OX=10116 GN=Matr3 PE=1 SV=1	Matr3	A0A0G2JSR7	2.25913433	2.189577341	16.6847534	15.9592457	16.6881256	15.8657064	19.3384476	19.0900898	18.253067	17.2745361
967	Membrane-associated progesterone receptor component 1 OS=Rattus norvegicus OX=10116 GN=Pgrmc1 PE=1 SV=1	Pgrmc1	A0A0H2UHK2	3.07768259	3.565978289	13.5371695	15.6261692	15.7857208	15.9249706	18.6880951	18.8993702	18.4765797	19.0738983
968	Membrane-associated progesterone receptor component 2 OS=Rattus norvegicus OX=10116 GN=Pgrmc2 PE=1 SV=1	Pgrmc2	Q5XIU9	5.06197124	4.511998415	17.1915035	16.5150642	16.9538212	15.9045286	20.7594624	21.4348125	21.0272369	21.3913994
969	Metalloproteinase inhibitor 3 OS=Rattus norvegicus OX=10116 GN=Timp3 PE=2 SV=1	Timp3	P48032	4.12765885	-4.061007738	21.0760994	20.6678123	20.8619804	20.080761	17.6045017	16.7034378	15.9516783	16.1830044
970	Metalloreductase STEAP3 OS=Rattus norvegicus OX=10116 GN=Steap3 PE=1 SV=1	Steap3	A0A0H2UI26	0.44812613	-0.767352104	18.3283939	16.0012417	17.8012428	18.6535835	15.4642487	17.5020924	17.3080502	17.4406624
971	Methanethiol oxidase OS=Rattus norvegicus OX=10116 GN=Selenbp1 PE=1 SV=2	LOC103689947	F1LRJ9	1.36066806	1.408211708	14.1341753	15.4491739	16.2294197	15.423214	15.9960709	17.6454563	16.6361485	16.5911541
972	Methionine aminopeptidase 2 OS=Rattus norvegicus OX=10116 GN=Metap2 PE=1 SV=2	Metap2	P38062	3.79009029	2.121218204	16.997282	16.6367092	17.2683945	17.2106476	19.4847069	19.4608841	19.0648594	18.5874557
973	Methionyl-tRNA synthetase OS=Rattus norvegicus OX=10116 GN=Mars PE=1 SV=1	Mars1	D3Z941	4.46593003	6.874545574	15.0141954	14.5301256	16.5501785	17.1421776	22.71175	22.3885784	22.7980328	22.8364983
974	Methylthioribose-1-phosphate isomerase OS=Rattus norvegicus OX=10116 GN=Mri1 PE=1 SV=1	Mri1	Q5HZE4	1.30104408	0.910980225	20.7973709	20.6068249	20.6653805	19.2144146	21.1805305	21.2428474	21.3150921	21.1894417

975	Methylthioribulose-1-phosphate dehydratase OS=Rattus norvegicus OX=10116 GN=Apip PE=1 SV=3	Apip	D3ZUI1	1.33340173	2.62357235	15.0330639	12.7891159	15.6178532	12.6289997	16.1196747	16.3097439	18.7134285	15.420475
976	Methyltransferase-like 3 OS=Rattus norvegicus OX=10116 GN=Mettl3 PE=1 SV=1	Mettl3	Q4V8G6	0.3960512	-1.066510677	20.3447952	21.6336594	19.4850044	19.5726852	20.3781738	20.6888523	19.6629868	16.0400887
977	MICOS complex subunit MIC60 OS=Rattus norvegicus OX=10116 GN=Immt PE=1 SV=1	Immt	A0A0G2JVH4	1.67726302	1.436350346	20.3440247	19.9298019	19.1350441	19.0698166	20.1057262	21.6083679	21.0048485	21.505146
978	Microfibril-associated glycoprotein 4-like OS=Rattus norvegicus OX=10116 GN=LOC102553715 PE=1 SV=3	Mfap4	D4A7W8	0.83768061	-0.340272427	19.1788616	19.6819229	19.7910061	19.0495205	19.2895851	18.9026356	18.9754829	19.1725178
979	Microtubule-actin cross-linking factor 1 OS=Rattus norvegicus OX=10116 GN=Macf1 PE=1 SV=1	Macf1	A0A0G2K9T4	2.78344297	1.84794569	21.3193378	22.0273399	22.1827621	22.5697861	23.4609661	24.4934998	23.8079929	23.72855
980	Microtubule-associated protein 1A OS=Rattus norvegicus OX=10116 GN=Map1a PE=1 SV=1	Map1a	A0A0G2K5C6	2.49680002	3.588082075	16.0329857	16.8215446	16.1373997	13.7306223	18.236927	19.5138206	19.6612339	19.662899
981	Microtubule-associated protein 1A OS=Rattus norvegicus OX=10116 GN=Map1a PE=1 SV=1	Map1a	P34926	2.96436478	4.72889185	20.0341148	19.7102623	18.5514812	17.1935196	22.2553196	24.5244007	24.0026531	23.6225719
982	Microtubule-associated protein 1B OS=Rattus norvegicus OX=10116 GN=Map1b PE=1 SV=3	Map1b	P15205	4.978129	2.878013611	19.2993622	19.8108006	19.1038208	19.0512409	21.9331932	22.5379257	22.168663	22.1374969
983	Microtubule-associated protein OS=Rattus norvegicus OX=10116 GN=Map4 PE=1 SV=1	Map4	A0A0G2JW88	6.34323273	6.067738533	19.785511	20.3089085	19.961319	19.7485504	25.4497128	26.5629616	26.1436825	25.9188862
984	Microtubule-associated protein RP/EB family member 1 OS=Rattus norvegicus OX=10116 GN=Mapre1 PE=1 SV=3	Mapre1	Q66HR2	4.09589649	6.876064539	13.4063683	16.7687168	15.8335171	15.8199663	22.5756493	22.3168297	22.4172115	22.0231361
985	Microtubule-associated protein RP/EB family member 2 OS=Rattus norvegicus OX=10116 GN=Mapre2 PE=1 SV=1	Mapre2	Q3B8Q0	3.97077166	6.850739002	15.7572184	12.6657076	15.6917553	13.8896275	21.0613823	21.1546402	21.6737957	21.5174465
986	Microtubule-associated serine/threonine kinase family member 4 OS=Rattus norvegicus OX=10116 GN=Mast4 PE=1 SV=2	Mast4	M0R3L1	0.15536265	-0.211497784	20.7532864	22.1051998	19.8937874	20.9552956	19.9886227	21.1454296	20.7574692	20.9700565
987	Misato 1, mitochondrial distribution and morphology regulator OS=Rattus norvegicus OX=10116 GN=Msto1 PE=1 SV=1	Msto1	D3ZMW3	0.54369707	0.371750355	22.6103954	21.9783707	21.996542	21.3179245	22.8461227	22.3034897	22.0216732	22.2189484
988	Mitochondrial brown fat uncoupling protein 1 OS=Rattus norvegicus OX=10116 GN=Ucp1 PE=1 SV=2	Ucp1	P04633	0.19850991	-0.376322508	16.7100506	19.00033	16.7968731	15.893569	16.1030197	17.6347828	16.2974548	16.8602753
989	Mitochondrial carnitine/acylcarnitine carrier protein OS=Rattus norvegicus OX=10116 GN=Slc25a20 PE=1 SV=1	Slc25a20	P97521	0.27165662	-0.82884264	18.981554	14.1750832	19.4764519	18.9762592	16.7938309	17.5680218	16.897541	17.034584
990	Mitochondrial fission 1 protein OS=Rattus norvegicus OX=10116 GN=Fis1 PE=1 SV=1	Fis1	P84817	3.45040393	4.536486626	17.7177696	15.8054333	17.3392143	16.1815281	21.8350868	20.0116978	21.6594887	21.6836185
991	Mitochondrial import receptor subunit TOM22 homolog OS=Rattus norvegicus OX=10116 GN=Tomm22 PE=1 SV=1	Tomm22	Q75Q41	1.91039257	2.523348331	16.2700329	17.1188717	15.6317482	15.5342331	16.8781872	19.5247459	18.8372154	19.4081306
992	Mitochondrial import receptor subunit TOM34 OS=Rattus norvegicus OX=10116 GN=Tomm34 PE=1 SV=1	Tomm34	Q3KRD5	6.65574637	5.338871002	18.7174397	17.9704018	18.489542	18.4368114	24.056612	23.4009171	23.7289391	23.7832108
993	Mitogen-activated protein kinase 1 OS=Rattus norvegicus OX=10116 GN=Mapk1 PE=1 SV=3	Mapk1	P63086	4.58192227	4.357021332	18.6689835	18.9944477	17.9587383	18.0131741	23.5084934	22.133707	22.6954765	22.7257519
994	Mitogen-activated protein kinase kinase 4 OS=Rattus norvegicus OX=10116 GN=Map2k4 PE=1 SV=3	Map2k4	F1LP57	1.91857491	1.284505367	19.0682507	20.4031067	19.2637577	20.3779144	21.1480999	20.8757591	21.0677319	21.1594601
995	Mitogen-activated protein kinase kinase 6 OS=Rattus norvegicus OX=10116 GN=Map2k6 PE=1 SV=1	Map2k6	Q925D6	4.7167897	3.122160912	17.2926025	17.3393269	17.2777348	17.5811672	21.2379055	20.2506599	20.2292461	20.2616634
996	Mitogen-activated protein kinase kinase kinase kinase 4 OS=Rattus norvegicus OX=10116 GN=Map4k4 PE=1 SV=1	Map4k4	A0A0G2K7W4	3.19949507	2.992006063	14.6931686	15.7838154	14.9690428	16.548811	19.0309143	18.4674244	18.2765083	18.188015
997	Mitogen-activated protein kinase OS=Rattus norvegicus OX=10116 GN=Mapk14 PE=1 SV=1	Mapk14	G3V617	3.86533884	4.076836824	17.2557297	16.6582603	16.897068	15.458066	21.3942623	20.3066196	20.1963539	20.6792355
998	Mitogen-activated protein kinase-activated protein kinase 2 OS=Rattus norvegicus OX=10116 GN=Mapkapk2 PE=1 SV=3	Mapkapk2	F1M9C0	4.81884006	4.335621357	17.5647678	16.537735	16.3804436	16.3814545	21.587101	20.8836117	21.0379868	20.6981869
999	MMS19 homolog, cytosolic iron-sulfur assembly component OS=Rattus norvegicus OX=10116 GN=Mms19 PE=1 SV=1	Mms19	M0R6T4	3.69549164	6.422482014	14.4738798	16.9192581	14.9588814	13.293519	20.5305347	21.5498123	21.6015625	21.6535568
1000	MOB kinase activator 1B OS=Rattus norvegicus OX=10116 GN=Mob1b PE=1 SV=1	Mob1b	D4A1V7	4.96474524	6.328649759	16.1629963	16.5729446	14.589757	15.0986881	22.1388054	21.6667023	22.1057434	21.827734
1001	MOB-like protein phocein OS=Rattus norvegicus OX=10116 GN=Mob4 PE=1 SV=1	Mob4	Q9QYW3	3.36399987	4.432203054	16.7904205	17.4261532	15.7445908	14.5267859	20.5578384	20.54813	20.6380367	20.4727573
1002	Moesin OS=Rattus norvegicus OX=10116 GN=Msn PE=1 SV=1	Msn	A0A096MK30	5.60604884	2.117798805	21.8818302	22.077446	21.6993446	21.6780739	24.1179352	24.0219574	23.7397881	23.9282093
1003	MON2 homolog, regulator of endosome-to-Golgi-trafficking OS=Rattus norvegicus OX=10116 GN=Mon2 PE=1 SV=3	Mon2	D3ZCG3	0.31736974	0.700213194	15.8223619	18.3887768	15.6004581	16.7472153	17.525526	18.6474972	17.7718334	15.4148083
1004	Monocarboxylate transporter 1 OS=Rattus norvegicus OX=10116 GN=Slc16a1 PE=1 SV=1	Slc16a1	P53987	3.8046122	2.296288013	20.0260677	20.7039852	20.4402313	20.5678234	22.0882721	23.1755257	22.910162	22.7493
1005	Monocarboxylate transporter 4 OS=Rattus norvegicus OX=10116 GN=Slc16a3 PE=1 SV=1	Slc16a3	O35910	1.78676558	1.936769247	17.142519	14.4349546	16.4773445	15.8730259	18.0398884	17.8953419	17.6378822	18.1018085
1006	Mortality factor 4-like protein 1 OS=Rattus norvegicus OX=10116 GN=Morf4l1 PE=2 SV=1	Morf4l1	Q6AYU1	2.07226014	-1.307759762	18.3561497	18.6987953	18.8717098	18.309309	16.5122967	17.9702015	17.4860859	17.0363407
1007	Muc1 protein OS=Rattus norvegicus OX=10116 GN=Muc1 PE=2 SV=1	Muc1	B2GV31	3.0915101	-2.050037384	18.8484001	19.7959156	20.3253708	19.2545395	17.3934307	17.5511398	17.3769913	17.7025146
1008	Multifunctional protein ADE2 OS=Rattus norvegicus OX=10116 GN=Paics PE=1 SV=3	Paics	P51583	3.01093006	2.588253975	21.6621914	21.4409389	21.1079788	21.3059158	25.0090847	22.9708939	23.9590816	23.9309807
1009	Multimerin 1 OS=Rattus norvegicus OX=10116 GN=Mmrn1 PE=4 SV=1	Mmrn1	D4A3E0	5.06534747	2.728958607	21.5905285	21.0488529	21.9193726	21.3113232	24.2749348	24.0441666	24.1597195	24.3070908
1010	Murinoglobulin-1 OS=Rattus norvegicus OX=10116 GN=LOC297568 PE=1 SV=1	LOC297568	A0A0G2K926	0.81383934	-2.377487421	16.9745216	14.2890587	19.7910957	20.6161366	15.1176834	15.3708029	15.5237312	16.1486454
1011	Murinoglobulin-1 OS=Rattus norvegicus OX=10116 GN=Mug1 PE=2 SV=1	Mug1	Q03626	5.30788885	-4.352707863	26.1046276	26.4962044	26.7519531	26.2005177	22.7227478	21.6544666	21.7289639	22.036293
1012	Muscular LMNA-interacting protein OS=Rattus norvegicus OX=10116 GN=Mlip PE=1 SV=1	Mlip	A0A096MK47	3.99300698	3.368170738	19.584753	19.2716885	19.6787224	18.0919151	22.479475	22.5312805	22.7091045	22.3799019
1013	Myadm protein OS=Rattus norvegicus OX=10116 GN=Myadm PE=1 SV=1	Myadm	Q05BA4	4.84776964	3.189391613	18.6329651	19.7021694	18.8696938	19.0532455	22.2930851	22.4873505	22.0053711	22.2298336
1014	Myl6 protein OS=Rattus norvegicus OX=10116 GN=Myl6 PE=2 SV=1	Myl6	B2GV99	4.34317598	5.233475685	20.2484188	20.6719894	20.1562233	18.5746822	25.5207481	25.4576778	24.7467098	24.8600807
1015	Myocardial ischemic preconditioning associated protein 7 OS=Rattus norvegicus OX=10116 GN=Pxn PE=1 SV=1	Pxn	Q1EG89	3.04351959	5.842567205	14.9752207	12.9352531	16.5797596	17.1633987	21.5592251	21.408392	21.282299	20.7739849
1016	Myocyte-specific enhancer factor 2A OS=Rattus norvegicus OX=10116 GN=Mef2a PE=1 SV=2	Mef2a	M0R6R7	0.26051748	0.232224464	18.2324486	17.6700821	17.5276127	16.5223923	17.9492397	17.6971741	17.6871529	17.5478668
1017	Myoglobin OS=Rattus norvegicus OX=10116 GN=Mb PE=1 SV=3	Mb	Q9QZ76	5.1224494	8.561638594	16.1004009	15.3524733	16.4146709	13.8656425	23.8742542	24.4677868	24.1140232	23.5236778
1018	Myopalladin OS=Rattus norvegicus OX=10116 GN=Mypn PE=1 SV=1	Mypn	A0A0G2K046	2.70545056	3.969206572	16.7679329	15.6274538	16.0059738	13.3926334	19.5253658	19.7606392	19.6334934	18.7513218
1019	Myosin heavy chain 14 OS=Rattus norvegicus OX=10116 GN=Myh14 PE=1 SV=1	Myh14	F1LNF0	1.09094382	1.357326508	16.2401218	16.5695915	17.0200539	16.6667252	16.9586983	19.7390804	17.2103844	18.0176353
1020	Myosin light chain 3 OS=Rattus norvegicus OX=10116 GN=Myl3 PE=1 SV=2	Myl3	P16409	4.99455202	5.419904709	20.0375805	21.0307484	19.4325809	20.585844	25.8704205	26.173645	25.2897816	25.4325256
1021	Myosin light chain 4 OS=Rattus norvegicus OX=10116 GN=Myl4 PE=2 SV=2	Myl4	P17209	3.29674143	8.098809242	14.6065111	14.0724602	15.1306067	19.1951065	24.5657158	23.6452732	23.3893528	23.7995796
1022	Myosin light chain 7 OS=Rattus norvegicus OX=10116 GN=Myl7 PE=1 SV=1	Myl7	A0A0G2K2W5	3.88379627	3.854202271	18.0068016	17.4375801	16.9222336	16.3176022	21.744957	20.7639694	20.5455666	21.0465336
1023	Myosin light chain kinase 3 OS=Rattus norvegicus OX=10116 GN=Mylk3 PE=1 SV=1	Mylk3	E9PT87	2.7277853	2.261230946	20.7328529	22.0903606	20.3301544	20.2896385	23.3064728	23.0462608	23.1729565	22.9622402
1024	Myosin phosphatase Rho-interacting protein OS=Rattus norvegicus OX=10116 GN=Mprip PE=1 SV=1	Mprip	A0A0G2JUR5	0.88193935	-0.976816416	16.5568237	17.0047474	17.0528851	17.4924946	15.7991409	14.6919718	17.0908298	16.6177425
1025	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform OS=Rattus norvegicus OX=10116 GN=Myl2 PE=1 SV=2	Myl2	P08733	7.55444181	7.061757088	18.9047394	18.274847	18.7691212	18.2937088	25.6325493	25.9122849	25.4304237	25.5141869
1026	Myosin regulatory light chain RLC-A OS=Rattus norvegicus OX=10116 GN=Rlc-a PE=2 SV=2	Myl12a	P13832	5.49742512	5.302511215	18.3405056	18.6853504	19.1798782	18.298584	23.9324341	24.6311417	23.5838718	23.5669155
1027	Myosin XVIIIa OS=Rattus norvegicus OX=10116 GN=Myo18a PE=1 SV=1	Myo18a	A0A0G2JY08	3.91034141	2.105966091	19.7388287	19.3029022	20.0179634	19.5783329	21.2027836	22.0005493	21.9194584	21.9391003
1028	Myosin XVIIIb OS=Rattus norvegicus OX=10116 GN=Myo18b PE=1 SV=2	Myo18b	M0R6Z9	1.48651131	1.256939888	17.8894558	17.7055244	18.7717819	19.1419182	19.0399628	19.2553463	20.3203468	19.920784
1029	Myosin, heavy polypeptide 10, non-muscle, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Myh10 PE=1 SV=1	Myh10	G3V9Y1	1.08853006	0.908413887	26.1102409	25.7601185	25.763979	24.4791737	26.8617401	26.8241291	25.8616199	26.1996784
1030	Myosin, heavy polypeptide 9, non-muscle OS=Rattus norvegicus OX=10116 GN=Myh9 PE=1 SV=1	Myh9	G3V6P7	4.27834765	3.088397026	23.2996178	23.883873	23.530962	24.0038223	26.5384274	27.5387783	26.4811535	26.513504
1031	Myosin-11 OS=Rattus norvegicus OX=10116 GN=Myh11 PE=1 SV=1	Myh11	A0A0G2K6S9	3.04157767	3.19810915	21.0132484	20.0199871	20.0440693	20.9499264	22.4417076	24.5661507	23.9787846	23.833025
1032	Myosin-6 OS=Rattus norvegicus OX=10116 GN=Myh6 PE=1 SV=2	Myh6	G3V885	1.06893558	2.833424568	24.0318069	19.3326416	19.8117867	18.3870373	22.2355766	24.9002934	22.9148369	22.8462639
1033	Myosin-7 OS=Rattus norvegicus OX=10116 GN=Myh7 PE=1 SV=1	Myh7	G3V8B0	3.8998721	5.778518677	21.4846268	21.2124443	21.2262001	21.3888245	25.4917068	28.7227726	27.0926323	27.1190586
1034	Myosin-binding protein C, cardiac-type OS=Rattus norvegicus OX=10116 GN=Mybpc3 PE=1 SV=2	Mybpc3	P56741	4.59637712	4.338863373	19.3654556	17.9828167	19.5873032	19.3727055	23.5177231	23.5578079	23.2443085	23.343895
1035	Myosin-binding protein C, slow-type OS=Rattus norvegicus OX=10116 GN=Mybpc1 PE=1 SV=1	Mybpc1	A0A0G2JUE5	0.43162111	-0.922810793	17.5262318	18.5902443	19.400692	18.5527706	18.41049	18.6384792	14.9857473	18.3439789

1036	Myotubularin related protein 2 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Mtmr2 PE=1 SV=1	Mtmr2	D3ZA31	0.55611907	0.838720798	15.661212	15.4451303	13.296361	16.5481262	16.3274937	16.0972939	16.1875401	15.6933851
1037	Myristoylated alanine-rich C-kinase substrate OS=Rattus norvegicus OX=10116 GN=Marcks PE=1 SV=2	Marcks	P30009	4.80905006	2.817830563	22.8182182	23.3931046	23.7963676	22.9622612	26.0149002	26.1661453	26.0265675	26.0336609
1038	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Rattus norvegicus OX=10116 GN=Ddah1 PE=1 SV=3	Ddah1	O08557	3.04626173	5.830260992	13.8235168	14.2714024	13.5586233	17.6560421	20.4593506	20.8254356	20.8056049	20.5402374
1039	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Rattus norvegicus OX=10116 GN=Ddah2 PE=1 SV=1	Ddah2	Q6MG60	2.46457831	1.427456379	18.450428	18.7432632	19.2023888	18.5411777	19.9903069	20.8422832	19.6226521	20.1918411
1040	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Rattus norvegicus OX=10116 GN=Slc9a3r1 PE=1 SV=3	Slc9a3r1	Q9JJ19	1.98787767	-2.255347729	19.3942432	19.1804428	20.2490406	17.9969158	17.6863365	15.9125004	16.7479839	17.4524307
1041	N-acetylgalactosamine kinase OS=Rattus norvegicus OX=10116 GN=Galk2 PE=2 SV=1	Galk2	Q5XIG6	1.40443687	1.93208456	14.7068119	17.4830437	16.9549637	15.6456661	17.0337467	18.2186165	18.7740803	18.4923801
1042	N-acetylneuraminate synthase OS=Rattus norvegicus OX=10116 GN=Nans PE=1 SV=1	Nans	B1WC26	1.5218645	3.281083584	16.3741302	18.5536785	17.6185379	15.7537956	17.447094	21.0388355	21.6059704	21.3325768
1043	NAD-dependent protein deacetylase OS=Rattus norvegicus OX=10116 GN=Sirt2 PE=1 SV=1	Sirt2	A0A0G2JWM2	3.62577397	3.224649429	18.5286827	17.1070786	17.9679356	18.9996891	21.4830494	21.143713	21.4331627	21.4420586
1044	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 5 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=	Ndufb5	D4A565	0.28377547	0.405562401	19.378891	19.0134754	17.9841633	17.2552185	17.8097687	19.3539181	18.9740868	19.1162243
1045	NADH dehydrogenase (Ubiquinone) Fe-S protein 8 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ndufs	Ndufs8	B0BNE6	0.76871208	-0.410510063	20.1947098	20.9733677	20.5512505	19.9566097	19.6021385	20.211256	20.0164089	20.2040939
1046	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Rattus norvegicus OX=10116 GN=Nd	Ndufa10	Q561S0	0.59473678	1.316121578	18.6016579	18.3016319	18.7029305	15.0525761	18.4923592	20.1562824	17.6276093	19.6470318
1047	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Rattus norvegicus OX=10116 GN=Ndufa12 PE=1 SV	Ndufa12	F1LXA0	2.94434989	3.448740959	16.9509506	16.8874321	15.3194046	15.1396008	18.521307	19.9101334	19.7745857	19.8863258
1048	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Rattus norvegicus OX=10116 GN=Ndufa6 PE=1 SV=1	Ndufa6	D4A3V2	0.3053762	0.397758484	19.4168987	16.9144173	18.7238941	18.7581959	18.5973816	19.1193638	18.8367805	18.850914
1049	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Rattus norvegicus OX=10116 GN=Ndufa8 PE=1 SV=1	Ndufa8	A0A0G2JVL6	2.09580574	3.813533068	16.9163246	16.4891453	15.8763733	13.7704191	17.5675526	20.6179886	20.2439899	19.8768635
1050	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndu	Ndufa9	Q5BK63	2.8569344	3.973716021	15.0840034	14.7797785	15.4915953	12.9479685	17.254528	19.0713596	18.8329334	19.0393887
1051	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufv1 PE=1 SV=1	Ndufv1	Q5XIH3	3.21420094	3.366953373	17.5471458	17.311039	17.0406055	16.0982895	19.2573967	21.0908718	20.2928753	20.8237495
1052	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufv2 PE=1 SV=2	Ndufv2	P19234	0.49282942	0.701394558	19.1724167	20.4171047	18.6911278	21.3442688	20.0484047	21.1884613	20.4181175	20.7755127
1053	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufs2 PE=1	Ndufs2	Q641Y2	2.16738396	2.602531672	15.8171244	16.1986866	17.2348747	16.6578388	17.4071178	19.9034843	19.3962593	19.6117897
1054	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Rattus norvegicus OX=10116 GN=LOC1009125	LOC679739	D3ZCZ9	2.97645435	4.304002523	15.9132204	15.6063595	15.9268265	13.3500214	18.352335	19.9126911	19.8604527	19.8869591
1055	NADH:ubiquinone oxidoreductase subunit A13 OS=Rattus norvegicus OX=10116 GN=Ndufa13 PE=1 SV=1	Ndufa13	D3ZE15	0.95999174	-1.383265734	19.7190971	18.9940205	18.7838478	18.4969482	18.2420731	17.5393009	18.9446793	15.7347975
1056	NADH:ubiquinone oxidoreductase subunit B10 OS=Rattus norvegicus OX=10116 GN=Ndufb10 PE=1 SV=1	Ndufb10	D4A0T0	3.66958997	4.290819883	15.9573774	17.9276581	17.7399483	16.5492191	20.5553303	21.6509361	21.4924679	21.6387482
1057	NADH-cytochrome b5 reductase 3 OS=Rattus norvegicus OX=10116 GN=Cyb5r3 PE=1 SV=2	Cyb5r3	P20070	2.16229724	2.522283316	15.3343992	17.5638847	17.0908337	17.1743832	20.1476917	19.4994488	18.3062553	19.2992382
1058	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufs1 PE=1 SV=1	Ndufs1	Q66HF1	1.08443952	1.428106308	21.2256355	21.4228001	21.3062096	19.0333405	21.0780354	22.6077919	22.2939491	22.7206345
1059	N-alpha-acetyltransferase 11 OS=Rattus norvegicus OX=10116 GN=Naa11 PE=2 SV=1	Naa11	Q4V8K3	2.53118496	4.095265388	13.8291531	15.6024466	15.4960594	15.3219271	16.9439487	20.0541019	19.7008228	19.9317741
1060	Nascent polypeptide-associated complex subunit alpha OS=Rattus norvegicus OX=10116 GN=Naca PE=1 SV=1	Naca	M0R9L0	5.27186949	4.833185196	20.8864155	20.229023	20.2891617	20.6017246	24.9882202	26.1244392	25.3500996	24.8763065
1061	Natriuretic peptides A OS=Rattus norvegicus OX=10116 GN=Nppa PE=1 SV=1	Nppa	P01161	6.18919234	5.383824348	17.8177338	17.7025013	17.480299	17.3014259	22.3592701	23.385704	23.1710567	22.9212265
1062	Nck-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Nckap1 PE=2 SV=1	Nckap1	P55161	2.16205769	0.710643768	20.4634628	19.9046345	20.0663815	20.1228199	20.6839657	21.026741	21.1172256	20.5719414
1063	NDUFA4, mitochondrial complex-associated OS=Rattus norvegicus OX=10116 GN=Ndufa4 PE=1 SV=1	Ndufa4	B2RZD6	2.50614111	3.155891895	19.1978302	19.1048279	18.2909584	16.9606304	20.3205509	22.1041851	21.7747307	21.9783478
1064	Nebulette OS=Rattus norvegicus OX=10116 GN=Nebl PE=1 SV=2	Nebl	D4A164	1.12103903	1.651252747	19.9903297	19.1860294	19.0726376	16.8755932	20.0197201	21.405405	20.6514244	19.6530514
1065	Nebulin-related-anchoring protein OS=Rattus norvegicus OX=10116 GN=Nrap PE=1 SV=1	Nrap	D4A4K6	2.882649	2.106750965	19.8927193	20.0246944	20.3809738	20.075634	22.7913666	21.8409176	22.802269	21.3664722
1066	Neprilysin OS=Rattus norvegicus OX=10116 GN=Mme PE=1 SV=2	Mme	P07861	0.37735248	-0.373283863	17.7524071	17.1638546	17.2856827	17.7337227	17.6035042	15.9055939	17.4422436	17.49119
1067	Neudesin OS=Rattus norvegicus OX=10116 GN=Nenf PE=2 SV=1	Nenf	Q6IUR5	2.70102739	2.75450182	16.6829929	16.3497524	15.5958347	17.9302807	19.4084682	19.8978195	18.8884296	19.3821507
1068	Neural cell adhesion molecule 1 OS=Rattus norvegicus OX=10116 GN=Ncam1 PE=1 SV=3	Ncam1	F1LUV9	5.41795016	3.090700626	18.8393364	19.3806477	19.596117	18.9884911	22.4180527	22.0679913	22.257082	22.4242687
1069	Neuroendocrine secretory protein 55 OS=Rattus norvegicus OX=10116 GN=Gnas PE=2 SV=1	Gnas	Q792G6	0.9475393	-0.735882759	18.1962109	18.1889706	18.2341919	17.7755756	17.9828396	16.3207798	17.2685108	17.8792877
1070	Neuromodulin OS=Rattus norvegicus OX=10116 GN=Gap43 PE=1 SV=1	Gap43	P07936	0.14237612	-0.062329769	19.1423721	19.3927135	19.4523888	19.3597813	19.4604435	19.4465981	18.8232327	19.3676624
1071	Neuron navigator 2 OS=Rattus norvegicus OX=10116 GN=Nav2 PE=1 SV=1	Nav2	A0A0G2K833	0.82494744	1.100558758	20.4194546	20.0706654	17.7830181	18.4561119	19.9983368	20.7959118	20.4434414	19.893795
1072	Neuroplastin OS=Rattus norvegicus OX=10116 GN=Nptn PE=1 SV=2	Nptn	P97546	0.25760583	0.705501556	13.2361736	17.6888351	17.4219131	17.3233757	17.4782639	17.6800919	17.2506733	16.0832748
1073	NHS-like 1 OS=Rattus norvegicus OX=10116 GN=Nhsl1 PE=4 SV=1	Nhsl1	A0A0G2JZL4	0.22882471	-0.111145496	21.1662292	21.0301113	20.999918	20.5474701	20.901392	20.4041119	20.9924335	21.0012093
1074	Niban-like protein 1 OS=Rattus norvegicus OX=10116 GN=Fam129b PE=1 SV=1	Niban2	B4F7E8	4.39409196	2.676528931	18.2521877	18.6848373	18.0843964	18.0832882	20.431076	20.8239212	21.1888771	21.366951
1075	Nicastrin OS=Rattus norvegicus OX=10116 GN=Ncstn PE=1 SV=1	Ncstn	Q8CGU6	2.23226818	2.932136297	15.7631321	14.9112263	16.2120495	13.1367788	17.6863403	18.4417973	17.6630859	17.9605083
1076	Nicotinamide nucleotide transhydrogenase OS=Rattus norvegicus OX=10116 GN=Nnt PE=1 SV=1	Nnt	Q5BJZ3	4.00090187	2.92249155	20.8631954	20.4553852	19.9251976	19.8043327	22.6982632	23.6975727	23.0715828	23.2706585
1077	Nicotinamide phosphoribosyltransferase OS=Rattus norvegicus OX=10116 GN=Nampt PE=1 SV=1	Nampt	Q80Z29	3.86504952	3.38644743	16.9849529	17.246933	17.5593987	16.1502953	19.7683945	20.1405048	20.7589512	20.819519
1078	Nidogen-1 OS=Rattus norvegicus OX=10116 GN=Nid1 PE=1 SV=1	Nid1	F1LM84	0.16751332	-0.151474953	19.6755276	18.5872974	19.1671429	19.433691	19.7420006	18.6261749	19.2004738	18.6891098
1079	NIMA-related kinase 9 OS=Rattus norvegicus OX=10116 GN=Nek9 PE=1 SV=1	Nek9	A0A0G2K8N9	3.53782472	4.865742922	16.5977497	14.8676376	14.2599459	16.8273239	20.1155605	20.6410999	20.7215767	20.5373917
1080	Nitric oxide synthase-interacting protein OS=Rattus norvegicus OX=10116 GN=Nosip PE=1 SV=1	Nosip	D3ZH12	0.05502916	0.166550398	16.7487164	14.2021952	16.7885876	19.2549591	16.3527813	16.5816402	17.512373	17.2138653
1081	NmrA-like family domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Nmral1 PE=1 SV=2	Nmral1	D3ZDB9	3.72922294	4.785319805	18.0216293	15.2614422	16.4552155	16.6415501	21.8572826	21.0988464	21.2937527	21.2712345
1082	N-myc downstream regulated gene 2, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Ndrg2 PE=1 SV=1	Ndrg2	A0A0G2JSU4	4.72280832	6.042081356	17.7051964	16.6382008	18.7407646	16.9472656	23.1460781	23.4690018	23.9546566	23.6300163
1083	Non-SMC condensin I complex, subunit G OS=Rattus norvegicus OX=10116 GN=Ncapg PE=1 SV=3	Ncapg	D3ZD72	0.77090869	-0.791598558	17.3405113	16.7611523	16.7641659	18.1191311	16.1134567	15.5261641	16.9139824	17.2649632
1084	Non-specific serine/threonine protein kinase OS=Rattus norvegicus OX=10116 GN=Mark2 PE=1 SV=1	Mark2	A0A0G2K6X6	4.44335646	5.464542627	15.8917828	14.889924	16.262989	14.2881794	20.5645523	21.3207474	20.9696541	20.336092
1085	Non-specific serine/threonine protein kinase OS=Rattus norvegicus OX=10116 GN=Mark3 PE=1 SV=1	Mark3	A0A0G2JU56	2.56418465	2.656744003	18.2060566	17.8498268	16.502203	16.3415756	19.9232864	20.6191044	19.6181831	19.3660641
1086	Non-specific serine/threonine protein kinase OS=Rattus norvegicus OX=10116 GN=Prkaa2 PE=1 SV=1	Prkaa2	G3V715	3.94854264	6.424316883	15.1612444	14.9229078	16.0056725	18.0429516	22.8125877	22.3073635	22.5271664	22.1829262
1087	Non-specific serine/threonine protein kinase OS=Rattus norvegicus OX=10116 GN=Stk38 PE=1 SV=3	Stk38	G3V9Q4	0.1374844	0.280046463	17.2266636	17.3621483	16.6538849	18.5041351	18.6482029	15.7654972	17.9788895	18.4744282
1088	NSF attachment protein gamma OS=Rattus norvegicus OX=10116 GN=Napg PE=1 SV=1	Napg	A0A0G2K350	3.36689926	3.206632137	16.679081	15.5891857	17.652359	16.5305958	20.3297539	19.8071537	19.6311569	19.5096855
1089	NSFL1 cofactor p47 OS=Rattus norvegicus OX=10116 GN=Nsfl1c PE=1 SV=1	Nsfl1c	O35987	3.84692553	3.263010025	18.2195168	18.8448658	18.8278027	17.4015484	21.5965366	21.5113697	21.1940689	22.0437984
1090	Nuclear autoantigenic sperm protein OS=Rattus norvegicus OX=10116 GN=Nasp PE=1 SV=1	Nasp	Q66HD3	3.71954966	1.742479324	20.5174313	21.2669716	20.8387089	20.6411476	22.8825512	22.2444401	22.6738262	22.4330561
1091	Nuclear factor 1 OS=Rattus norvegicus OX=10116 GN=Nfib PE=1 SV=2	Nfib	O70185	0.93677588	2.38708806	18.3698349	20.303791	17.6534977	14.1157732	20.3182678	20.0647068	19.8728466	19.7354279
1092	Nuclear factor kappaB subunit p65 OS=Rattus norvegicus OX=10116 GN=Rela PE=1 SV=1	Rela	Q7TQN4	2.30251066	3.69568038	16.8544483	17.8767567	17.0508289	13.9710226	20.3121815	19.9250851	20.176981	20.1215305
1093	Nuclear factor NF-kappa-B p105 subunit OS=Rattus norvegicus OX=10116 GN=Nfkb1 PE=1 SV=2	Nfkb1	F1LQH2	4.84782587	1.364881039	20.0149307	20.1521511	20.1456661	20.2354412	21.7295628	21.3833237	21.5897045	21.3051224
1094	Nuclear migration protein nudC OS=Rattus norvegicus OX=10116 GN=Nudc PE=1 SV=1	Nudc	Q63525	3.24555832	2.040364742	19.3549557	19.5467243	19.4458504	19.0742397	21.8749352	20.5572338	21.6638699	21.4871902
1095	Nuclear pore complex protein Nup88 OS=Rattus norvegicus OX=10116 GN=Nup88 PE=1 SV=1	Nup88	O08658	3.51633124	5.018681526	15.5602646	15.8401003	15.1061115	12.8796663	19.7805061	19.7803955	19.9006958	19.9992714
1096	Nuclear pore glycoprotein p62 OS=Rattus norvegicus OX=10116 GN=Nup62 PE=1 SV=1	Nup62	P17955	1.40236663	2.790351629	17.9294777	17.4827309	18.4326897	13.9892492	20.6292248	18.9685822	19.7900391	19.607708

1097	Nuclear protein localization protein 4 homolog OS=Rattus norvegicus OX=10116 GN=Nploc4 PE=1 SV=1	Nploc4	A0A0G2JU66	4.74765708	4.663636923	15.890152	16.0350208	15.9996519	15.106266	21.1131153	19.6027966	20.5008774	20.4688492
1098	Nuclear transport factor 2 OS=Rattus norvegicus OX=10116 GN=Nutf2 PE=1 SV=1	Nutf2	P61972	1.21663056	1.699038506	16.3160439	17.7590389	14.3430862	16.6037769	18.5397224	17.8810139	17.6747227	17.722641
1099	Nuclease-sensitive element-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ybx1 PE=1 SV=1	Ybx1	Q3ZAV2	1.93795549	3.064237118	21.635231	21.859808	21.7840691	18.5858536	23.2542896	24.782177	23.9936447	24.0917988
1100	Nucleobindin 2, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Nucb2 PE=1 SV=1	Nucb2	G3V8R1	0.67442818	0.722888947	17.597683	16.6651382	16.184763	16.634346	16.2799568	17.7348003	17.7065849	18.2521439
1101	Nucleobindin-1 OS=Rattus norvegicus OX=10116 GN=Nucb1 PE=1 SV=1	Nucb1	Q63083	2.87343754	2.886666298	17.9559765	17.4288597	17.1387806	16.5411205	19.090004	21.0893269	20.0023899	20.4296818
1102	Nucleolin OS=Rattus norvegicus OX=10116 GN=Ncl PE=1 SV=1	Ncl	Q5U328	5.1456844	4.442286968	19.5212727	18.7306843	18.6154346	19.2398891	22.8729153	23.958971	23.5455627	23.4989796
1103	Nucleophosmin OS=Rattus norvegicus OX=10116 GN=Npm1 PE=1 SV=1	Npm1	P13084	1.90890806	3.519624472	15.841073	13.9099264	15.4046087	16.0900078	21.1675205	18.9390144	17.0628986	18.1546803
1104	Nucleoside diphosphate kinase A OS=Rattus norvegicus OX=10116 GN=Nme1 PE=1 SV=1	Nme1	Q05982	3.68667239	1.945353508	16.3907814	16.023695	16.005518	16.9159966	18.4856148	18.4390335	18.2214699	17.9712868
1105	Nucleoside diphosphate kinase B OS=Rattus norvegicus OX=10116 GN=Nme2 PE=1 SV=1	Nme2	P19804	3.22736691	3.412282944	20.9423084	21.0958195	21.3675804	19.2443905	23.5613594	24.254961	24.4692039	24.0137062
1106	Nucleosome assembly protein 1-like 1 OS=Rattus norvegicus OX=10116 GN=Nap1l1 PE=1 SV=1	Nap1l1	G3V6H9	2.52464548	3.177508354	17.1766682	16.5099316	15.4512138	18.3465118	20.5728226	19.3295441	20.0415173	20.2504749
1107	Nucleosome assembly protein 1-like 4 OS=Rattus norvegicus OX=10116 GN=Nap1l4 PE=1 SV=1	Nap1l4	A0A0H2UHZ2	4.11730727	5.405958891	15.3438644	14.8998308	16.4028072	17.3568363	21.7820969	21.1671886	21.4185963	21.2592926
1108	Obg-like ATPase 1 OS=Rattus norvegicus OX=10116 GN=Ola1 PE=2 SV=1	Ola1	A0JPJ7	5.18129448	3.73633194	18.1010208	17.9769344	18.9120464	18.5022259	21.8955154	21.8544674	22.469532	22.2180405
1109	Obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF OS=Rattus norvegicus OX=10116 GN=Obscn PE=1 SV=1	Obscn	A0A0G2JUP3	3.52152979	2.604373932	18.5266914	18.2961044	17.6726742	19.3051949	20.9876442	21.0927963	21.2857494	20.8519707
1110	Obscurin-like protein 1 OS=Rattus norvegicus OX=10116 GN=Obsl1 PE=2 SV=3	Obsl1	D3ZZ80	1.26385303	-1.556364536	20.6028271	21.7273045	21.0550804	19.3298035	19.354826	20.1780453	18.3206406	18.6360455
1111	OCIA domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Ociad1 PE=1 SV=1	Ociad1	Q5XIG4	0.16528471	0.20650816	18.0523338	17.8781872	18.2884598	19.7436848	18.4669838	19.3443699	18.3239517	18.6533928
1112	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase	Ogt	G3V6F4	4.20079265	3.499290466	17.9163876	17.108078	17.5511627	18.3328476	20.7702904	21.6203327	21.6644421	20.8505726
1113	Omega-amidase NIT2 OS=Rattus norvegicus OX=10116 GN=Nit2 PE=1 SV=1	Nit2	Q497B0	2.87325096	1.361182213	18.2063751	17.929985	17.5375595	18.1155262	18.944313	19.8379841	19.1540833	19.2977943
1114	Oncoprotein-induced transcript 3 protein OS=Rattus norvegicus OX=10116 GN=Oit3 PE=2 SV=1	Oit3	Q6V0K7	2.8306071	-3.070522785	21.4104557	21.0613327	19.6698456	20.0120087	17.5660038	18.0950184	16.4081039	17.8024254
1115	Osteopontin OS=Rattus norvegicus OX=10116 GN=Spp1 PE=1 SV=2	Spp1	P08721	1.45914149	-1.605611324	17.7371693	17.3528481	18.2951431	17.8793831	17.7440071	16.2472782	15.6974487	15.1533642
1116	Out at first protein homolog OS=Rattus norvegicus OX=10116 GN=Oaf PE=2 SV=1	Oaf	Q6AYE5	1.24065475	1.439298391	16.4110584	14.3698225	17.1456299	16.486805	17.6680565	17.1998329	17.5269527	17.7756672
1117	Oxidative stress-responsive kinase 1 OS=Rattus norvegicus OX=10116 GN=Oxsr1 PE=1 SV=1	Oxsr1	D3ZUC9	3.47820385	5.543676376	15.5566607	14.4193277	17.4654388	17.2666187	22.2925644	21.3221912	21.813406	21.4545898
1118	Oxysterol-binding protein OS=Rattus norvegicus OX=10116 GN=Osbp PE=1 SV=2	Osbp	D4A9D8	2.89357116	4.367497444	17.3374119	14.15592	17.2668839	17.0480042	20.8757877	20.8154793	20.8330555	20.7538872
1119	Oxysterol-binding protein OS=Rattus norvegicus OX=10116 GN=Osbpl11 PE=1 SV=1	Osbpl11	B5DF74	4.38018881	5.196511745	14.7236443	14.4194059	14.1928282	16.2616558	20.512291	19.7930546	20.0325127	20.045723
1120	Pachytene checkpoint protein 2 homolog OS=Rattus norvegicus OX=10116 GN=Trip13 PE=2 SV=1	Trip13	Q5XHZ9	3.11511293	4.785377502	13.5016155	15.9304295	16.5476875	16.8417149	20.6507359	20.4408855	20.6036816	20.2676544
1121	Pantothenate kinase 4 OS=Rattus norvegicus OX=10116 GN=Pank4 PE=1 SV=1	Pank4	G3V7T3	3.48379521	4.743910074	18.1392288	16.3438339	16.6943817	15.0765257	21.3440418	20.8940411	21.4040165	21.5875111
1122	Paralemmin 2 OS=Rattus norvegicus OX=10116 GN=Palm2 PE=1 SV=1	Palm2	A0A096MIZ1	2.5482826	4.98568058	15.0325117	17.085062	14.1246967	12.235013	19.7099056	20.0397816	19.0953979	19.5749207
1123	Paralemmin-1 OS=Rattus norvegicus OX=10116 GN=Palm PE=1 SV=1	Palm	Q920Q0	1.79084838	-0.862651825	19.212925	18.7013817	19.2253666	19.2733669	18.5323963	18.4415741	17.5757122	18.4127502
1124	Parvin, beta OS=Rattus norvegicus OX=10116 GN=Parvb PE=1 SV=1	Parvb	D3ZKG5	2.67397912	2.200222015	18.168129	17.9727726	19.4452877	18.6652489	21.1517487	20.0227623	21.2010708	20.6767445
1125	PDZ and LIM domain 3, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Pdlim3 PE=1 SV=1	Pdlim3	A0A0G2JSM3	4.23935145	5.781368971	17.7256832	17.1904678	15.6982298	18.2952175	23.3923111	22.6516342	23.0130596	22.9780693
1126	PDZ and LIM domain protein 1 OS=Rattus norvegicus OX=10116 GN=Pdlim1 PE=1 SV=4	Pdlim1	P52944	3.72545781	4.663633585	17.4430504	15.2902021	15.0952101	15.8207769	21.0545502	20.0167923	20.6989346	20.5334969
1127	PDZ and LIM domain protein 5 OS=Rattus norvegicus OX=10116 GN=Pdlim5 PE=1 SV=2	Pdlim5	Q62920	5.52096117	8.19900322	18.5671673	17.1761093	17.6763687	16.2516937	25.6249886	25.686306	25.8037071	25.3523502
1128	Peflin OS=Rattus norvegicus OX=10116 GN=Pef1 PE=2 SV=1	Pef1	Q641Z8	1.27769511	1.471954346	16.6793232	16.8013687	17.8700237	17.4032307	19.9708443	18.4254951	17.3430481	18.9023762
1129	Peptide-methionine (R)-S-oxide reductase OS=Rattus norvegicus OX=10116 GN=Msrb3 PE=1 SV=3	Msrb3	D4A650	3.92135432	2.591154575	18.3042507	17.099987	17.4481812	18.0295258	20.6030197	20.2165527	20.3418064	20.0851841
1130	Peptidoglycan recognition protein 2 OS=Rattus norvegicus OX=10116 GN=Pglyrp2 PE=1 SV=2	Pglyrp2	M0R485	3.22667534	-3.932605743	21.5915909	21.242588	22.0824013	22.126955	18.8821259	18.0971203	16.2450123	18.0888538
1131	Peptidyl-glycine alpha-amidating monooxygenase OS=Rattus norvegicus OX=10116 GN=Pam PE=1 SV=1	Pam	P14925	6.27486651	5.407729626	16.8053913	16.9818211	16.0081348	16.6852531	22.019825	22.3381367	21.7782993	21.9752579
1132	Peptidyl-prolyl cis-trans isomerase A OS=Rattus norvegicus OX=10116 GN=Ppia PE=1 SV=2	Ppia	P10111	5.07286596	1.756280899	22.0360451	21.9865875	22.267725	22.3489914	23.6638145	24.033062	24.0577488	23.9098473
1133	Peptidyl-prolyl cis-trans isomerase B OS=Rattus norvegicus OX=10116 GN=Ppib PE=1 SV=3	Ppib	P24368	4.90338166	2.414253235	19.5211926	20.0768757	19.4950657	19.4689102	21.7928543	22.3189487	21.9608688	22.1463852
1134	Peptidyl-prolyl cis-trans isomerase D OS=Rattus norvegicus OX=10116 GN=Ppid PE=1 SV=3	Ppid	Q6DGG0	3.23780466	3.739678383	16.0835495	17.5247536	18.5068493	18.21171	21.3323307	20.8546696	21.654417	21.4441586
1135	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Rattus norvegicus OX=10116 GN=Fkbp1a PE=1 SV=3	Fkbp1a	Q62658	7.27283381	5.423097134	17.7096958	17.9976864	18.2207241	17.9771385	23.5817413	23.0204964	23.482193	23.5132027
1136	Peptidyl-prolyl cis-trans isomerase OS=Rattus norvegicus OX=10116 GN=Ppic PE=1 SV=1	Ppic	Q6AYQ9	3.09253304	-1.905737877	21.8494892	21.3823299	21.7032814	21.8902454	19.7591839	20.4754066	19.0870514	19.8807526
1137	Peptidylprolyl isomerase OS=Rattus norvegicus OX=10116 GN=Fkbp3 PE=1 SV=1	Fkbp3	G3V6L9	5.35129288	4.053910732	17.2361698	17.5155029	16.8771839	17.623867	21.9074001	20.9402466	21.3169651	21.3037548
1138	Pericentriolar material 1 OS=Rattus norvegicus OX=10116 GN=Pcm1 PE=1 SV=1	Pcm1	A0A0G2K0X1	1.3256045	1.310995102	18.7451363	19.9105549	18.5208588	18.7450047	19.6530132	21.5354557	20.0350437	19.9420223
1139	Perilipin 4 OS=Rattus norvegicus OX=10116 GN=Plin4 PE=4 SV=2	Plin4	M0R7S5	1.83110532	1.38556242	20.2650566	21.1957626	19.3008099	19.8337917	21.7271881	21.4877033	21.335413	21.5873661
1140	Perilipin OS=Rattus norvegicus OX=10116 GN=Plin3 PE=1 SV=1	Plin3	M0RA08	5.3188073	2.642480373	21.3692036	21.6929474	21.5236435	21.7771416	24.5571613	23.9897957	24.4034691	23.9824314
1141	Periostin OS=Rattus norvegicus OX=10116 GN=Postn PE=1 SV=1	Postn	D3ZAF5	1.38293727	0.801831722	21.1611309	21.2523327	22.0879154	21.9406185	22.8902035	22.2564754	21.9499722	22.5526733
1142	Peroxiredoxin 5, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Prdx5 PE=1 SV=1	Prdx5	A0A0G2JSS8	1.3346009	0.698599815	18.4350529	18.0037327	18.2331352	18.8174915	18.420332	19.2010555	19.3540573	19.3083668
1143	Peroxiredoxin-1 OS=Rattus norvegicus OX=10116 GN=Prdx1 PE=1 SV=1	Prdx1	Q63716	4.86403692	3.583936691	21.9075108	22.3611031	21.5012341	22.3323059	26.040844	25.113205	25.597002	25.6868496
1144	Peroxiredoxin-2 OS=Rattus norvegicus OX=10116 GN=Prdx2 PE=1 SV=1	Prdx2	A0A0G2JSH9	4.95409848	2.904745579	22.4895649	22.5773449	22.7705803	23.2559109	26.0486298	25.4010944	25.6073246	25.6553345
1145	Peroxiredoxin-4 OS=Rattus norvegicus OX=10116 GN=Prdx4 PE=2 SV=1	Prdx4	Q9Z0V5	0.14298344	0.140698433	19.1516018	20.634161	19.348074	19.1617165	19.680172	19.430933	19.7738171	19.9734249
1146	Peroxiredoxin-6 OS=Rattus norvegicus OX=10116 GN=Prdx6 PE=1 SV=3	Prdx6	O35244	4.01956298	2.52941227	18.2103291	19.1863632	19.1136532	19.3958225	21.5450954	21.2818508	21.7019615	21.4949093
1147	Peroxisomal biogenesis factor 19 OS=Rattus norvegicus OX=10116 GN=LOC100911356 PE=1 SV=1	Pex19	G3V907	3.41422997	4.426113129	16.2687473	17.6453648	16.3707047	15.6866398	22.1426659	19.8834686	20.7876186	20.8621559
1148	Phenylalanine--tRNA ligase alpha subunit OS=Rattus norvegicus OX=10116 GN=Farsa PE=1 SV=1	Farsa	Q505J8	1.70613573	3.265583515	20.3843575	16.6425571	17.1512222	18.9677162	19.8380356	22.1667862	22.2941456	21.9092197
1149	Phosducin-like protein 3 OS=Rattus norvegicus OX=10116 GN=Pdcl3 PE=1 SV=1	Pdcl3	Q4KLJ8	0.32352753	1.255753994	19.2286797	19.5696049	19.7612896	13.1431904	20.0797348	18.196455	18.9609852	19.4886055
1150	Phosphatase domain-containing, paladin 1 OS=Rattus norvegicus OX=10116 GN=Pald1 PE=1 SV=1	Pald1	D3ZCT5	1.87538079	2.313180685	17.2055225	15.0884848	16.2576981	17.3639202	19.0743141	17.6074848	18.966814	19.5197353
1151	Phosphate carrier protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Slc25a3 PE=1 SV=1	Slc25a3	Q6IRH6	2.61991311	3.117252827	19.9178352	21.033289	19.4157467	18.4564705	21.9329662	23.3758163	22.9005489	23.0830212
1152	Phosphatidylethanolamine-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Pebp1 PE=1 SV=3	Pebp1	P31044	3.7245219	3.450903416	19.0680122	18.9739456	20.0128593	17.9513569	22.2757931	22.511982	22.5201015	22.5019112
1153	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Rattus norvegicus OX=10116 GN=Inppl1 PE=1 SV=1	Inppl1	Q9WVR3	6.5572149	3.711112499	18.342802	18.6476212	18.1784344	18.36553	22.3071918	22.1732826	22.1215611	21.7768021
1154	Phosphatidylinositol 4-kinase type 2-alpha OS=Rattus norvegicus OX=10116 GN=Pi4k2a PE=1 SV=1	Pi4k2a	Q99M64	0.00233797	-0.002371788	18.6693573	17.8928394	18.3394852	19.1056137	18.7576389	17.9105263	18.4259491	18.9036942
1155	Phosphatidylinositol binding clathrin assembly protein, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Picalm PE=1 S	Picalm	A0A0G2JTT2	1.77945217	2.791627407	18.0482197	21.2300262	17.8258743	18.4369125	22.5835342	21.3385124	21.4945316	21.2909641
1156	Phosphatidylinositol transfer protein alpha isoform OS=Rattus norvegicus OX=10116 GN=Pitpna PE=1 SV=2	Pitpna	P16446	4.3142433	4.759304047	17.0286045	15.6145601	15.1548815	16.2350178	21.0497761	20.1749096	21.1458225	20.6997719
1157	Phosphodiesterase OS=Rattus norvegicus OX=10116 GN=Pde8b PE=2 SV=1	Pde8b	Q76KC5	1.73456325	-1.237419128	24.0591526	25.4725552	24.070549	24.8727074	23.5511761	23.7895527	23.1826	23.0019588

1158	Phosphofurin acidic cluster sorting protein 1 OS=Rattus norvegicus OX=10116 GN=Pacs1 PE=1 SV=1	Pacs1	F1LPG3	5.83987285	5.549150705	13.6849003	14.0503349	14.6494827	14.962863	19.9867973	19.7506428	19.9915447	19.8151989
1159	Phosphoglucomutase 1 OS=Rattus norvegicus OX=10116 GN=Pgm1 PE=1 SV=2	Pgm1	Q499Q4	4.14122617	5.920761347	14.7074003	16.8996334	17.4817085	16.6643677	22.7195816	22.3660698	22.1773148	22.1731892
1160	Phosphoglycerate kinase 1 OS=Rattus norvegicus OX=10116 GN=Pgk1 PE=1 SV=2	Pgk1	P16617	4.61763798	3.3857131	20.4031506	20.4673672	21.3049088	20.4067936	23.5101013	24.2553558	24.3608856	23.9987297
1161	Phosphoglycerate mutase 1 OS=Rattus norvegicus OX=10116 GN=Pgam1 PE=1 SV=4	Pgam1	P25113	6.29335707	3.58994627	19.7257004	19.9100857	19.6525841	20.1435146	23.4296837	23.1258049	23.602808	23.6333733
1162	Phosphoglycerate mutase 2 OS=Rattus norvegicus OX=10116 GN=Pgam2 PE=1 SV=2	Pgam2	P16290	3.04746201	1.148025036	18.4977531	18.3327084	18.7318058	18.8229656	19.4681511	19.4993572	20.0607357	19.9490891
1163	Phosphoinositide phospholipase C OS=Rattus norvegicus OX=10116 GN=Plcd3 PE=1 SV=1	Plcd3	D4A978	0.86021889	-0.947881222	19.8977432	21.8401108	19.5478077	20.6280479	19.5335121	20.1547127	19.3111801	19.1227798
1164	Phospholipase A2, group XIIB OS=Rattus norvegicus OX=10116 GN=Pla2g12b PE=1 SV=1	Pla2g12b	M0RCI5	0.96533828	0.941639662	16.8406792	15.1770334	16.7788906	17.4751301	17.5555325	17.5085602	17.249464	17.7247353
1165	Phospholipase A2, membrane associated OS=Rattus norvegicus OX=10116 GN=Pla2g2a PE=1 SV=2	Pla2g2a	P14423	2.44504419	-3.719406128	22.2354355	21.0331516	21.7434998	20.2421703	19.4136772	16.1420135	17.4648724	17.3560696
1166	Phospholipase A-2-activating protein OS=Rattus norvegicus OX=10116 GN=Plaa PE=1 SV=3	Plaa	P54319	3.65889197	5.324482441	16.4261971	16.7367172	19.3317318	17.1832943	22.2966461	22.8333111	23.0330563	22.8128567
1167	Phospholipid transfer protein OS=Rattus norvegicus OX=10116 GN=Pltp PE=1 SV=1	Pltp	E9PSP1	7.26693192	-4.075182915	22.0452423	21.720335	21.6890736	21.7831764	17.5847549	18.0051537	17.7193451	17.6278419
1168	Phosphomannomutase OS=Rattus norvegicus OX=10116 GN=Pmm2 PE=1 SV=1	Pmm2	B5DF46	2.62305694	3.08696866	14.5643911	16.9062004	17.202137	16.5646954	19.4914474	19.3249931	19.7331314	19.0357265
1169	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Prpsap2 PE=1 SV=1	Prpsap2	O08618	3.59114087	5.288260937	14.0762138	13.7527361	14.6105795	16.6710339	20.3541336	19.4472637	20.3427429	20.1194668
1170	Phosphorylase b kinase regulatory subunit OS=Rattus norvegicus OX=10116 GN=Phkb PE=1 SV=1	Phkb	Q5RKH5	3.75991974	4.00996685	16.8433685	15.6311378	16.9798203	16.0681362	19.3269386	20.8585682	20.8988914	20.477932
1171	Phytanoyl-CoA dioxygenase, peroxisomal OS=Rattus norvegicus OX=10116 GN=Phyh PE=1 SV=2	Phyh	P57093	3.25699618	2.566815853	17.5189953	18.5826416	18.3730068	17.4576111	19.8478489	20.8670826	20.5066528	20.9779339
1172	Plasma kallikrein OS=Rattus norvegicus OX=10116 GN=Klkb1 PE=1 SV=1	Klkb1	P14272	4.10984833	-2.123916149	23.1387119	23.0471153	23.6130962	22.6591702	21.230278	20.841692	20.7789135	21.1115456
1173	Plasma membrane calcium-transporting ATPase 4 OS=Rattus norvegicus OX=10116 GN=Atp2b4 PE=1 SV=1	Atp2b4	Q64542	0.06339189	0.166026354	18.7241478	18.8888721	15.9190989	20.2535858	18.1836548	18.4545441	18.7163219	19.0952892
1174	Plasma protease C1 inhibitor OS=Rattus norvegicus OX=10116 GN=Serping1 PE=2 SV=1	Serping1	Q6P734	4.0578379	-3.247068882	22.2057495	22.402401	22.4350109	22.0396996	19.6041012	18.0504093	19.2188187	19.2212563
1175	Plasminogen activator inhibitor 1 RNA-binding protein OS=Rattus norvegicus OX=10116 GN=Serbp1 PE=1 SV=2	Serbp1	Q6AXS5	6.24250828	4.427670956	19.0587292	18.5827808	18.4121933	18.4894047	23.3659801	23.2235355	22.8936462	22.7706299
1176	Plasminogen OS=Rattus norvegicus OX=10116 GN=Plg PE=2 SV=2	Plg	Q01177	4.69037183	-3.851696968	26.0039825	25.5314293	26.3833694	26.4130192	22.2688675	22.1733875	21.6398544	22.8429031
1177	Plastin 3 (T-isoform), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Pls3 PE=1 SV=2	Pls3	F1LPK7	3.30529102	2.50338316	17.0043468	17.9826355	18.3678417	17.9780064	20.9784279	19.9435959	20.2913246	20.1330147
1178	Platelet endothelial cell adhesion molecule OS=Rattus norvegicus OX=10116 GN=Pecam1 PE=1 SV=1	Pecam1	Q3SWT0	2.28186044	4.371086836	17.7938347	14.0593634	17.9834232	14.7165127	20.5753555	20.5295773	20.3257618	20.6067867
1179	Platelet factor 4 OS=Rattus norvegicus OX=10116 GN=Pf4 PE=1 SV=1	Pf4	P06765	5.45436215	-5.142669201	23.7399063	23.0583267	24.0863438	23.5260563	18.9823227	18.1115551	18.0235996	18.7224789
1180	Platelet glycoprotein 4 OS=Rattus norvegicus OX=10116 GN=Cd36 PE=1 SV=3	Cd36	Q07969	3.97117618	1.751223564	20.1659126	20.5537167	20.4715672	20.2516174	22.0973434	22.6044407	21.8868103	21.8591137
1181	Platelet-activating factor acetylhydrolase OS=Rattus norvegicus OX=10116 GN=Pla2g7 PE=2 SV=1	Pla2g7	Q5M7T7	3.14706005	-1.369517326	19.661171	19.7072678	19.7906933	19.900753	18.0226173	18.5246201	18.9289703	18.105608
1182	Pleckstrin homology domain-containing A2 OS=Rattus norvegicus OX=10116 GN=Plekha2 PE=1 SV=2	Plekha2	F1LXA9	0.50970646	0.537896633	19.9572506	18.502821	18.1518497	18.2483711	19.9675636	18.9551983	19.0966587	18.9924583
1183	Pleckstrin homology-like domain family B member 1 OS=Rattus norvegicus OX=10116 GN=Phldb1 PE=1 SV=2	Phldb1	D3ZNS1	4.19622459	4.627188921	16.841692	14.9232225	15.8991947	16.2475376	20.1927509	21.1654339	20.865345	20.1968727
1184	Pleckstrin OS=Rattus norvegicus OX=10116 GN=Plek PE=1 SV=1	Plek	Q4KM33	0.93074089	0.759925842	18.2148685	16.6845627	18.313797	17.3549232	18.0601273	18.6636314	18.6726685	18.2114277
1185	Plectin OS=Rattus norvegicus OX=10116 GN=Plec PE=1 SV=1	Plec	Q6S3A0	2.33971433	0.514879227	19.8265705	20.037775	20.012104	20.3128662	20.7272472	20.4808445	20.4635067	20.5772343
1186	Plexin B2 OS=Rattus norvegicus OX=10116 GN=Plxnb2 PE=1 SV=1	Plxnb2	D3ZQ57	4.98320053	2.583422184	17.7726288	17.511919	17.9142876	18.0990448	19.9906731	20.4981327	20.4660759	20.6766872
1187	Poly (A) polymerase alpha OS=Rattus norvegicus OX=10116 GN=Papola PE=1 SV=1	Papola	A0A0G2K0C9	0.71912668	-0.864506721	16.6709881	15.9533978	16.4405079	18.4428368	16.6439457	15.6447229	15.7770624	15.9839725
1188	Poly [ADP-ribose] polymerase 1 OS=Rattus norvegicus OX=10116 GN=Parp1 PE=1 SV=4	Parp1	P27008	0.31378317	-0.319484234	20.9093781	20.2329159	18.9235153	19.9926529	20.0023403	19.7166309	19.4073391	19.6542149
1189	Poly(rC)-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Pcbp2 PE=1 SV=1	Pcbp2	Q6AYU5	6.29578754	4.169225216	21.8692875	21.6120281	21.1405621	21.4946384	25.993763	25.5017052	25.7077961	25.5901527
1190	Poly(rC)-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Pcbp3 PE=1 SV=1	Pcbp3	Q6AY48	0.82186445	2.309187174	19.3335361	18.5908756	19.3215866	13.5933084	20.5180435	19.5642643	19.6942291	20.2995186
1191	Poly(rC)-binding protein 4 OS=Rattus norvegicus OX=10116 GN=Pcbp4 PE=4 SV=1	Pcbp4	D3ZCS3	4.90738105	3.975305557	18.901289	18.4437351	18.495018	19.6353569	23.1818848	22.7306633	22.5750637	22.8890095
1192	Poly(U)-binding-splicing factor PUF60 OS=Rattus norvegicus OX=10116 GN=Puf60 PE=2 SV=2	Puf60	Q9WV25	4.39183232	4.796764851	15.0606918	16.8025341	15.7330666	16.318697	21.4136524	20.4148064	20.9236641	20.349926
1193	Polyadenylate-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Pabpc1 PE=1 SV=1	Pabpc1	Q9EPH8	4.54839044	1.835752964	22.3668652	22.3235645	22.5621948	22.7761002	24.3396549	24.6780014	24.2742672	24.079813
1194	Polyadenylate-binding protein OS=Rattus norvegicus OX=10116 GN=Pabpc4 PE=1 SV=2	Pabpc4	G3V9N0	5.62394213	4.838628769	17.8126297	17.9505615	17.8121567	17.7200584	22.1586857	23.4475555	22.511795	22.5318851
1195	Polypyrimidine tract binding protein 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ptbp1 PE=1 SV=1	Ptbp1	Q6P736	2.15329459	3.89384985	16.2459602	19.5366898	17.2578506	20.0375271	22.7561092	22.7767754	21.5354652	21.5850773
1196	Polysaccharide biosynthesis domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Pbdc1 PE=1 SV=1	Pbdc1	G3V6C3	5.86543015	4.093852043	18.5996075	17.8737755	18.3383999	18.6045933	22.8359375	22.2985649	22.3414497	22.3158321
1197	PPFIA-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ppfibp1 PE=1 SV=1	Ppfibp1	A0A0G2K781	2.57250821	1.773624897	18.8775082	19.3005962	20.3287868	20.100687	21.4762688	21.7426815	21.3139648	21.1691628
1198	Ppm1b protein OS=Rattus norvegicus OX=10116 GN=Ppm1b PE=1 SV=1	Ppm1b	Q99ND8	4.31750779	3.641523361	18.7817116	18.8621998	17.697113	18.8795815	22.8021736	21.8960724	22.0655499	22.0229034
1199	PRA1 family protein OS=Rattus norvegicus OX=10116 GN=Arl6ip5 PE=1 SV=1	Arl6ip5	A0A0H2UHF6	2.81236855	2.279000282	18.1615295	19.1132565	18.0733337	17.1504116	20.1890335	20.5618038	20.619873	20.2438221
1200	Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Pbxip1 PE=1 SV=1	Pbxip1	A2VD12	2.47970405	3.449185371	17.2135906	17.8564339	15.7339458	14.6545258	19.8843727	20.1313229	19.5798626	19.6596794
1201	Preferentially-expressed antigen in melanoma-like 3 OS=Rattus norvegicus OX=10116 GN=LOC100912836 PE=4 SV=3	Pramel3	D4A8C3	1.20081133	-0.87831068	19.1246567	18.1526127	18.7459965	18.2090931	18.008543	16.7558765	18.0141354	17.9405613
1202	Prefoldin 5 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Pfdn5 PE=1 SV=1	Pfdn5	B5DFN4	0.94628185	1.293030262	19.2333984	18.219759	18.6038361	17.4738407	20.8359871	18.2437229	19.1878662	20.435379
1203	Prenylcysteine oxidase OS=Rattus norvegicus OX=10116 GN=Pcyox1 PE=1 SV=1	Pcyox1	Q99ML5	1.9237768	0.912109852	17.0814018	16.7990265	16.9537182	16.8369675	18.4349461	17.2376842	17.7188625	17.9280605
1204	Probable E3 ubiquitin-protein ligase HERC4 OS=Rattus norvegicus OX=10116 GN=Herc4 PE=2 SV=1	Herc4	Q5PQN1	1.89871424	3.254150152	17.518734	14.9159107	13.4198484	16.034317	19.2486439	18.073637	18.2605228	17.3223608
1205	Procollagen C-endopeptidase enhancer 1 OS=Rattus norvegicus OX=10116 GN=Pcolce PE=1 SV=1	Pcolce	O08628	1.00321484	-0.18698597	21.1779079	21.089901	21.3377647	21.3691139	21.2621002	20.9743881	20.9686642	21.0215912
1206	Profilin-1 OS=Rattus norvegicus OX=10116 GN=Pfn1 PE=1 SV=2	Pfn1	P62963	2.84535284	1.959425926	21.8822422	21.9021912	22.4343548	23.2468815	24.5893803	23.9079628	24.438797	24.3672333
1207	Programmed cell death 6-interacting protein OS=Rattus norvegicus OX=10116 GN=Pdcd6ip PE=1 SV=1	Pdcd6ip	A0A140TAA4	7.08376901	4.394198418	19.6763477	19.287405	19.1650887	19.5350666	24.0501785	23.6498947	23.7945194	23.746109
1208	Programmed cell death protein 10 OS=Rattus norvegicus OX=10116 GN=Pdcd10 PE=2 SV=1	Pdcd10	Q6NX65	3.92337906	3.741826773	16.914196	15.6196737	15.3539791	15.247509	19.7652912	18.9897041	19.711401	19.6362686
1209	Prohibitin OS=Rattus norvegicus OX=10116 GN=Phb PE=1 SV=1	Phb1	P67779	2.06981715	2.04774332	19.5734806	19.8757687	18.2108059	18.8338509	20.119051	21.732378	21.1193848	21.7140656
1210	Prohibitin-2 OS=Rattus norvegicus OX=10116 GN=Phb2 PE=1 SV=1	Phb2	Q5XIH7	2.24397566	2.494683743	19.9289188	20.1225662	18.6448994	17.6838112	21.1672497	21.8498344	21.5403233	21.8015232
1211	Proliferating cell nuclear antigen OS=Rattus norvegicus OX=10116 GN=Pcna PE=1 SV=1	Pcna	P04961	1.73321298	2.89887476	18.5021591	18.4976406	17.9853382	17.5752029	19.7281952	19.3869209	22.0851479	22.9555759
1212	Proliferation-associated protein 2G4 OS=Rattus norvegicus OX=10116 GN=Pa2g4 PE=1 SV=1	Pa2g4	Q6AYD3	1.91942267	1.724092007	16.6942558	17.0920448	16.9354954	16.2998886	18.3329697	18.9682331	19.3454571	17.2713628
1213	Prolyl endopeptidase OS=Rattus norvegicus OX=10116 GN=Prep PE=1 SV=1	Prep	O70196	1.9392098	3.768385172	13.9497623	16.0984364	15.644002	15.7594166	16.3323193	20.0804863	20.0802021	20.0321503
1214	Prosaposin OS=Rattus norvegicus OX=10116 GN=Psap PE=1 SV=2	Psap	F7EPE0	0.54799958	-0.37833786	21.2751045	20.8110161	21.3964634	21.1541309	21.3917942	21.1616859	20.1522655	20.4176178
1215	Prostaglandin E synthase 3 OS=Rattus norvegicus OX=10116 GN=Ptges3 PE=1 SV=2	Ptges3	P83868	5.08437467	4.427408695	16.8535805	16.7156601	16.1506863	16.2486782	21.1645107	20.1257267	21.2092266	21.1787758
1216	Prostaglandin reductase 1 OS=Rattus norvegicus OX=10116 GN=Ptgr1 PE=2 SV=3	Ptgr1	P97584	1.35507755	-0.829675198	20.1636639	19.7927647	20.7412376	20.8490067	19.0749893	19.3265629	19.8995018	19.926918
1217	Proteaseome (Prosome, macropain) 28 subunit, 3 OS=Rattus norvegicus OX=10116 GN=Psme3 PE=1 SV=1	Psme3	Q5FVM2	2.75182463	5.210413694	15.9687014	13.4795771	17.1391697	13.3939619	20.8215199	19.4055977	20.3577747	20.2381725
1218	Proteasomal ubiquitin receptor ADRM1 OS=Rattus norvegicus OX=10116 GN=Adrm1 PE=1 SV=2	Adrm1	Q9JMB5	1.36836318	1.438838482	20.6097679	19.7159672	20.1037464	21.7083588	22.7297688	20.9993248	22.0468674	22.1172333

1219	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 12 OS=Rattus norvegicus OX=10116 GN=Psmd12 PE=1 SV=1	Psmd12	Q5XIC6	5.37321701	5.521754742	17.6395111	18.2982559	17.2077103	17.1148186	23.5998974	22.500473	23.1502018	23.0967426
1220	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 14 OS=Rattus norvegicus OX=10116 GN=Psmd14 PE=1 SV=1	Psmd14	Q4V8E2	2.063327	5.575701475	15.6561022	19.6916027	13.1973677	14.3080339	21.9880219	20.620882	21.6862545	20.860754
1221	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 3 OS=Rattus norvegicus OX=10116 GN=Psmd3 PE=1 SV=1	Psmd3	Q5U2S7	5.0975431	5.285455704	16.8249798	18.2973652	17.9853001	17.8107643	23.4397717	22.4820099	23.125351	23.0130997
1222	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 5 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116	Psmd5	G3V8G2	2.6386927	3.958520174	16.9355068	15.0747004	16.0750256	18.5847607	21.3256416	20.2325535	20.4520016	20.4938774
1223	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 6 OS=Rattus norvegicus OX=10116 GN=Psmd6 PE=1 SV=1	Psmd6	Q6PCT9	6.2145383	5.722863674	17.1509171	16.8315411	16.9881039	16.8147411	23.3515892	22.1471958	22.5526066	22.6253662
1224	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 7 (Predicted) OS=Rattus norvegicus OX=10116 GN=Psmd7 PE=	Psmd7	D4AEH3	3.56150365	6.066121101	16.2457542	16.281229	16.6838589	13.4160519	22.4087257	21.2637157	21.9006824	21.3182545
1225	Proteasome (Prosome, macropain) activator subunit 1 OS=Rattus norvegicus OX=10116 GN=Psme1 PE=1 SV=1	Psme1	Q6P9V7	0.8815604	0.702926636	26.7180309	26.3309708	26.1252995	24.9368515	26.9818325	26.3991985	26.7710629	26.7707653
1226	Proteasome 26S subunit, ATPase 6 OS=Rattus norvegicus OX=10116 GN=Psmc6 PE=1 SV=1	Psmc6	G3V6W6	3.27618307	2.652598381	22.7982006	20.9220524	21.5130424	21.5882549	24.3133621	24.3065739	24.4496899	24.362318
1227	Proteasome 26S subunit, non-ATPase 8 OS=Rattus norvegicus OX=10116 GN=Psmd8 PE=1 SV=1	Psmd8	F1LMQ3	0.03189371	-0.016918659	22.2025051	22.3086033	22.0177116	21.7307262	22.1879082	21.6534061	22.1852913	22.165266
1228	Proteasome activator complex subunit 2 OS=Rattus norvegicus OX=10116 GN=Psme2 PE=2 SV=3	Psme2	Q63798	2.98019898	5.360818863	17.9347534	14.1072788	17.0648041	17.5979233	21.4058342	21.9167976	22.4577351	22.3676682
1229	Proteasome maturation protein OS=Rattus norvegicus OX=10116 GN=Pomp PE=1 SV=1	Pomp	A5HKJ3	3.80272642	2.342795372	17.2768631	16.2427902	16.2778397	16.6743355	19.336462	18.8491917	18.996645	18.6607113
1230	Proteasome subunit alpha type OS=Rattus norvegicus OX=10116 GN=Psma7 PE=1 SV=1	Psma7	A0A0G2K0W9	1.56454446	0.932166576	19.1786957	20.0454807	18.8393745	19.0276775	20.5491447	19.8772602	19.9155445	20.4779453
1231	Proteasome subunit alpha type-1 OS=Rattus norvegicus OX=10116 GN=Psma1 PE=1 SV=2	Psma1	P18420	0.01222364	-0.012448788	20.044836	20.9066296	20.5795155	19.6285019	20.835495	19.9419346	20.2074833	20.1247749
1232	Proteasome subunit alpha type-2 OS=Rattus norvegicus OX=10116 GN=Psma2 PE=1 SV=3	Psma2	P17220	0.09151171	0.159459114	17.0725937	17.1288605	17.7086239	17.720047	18.0520535	16.0795326	17.2006397	18.9357357
1233	Proteasome subunit alpha type-3 OS=Rattus norvegicus OX=10116 GN=Psma3 PE=1 SV=3	Psma3	P18422	0.27368458	0.449790001	17.2644348	19.1028595	18.8227997	18.6699028	17.326334	19.5134258	19.6819706	19.1374264
1234	Proteasome subunit alpha type-4 OS=Rattus norvegicus OX=10116 GN=Psma4 PE=1 SV=1	Psma4	P21670	2.53266141	2.017221451	19.8384457	20.1884651	20.2739754	18.7352123	21.2880402	21.5846233	22.3277817	21.9045391
1235	Proteasome subunit alpha type-5 OS=Rattus norvegicus OX=10116 GN=Psma5 PE=1 SV=1	Psma5	P34064	1.28168034	1.526521206	18.3177319	20.6969757	18.0383377	18.4535236	20.4167194	20.0858269	20.8226318	20.2874756
1236	Proteasome subunit alpha type-6 OS=Rattus norvegicus OX=10116 GN=Psma6 PE=1 SV=1	Psma6	P60901	3.5532003	2.06111002	19.1634541	20.0759048	19.090374	18.9392605	21.5317192	21.2128754	21.5414829	21.227356
1237	Proteasome subunit beta OS=Rattus norvegicus OX=10116 GN=LOC100360846 PE=3 SV=1	LOC100360846	A0A0G2JSL0	0.08005873	-0.070817471	20.0780487	20.5268688	19.0659142	20.1174431	19.8896656	19.8226223	20.0667706	19.7259464
1238	Proteasome subunit beta OS=Rattus norvegicus OX=10116 GN=Psmb5 PE=1 SV=1	Psmb5	G3V7Q6	1.87560267	1.005904675	18.5876236	18.2937756	18.9927502	17.9431782	19.8085785	19.7025337	19.3376522	18.9921818
1239	Proteasome subunit beta type-1 OS=Rattus norvegicus OX=10116 GN=Psmb1 PE=1 SV=3	Psmb1	P18421	0.78101088	-0.821872234	19.1769333	20.3919926	20.5596733	21.6402855	19.3436298	19.9682617	19.6087723	19.5607319
1240	Proteasome subunit beta type-2 OS=Rattus norvegicus OX=10116 GN=Psmb2 PE=1 SV=1	Psmb2	P40307	0.97155463	-0.879876614	17.2466297	18.68013	18.1451073	17.9451466	17.4868622	17.9537621	16.5084076	16.5484753
1241	Proteasome subunit beta type-3 OS=Rattus norvegicus OX=10116 GN=Psmb3 PE=1 SV=1	Psmb3	P40112	2.47994324	0.822465897	16.4964275	17.1839561	16.6316204	17.0080376	17.4688282	17.618721	17.7800102	17.7423458
1242	Proteasome subunit beta type-4 OS=Rattus norvegicus OX=10116 GN=Psmb4 PE=1 SV=2	Psmb4	P34067	0.37336233	0.340751171	17.340519	18.9120178	18.6499958	17.7811928	18.6735764	18.0726166	18.7223587	18.5781784
1243	Proteasome subunit beta type-7 OS=Rattus norvegicus OX=10116 GN=Psmb7 PE=1 SV=1	Psmb7	Q9JHW0	0.09261173	0.179890156	17.0697117	19.5939217	17.1405334	17.7560902	19.2217846	17.9307384	17.6036835	17.5236111
1244	Protein AMBP OS=Rattus norvegicus OX=10116 GN=Ambp PE=1 SV=1	Ambp	Q64240	4.31899568	-4.92456007	24.3792477	23.8462753	24.3893299	24.7355022	20.3542671	18.8758831	18.4815578	19.9404068
1245	Protein arginine methyltransferase 1-like OS=Rattus norvegicus OX=10116 GN=LOC100361025 PE=3 SV=1	LOC100361025	A0A0G2K9I8	1.18594873	2.204847813	14.0147419	17.8834248	16.3896046	17.5878468	17.4881325	18.8824387	18.7854996	19.5389385
1246	Protein arginine N-methyltransferase 3 OS=Rattus norvegicus OX=10116 GN=Prmt3 PE=1 SV=1	Prmt3	A0A0G2JW52	0.38090123	1.042164326	16.9617577	16.8106747	17.0095253	12.3706799	16.6087437	16.6494064	16.2169724	17.8461723
1247	Protein arginine N-methyltransferase 5 OS=Rattus norvegicus OX=10116 GN=Prmt5 PE=1 SV=1	Prmt5	D4A0E8	1.12805304	1.669190645	15.0588369	15.82059	13.1243773	16.5097504	16.5160141	17.5001678	16.8335838	16.3405514
1248	Protein argonaute-2 OS=Rattus norvegicus OX=10116 GN=Ago2 PE=1 SV=2	Ago2	F1LRP7	0.9465178	0.59653759	20.523386	20.1496086	20.0723648	19.1007862	20.5541325	20.7665977	20.6471062	20.2644596
1249	Protein DEK OS=Rattus norvegicus OX=10116 GN=Dek PE=1 SV=1	Dek	Q6AXS3	4.83205786	-2.739202023	20.0090523	19.943079	20.3496113	20.1530895	17.7464962	17.1684055	16.9256783	17.657444
1250	Protein delta homolog 1 OS=Rattus norvegicus OX=10116 GN=Dlk1 PE=1 SV=1	Dlk1	O70534	4.9694263	-3.562798023	20.123024	20.797472	21.1909866	20.1484337	17.0319653	17.0902481	16.8461018	17.0404091
1251	Protein diaphanous homolog 1 OS=Rattus norvegicus OX=10116 GN=Diaph1 PE=1 SV=3	Diaph1	F1M775	0.39614231	-0.260382175	18.6785431	17.841095	18.9882469	18.1767673	18.5096493	18.196907	17.8730984	18.0634689
1252	Protein disulfide-isomerase A4 OS=Rattus norvegicus OX=10116 GN=Pdia4 PE=1 SV=1	Pdia4	G3V6T7	2.00124728	3.923069715	14.1571465	17.1969185	15.2537432	18.8923569	20.03862	20.2770348	20.1902828	20.6865063
1253	Protein disulfide-isomerase A6 OS=Rattus norvegicus OX=10116 GN=Pdia6 PE=1 SV=1	Pdia6	A0A0G2JSZ5	4.70779554	3.323873997	20.0251732	20.4442329	19.4150925	19.6607227	22.9487534	23.3558941	22.9442539	23.5918159
1254	Protein disulfide-isomerase OS=Rattus norvegicus OX=10116 GN=P4hb PE=1 SV=2	P4hb	P04785	2.55069609	2.404473782	22.1375732	22.5966167	21.4833221	20.4615479	23.7075539	24.3862839	23.848835	24.3542824
1255	Protein disulfide-isomerase OS=Rattus norvegicus OX=10116 GN=Pdia3 PE=1 SV=1	Pdia3	A0A0H2UHM5	3.75688065	2.797533989	22.0595379	22.2680931	21.7377949	20.8587551	24.2802773	24.7962742	24.296051	24.7417145
1256	Protein ERGIC-53 OS=Rattus norvegicus OX=10116 GN=Lman1 PE=1 SV=1	Lman1	A0A0G2JXC1	3.38891179	2.068640709	18.311451	17.8778057	18.3288021	18.2369823	20.436758	20.9096622	19.6213779	20.0618057
1257	Protein ERGIC-53 OS=Rattus norvegicus OX=10116 GN=Lman1 PE=1 SV=1	Lman1	Q62902	4.70178602	2.705012321	19.7105885	19.7779217	19.6097374	19.5426083	22.310257	22.9950924	22.1386833	22.0168724
1258	Protein FAM210A OS=Rattus norvegicus OX=10116 GN=Fam210a PE=2 SV=1	Fam210a	Q5XIJ4	0.45505845	1.126944065	17.3278656	18.8994942	16.2156429	18.8925476	20.8658333	19.9315338	18.2478695	16.79809
1259	Protein kinase AMP-activated non-catalytic subunit gamma 2 OS=Rattus norvegicus OX=10116 GN=Prkag2 PE=1 SV=1	Prkag2	A0A140UHX4	1.36632299	1.592381001	20.8699551	20.2675934	18.5173893	20.4741669	22.6297626	21.1846085	21.2020626	21.4821949
1260	Protein kinase C and casein kinase substrate in neurons 2 protein OS=Rattus norvegicus OX=10116 GN=Pacsin2 PE=1 SV=2	Pacsin2	Q9QY17	6.52136759	5.304401398	16.0661507	16.9677525	16.595293	16.6931038	22.1480598	21.8497906	21.9066315	21.6354237
1261	Protein kinase C delta type OS=Rattus norvegicus OX=10116 GN=Prkcd PE=1 SV=1	Prkcd	A0A140UHX0	4.11012736	4.684659004	17.9036999	19.2958908	19.28578	17.3803215	23.2325459	22.9505291	23.2787094	23.1425438
1262	Protein kinase C OS=Rattus norvegicus OX=10116 GN=Prkca PE=1 SV=3	Prkca	F1LS98	2.85821704	4.188305855	17.931715	18.7387314	17.5430508	16.0481129	20.2828045	22.1309528	22.2516136	22.3494625
1263	Protein kinase C substrate 80K-H OS=Rattus norvegicus OX=10116 GN=Prkcsh PE=1 SV=1	Prkcsh	B1WC34	3.43278704	4.81209445	16.7076931	18.0227299	17.2649174	14.9372511	21.3582802	21.9126015	21.3249702	21.5851173
1264	Protein kinase, cAMP-dependent, catalytic, alpha OS=Rattus norvegicus OX=10116 GN=Prkaca PE=1 SV=1	Prkaca	A1L1M0	4.36002429	6.749175072	17.2627029	14.4904289	16.7801018	16.943512	23.2955933	23.1719284	23.1809044	22.8250198
1265	Protein kish OS=Rattus norvegicus OX=10116 GN=Tmem167a PE=3 SV=2	Tmem167a	D3ZKR8	4.75554714	2.163282871	15.8642673	15.8924704	15.9731493	16.4549103	18.183794	18.5209084	18.0260124	18.107214
1266	Protein NDRG1 OS=Rattus norvegicus OX=10116 GN=Ndrg1 PE=1 SV=1	Ndrg1	Q6JE36	6.30713945	4.523233414	16.3621502	16.2830811	15.6288853	16.4736099	20.7898369	20.7383823	20.524416	20.7880249
1267	Protein NDRG4 OS=Rattus norvegicus OX=10116 GN=Ndrg4 PE=1 SV=1	Ndrg4	D3ZUT8	2.98149584	4.468013287	14.5670433	17.7268353	15.4874773	14.6204195	19.9602852	19.8851452	20.5359116	19.8924866
1268	Protein phosphatase 1 regulatory subunit 12A OS=Rattus norvegicus OX=10116 GN=Ppp1r12a PE=1 SV=1	Ppp1r12a	A0A0G2JWJ0	3.1274423	4.968072414	15.2716541	13.2214127	15.3355465	17.0190239	20.2644768	20.3839855	20.2866077	19.7848568
1269	Protein phosphatase 1 regulatory subunit 14C OS=Rattus norvegicus OX=10116 GN=Ppp1r14c PE=1 SV=1	Ppp1r14c	Q8R4R9	0.21591734	0.517533302	15.2349873	18.1993484	18.2945938	14.7181168	17.1389751	16.9580784	17.4566002	16.9635258
1270	Protein phosphatase 1 regulatory subunit 36 OS=Rattus norvegicus OX=10116 GN=Ppp1r36 PE=2 SV=1	Ppp1r36	Q68FW6	0.15813089	0.410827637	17.6269455	16.7518578	17.0090084	13.3382053	17.2293758	16.1430149	16.2375145	16.7594223
1271	Protein phosphatase 1 regulatory subunit 3B OS=Rattus norvegicus OX=10116 GN=Ppp1r3b PE=1 SV=1	Ppp1r3b	Q6IN01	0.05152439	0.129247189	18.1018295	18.1165829	17.8062439	14.7044544	16.7253323	18.1391773	17.2197285	17.1618614
1272	Protein phosphatase 1, regulatory subunit 12C OS=Rattus norvegicus OX=10116 GN=Ppp1r12c PE=1 SV=1	Ppp1r12c	A0A0G2K4R1	3.36226072	-1.826972961	21.2463551	21.438076	21.288229	21.6652908	19.7219048	19.7065659	18.881609	20.0199795
1273	Protein phosphatase 1A OS=Rattus norvegicus OX=10116 GN=Ppm1a PE=1 SV=1	Ppm1a	A0A0H2UHE5	4.26645611	4.223095179	15.9314184	16.2407303	16.0737305	16.3094501	21.4571457	19.9393864	20.4723053	19.5788727
1274	Protein phosphatase 1F OS=Rattus norvegicus OX=10116 GN=Ppm1f PE=2 SV=1	Ppm1f	Q9WVR7	0.5815039	1.015244961	17.8702259	20.2963219	16.6808243	18.2548103	19.5207672	18.3372192	19.8269386	19.4782372
1275	Protein phosphatase 2 (Formerly 2A), regulatory subunit A (PR 65), alpha isoform, isoform CRA_a OS=Rattus norvegicus OX=	Ppp2r1a	Q5XI34	6.00428543	5.275397778	18.7461185	19.2692318	19.9602795	19.2444019	24.4942303	24.3946609	24.7521477	24.680584
1276	Protein phosphatase 2 (Formerly 2A), regulatory subunit B", alpha OS=Rattus norvegicus OX=10116 GN=Ppp2r3a PE=2 SV=1	Ppp2r3a	Q5PQN8	3.0220499	2.728353977	19.0902996	17.6835442	18.5121326	19.3807259	20.6977577	21.8497143	21.6971188	21.3355274
1277	Protein phosphatase 2 (Formerly 2A), regulatory subunit B", alpha, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ppp	Ppp2r3a	D3ZLD7	0.71988941	0.517918587	20.7778015	19.6946297	20.071928	21.0401649	21.1731796	20.4407597	21.0814209	20.9608383
1278	Protein phosphatase 6, regulatory subunit 3 OS=Rattus norvegicus OX=10116 GN=Ppp6r3 PE=1 SV=3	Ppp6r3	F1MAH5	4.96483755	3.624742508	17.941782	17.9938869	17.8768196	17.1831284	21.5687828	20.7938156	21.5546627	21.5773258
1279	Protein PRRC1 OS=Rattus norvegicus OX=10116 GN=Prrc1 PE=1 SV=1	Prrc1	G3V834	0.13473439	0.152852535	20.8241253	19.4231052	20.41119	20.510561	21.1674156	20.3095646	19.7119465	20.591465

1280	Protein PRRC2A OS=Rattus norvegicus OX=10116 GN=Prrc2a PE=1 SV=1	Prrc2a	A0A0U1RRZ5	0.67398602	0.615056992	17.7423935	18.067318	17.4769058	16.8127728	17.94347	19.0436039	18.2158661	17.356678
1281	Protein quaking-like OS=Rattus norvegicus OX=10116 GN=LOC108348175 PE=4 SV=1	Qk	A0A0G2JXZ5	5.48520095	4.23036623	19.202177	18.8322449	19.373539	19.269886	24.0686817	23.0734348	23.3266315	23.1305637
1282	Protein S (Alpha), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Pros1 PE=1 SV=1	Pros1	M0R5R0	3.47843638	-1.554321289	22.4626884	21.7456856	22.1312542	22.4219055	21.0286083	20.5295601	20.4386044	20.5474758
1283	Protein S100-A10 OS=Rattus norvegicus OX=10116 GN=S100a10 PE=1 SV=2	S100a10	P05943	5.21122707	3.122178555	18.1358242	18.9835682	18.7108326	18.3684597	21.6031532	21.4272823	21.8880367	21.7689266
1284	Protein S100-A11 OS=Rattus norvegicus OX=10116 GN=S100a11 PE=3 SV=1	S100a11	Q6B345	5.68359646	3.552076817	18.0553513	18.8322601	18.4977341	18.8412151	21.9997578	22.0747871	22.3335361	22.0267868
1285	Protein S100-A4 OS=Rattus norvegicus OX=10116 GN=S100a4 PE=2 SV=1	S100a4	P05942	4.87493388	5.565426826	15.1120062	14.9118948	15.8120728	16.5849228	20.5714111	21.3676071	21.2541656	21.4894199
1286	Protein SEC13 homolog OS=Rattus norvegicus OX=10116 GN=Sec13 PE=1 SV=1	Sec13	Q5XFW8	6.22682419	6.013095856	18.0101662	17.2109032	17.5090065	16.7200928	23.4722786	23.4120426	23.376379	23.2418518
1287	Protein SGT1 homolog OS=Rattus norvegicus OX=10116 GN=Sugt1 PE=2 SV=1	Sugt1	B0BN85	5.64652015	5.161410332	17.6630192	17.2028389	17.5749626	18.0707989	23.4255772	22.2908192	22.6764603	22.7644043
1288	Protein TANC1 OS=Rattus norvegicus OX=10116 GN=Tanc1 PE=1 SV=3	Tanc1	G3V917	4.80149442	2.498245716	17.2815876	16.8209858	17.4664364	17.6547318	19.8802128	19.7545471	19.9972992	19.5846653
1289	Protein transport protein SEC23 OS=Rattus norvegicus OX=10116 GN=Sec23a PE=1 SV=1	Sec23a	A0A0G2JZM2	3.90461157	3.186042786	18.8633938	19.8757248	19.2642841	18.207468	22.5301914	22.1165867	22.0836239	22.2246399
1290	Protein transport protein Sec31A OS=Rattus norvegicus OX=10116 GN=Sec31a PE=1 SV=1	Sec31a	G3V699	7.41494235	5.374117374	18.8645325	19.087389	18.5582142	19.0623608	24.4807472	24.3526211	24.1942272	24.0413704
1291	Protein tyrosine kinase 9-like (A6-related protein) (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Twf2 PI	Twf2	B0BMY7	2.80702425	2.888589859	16.0755024	17.9743652	17.1662788	16.6577606	20.6487675	18.9825745	19.961174	19.8357506
1292	Protein Z, vitamin K-dependent plasma glycoprotein OS=Rattus norvegicus OX=10116 GN=Proz PE=3 SV=4	Proz	G3V8K8	2.03449935	-2.271550179	21.3429642	21.2648792	20.7006836	20.5681953	19.4493351	17.0956688	18.6796989	19.5658188
1293	Protein Z-dependent protease inhibitor OS=Rattus norvegicus OX=10116 GN=Serpina10 PE=2 SV=2	Serpina10	Q62975	2.73053308	-1.309079647	21.5391903	21.1855888	20.7814751	20.8279076	20.0354538	19.2639732	19.9333687	19.8650475
1294	Protein/nucleic acid deglycase DJ-1 OS=Rattus norvegicus OX=10116 GN=Park7 PE=1 SV=1	Park7	O88767	5.56387075	2.238272667	19.2030182	19.6117134	19.354948	19.0930443	21.4551773	21.6992016	21.6464062	21.4150295
1295	Protein-glutamine gamma-glutamyltransferase K OS=Rattus norvegicus OX=10116 GN=Tgm1 PE=1 SV=1	Tgm1	P23606	0.11497063	-0.242692471	18.8107166	21.0414104	17.4425507	18.8360271	18.3195934	19.4828777	18.6526413	18.7048225
1296	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Rattus norvegicus OX=10116 GN=Pcmt1 PE=1 SV=2	Pcmt1	P22062	0.5158799	0.393640518	20.6971607	21.0082855	21.4871349	21.9586868	22.1470528	21.106041	21.7962952	21.6764412
1297	Proteolipid protein 2 OS=Rattus norvegicus OX=10116 GN=Plp2 PE=2 SV=1	Plp2	Q6P742	6.72702752	3.638806343	17.0432987	17.3200188	17.2984238	17.3040066	21.1935043	20.9311123	20.6462193	20.7501373
1298	Prothrombin OS=Rattus norvegicus OX=10116 GN=F2 PE=1 SV=1	F2	G3V843	3.91492869	-2.354382038	25.2305546	25.1068668	25.9331779	25.5816765	23.5318928	22.6520252	22.9518394	23.2989902
1299	Protocadherin 12 OS=Rattus norvegicus OX=10116 GN=Pcdh12 PE=1 SV=2	Pcdh12	F1MA46	0.2264615	-0.259765625	20.2692547	18.8391266	18.6912785	18.6158371	19.5558987	18.5286064	18.5217323	18.7701969
1300	PTPRF-interacting protein alpha 1 OS=Rattus norvegicus OX=10116 GN=Ppfia1 PE=1 SV=1	Ppfia1	A0A0G2K3L9	0.03306473	-0.065361738	16.9104633	18.7687874	15.9461966	18.3676491	17.2359524	18.0067024	17.2994671	17.1895275
1301	Pulmonary surfactant-associated protein B OS=Rattus norvegicus OX=10116 GN=Sftpb PE=2 SV=1	Sftpb	P22355	3.60618693	-2.826137781	19.3258133	18.4573765	18.386507	19.4654846	15.8845482	16.5964432	16.3084545	15.5411844
1302	Purine nucleoside phosphorylase OS=Rattus norvegicus OX=10116 GN=Pnp PE=1 SV=1	Pnp	P85973	0.23196312	-0.381717682	14.6852369	17.473999	17.3806686	16.8960037	16.3412571	16.1271191	16.4833431	15.9573183
1303	Pyridoxal-dependent decarboxylase domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Pdxdc1 PE=1 SV=1	Pdxdc1	G3V6B0	6.81865301	3.542577744	17.2456474	17.5629883	17.0112514	17.3229752	20.9107399	20.8924599	20.8594322	20.6505413
1304	Pyrophosphatase (inorganic) 1 OS=Rattus norvegicus OX=10116 GN=Ppa1 PE=1 SV=1	Ppa1	F7EPH4	3.61836486	1.827504635	19.4753532	18.809454	19.0292492	19.59445	20.9873829	20.8039665	21.4757462	20.9514294
1305	Pyrroline-5-carboxylate reductase 3 OS=Rattus norvegicus OX=10116 GN=Pycr3 PE=2 SV=1	Pycr3	Q5PQJ6	6.3625581	5.891266823	17.894455	18.6059151	18.4718971	18.8531361	24.7880859	24.132761	24.3364239	24.1331997
1306	Pyruvate dehydrogenase E1 component subunit alpha OS=Rattus norvegicus OX=10116 GN=Pdha1 PE=1 SV=1	Pdha1	A0A0G2JW90	2.00452381	2.064448357	18.1620884	18.3711414	18.2057362	18.3769836	18.6985817	21.0878315	20.7707672	20.8165627
1307	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pdhb PE=1 SV=1	Pdhb	A0A0G2KAM3	2.65922207	2.117236614	18.2986832	18.132616	18.4814796	19.0320911	19.5568428	21.1991711	20.9820766	20.6757259
1308	Pyruvate kinase OS=Rattus norvegicus OX=10116 GN=Pkm PE=1 SV=1	Pkm	A0A0G2JVG3	2.08781122	1.423707485	17.8739395	18.1425056	18.5875454	18.7279663	20.6052685	19.1301975	19.5731049	19.7182159
1309	Pyruvate kinase PKLR OS=Rattus norvegicus OX=10116 GN=Pklr PE=1 SV=2	Pklr	P12928	4.17338321	-3.088516712	20.7956619	19.3431625	20.0981827	19.9942589	17.2590256	16.9913597	16.7378483	16.8889656
1310	Pyruvate kinase PKM OS=Rattus norvegicus OX=10116 GN=Pkm PE=1 SV=3	Pkm	P11980	5.20228022	2.328197479	22.5241375	22.5492229	22.5472145	22.6964512	25.2502003	24.5065041	24.9767094	24.8964024
1311	Rab GDP dissociation inhibitor beta OS=Rattus norvegicus OX=10116 GN=Gdi2 PE=1 SV=2	Gdi2	P50399	3.69657405	2.105190277	19.3668213	20.4568977	19.8861809	19.351511	21.887825	21.8202362	21.911375	21.8627357
1312	Rab GTPase-binding effector protein 2 OS=Rattus norvegicus OX=10116 GN=Rabep2 PE=1 SV=1	Rabep2	Q5EBC7	3.29215279	-2.710800171	20.9520226	20.3975048	21.0861645	20.6450672	18.5906906	18.7842102	17.5798836	17.282774
1313	RAB10, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab10 PE=1 SV=1	Rab10	Q5RKJ9	5.55397796	4.144804001	19.0742817	19.4930172	20.068121	19.1544132	23.8497868	23.449728	23.636013	23.4335213
1314	RAB14, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab14 PE=1 SV=1	Rab14	B0BMW0	4.69481517	4.092263699	18.7353706	18.8691616	17.9441833	18.973362	23.4478226	22.4500885	22.6268387	22.3663826
1315	RAB22A, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab22a PE=1 SV=1	Rab22a	B0BN19	2.68364677	4.042515278	16.1614494	16.0710602	16.0284252	19.1592751	21.1859245	20.7046909	21.0944748	20.6051807
1316	RAB3A interacting protein (Rabin3) OS=Rattus norvegicus OX=10116 GN=Rab3ip PE=1 SV=1	Rab3ip	A1L127	3.14498053	3.753329039	16.0655003	15.5844965	16.5085907	14.0708561	18.5430794	19.6482201	19.4113808	19.6400795
1317	RAB5B, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab5b PE=1 SV=1	Rab5b	A1L1J8	5.24254568	4.4320364	18.442667	19.0674839	19.2694588	19.5647774	24.0054607	23.1467152	23.4765663	23.4437904
1318	Rac family small GTPase 2 OS=Rattus norvegicus OX=10116 GN=Rac2 PE=1 SV=1	Rac2	Q5U1Y2	4.38559778	2.5588274	17.8764095	16.87677	17.7999649	17.3486233	20.1459599	20.1384716	19.9969463	19.8556995
1319	RAC-alpha serine/threonine-protein kinase OS=Rattus norvegicus OX=10116 GN=Akt1 PE=1 SV=1	Akt1	P47196	3.98192247	5.457340956	16.7353249	16.8050404	14.3368349	15.2034016	21.3056202	21.2848492	21.1714478	21.1480484
1320	Radixin OS=Rattus norvegicus OX=10116 GN=Rdx PE=1 SV=2	Rdx	E9PT65	0.85800919	0.802763939	20.6494293	22.1291752	19.9004593	20.872406	21.6733913	21.8771286	21.4809151	21.7310905
1321	Ragulator complex protein LAMTOR1 OS=Rattus norvegicus OX=10116 GN=Lamtor1 PE=1 SV=1	Lamtor1	Q6P791	2.93902486	-1.269298077	20.4436111	20.21451	19.9456196	19.8203278	18.734766	19.3314838	18.5726547	18.7079716
1322	RAN GTPase-activating protein 1 OS=Rattus norvegicus OX=10116 GN=Rangap1 PE=1 SV=2	Rangap1	F1MAA5	4.08364016	4.924204826	16.8852654	15.1804333	16.8529587	17.5399055	21.5164223	21.1407413	21.7009983	21.7972202
1323	RAN-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ranbp1 PE=1 SV=1	Ranbp1	D4A2G9	4.22726917	4.030610561	16.4766369	18.1879387	17.0012474	17.605957	21.5916862	20.8739128	21.519186	21.4094372
1324	RAN-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Ranbp3 PE=1 SV=2	Ranbp3	M0R5Q3	4.17793346	5.735748291	14.045928	15.9430857	16.2848721	16.5083389	21.6784248	21.5467281	21.5748329	20.9252319
1325	Rap guanine nucleotide exchange factor 1 OS=Rattus norvegicus OX=10116 GN=Rapgef1 PE=1 SV=3	Rapgef1	F1M8L9	5.30035826	3.586690664	14.4184561	14.2146101	15.2004576	14.9838066	18.1981945	18.3752441	18.3246822	18.2659721
1326	RAP1, GTP-GDP dissociation stimulator 1 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Rap1gds1 PE=1	Rap1gds1	A0A0G2K1D2	1.59479037	1.6265378	18.1280937	19.3052826	17.8482533	19.026432	19.0121765	20.3017139	21.0169144	20.483408
1327	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 OS=Rattus norvegicus OX=10116 GN=Raph1 PE=1 SV=2	Raph1	D4ADX8	1.58673971	1.438920021	20.9530983	21.7307034	20.6192379	19.5506763	21.6413746	22.5269661	22.1584854	22.2825699
1328	Ras homolog family member G OS=Rattus norvegicus OX=10116 GN=Rhog PE=1 SV=1	Rhog	Q32PX6	4.00658395	2.214942455	18.1378212	18.1568966	17.6133957	17.2989159	19.8251801	20.3049641	19.7980061	20.138649
1329	RAS protein activator-like 2 OS=Rattus norvegicus OX=10116 GN=Rasal2 PE=1 SV=1	Rasal2	A0A0G2JTA7	3.20688621	3.642535686	18.0977974	17.8670044	18.852602	16.4064713	20.9991932	22.0456314	21.5035839	21.2456093
1330	Ras suppressor protein 1 OS=Rattus norvegicus OX=10116 GN=Rsu1 PE=1 SV=3	Rsu1	D4A8F2	4.70801412	3.554429531	18.9107552	18.2513084	18.1232815	17.6902905	22.2510166	21.6307545	21.6421986	21.669384
1331	RAS-related 2 OS=Rattus norvegicus OX=10116 GN=Rras2 PE=1 SV=1	Rras2	Q5BJU0	4.5397811	3.417336941	17.6783752	16.8823776	17.7977371	18.1516666	21.1671333	21.2679844	21.1100445	20.6343422
1332	Ras-related C3 botulinum toxin substrate 1 OS=Rattus norvegicus OX=10116 GN=Rac1 PE=1 SV=1	Rac1	Q6RUV5	2.77594279	1.168158054	21.8795776	21.8863811	21.8487682	21.4155293	23.4758282	22.7753639	22.7019711	22.7497253
1333	Ras-related protein Rab-11B OS=Rattus norvegicus OX=10116 GN=Rab11b PE=1 SV=4	Rab11b	O35509	5.23946693	4.557701588	20.8861008	20.807375	20.0190887	19.7316418	25.223093	24.842802	24.8787727	24.7303448
1334	Ras-related protein Rab-12 OS=Rattus norvegicus OX=10116 GN=Rab12 PE=1 SV=2	Rab12	P35284	5.00104769	3.645754814	17.0632305	17.3339481	17.4099655	16.618042	21.3312721	20.5680161	20.4210835	20.6878338
1335	Ras-related protein Rab-13 OS=Rattus norvegicus OX=10116 GN=Rab13 PE=1 SV=2	Rab13	P35286	1.68706767	3.098829508	18.6803932	14.9739008	17.0721207	14.7533817	20.4814968	19.3107643	19.1413784	18.9414749
1336	Ras-related protein Rab-18 OS=Rattus norvegicus OX=10116 GN=Rab18 PE=2 SV=1	Rab18	Q5EB77	3.59770412	3.325101852	18.1256237	17.4472084	16.7018452	17.9753838	21.258358	21.4266224	20.7138329	20.1516552
1337	Ras-related protein Rab-1A OS=Rattus norvegicus OX=10116 GN=Rab1A PE=1 SV=3	Rab1a	Q6NYB7	5.95542931	3.555360794	21.8653164	22.0795231	21.4410801	22.0776405	25.6287174	25.148592	25.4422359	25.4654579
1338	Ras-related protein Rab-21 OS=Rattus norvegicus OX=10116 GN=Rab21 PE=2 SV=1	Rab21	Q6AXT5	4.62403427	6.026854992	15.0518236	14.6393909	14.2442245	15.9635916	21.4994373	21.0998344	21.4556217	19.9515572
1339	Ras-related protein Rab-2A OS=Rattus norvegicus OX=10116 GN=Rab2a PE=2 SV=1	Rab2a	P05712	3.98901468	3.665994644	18.9519634	18.2941933	17.8483276	19.5849552	22.5714588	21.9304199	22.3689117	22.4726276
1340	Ras-related protein Rab-35 OS=Rattus norvegicus OX=10116 GN=Rab35 PE=1 SV=1	Rab35	Q5U316	3.42854528	1.505207062	18.7486057	18.8704224	19.4094734	19.3336239	20.71525	20.3013306	20.8917484	20.4746246

1341	Ras-related protein Rab-3A OS=Rattus norvegicus OX=10116 GN=Rab3a PE=1 SV=1	Rab3a	P63012	1.70994531	4.439693689	19.6115894	17.6966858	13.0127821	16.0426731	21.2549992	20.6681271	21.1557236	21.0436554
1342	Ras-related protein Rab-4A OS=Rattus norvegicus OX=10116 GN=Rab4a PE=1 SV=3	Rab4a	P05714	5.01771539	2.975238323	17.9029007	18.1318626	18.2232647	17.4311829	20.9988861	21.2092876	20.6662064	20.7157841
1343	Ras-related protein Rab-5A OS=Rattus norvegicus OX=10116 GN=Rab5a PE=2 SV=1	Rab5a	M0RC99	3.787352	5.416590691	15.5741425	16.2144375	16.7259979	13.8769035	21.4922733	20.5263748	21.0204296	21.0187664
1344	Ras-related protein Rab-6A OS=Rattus norvegicus OX=10116 GN=Rab6a PE=1 SV=2	Rab6a	Q9WVB1	5.67857624	4.136946678	19.5381088	18.5753422	18.8397121	18.5390129	22.9235058	23.0443115	22.9993019	23.0728436
1345	Ras-related protein Rab-7a OS=Rattus norvegicus OX=10116 GN=Rab7a PE=1 SV=2	Rab7a	P09527	6.07364442	4.473310471	18.8717861	19.7427769	19.2101135	19.068718	24.0061283	23.6587601	23.6403847	23.4813633
1346	Ras-related protein Rab-8A OS=Rattus norvegicus OX=10116 GN=Rab8a PE=1 SV=2	Rab8a	P35280	3.95517053	2.795735836	18.8014393	17.9425545	18.6043968	17.5894527	21.41712	20.8999615	20.8011551	21.0025501
1347	Ras-related protein Rab-8B OS=Rattus norvegicus OX=10116 GN=Rab8b PE=1 SV=1	Rab8b	P70550	1.31301476	1.041287899	16.7745647	17.8281384	18.2840805	17.1891766	18.5385075	19.2470932	18.0038719	18.4516392
1348	Ras-related protein Ral-A OS=Rattus norvegicus OX=10116 GN=Rala PE=1 SV=1	Rala	P63322	4.76984868	2.849429131	18.272398	18.7116203	18.7770653	18.77668	21.432333	21.9682312	21.5201035	21.0148125
1349	Ras-related protein Ral-B OS=Rattus norvegicus OX=10116 GN=Ralb PE=2 SV=1	Ralb	P36860	2.8599244	1.677278042	18.7479668	18.440094	18.4948521	18.4774284	19.3897152	20.7010994	20.2494888	20.52915
1350	Ras-related protein Rap-1A OS=Rattus norvegicus OX=10116 GN=Rap1a PE=1 SV=1	Rap1a	P62836	2.25662046	2.393850327	16.5461006	17.3065414	17.2099667	18.9382496	20.2366924	19.8666286	19.1948185	20.27812
1351	Ras-related protein Rap-1b OS=Rattus norvegicus OX=10116 GN=Rap1b PE=1 SV=2	Rap1b	Q62636	5.44212011	1.125005245	21.7647514	21.9194794	21.9810219	21.9405975	22.8940868	23.08288	23.0015106	23.1273937
1352	RCG20603 OS=Rattus norvegicus OX=10116 GN=Serpina3c PE=3 SV=1	Serpina3c	A0A0G2JSK1	4.46227568	-3.524739742	24.527813	24.6971836	25.2626133	25.3004475	21.9572067	20.7858715	21.2668304	21.6791897
1353	RCG20801, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Vipas39 PE=1 SV=1	Vipas39	A0A0G2K5Y1	3.22779679	-2.549473524	17.8499908	17.0354061	17.1750393	17.4150982	15.1175404	15.5430593	14.6861668	13.9308739
1354	RCG30099, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tex52 PE=4 SV=1	Tex52	D4ABA3	3.27321519	-1.983694077	19.4891968	19.0751572	19.3349724	19.8970623	17.9415874	16.8359718	17.7145958	17.3694572
1355	RCG31562, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Tardbp PE=1 SV=1	Tardbp	I6L9G6	3.74093443	3.889132023	17.8321037	16.3813782	16.6679497	18.0667381	21.7670422	20.7442036	20.8672028	21.1262493
1356	RCG40648, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Sec23ip PE=1 SV=1	Sec23ip	G3V8Q8	3.51440111	2.74706316	19.9739437	19.3785515	18.6365547	20.1675701	22.6854496	22.2004776	22.1236267	22.1353188
1357	RCG43947 OS=Rattus norvegicus OX=10116 GN=Txndc5 PE=1 SV=1	Txndc5	D3ZZC1	3.55665009	3.528009415	16.0527229	16.0814552	16.6087379	17.2501717	19.1753101	20.3929691	19.6828671	20.8539791
1358	RCG45489, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Stom PE=1 SV=1	Stom	Q5XI04	2.22682671	-1.372736454	19.0993042	19.0818443	18.4234295	19.0435905	17.8927994	17.7235298	16.6864719	17.8544216
1359	RCG48149, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=LOC100363782 PE=1 SV=1	Rab1b	G3V6H0	5.27584711	4.27445507	18.5812931	18.25951	19.2207355	17.9928112	23.0832577	22.7020988	22.6416473	22.7251663
1360	RCG52996, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tfg PE=1 SV=1	Tfg	Q6AYR1	3.95550145	3.472850323	18.5298634	18.1534405	18.5857582	17.45541	22.0992546	21.0394325	21.2822838	22.1949024
1361	RCG53953, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=LOC103690005 PE=1 SV=1	Tbcb	Q1RP74	5.41542468	4.017595291	17.2092247	17.5024242	18.1661358	17.4658203	21.8660088	21.1821899	21.709877	21.6559105
1362	RCG55135, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Tln1 PE=1 SV=1	Tln1	G3V852	5.23055196	2.349771023	23.8504238	23.7876854	24.3460464	23.7249336	26.1470509	26.3274269	26.4517746	26.181921
1363	RCG55706 OS=Rattus norvegicus OX=10116 GN=Stam PE=1 SV=1	Stam	B5DF55	3.95617623	5.413751125	15.9088135	13.5702562	16.0423336	15.6160612	21.2491493	20.4902706	20.5450401	20.508009
1364	RCG56113, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Smyd1 PE=4 SV=1	Smyd1	D4A3D2	2.21498317	2.626778126	14.9664965	15.0842123	16.1492996	16.1532326	16.6308479	18.5703526	19.1218834	18.5372696
1365	RCG57812, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Slk PE=1 SV=1	Slk	G3V7I8	4.22516724	2.11955452	20.5059662	20.0419464	20.5598087	20.9994011	22.4402981	22.8342113	22.7123489	22.5984821
1366	RCG61894, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Strn PE=1 SV=1	Strn	G3V6L8	3.93396823	6.127975225	13.8063145	15.2651167	15.2215109	12.3580446	20.2289619	20.3871307	20.3996544	20.1471405
1367	RCSD domain containing 1 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Rcsd1 PE=1 SV=1	Rcsd1	A0A0G2K7I4	5.17424381	4.922084332	16.8179359	17.3683548	17.1257954	17.5529804	23.0102158	21.6487293	21.9854794	21.9089794
1368	Receptor expression-enhancing protein 5 OS=Rattus norvegicus OX=10116 GN=Reep5 PE=1 SV=1	Reep5	B2RZ37	2.27511957	2.645822525	19.6161079	20.0849152	19.6614075	17.3728752	21.7412415	22.0574303	21.6051369	21.9147873
1369	Receptor of activated protein C kinase 1 OS=Rattus norvegicus OX=10116 GN=Rack1 PE=1 SV=3	Rack1	P63245	2.112671	3.827854156	18.5895195	18.9544144	18.2219868	19.4380016	19.8184757	23.7237244	23.5502186	23.4229202
1370	Receptor protein-tyrosine kinase OS=Rattus norvegicus OX=10116 GN=Egfr PE=1 SV=1	Egfr	G3V6K6	0.10036695	-0.063464165	18.2740479	18.7034264	18.7441483	17.9519444	18.2865505	18.5334435	18.0016384	18.5980778
1371	Reelin OS=Rattus norvegicus OX=10116 GN=Reln PE=4 SV=3	Reln	F1LZI7	2.14976493	-0.815813541	19.3852921	19.3854065	19.1075859	19.1714535	18.7569313	17.9629936	18.7458649	18.320694
1372	Regulatory-associated protein of MTOR, complex 1 OS=Rattus norvegicus OX=10116 GN=Rptor PE=1 SV=2	Rptor	D3ZDU2	3.79439949	2.785362244	16.3892765	16.4094658	17.4857502	16.3838806	18.9857464	19.2901402	19.7683868	19.7655487
1373	Replication protein A subunit OS=Rattus norvegicus OX=10116 GN=Rpa1 PE=1 SV=1	Rpa1	A0A0G2KAT3	3.96382508	5.097275496	16.4043427	16.3581161	16.476532	14.2571001	21.3145523	20.9223461	21.1680279	20.4802666
1374	Resistin OS=Rattus norvegicus OX=10116 GN=Retn PE=2 SV=1	Retn	Q8K4J7	2.53180942	-2.758833408	19.8801651	19.2442131	18.1854763	17.3761501	15.6236753	15.9473314	16.2750111	15.8046532
1375	Reticulocalbin 1 OS=Rattus norvegicus OX=10116 GN=Rcn1 PE=1 SV=1	Rcn1	D3ZUB0	0.23774195	0.203207016	19.8390255	19.8694401	20.0154591	19.0476761	19.1659184	19.9071541	20.0659084	20.4454479
1376	Reticulon OS=Rattus norvegicus OX=10116 GN=Rtn4 PE=1 SV=1	Rtn4	F1LQN3	5.32361465	3.939647198	19.1797276	19.9401417	19.8683834	19.6359005	23.2648258	24.1366863	23.4256077	23.5556221
1377	Reticulon-3 OS=Rattus norvegicus OX=10116 GN=Rtn3 PE=1 SV=1	Rtn3	Q6RJR6	3.96075894	2.612561226	17.8942261	17.8604202	17.4431744	17.293335	20.0629234	20.9798241	19.8913155	20.0073376
1378	Retinol-binding protein 4 OS=Rattus norvegicus OX=10116 GN=Rbp4 PE=1 SV=1	Rbp4	P04916	1.00820991	-2.44217205	22.724865	22.1527233	22.9329281	22.2499561	23.5349693	19.4186554	19.6477203	17.6904392
1379	RGD1563325 protein OS=Rattus norvegicus OX=10116 GN=Tmem263 PE=1 SV=1	Tmem263	B2RZ08	6.05816995	2.608972549	20.6075897	20.726923	21.0194073	20.6406002	23.1218948	23.4039192	23.5336971	23.3708992
1380	Rho family-interacting cell polarization regulator 1 OS=Rattus norvegicus OX=10116 GN=Ripor1 PE=1 SV=1	Ripor1	A0A0G2JVR9	3.4290589	4.384809971	16.5394039	16.6355896	14.4990234	16.4048367	20.7977715	20.9784412	20.3840351	19.4578457
1381	Rho family-interacting cell polarization regulator 2 OS=Rattus norvegicus OX=10116 GN=Ripor2 PE=1 SV=1	Ripor2	Q7TP54	1.10701036	0.461602688	20.9376163	20.4023991	20.2756691	20.7945957	21.4686279	20.9881668	21.0563812	20.743515
1382	Rho GDP-dissociation inhibitor 1 OS=Rattus norvegicus OX=10116 GN=Arhgdia PE=1 SV=1	Arhgdia	Q5XI73	5.55685215	2.961260319	20.3006897	20.2444477	20.5949345	20.4583244	23.7460327	22.9987049	23.2639046	23.4347954
1383	Rho GTPase-activating protein 1 OS=Rattus norvegicus OX=10116 GN=Arhgap1 PE=1 SV=1	Arhgap1	D4A6C5	5.35783994	7.625285625	17.4533577	18.3508282	16.072155	17.0180264	25.1030598	24.5244827	24.9147186	24.8532486
1384	Rho guanine nucleotide exchange factor (GEF) 17 OS=Rattus norvegicus OX=10116 GN=Arhgef17 PE=1 SV=1	NEWGENE_1309890	A0A0G2JXT9	0.04379549	0.074213982	21.2910461	20.5663242	20.7398338	18.8318138	21.0225945	19.767313	20.4493637	20.4866028
1385	Rho guanine nucleotide exchange factor 1 OS=Rattus norvegicus OX=10116 GN=Arhgef1 PE=2 SV=1	Arhgef1	Q9Z1I6	3.41570585	4.540038109	16.5242825	14.0108671	14.3252182	14.8831549	20.0543213	19.7153072	19.5077572	18.6262894
1386	Rho guanine nucleotide exchange factor 12 OS=Rattus norvegicus OX=10116 GN=Arhgef12 PE=1 SV=1	Arhgef12	A0A0G2K860	1.17601611	-1.004985809	18.5032787	17.6438828	19.0992088	18.9882965	17.2601204	18.0050163	18.1089554	16.8406315
1387	Rho guanine nucleotide exchange factor 2 OS=Rattus norvegicus OX=10116 GN=Arhgef2 PE=1 SV=1	Arhgef2	A0A0G2K0V4	2.51571974	1.794757366	18.6412163	18.069912	19.6579342	18.921896	20.7521782	20.8880196	20.7376385	20.0921516
1388	Rho guanine nucleotide exchange factor 6 OS=Rattus norvegicus OX=10116 GN=Arhgef6 PE=1 SV=3	Arhgef6	D3ZWQ8	3.59949891	5.308792114	14.5282154	15.0857716	13.3994999	16.4004326	19.383688	20.6620007	20.5693665	20.0340328
1389	Rho guanine nucleotide exchange factor 7 OS=Rattus norvegicus OX=10116 GN=Arhgef7 PE=1 SV=1	Arhgef7	A0A0G2QC21	6.34777162	3.547375202	22.0108643	22.0092907	22.0250645	21.5097427	25.3746529	25.3799419	25.6965504	25.2933178
1390	Rho-associated protein kinase OS=Rattus norvegicus OX=10116 GN=Rock2 PE=1 SV=1	Rock2	A0A0G2K5N6	1.96806863	0.84414196	22.0733585	22.8338528	22.359108	21.8064232	23.25737	23.0513859	23.203846	22.9367085
1391	Ribonuclease inhibitor OS=Rattus norvegicus OX=10116 GN=Rnh1 PE=1 SV=1	Rnh1	E2RUH2	1.81215357	4.536646366	19.575388	20.0926685	20.6215248	15.1493607	21.8769093	23.8528385	24.018549	23.8372307
1392	Ribonucleoside-diphosphate reductase OS=Rattus norvegicus OX=10116 GN=Rrm1 PE=1 SV=1	Rrm1	Q5U2Q5	5.68451249	4.257564068	18.4092407	17.8281002	18.120842	18.3875999	22.8682461	21.9172935	22.5522251	22.4382744
1393	Ribose-phosphate pyrophosphokinase I -like OS=Rattus norvegicus OX=10116 GN=LOC314140 PE=1 SV=1	LOC314140	A0A0G2JSV3	6.16289769	4.193219185	17.1603813	17.486763	17.9211388	17.7868671	21.8148651	21.679884	22.0457973	21.5874805
1394	Ribosomal protein L37 OS=Rattus norvegicus OX=10116 PE=3 SV=2	D4A7Z2_RAT	D4A7Z2	5.0644612	3.591021061	16.9762669	17.8004608	17.8749886	17.1314087	20.7322178	21.3133831	21.0778389	21.0237694
1395	Ribosomal protein S19-like2 OS=Rattus norvegicus OX=10116 GN=Rps19l2 PE=4 SV=1	Rps19	A0A0H2UI38	4.49085974	4.304280281	20.170887	20.6778202	20.7707024	19.9778614	23.7145061	25.2371902	24.9543514	24.9083443
1396	Ribosomal protein S6 kinase beta-1 OS=Rattus norvegicus OX=10116 GN=Rps6kb1 PE=1 SV=1	Rps6kb1	P67999	1.71701567	2.044225216	17.4261608	15.8148632	17.1626892	18.0471058	17.8402271	19.6181602	19.6200676	19.5492649
1397	Ribosomal protein S6 kinase OS=Rattus norvegicus OX=10116 GN=Rps6ka3 PE=1 SV=2	Rps6ka3	D3Z8E0	2.73563666	2.70404768	19.2647572	20.2021847	17.8442707	18.9622154	22.0541782	21.3959618	22.0065441	21.6329346
1398	Ribosomal protein S6 kinase OS=Rattus norvegicus OX=10116 GN=Rps6ka5 PE=1 SV=1	Rps6ka5	A0A0G2K366	0.80983886	-0.721905231	20.0664959	18.7067547	18.9163818	20.4530563	19.0749512	18.6618366	18.5690479	18.9492321
1399	Ribosome-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Rrbp1 PE=1 SV=3	Rrbp1	F1M853	3.74381394	2.36787653	19.1835766	19.2787132	19.3437099	18.3147755	21.3042812	21.8658485	21.1281757	21.2939758
1400	RILP-like protein 1 OS=Rattus norvegicus OX=10116 GN=Rilpl1 PE=1 SV=1	Rilpl1	D3ZUQ0	7.20677064	2.870383739	18.5973701	18.2399025	18.2486763	18.4623375	21.2993584	21.2505054	21.2820816	21.197876
1401	Ring finger protein 31 OS=Rattus norvegicus OX=10116 GN=Rnf31 PE=1 SV=2	Rnf31	E9PU29	2.18750952	3.012519836	16.9808369	15.7684374	15.4614687	13.6469097	17.8414574	18.4679127	19.1394558	18.4589062

1402	RNA 3'-terminal phosphate cyclase OS=Rattus norvegicus OX=10116 GN=Rtca PE=1 SV=1	Rtca	Q68FS8	3.1449495	6.809185266	15.0148678	18.9471626	14.9173126	14.5513315	21.8661976	23.1077614	23.0223465	22.6711102
1403	RNA-binding motif protein 38 OS=Rattus norvegicus OX=10116 GN=Rbm38 PE=1 SV=3	Rbm38	D3ZGE9	2.05494473	2.078657866	16.4855309	15.9063892	16.0784988	14.572053	17.6456318	18.880722	17.5165806	17.3141689
1404	RuvB-like 1 OS=Rattus norvegicus OX=10116 GN=Ruvbl1 PE=1 SV=1	Ruvbl1	P60123	5.84467343	6.115437031	14.9159498	13.6120129	14.8624811	14.4415817	20.8347015	20.2882423	20.4831944	20.6876354
1405	RuvB-like helicase OS=Rattus norvegicus OX=10116 GN=Ruvbl2 PE=1 SV=1	Ruvbl2	G3V8T5	0.85393182	1.734492779	21.2644405	21.3820972	19.3078556	22.0911789	25.2195015	21.7256756	22.0522594	21.9861069
1406	Ryanodine receptor 2 OS=Rattus norvegicus OX=10116 GN=Ryr2 PE=1 SV=2	Ryr2	B0LPN4	0.62874093	0.598298073	20.498085	21.2020893	19.4409389	19.9048843	21.3709335	21.1544971	20.6197605	20.2939987
1407	S-adenosylmethionine synthase OS=Rattus norvegicus OX=10116 GN=Mat2a PE=1 SV=2	Mat2a	F1LRB8	4.50235073	3.31302309	19.1100979	18.5797901	19.0138073	19.7093506	22.3204689	21.9313736	22.7381573	22.6751385
1408	SAP domain-containing ribonucleoprotein OS=Rattus norvegicus OX=10116 GN=Sarnp PE=1 SV=3	Sarnp	Q498U4	0.66894334	0.583875179	19.8887138	19.6951771	19.7956333	18.8136349	21.080101	19.4937611	20.0984249	19.8563728
1409	SAR1 gene homolog A (S. cerevisiae), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Sar1a PE=1 SV=1	Sar1a	Q6AY18	8.30409473	2.998474598	21.6821442	21.5324745	21.7260132	21.7110538	24.662426	24.6470261	24.5648079	24.7713242
1410	Sarcalumenin OS=Rattus norvegicus OX=10116 GN=Srl PE=1 SV=3	Srl	F1LWG8	4.13117043	4.136120796	19.8641796	20.7616901	20.1100025	18.8567619	24.1544399	24.4705257	23.733408	23.7787437
1411	Sarcolemmal membrane-associated protein OS=Rattus norvegicus OX=10116 GN=Slmap PE=1 SV=1	Slmap	A0A0G2JWA5	5.24087813	2.406037807	20.9527721	20.7731838	20.8326759	21.2661438	23.4185276	23.6077881	23.0397091	23.3829021
1412	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Rattus norvegicus OX=10116 GN=Atp2a1 PE=1 SV=1	Atp2a1	Q64578	4.00276379	-2.998961449	22.2778149	23.4742794	22.9035587	22.0440159	19.5573845	19.5550156	19.7726955	19.8187275
1413	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Rattus norvegicus OX=10116 GN=Atp2a2 PE=1 SV=1	Atp2a2	P11507	5.43177917	4.79348135	23.1573753	23.3429642	22.5497227	22.2070999	27.7286358	27.9117851	27.2620277	27.5286388
1414	SCY1-like pseudokinase 2 OS=Rattus norvegicus OX=10116 GN=Scyl2 PE=1 SV=1	Scyl2	A0A0G2JVC2	0.742763	1.04591608	18.6126747	17.6804256	18.049427	18.0294228	20.3052559	17.2433567	19.3274422	19.6795597
1415	SECIS binding protein 2, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Secisbp2 PE=1 SV=2	Secisbp2	F1LPQ8	0.17507736	-0.156311035	23.0945263	22.5990982	21.8246174	22.978075	22.8101444	22.777029	22.0123196	22.2715797
1416	Secreted phosphoprotein 24 OS=Rattus norvegicus OX=10116 GN=Spp2 PE=1 SV=2	Spp2	Q62740	4.48545765	-3.840986729	21.2309036	20.9642811	20.9964352	20.1272526	16.4366474	17.5933533	17.1599636	16.7649612
1417	Secretory carrier-associated membrane protein 1 OS=Rattus norvegicus OX=10116 GN=Scamp1 PE=1 SV=1	Scamp1	P56603	2.22935359	2.296896458	17.3403931	19.6724148	19.1791306	19.3159275	21.4603062	21.4776802	20.9772015	20.7802639
1418	Secretory carrier-associated membrane protein OS=Rattus norvegicus OX=10116 GN=Scamp2 PE=1 SV=1	Scamp2	Q5U2U4	3.68436223	2.321336269	16.4099636	17.5979691	16.4894867	16.8871269	19.0530834	19.4809647	19.0477295	19.0881138
1419	Secretory carrier-associated membrane protein OS=Rattus norvegicus OX=10116 GN=Scamp3 PE=1 SV=2	Scamp3	E9PTW1	2.99696756	4.859635592	16.5772514	16.4121265	17.1807213	13.6341429	20.543457	21.4192333	20.7340488	20.5460453
1420	Selenoprotein P OS=Rattus norvegicus OX=10116 GN=Selenop PE=1 SV=2	Selenop	P25236	3.41590371	-3.583891153	19.8991108	19.4130516	19.8534031	19.4986324	17.5267467	15.7754526	15.6225548	15.4038792
1421	Sepiapterin reductase OS=Rattus norvegicus OX=10116 GN=Spr PE=1 SV=1	Spr	P18297	0.78068259	1.257621288	16.6494389	18.2775211	18.1379547	17.9942074	19.0681953	17.0501671	19.6871433	20.2841015
1422	Septin-11 OS=Rattus norvegicus OX=10116 GN=Sept11 PE=1 SV=1	Septin11	B3GNI6	2.72349151	3.43998909	18.7879047	20.3938351	19.07687	17.217123	22.377573	22.3238945	22.3320274	22.2021942
1423	Septin-2 OS=Rattus norvegicus OX=10116 GN=Sept2 PE=1 SV=1	Septin2	Q91Y81	4.24627206	5.1596632	18.2319069	16.301918	18.1858654	18.4925804	22.741745	23.1247501	23.1247482	22.8596802
1424	Septin-7 OS=Rattus norvegicus OX=10116 GN=Sept7 PE=1 SV=3	Septin7	F1LMC7	6.33680231	5.442133427	17.5923004	18.5534821	17.6635685	18.0836086	23.3428097	23.647646	23.432909	23.2381287
1425	Septin-8 OS=Rattus norvegicus OX=10116 GN=Sept8 PE=1 SV=1	Septin8	A0A0G2K7G7	3.96003755	4.323587418	14.3266935	15.9860268	14.3653584	14.8132849	19.2903461	19.7757301	19.3288956	18.3907413
1426	Septin-9 OS=Rattus norvegicus OX=10116 GN=Sept9 PE=1 SV=3	Septin9	F1LN75	5.09640836	5.192127705	17.9388847	16.4534359	16.4396572	16.9241333	21.9284954	22.3680382	22.270256	21.9578323
1427	Serine (Or cysteine) peptidase inhibitor, clade B, member 6a OS=Rattus norvegicus OX=10116 GN=Serpinb6a PE=1 SV=1	Serpinb6a	Q6P9U0	4.00429967	4.337966204	17.7427616	17.2011433	17.1708965	15.6493959	20.8769016	21.2907715	21.6449585	21.3034306
1428	Serine (Or cysteine) peptidase inhibitor, clade C (Antithrombin), member 1 OS=Rattus norvegicus OX=10116 GN=Serpinc1 P	Serpinc1	Q5M7T5	6.14575881	-2.979513168	24.3579369	24.1859512	24.7243748	24.5561962	21.2819996	21.464819	21.4999161	21.6596718
1429	Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 4 OS=Rattus norvegicus OX=	Serpina4	Q5M8C3	2.98016022	-3.678024769	22.5809765	22.0534515	22.3551846	22.3694916	19.1373482	17.5981426	20.1765671	17.7349472
1430	Serine protease inhibitor A3K OS=Rattus norvegicus OX=10116 GN=Serpina3k PE=1 SV=3	Serpina3c	P05545	3.26943935	-2.727348328	21.0210896	20.0247688	21.1631126	20.813755	18.8474712	18.1152725	17.8272648	17.3233242
1431	Serine protease inhibitor A3N OS=Rattus norvegicus OX=10116 GN=LOC299282 PE=1 SV=1	LOC299282	A0A0G2K1T8	4.02398995	-3.423492908	23.4509468	23.5565529	23.3637867	22.5294247	19.4467907	19.5372009	19.5545158	20.668232
1432	Serine protease inhibitor A3N OS=Rattus norvegicus OX=10116 GN=LOC299282 PE=1 SV=1	LOC299282	F1LM05	5.23559321	-3.8991642	26.6578426	26.3520832	26.9771404	26.7558823	23.046896	22.2687492	22.5591164	23.2715302
1433	Serine protease inhibitor A3N OS=Rattus norvegicus OX=10116 GN=Serpina3n PE=1 SV=3	Serpina3n	P09006	4.5336634	-3.581130981	23.601675	23.8551598	23.8019123	23.6541977	20.5859756	19.2634258	20.1488647	20.5901546
1434	Serine racemase OS=Rattus norvegicus OX=10116 GN=Srr PE=1 SV=1	Srr	Q76EQ0	2.82439994	3.549580336	15.6874485	14.626133	16.268816	13.3787756	18.3582344	18.3744164	18.6590214	18.7678223
1435	Serine/arginine-rich splicing factor 2 OS=Rattus norvegicus OX=10116 GN=Srsf2 PE=1 SV=3	Srsf2	Q6PDU1	2.3996498	3.379166603	16.7467556	17.122221	19.906168	18.3504181	20.7479744	21.5770245	21.6429806	21.6742496
1436	Serine/threonine kinase 3 (STE20 homolog, yeast) OS=Rattus norvegicus OX=10116 GN=Stk3 PE=1 SV=1	Stk3	B1WBQ5	2.95793644	1.876636982	17.3034	17.8274078	18.5317211	17.4360809	20.0990868	19.3190594	19.6431465	19.5438652
1437	Serine/threonine-protein kinase MRCK beta OS=Rattus norvegicus OX=10116 GN=Cdc42bpb PE=1 SV=1	Cdc42bpb	Q7TT49	6.74521919	3.944111347	16.1070213	16.2643108	16.6494751	16.090662	20.3041897	20.367424	20.0616531	20.1546478
1438	Serine/threonine-protein kinase N2 OS=Rattus norvegicus OX=10116 GN=Pkn2 PE=1 SV=2	Pkn2	O08874	2.81627406	4.792096615	16.7865429	15.6789036	17.4470863	14.2731895	21.7078571	20.9704208	21.3562012	19.3196297
1439	Serine/threonine-protein kinase PAK 2 OS=Rattus norvegicus OX=10116 GN=Pak2 PE=1 SV=1	Pak2	Q64303	5.3809784	4.22908783	18.3161163	18.3727932	18.2975674	17.7037487	22.9721298	21.9256916	22.4352264	22.2735291
1440	Serine/threonine-protein kinase WNK1 OS=Rattus norvegicus OX=10116 GN=Wnk1 PE=1 SV=1	Wnk1	A0A0G2K3A0	3.65823337	5.286842823	16.624033	18.9993763	18.1159859	16.1282558	22.9565315	22.803896	22.7684765	22.4861183
1441	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Rattus norvegicus OX=10116 GN=Pp	Ppp2r2a	P36876	5.62918796	3.599976063	18.7127457	18.1997948	18.8782406	18.6061478	22.0088253	22.250946	22.5984497	21.938612
1442	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit OS=Rattus norvegicus OX=10116 GN=Ppp2r5a PE=1 SV=	Ppp2r5a	D3ZDI7	2.2131811	2.680766821	17.5398846	16.9078407	16.8393269	14.7514143	18.7062283	19.7215176	19.4003448	18.9334431
1443	Serine/threonine-protein phosphatase 2A activator OS=Rattus norvegicus OX=10116 GN=Ptpa PE=1 SV=1	Ptpa	B2RYQ2	3.98384288	3.999237776	15.4623346	16.4893208	16.9122562	16.8912373	20.9960957	19.6617584	20.6791325	20.4151134
1444	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Rattus norvegicus OX=10116 GN=Ppp3ca PE=1	Ppp3ca	P63329	3.07006304	3.377613783	16.8280506	15.4787941	15.6012325	14.3841963	19.382782	18.3126469	18.9732113	19.1340885
1445	Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Rattus norvegicus OX=10116 GN=Ppp4r1 PE=1 SV=1	Ppp4r1	Q8VI02	3.15361306	1.539112568	17.4850903	17.339077	16.5546875	16.6637783	18.682291	18.527874	18.5806541	18.4082642
1446	Serine/threonine-protein phosphatase OS=Rattus norvegicus OX=10116 GN=LOC100362453 PE=3 SV=1	LOC100362453	A0A0G2JYA4	2.67039531	3.542982101	17.5067406	16.5661221	16.2323551	19.2711124	20.7339458	21.2050362	20.992157	20.8171196
1447	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Rattus norvegicus OX=10116 GN=Ppp1ca PE=1 SV=1	Ppp1ca	P62138	3.88717403	4.31816268	15.4043779	15.5008469	14.9608088	13.3678885	19.1767979	18.957901	19.1414375	19.2304363
1448	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Rattus norvegicus OX=10116 GN=Ppp1cb PE=1 SV=3	Ppp1cb	P62142	0.12821773	0.047556877	22.0579872	21.7927914	22.3137417	22.1827908	22.0295792	22.3838692	22.0395222	22.084568
1449	Serine-threonine kinase receptor-associated protein OS=Rattus norvegicus OX=10116 GN=Strap PE=1 SV=1	Strap	Q5XIG8	2.70972789	3.938250065	17.3889847	17.1328449	16.7534752	14.1946182	20.2010975	20.1280594	20.7739487	20.1198177
1450	Serine--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Sars PE=1 SV=1	Sars1	A0A0G2JZG7	3.7386423	3.174908638	15.547349	16.043354	16.6052189	15.8302679	19.9844341	18.6373806	18.7044392	19.3995705
1451	Serotransferrin OS=Rattus norvegicus OX=10116 GN=Tf PE=1 SV=1	Tf	A0A0G2QC06	6.47710259	-4.207471848	29.3884373	29.3965092	29.771431	29.4303322	25.5860348	25.4823189	24.9494724	25.1389961
1452	Serotransferrin OS=Rattus norvegicus OX=10116 GN=Tf PE=1 SV=3	Tf	P12346	3.81067681	-3.129985809	24.6465454	24.9333973	24.9161835	23.5943909	21.8045425	21.6251831	20.9428806	21.1979675
1453	Serpin family F member 2 OS=Rattus norvegicus OX=10116 GN=Serpinf2 PE=1 SV=1	Serpinf2	F7FHF3	4.57484854	-3.730041504	24.166626	24.1388779	24.387825	23.8828545	21.0100479	19.9150219	19.8477535	20.883194
1454	Serpin H1 OS=Rattus norvegicus OX=10116 GN=Serpinh1 PE=1 SV=1	Serpinh1	P29457	5.2363346	3.095963001	21.7339935	21.8333073	21.721735	21.0323257	24.4654179	24.8511181	24.5600395	24.8286381
1455	Serum albumin OS=Rattus norvegicus OX=10116 GN=Alb PE=1 SV=1	Alb	A0A0G2JSH5	3.22830828	-3.78133297	24.2650414	26.3487301	25.1854572	26.4119244	22.2181587	22.0763931	21.0618114	21.7294579
1456	Serum albumin OS=Rattus norvegicus OX=10116 GN=Alb PE=1 SV=2	Alb	P02770	6.68137363	-3.768480301	31.5012875	31.4631805	31.5613518	31.5005035	28.1126804	27.741991	27.4201927	27.6775379
1457	Serum amyloid P-component OS=Rattus norvegicus OX=10116 GN=Apcs PE=1 SV=1	Apcs	A0A0H2UHH2	5.03146637	-6.645079613	22.6718712	23.139967	23.1405697	22.828537	15.4953775	17.2886791	15.4987402	16.9178295
1458	Serum paraoxonase/arylesterase 1 OS=Rattus norvegicus OX=10116 GN=Pon1 PE=1 SV=3	Pon1	P55159	3.5372937	-1.9540658	21.0073376	21.5557785	20.5061874	21.3122997	19.3558712	19.0542774	18.8143768	19.3408146
1459	SH2B adapter protein 1 OS=Rattus norvegicus OX=10116 GN=Sh2b1 PE=1 SV=1	Sh2b1	Q62985	4.68338954	4.074895859	15.923811	15.8475771	16.6625767	15.0901842	19.8453579	20.2593956	19.9849968	19.7339821
1460	SH3 and PX domains 2A OS=Rattus norvegicus OX=10116 GN=Sh3pxd2a PE=1 SV=1	Sh3pxd2a	A0A0G2JX92	4.14490176	2.177812576	18.6347218	18.4318161	18.196661	17.8793907	20.1831207	20.8838844	20.5197525	20.2670822
1461	SH3 domain binding glutamic acid-rich protein-like 3 OS=Rattus norvegicus OX=10116 GN=Sh3bgrl3 PE=1 SV=1	Sh3bgrl3	B2RZ27	0.20905459	-0.459482431	15.5250158	17.1706409	15.9792366	17.1746712	13.813982	17.3941746	16.4170723	16.3864059
1462	SH3 domain-containing kinase-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Sh3kbp1 PE=1 SV=2	Sh3kbp1	Q925Q9	2.30408968	2.488090038	17.7951851	18.9289417	17.1573944	16.3748894	20.5140266	19.9413166	19.5672493	20.1861782

1463	Signal recognition particle 54 kDa protein OS=Rattus norvegicus OX=10116 GN=Srp54 PE=2 SV=1	Srp54a	Q6AYB5	4.36987117	3.555235386	18.9469376	18.2536011	19.1515121	17.9263248	22.5489216	22.2140045	22.0244102	21.7119808
1464	Signal recognition particle subunit SRP68 OS=Rattus norvegicus OX=10116 GN=Srp68 PE=1 SV=1	Srp68	B2RYI2	5.85849907	3.103891373	17.038023	17.5045967	17.1801128	17.5282116	20.3220272	20.7195568	20.2066002	20.4183254
1465	Signal recognition particle subunit SRP72 OS=Rattus norvegicus OX=10116 GN=LOC108348180 PE=1 SV=2	Srp72	D4A7R0	4.63197796	3.942627907	15.6025753	15.6086788	15.8094587	14.4739084	19.390707	18.9400539	19.6395092	19.2948627
1466	Signal transducer and activator of transcription 3 OS=Rattus norvegicus OX=10116 GN=Stat3 PE=1 SV=1	Stat3	P52631	6.10882311	4.985277176	18.5123615	17.9617023	18.2305889	17.5897541	22.7220802	23.3702526	23.1322784	23.0109043
1467	Signal transducer and activator of transcription OS=Rattus norvegicus OX=10116 GN=Stat1 PE=1 SV=2	Stat1	F1M9D6	2.59520876	3.713376284	15.2050104	18.4165707	15.8957977	17.5306911	20.4032211	20.3534431	20.8646545	20.2802563
1468	Signal transducer and activator of transcription OS=Rattus norvegicus OX=10116 GN=Stat2 PE=1 SV=1	Stat2	Q5XI26	0.27812053	-1.096728802	18.7845783	19.963541	18.9886398	13.0206861	15.3237333	16.947361	16.9262009	17.1732349
1469	Signal transducing adapter molecule 2 OS=Rattus norvegicus OX=10116 GN=Stam2 PE=2 SV=1	Stam2	Q5XHY7	3.20983531	3.142166853	14.9926128	14.9756145	15.3414965	13.4543667	17.1938744	18.3170204	17.8903675	17.9314957
1470	Similar to 60S ribosomal protein L23a OS=Rattus norvegicus OX=10116 GN=LOC689899 PE=3 SV=1	LOC689899	D3ZTH8	4.74390493	4.035535336	19.6407948	19.7157364	18.8187466	19.3207417	22.7033005	23.9412174	23.5552979	23.438345
1471	Similar to alpha-fetoprotein OS=Rattus norvegicus OX=10116 GN=LOC360919 PE=1 SV=1	LOC360919	F7FAY5	0.17590108	-0.189500332	18.3927422	18.8993282	19.1441269	17.5307293	18.6752796	17.6972179	18.5754223	18.2610054
1472	Similar to CG3740-PA OS=Rattus norvegicus OX=10116 GN=LOC690000 PE=1 SV=1	LOC690000	D3ZWS2	3.7287814	4.915032387	14.7495031	15.9379301	14.3713341	17.0017414	20.5087051	20.2641792	20.6622486	20.2855053
1473	Similar to DNA segment, Chr 8, ERATO Doi 531, expressed, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Vps37a P	Vps37a	Q4V794	2.14980935	3.26712513	18.0972652	17.7708454	16.3077316	15.610815	18.5513287	20.5132542	20.9637203	20.8268547
1474	Similar to RIKEN cDNA 0610038D11 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Trmt112 PE=1 SV=	Trmt112	B2RYS9	1.24787129	2.520060301	19.270052	18.8489647	18.6370754	14.7097578	20.0809174	20.7368393	20.4186821	20.3096523
1475	Similar to RIKEN cDNA 1300017J02 OS=Rattus norvegicus OX=10116 GN=RGD1310507 PE=1 SV=1	Inhca	A0A0G2K896	4.78206638	-4.003960609	23.699873	23.4737511	24.4039974	23.8075962	19.3253231	20.2193985	19.4927845	20.3318691
1476	Similar to RIKEN cDNA 2310022B05 OS=Rattus norvegicus OX=10116 GN=RGD1559896 PE=1 SV=1	RGD1559896	D3ZY47	5.54655882	5.597409725	14.8614845	14.6365395	14.6026344	13.4418907	20.2329197	19.782793	19.9339161	19.9825592
1477	Similar to RIKEN cDNA 2810055F11 (Predicted) OS=Rattus norvegicus OX=10116 GN=L3hypdh PE=1 SV=1	L3hypdh	D3ZV91	1.28641182	1.673395634	17.024641	19.7766323	19.6073017	18.7960873	19.6896057	20.6614838	21.038414	20.5087414
1478	Similar to RIKEN cDNA 5830475I06 OS=Rattus norvegicus OX=10116 GN=RGD1311744 PE=1 SV=3	RGD1311744	D4A1U8	1.81831255	2.601922274	13.5126085	15.5790844	15.3360939	17.1581116	18.566082	17.6989937	18.0236588	17.7048531
1479	Similar to TBC1 domain family, member 8;BUB2-like protein 1;vascular Rab-GAP/TBC-containing (Predicted), isoform CRA_	Tbc1d9b	F1LRL4	2.62033617	-0.91408205	21.4232769	21.0865326	21.5913849	21.1418648	20.3106365	20.0453014	20.5974483	20.6333447
1480	Similar to THUMP domain containing 3 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Thumpd3 PE=1 S	Thumpd3	D3ZSV7	1.14474762	2.107132435	17.3484383	14.8213844	15.2380371	14.2240906	18.1585827	15.4726372	18.0345306	18.3947296
1481	Similar to Tripartite motif protein 47 OS=Rattus norvegicus OX=10116 GN=Trim47 PE=1 SV=1	Trim47	D3ZA22	4.65696227	3.951337814	18.0083637	17.9596233	17.741291	17.4859982	20.9585342	22.3563385	22.1221581	21.5635967
1482	SLAIN motif family, member 2 OS=Rattus norvegicus OX=10116 GN=Slain2 PE=1 SV=1	Slain2	G3V6A2	1.76906475	-0.954773903	21.9808941	22.3175697	22.4054985	22.0390701	21.0760517	21.9877796	21.1704388	20.6896667
1483	SLIT-ROBO Rho GTPase-activating protein 2 OS=Rattus norvegicus OX=10116 GN=Srgap2 PE=1 SV=1	Srgap2	D4A208	0.01371372	0.021584988	21.5293655	19.2053356	20.5016327	20.6514053	21.1035767	20.4188347	20.4622726	19.9893951
1484	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Rattus norvegicus OX=10116 GN=Sgta PE=1 SV=	Sgta	O70593	2.52039892	4.17925024	16.8883457	16.9103394	17.2901669	20.1722183	22.8695984	21.1812744	21.6643143	22.2628841
1485	Small proline-rich protein 2D OS=Rattus norvegicus OX=10116 GN=Sprr2d PE=4 SV=2	Sprr2d	D3ZAR3	0.7450966	1.414310694	15.804554	17.5054245	16.3761635	14.3338118	17.4452095	19.27071	16.5351257	16.4261513
1486	Sodium/calcium exchanger 1 OS=Rattus norvegicus OX=10116 GN=Slc8a1 PE=1 SV=3	Slc8a1	Q01728	0.66054398	0.590274334	22.8861656	22.9472542	23.0455418	21.3833408	23.5619221	23.2079735	23.1069965	22.7465076
1487	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Rattus norvegicus OX=10116 GN=Atp1a1 PE=1 SV=1	Atp1a1	P06685	6.28971414	3.638342857	22.002285	22.037405	21.6958523	21.5914974	25.719965	25.6194706	25.2279911	25.3129845
1488	Sodium/potassium-transporting ATPase subunit alpha-3 OS=Rattus norvegicus OX=10116 GN=Atp1a3 PE=1 SV=2	Atp1a3	P06687	2.79714498	4.588281155	16.8841267	18.3430347	17.789896	14.6318035	21.8497047	21.7653809	21.4410686	20.9458313
1489	Sodium/potassium-transporting ATPase subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Atp1b1 PE=1 SV=1	Atp1b1	P07340	4.76116806	5.892735004	18.3782043	18.1682816	17.277668	16.3568039	23.7047081	23.5772057	23.215416	23.2545681
1490	Sodium/potassium-transporting ATPase subunit beta-3 OS=Rattus norvegicus OX=10116 GN=Atp1b3 PE=2 SV=1	Atp1b3	Q63377	1.16171628	1.57852149	18.5191841	15.6993475	18.091217	17.9236431	19.4198837	19.5861759	18.1534977	19.3879204
1491	Sodium-dependent phosphate transporter 2 OS=Rattus norvegicus OX=10116 GN=Slc20a2 PE=1 SV=1	Slc20a2	Q63488	2.92756967	4.34979701	17.5796165	16.0354424	15.9899902	13.959691	20.2347488	20.599905	19.9825153	20.146759
1492	Solute carrier family 12 member 4 OS=Rattus norvegicus OX=10116 GN=Slc12a4 PE=1 SV=1	Slc12a4	Q63632	0.26014226	-0.216825485	17.627161	17.1876183	17.2705593	17.9927635	16.9766884	18.1623802	17.0963058	16.9754257
1493	Solute carrier family 18 (Vesicular acetylcholine), member 3 OS=Rattus norvegicus OX=10116 GN=Slc18a3 PE=4 SV=1	Slc18a3	A0A1B0GWU4	0.62717238	1.094976902	16.4780712	17.2932167	17.9862843	14.2400608	17.3976154	18.081686	17.321064	17.5771751
1494	Solute carrier family 2, facilitated glucose transporter member 1 OS=Rattus norvegicus OX=10116 GN=Slc2a1 PE=1 SV=1	Slc2a1	P11167	2.7150291	4.207069397	18.4656944	14.9441471	16.7544765	18.1114883	21.3907127	21.0687027	21.2673798	21.3772888
1495	Solute carrier family 2, facilitated glucose transporter member 3 OS=Rattus norvegicus OX=10116 GN=Slc2a3 PE=1 SV=1	Slc2a3	A0A0G2JVB0	0.72106976	-1.139541626	18.0289764	20.2763863	19.3350506	17.9120579	18.5433788	16.7051697	16.9864712	18.759285
1496	Sorbin and SH3 domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Sorbs2 PE=1 SV=2	Sorbs2	F1LPM3	5.44684771	4.128706932	20.0087204	19.4633999	19.9133549	20.0111465	23.6293411	24.3714714	24.3435841	23.5670528
1497	Sorting nexin 2 OS=Rattus norvegicus OX=10116 GN=Snx2 PE=1 SV=1	Snx2	B2RYP4	3.88243821	4.029281139	17.4070625	17.3363209	16.0416069	18.2333546	21.048502	21.2683887	21.573576	21.2450027
1498	Sorting nexin OS=Rattus norvegicus OX=10116 GN=Snx6 PE=1 SV=1	Snx6	B5DEY8	0.25157238	-0.364106178	19.6315289	19.5761871	20.2423706	17.5979557	18.8206902	18.7621346	18.7083054	19.3004875
1499	Sorting nexin OS=Rattus norvegicus OX=10116 GN=Snx9 PE=1 SV=2	Snx9	M0R9L3	0.56444233	-0.88190484	18.7889843	15.8074265	18.0872726	16.5249004	16.9607468	16.714653	15.9451551	16.0604095
1500	Sorting nexin-1 OS=Rattus norvegicus OX=10116 GN=Snx1 PE=1 SV=1	Snx1	Q99N27	2.9571128	5.154802561	16.9595737	16.053339	15.422081	12.9348326	20.6447849	20.9406109	20.1318836	20.2717571
1501	Sorting nexin-3 OS=Rattus norvegicus OX=10116 GN=Snx3 PE=1 SV=1	Snx3	Q5U211	3.21803699	5.463587999	16.7943554	16.1730347	16.8680096	13.4474039	21.6865883	20.6818256	21.3834629	21.3852787
1502	Sorting nexin-5 OS=Rattus norvegicus OX=10116 GN=Snx5 PE=1 SV=1	Snx5	B1H267	3.343531	3.076819897	18.0695114	17.2547016	18.3807793	18.3972015	22.0165329	20.4472427	20.6422138	21.303484
1503	SOS Ras/Rac guanine nucleotide exchange factor 1 OS=Rattus norvegicus OX=10116 GN=Sos1 PE=1 SV=2	Sos1	D4A3T0	2.47279448	2.168762922	15.0118656	15.4613171	15.5721531	15.7045488	16.2949905	18.0705109	17.9904079	18.0690269
1504	SPARC OS=Rattus norvegicus OX=10116 GN=Sparc PE=1 SV=4	Sparc	P16975	0.01102482	0.015888214	19.5703869	19.8877773	19.9440575	18.0987988	19.1196423	20.0419674	19.2227745	19.1801891
1505	Spartin OS=Rattus norvegicus OX=10116 GN=Spart PE=1 SV=3	Spart	E9PT90	5.04546934	0.530981541	20.6094418	20.6685772	20.6803455	20.7032185	21.2527523	21.1674824	21.2481289	21.1171455
1506	SPC24, NDC80 kinetochore complex component OS=Rattus norvegicus OX=10116 GN=Spc24 PE=4 SV=3	Spc24	D4A1C5	2.81635984	1.053228855	19.2358456	18.7429523	18.8127766	19.1999493	20.447813	19.8104324	20.0657253	19.8804684
1507	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus OX=10116 GN=Sptan1 PE=1 SV=1	Sptan1	A0A0G2K1Y8	4.57296402	4.478692055	19.3398914	18.623991	18.4129868	20.1104851	23.761734	23.4480591	23.6792164	23.513113
1508	Spectrin beta chain OS=Rattus norvegicus OX=10116 GN=Sptb PE=1 SV=1	Sptb	A0A140UHX6	1.7633945	-1.113019943	22.7258587	23.263628	22.4579468	23.7831841	21.471365	22.0832367	22.2863159	21.9376202
1509	Spectrin beta chain OS=Rattus norvegicus OX=10116 GN=Sptbn1 PE=1 SV=1	Sptbn1	A0A0G2K8W9	5.11601897	3.014992237	20.8073769	20.4712238	20.2144279	19.9382935	23.0894299	23.4990921	23.555397	23.3473721
1510	Spectrin, alpha, erythrocytic 1 OS=Rattus norvegicus OX=10116 GN=Spta1 PE=1 SV=3	Spta1	D4A678	1.56462737	-0.940979004	22.1630535	22.5031757	21.0302906	22.0484409	20.9579487	21.1678429	21.0137577	20.8414955
1511	Sperm-associated antigen 9 OS=Rattus norvegicus OX=10116 GN=Spag9 PE=1 SV=1	Spag9	A0A0G2K6E8	3.83023325	1.663364887	18.8052597	18.6763039	19.2416286	18.943882	20.9517136	20.2150898	20.6625957	20.4911346
1512	Spermidine synthase OS=Rattus norvegicus OX=10116 GN=LOC100912604 PE=1 SV=1	Srm	Q99MI5	3.84774554	2.864197254	17.7386398	17.4016647	17.4380608	17.5175819	19.6748428	19.993515	20.8921375	20.9922409
1513	S-phase kinase-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Skp1 PE=1 SV=1	Skp1	A0A0G2K4X8	4.60287652	6.582421064	14.4163847	16.8580608	16.0936279	16.7185574	22.8633499	22.5801888	22.5716438	22.4011326
1514	Splicing factor proline and glutamine rich OS=Rattus norvegicus OX=10116 GN=Sfpq PE=1 SV=1	Sfpq	A0A0G2K8K0	0.666923	1.591660261	17.1702995	19.1485004	17.4341125	13.7746496	19.1365337	18.0788517	18.2096043	18.4692135
1515	SPRY domain-containing protein 7 OS=Rattus norvegicus OX=10116 GN=Spryd7 PE=2 SV=1	Spryd7	Q5M7T2	3.99457952	4.866032839	14.9449329	14.503727	14.2834272	16.5861206	19.8236313	20.312933	19.9383354	19.7074394
1516	Stathmin OS=Rattus norvegicus OX=10116 GN=Stmn1 PE=1 SV=2	Stmn1	P13668	5.18610934	1.728996754	19.7477169	19.802639	20.0204792	19.7747822	21.8240376	21.5670185	21.3324223	21.538126
1517	STE20/SPS1-related proline-alanine-rich protein kinase OS=Rattus norvegicus OX=10116 GN=Stk39 PE=1 SV=2	Stk39	O88506	5.92664643	8.997261286	14.4921331	14.802721	13.4817724	15.6288271	23.270977	23.5584469	23.8840179	23.681057
1518	STIP1 homology and U-Box containing protein 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Stub1 PE=1 SV=1	Stub1	D4A4T0	5.47079883	4.152372837	16.2775764	17.1452351	17.0267754	16.6016121	21.2202091	20.7586098	21.1340961	20.5477753
1519	Stress-70 protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hspa9 PE=1 SV=1	Hspa9	F1M953	1.94511851	2.490077972	21.1014957	20.4000931	18.7096729	19.7919006	21.110796	23.1712322	22.6945572	22.9868889
1520	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus OX=10116 GN=Stip1 PE=1 SV=1	Stip1	O35814	2.85284544	3.041930676	22.158844	22.0216923	22.281908	20.8575974	26.025589	23.9163532	24.724329	24.8214931
1521	Striated muscle-specific serine/threonine-protein kinase OS=Rattus norvegicus OX=10116 GN=Speg PE=1 SV=2	Speg	Q63638	0.82303694	-0.330672741	22.9822826	23.4516697	23.1974983	23.3712025	22.7677307	23.427393	22.8103123	22.6745262
1522	Striatin 4 OS=Rattus norvegicus OX=10116 GN=Strn4 PE=1 SV=1	Strn4	F1M6V8	3.07401066	1.187521458	19.2491188	18.7063961	18.7061539	18.4559078	19.7160492	20.1835403	19.9953785	19.9726944
1523	Structural maintenance of chromosomes protein OS=Rattus norvegicus OX=10116 GN=Smc2 PE=1 SV=1	Smc2	D4A5Q2	1.14699433	2.664728165	19.4757423	14.0225143	18.7331448	17.2181931	19.6949043	19.9079399	20.4173679	20.088295

1524	Structural maintenance of chromosomes protein OS=Rattus norvegicus OX=10116 GN=Smc4 PE=1 SV=1	Smc4	F1MAD9	4.77645729	3.446092129	20.4427166	20.52701	19.5147781	20.6532021	23.8963966	23.5471172	23.5778866	23.9006748
1525	STT3A, catalytic subunit of the oligosaccharyltransferase complex OS=Rattus norvegicus OX=10116 GN=Stt3a PE=1 SV=1	Stt3a	A0A0G2JWH5	2.97007032	2.255108356	15.671279	15.8011541	15.4618759	16.4559536	17.5486698	18.9213066	17.653841	18.2868786
1526	Submandibular gland protein C OS=Rattus norvegicus OX=10116 GN=Smgc PE=4 SV=3	Smgc	E9PTP9	5.44482742	-6.303473949	24.1359406	23.5342102	24.0392342	25.2867451	18.0283012	18.0034714	17.588377	18.1620846
1527	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sdha PE=1	Sdha	Q920L2	2.67683135	4.332140923	19.2638206	19.668354	16.3716526	17.3504314	21.6229229	23.0281677	22.5564575	22.7752743
1528	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sdhb PE=2 S	Sdhb	P21913	2.68412188	4.359994888	16.5423622	16.5043297	13.5086594	16.9787807	19.4804726	20.7320328	20.3144169	20.4471893
1529	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Oxct1 PE=1 SV=1	Oxct1	B2GV06	1.40819818	-1.097087383	21.0757942	20.9935188	21.4931526	21.0815487	18.9095306	20.7347775	20.1700325	20.4413242
1530	Sulfhydryl oxidase 1 OS=Rattus norvegicus OX=10116 GN=Qsox1 PE=1 SV=1	Qsox1	Q6IUU3	4.76909861	-3.10261488	22.2918186	21.8925209	21.8738823	22.0149555	19.3083973	19.2534771	18.7828693	18.3179741
1531	Superoxide dismutase [Cu-Zn] OS=Rattus norvegicus OX=10116 GN=Sod1 PE=1 SV=2	Sod1	P07632	1.75219925	1.276257038	20.2390366	19.5588684	20.7882328	19.1896286	21.2832623	21.6238022	21.1730404	20.8006897
1532	Suprabasin OS=Rattus norvegicus OX=10116 GN=Sbsn PE=1 SV=1	Sbsn	F7FEM5	0.7781845	-0.700039864	21.472887	20.2172966	20.8454132	19.4092464	19.826973	19.8115044	19.8868465	19.61936
1533	Synapse associated protein 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Syap1 PE=1 SV=1	Syap1	F7F350	3.86977296	6.807922363	14.1960382	14.6095324	17.2194061	13.8254013	21.6419754	21.3906746	22.2616234	21.7877941
1534	Synaptic vesicle membrane protein VAT-1 homolog OS=Rattus norvegicus OX=10116 GN=Vat1 PE=1 SV=1	Vat1	Q3MIE4	4.44287548	2.335924149	21.4802971	21.57827	20.9582329	21.0637493	24.0544147	23.5011692	23.4839439	23.3847179
1535	Synaptophysin-like 1 OS=Rattus norvegicus OX=10116 GN=Sypl1 PE=1 SV=1	Sypl1	A0A0G2KA82	3.72070622	3.803692341	17.2672653	18.9709129	16.9111786	17.2581482	21.5491638	21.5188408	21.2786465	21.2756233
1536	Synaptopodin 2-like OS=Rattus norvegicus OX=10116 GN=Synpo2l PE=1 SV=1	Synpo2l	D3ZZ68	2.08946446	1.825805664	19.9375153	21.2721958	19.3864708	19.4939289	21.7873039	22.3215046	21.8509445	21.4335804
1537	Synaptopodin-2 OS=Rattus norvegicus OX=10116 GN=Synpo2 PE=1 SV=2	Synpo2	D4A702	1.22359124	0.957649708	18.6408272	18.1543045	18.3734436	18.197979	20.0571995	19.8870602	18.8261738	18.4267197
1538	Synergin gamma OS=Rattus norvegicus OX=10116 GN=Synrg PE=1 SV=3	Synrg	Q9JKC9	0.9176995	1.81304574	17.6463032	18.4279823	17.9632835	14.0617018	18.7060986	18.8345852	19.0556831	18.7550869
1539	Syntaxin 16 OS=Rattus norvegicus OX=10116 GN=Stx16 PE=1 SV=1	Stx16	A0A0G2K528	0.32766381	0.999271393	19.5966892	18.9817162	19.6420555	14.4160271	19.7906857	19.5737648	18.3991528	18.8699703
1540	Syntaxin-12 OS=Rattus norvegicus OX=10116 GN=Stx12 PE=1 SV=1	Stx12	A0A0G2JVB6	3.64239782	3.96005106	18.6991119	18.5542698	17.5827885	19.9607906	22.6976604	23.0098419	22.5090809	22.4205818
1541	Syntaxin-7 OS=Rattus norvegicus OX=10116 GN=Stx7 PE=1 SV=4	Stx7	O70257	3.08400746	1.557224751	18.8580132	18.7287693	18.8779011	19.5319576	21.0003605	20.6345444	20.1722565	20.4183788
1542	Syntaxin-8 OS=Rattus norvegicus OX=10116 GN=Stx8 PE=1 SV=1	Stx8	Q9Z2Q7	3.86684184	-3.417289257	20.9394951	19.8295097	20.3043079	21.2999821	17.7164135	17.337122	16.9742641	16.6763382
1543	Syntaxin-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Stxbp1 PE=1 SV=1	Stxbp1	P61765	3.09397418	2.821175337	13.4337664	14.8923616	14.817625	14.9552584	17.1478691	17.9490814	16.6984272	17.588335
1544	Syntenin-1 OS=Rattus norvegicus OX=10116 GN=Sdcbp PE=1 SV=1	Sdcbp	Q9JI92	2.20579716	3.935983896	13.233078	15.5926332	17.9007607	15.6468468	19.6375294	19.4551868	19.66008	19.3644581
1545	Talin 2 OS=Rattus norvegicus OX=10116 GN=Tln2 PE=1 SV=3	Tln2	D3ZA84	5.04871301	4.715895176	18.1186237	17.3981895	18.3687191	18.7779331	22.3782063	22.9098644	23.0124092	23.2265663
1546	Tankyrase 1-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Tnks1bp1 PE=1 SV=1	Tnks1bp1	D3ZF26	0.47099306	-0.498831749	18.9772568	19.6443081	18.6171741	19.6675167	17.8157711	19.7822552	18.6511536	18.6617489
1547	Target of myb1 homolog (Chicken) OS=Rattus norvegicus OX=10116 GN=Tom1 PE=1 SV=1	Tom1	Q5XI21	4.19490723	4.469457626	17.3085976	17.7650852	16.0632305	17.4487839	22.3677959	21.1959629	21.5200386	21.3797302
1548	Target of myb1-like 2 membrane-trafficking protein OS=Rattus norvegicus OX=10116 GN=Tom1l2 PE=1 SV=1	Tom1l2	A0A0G2K9L2	2.42879827	3.929623127	18.9057617	18.3552551	17.5568314	15.0969982	21.8470554	21.0899429	21.4012051	21.2951355
1549	Taxilin alpha OS=Rattus norvegicus OX=10116 GN=Txlna PE=1 SV=1	Txlna	B2GV14	1.53237083	3.04912591	16.8253365	15.7994385	15.7886868	13.9843969	16.3783722	20.328392	19.792696	18.094902
1550	Taxilin beta OS=Rattus norvegicus OX=10116 GN=Txlnb PE=1 SV=1	Txlnb	A0A0G2K2T1	3.17773872	1.821166515	21.8441277	21.8680859	22.1567154	21.6007538	22.9445858	24.0895119	23.9859028	23.7343483
1551	TBC1 domain family member 1 OS=Rattus norvegicus OX=10116 GN=Tbc1d1 PE=1 SV=1	Tbc1d1	D4AC16	4.21953699	3.743184328	16.6832027	16.3089466	16.4295139	15.0537615	19.9508495	19.721405	20.1011829	19.6747246
1552	TBC1 domain family, member 15 OS=Rattus norvegicus OX=10116 GN=Tbc1d15 PE=1 SV=2	Tbc1d15	F7EZ89	4.9286532	2.83834219	17.2714958	17.7749767	17.8810425	17.0861511	20.5517559	20.146862	20.21134	20.457077
1553	TBC1 domain family, member 17 OS=Rattus norvegicus OX=10116 GN=Tbc1d17 PE=1 SV=1	Tbc1d17	B1H264	6.88546113	5.180052757	15.3863792	15.2590141	14.7268429	15.1241665	20.3839359	19.9660168	20.3856068	20.4810543
1554	TBC1 domain family, member 4 OS=Rattus norvegicus OX=10116 GN=Tbc1d4 PE=1 SV=3	Tbc1d4	D3ZGN0	2.77205495	1.56118536	19.5063782	19.4407597	19.9410343	19.1270466	21.7057915	20.8840599	21.0830498	20.587059
1555	T-complex protein 1 subunit alpha OS=Rattus norvegicus OX=10116 GN=Tcp1 PE=1 SV=1	Tcp1	P28480	4.91469868	4.582304478	20.410305	20.4158134	19.821413	20.1079845	24.0825462	24.439106	25.0372334	25.5258484
1556	T-complex protein 1 subunit beta OS=Rattus norvegicus OX=10116 GN=Cct2 PE=1 SV=3	Cct2	Q5XIM9	4.76112825	4.881971359	19.8841572	20.1554794	20.1189995	19.5198231	24.4415092	23.9926548	25.1061802	25.6660004
1557	T-complex protein 1 subunit delta OS=Rattus norvegicus OX=10116 GN=Cct4 PE=1 SV=3	Cct4	Q7TPB1	3.59715416	3.861441612	21.454668	20.7718391	21.0549698	21.0003414	24.23699	23.9853477	25.5849609	25.9202862
1558	T-complex protein 1 subunit epsilon OS=Rattus norvegicus OX=10116 GN=Cct5 PE=1 SV=1	Cct5	Q68FQ0	5.01531099	5.685292721	18.0707893	19.0960407	19.4150944	19.6218739	24.5997658	24.1365337	25.0177879	25.1908817
1559	T-complex protein 1 subunit eta OS=Rattus norvegicus OX=10116 GN=Cct7 PE=1 SV=1	Cct7	D4AC23	4.3422765	4.893792152	19.3748894	19.748497	19.6285973	19.5535679	23.7746468	23.6463299	24.8761349	25.5836086
1560	T-complex protein 1 subunit gamma OS=Rattus norvegicus OX=10116 GN=Cct3 PE=1 SV=1	Cct3	Q6P502	4.76000334	5.14040947	19.1338673	19.7131805	19.7761288	19.8034763	24.1223888	24.0612392	25.2219715	25.5826912
1561	Tenascin C OS=Rattus norvegicus OX=10116 GN=Tnc PE=1 SV=1	Tnc	A0A0G2K1L0	1.80157329	-0.562065601	20.22785	20.3677006	20.6160755	20.1238155	20.1273479	19.7656498	19.6921444	19.502037
1562	Tensin 1 OS=Rattus norvegicus OX=10116 GN=Tns1 PE=1 SV=2	Tns1	F1LN42	5.22449119	6.851547718	17.274437	16.7603951	18.5162163	16.5293026	24.0577564	24.3859081	24.2597065	23.7831707
1563	Tetraspanin OS=Rattus norvegicus OX=10116 GN=Cd81 PE=1 SV=1	Cd81	Q6P9V1	1.92384968	3.304959297	17.8036594	17.502346	17.5955219	14.253767	20.5851402	18.9858665	20.2250538	20.579071
1564	Tetraspanin OS=Rattus norvegicus OX=10116 GN=Tspan6 PE=1 SV=1	Tspan6	B0BN20	1.6915587	1.052896023	18.6693554	18.7171936	18.3036442	17.732048	19.5418892	19.783308	18.6797924	19.6288357
1565	Tetratricopeptide repeat domain 1 OS=Rattus norvegicus OX=10116 GN=Ttc1 PE=1 SV=1	Ttc1	Q66H09	2.38693655	2.779871464	16.8776073	17.2194958	17.4567585	15.8112411	20.745039	18.3228798	19.5842953	19.8323746
1566	Tetratricopeptide repeat domain 38 OS=Rattus norvegicus OX=10116 GN=Ttc38 PE=1 SV=2	Ttc38	D4ACL2	0.5015677	1.042877674	16.4833736	16.9637547	16.9921017	13.5376854	16.0045166	17.3628559	18.1754265	16.6056271
1567	Tetratricopeptide repeat domain 7B OS=Rattus norvegicus OX=10116 GN=Ttc7b PE=1 SV=3	Ttc7b	F1LUY5	3.96742674	-4.010570765	20.4847107	20.4243031	20.3577213	20.6659279	15.199605	17.2231865	16.8563404	16.611248
1568	Thioredoxin domain containing 9 OS=Rattus norvegicus OX=10116 GN=Txndc9 PE=1 SV=1	Txndc9	Q5M8C7	0.52166944	0.834051847	14.7921467	17.6410999	14.5542231	16.3372002	17.0637512	16.5964127	16.335474	16.6652393
1569	Thioredoxin OS=Rattus norvegicus OX=10116 GN=Txn PE=1 SV=2	Txn1	P11232	4.0077485	2.634186745	19.5196934	20.8532352	20.3215179	20.3716106	23.0931969	22.7397575	22.7763786	22.9934711
1570	Thioredoxin-interacting protein OS=Rattus norvegicus OX=10116 GN=Txnip PE=2 SV=1	Txnip	Q5M7W1	0.76949234	1.012991428	15.9509821	16.1871548	15.7140512	15.0213699	18.4491348	15.6973076	16.2261982	16.5528831
1571	Thioredoxin-like protein 1 OS=Rattus norvegicus OX=10116 GN=Txnl1 PE=1 SV=1	Txnl1	A0A0G2K737	1.0884675	2.923414469	19.9421101	14.1739702	19.9065247	19.1747799	20.805439	21.0977859	21.6800175	21.3078003
1572	Thioredoxin-related transmembrane protein 2 OS=Rattus norvegicus OX=10116 GN=Tmx2 PE=2 SV=1	Tmx2	Q5XIK2	4.14225777	4.673810005	15.6662073	15.0959396	14.9002266	15.6658297	20.0139771	20.5550041	18.7503967	20.7040653
1573	Thrombospondin 1 OS=Rattus norvegicus OX=10116 GN=Thbs1 PE=1 SV=2	Thbs1	M0R979	5.41128452	-4.826693058	25.3523617	25.0040092	25.668993	25.0218124	20.886919	19.6962109	20.5020008	20.6552734
1574	Thrombospondin-4 OS=Rattus norvegicus OX=10116 GN=Thbs4 PE=4 SV=1	Thbs4	A0A0G2K7L8	3.97963844	-2.686023235	21.0910282	20.5093193	21.2730751	21.4241581	18.6730118	18.7391224	18.3705482	17.7708054
1575	Thymosin beta-10 OS=Rattus norvegicus OX=10116 GN=Tmsb10 PE=1 SV=2	Tmsb10	P63312	0.37032485	1.299419165	14.1723719	19.5018501	17.0841503	19.6039181	17.2675495	20.3535404	17.6663208	20.2725563
1576	Thymosin beta-4 OS=Rattus norvegicus OX=10116 GN=Tmsb4x PE=1 SV=2	Tmsb4x	P62329	3.17154521	1.263147354	20.9751091	21.3077297	21.4841537	20.6607571	22.4765835	22.3372555	22.174881	22.4916191
1577	Thyroid hormone receptor interactor 11 OS=Rattus norvegicus OX=10116 GN=Trip11 PE=1 SV=3	Trip11	D4ABD7	4.43418031	5.244531631	15.8347683	14.2883606	15.1321297	16.3246613	21.0646248	20.546875	20.1410065	20.8055401
1578	Thyroxine-binding globulin OS=Rattus norvegicus OX=10116 GN=Serpina7 PE=3 SV=1	Serpina7	A0A140TAB0	0.0838523	0.320981741	18.9644375	19.9332352	18.827076	13.8089094	18.4387894	18.140543	17.9194946	18.318758
1579	Tia1 cytotoxic granule-associated RNA-binding protein-like 1 OS=Rattus norvegicus OX=10116 GN=Tial1 PE=1 SV=1	Tial1	Q5BJN3	3.23980394	3.158840179	15.6292572	15.8281898	15.8054333	14.7086468	19.5670795	18.1811981	19.0360603	17.8225498
1580	Tight junction protein ZO-1 OS=Rattus norvegicus OX=10116 GN=Tjp1 PE=1 SV=1	Tjp1	A0A0G2K2P5	1.96612652	-0.834496498	21.4644756	21.0840778	21.6784744	21.2468243	20.5800247	21.012207	20.0974674	20.446167
1581	Tight junction-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Tjap1 PE=1 SV=1	Tjap1	A0A0G2K0W5	0.44640476	-0.58438158	19.6677208	19.652113	19.2048798	17.2236443	18.4038067	18.5598755	18.2390995	18.2080498
1582	Tissue specific transplantation antigen P35B (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tsta3 PE=1 S	Gfus	G3V762	1.96900045	2.276595831	16.87397	14.396203	16.6639194	16.2867184	17.8436909	18.1600323	19.0757675	18.2477036
1583	Tissue-type transglutaminase OS=Rattus norvegicus OX=10116 GN=Tgm2 PE=1 SV=1	Tgm2	Q9WVJ6	5.18546746	7.118671417	20.3199291	19.435791	19.1540146	18.8928242	25.4652367	26.7673111	27.15625	26.8884468
1584	T-kininogen 1 OS=Rattus norvegicus OX=10116 GN=Map1 PE=1 SV=2	Kng2	P01048	5.29084467	-2.866526604	26.1519909	26.224741	26.299305	25.9375401	23.7035275	23.1605568	22.8945637	23.3888226

1585	T-kininogen 2 OS=Rattus norvegicus OX=10116 PE=1 SV=2	Kng1	P08932	5.1838079	-2.6845994	28.3263569	28.60849	28.5680847	28.3114605	25.9686604	25.8311977	25.2805023	25.9956341
1586	Toll-interacting protein OS=Rattus norvegicus OX=10116 GN=Tollip PE=1 SV=1	Tollip	A2RUW1	2.17671114	2.926847696	17.7603054	15.4264631	16.1512394	14.4538784	19.3921223	18.630703	18.5892506	18.8872013
1587	Trafficking kinesin-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Trak2 PE=1 SV=2	Trak2	Q8R2H7	3.73575126	2.88465023	17.8211708	17.4873142	16.8829021	16.268898	19.9628639	20.2142735	19.7808285	20.0409203
1588	Trafficking protein particle complex subunit 3 OS=Rattus norvegicus OX=10116 GN=Trappc3 PE=2 SV=1	Trappc3	Q5U1Z2	1.86050913	1.443196297	19.0331421	19.4079876	18.8882599	17.7365551	19.5829487	20.5129032	20.460474	20.2824039
1589	Transcription elongation factor A protein 1 OS=Rattus norvegicus OX=10116 GN=Tcea1 PE=1 SV=1	Tcea1	Q4KLL0	0.5910751	-1.085207939	19.21632	19.8571835	19.7640553	18.7943096	20.0992413	16.3208733	19.1609917	17.7099304
1590	Transcription intermediary factor 1-beta OS=Rattus norvegicus OX=10116 GN=Trim28 PE=1 SV=2	Trim28	O08629	4.62847421	3.863828182	18.1234417	18.0481052	19.3273201	19.0043392	22.4621563	22.5302753	22.6891785	22.2769089
1591	Transferrin receptor protein 1 OS=Rattus norvegicus OX=10116 GN=Tfrc PE=1 SV=1	Tfrc	G3V679	1.9573991	-1.22342062	25.0913868	24.1029835	24.66222	25.3223743	23.608139	24.1319103	23.3442726	23.2009602
1592	Transforming protein RhoA OS=Rattus norvegicus OX=10116 GN=Rhoa PE=1 SV=1	Rhoa	P61589	4.64872954	3.265313148	19.7837391	20.9974842	20.4590073	20.0072689	23.7551994	23.5425529	23.4238873	23.5871124
1593	Transforming, acidic coiled-coil-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Tacc2 PE=1 SV=1	Tacc2	A0A0G2K598	1.77660517	1.622085094	19.1642532	19.0762024	17.2119751	18.323988	19.5874538	20.5031948	20.2526283	19.9214821
1594	Transgelin OS=Rattus norvegicus OX=10116 GN=Tagln PE=1 SV=1	Tagln	A0A0G2JWK7	3.35800512	2.126439571	21.8600178	21.5515919	21.1508121	20.77281	23.9710255	23.0637207	23.2923794	23.5138645
1595	Transgelin-2 OS=Rattus norvegicus OX=10116 GN=Tagln2 PE=1 SV=1	Tagln2	Q5XFX0	4.88373744	4.091300964	20.2830067	21.4011612	20.2644234	20.6073265	25.1355782	24.3034534	24.7038326	24.7782574
1596	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus OX=10116 GN=Vcp PE=1 SV=3	Vcp	P46462	4.62233652	3.3367486	20.0003529	20.8294945	20.7298756	21.0599041	24.3781071	23.5992508	23.8379459	24.1513176
1597	Transketolase OS=Rattus norvegicus OX=10116 GN=Tkt PE=1 SV=1	Tkt	G3V826	0.12583754	-0.19302845	19.833292	19.3828182	20.2214622	20.5686016	20.7717323	18.3497601	20.0039539	20.108614
1598	Translation initiation factor eIF-2B subunit delta OS=Rattus norvegicus OX=10116 GN=Eif2b4 PE=2 SV=1	Eif2b4	Q63186	2.6605528	5.458206654	17.387291	15.9657278	16.5330639	12.8711634	19.9225273	21.598629	21.6714954	21.3974209
1599	Translation initiation factor eIF-2B subunit epsilon OS=Rattus norvegicus OX=10116 GN=Eif2b5 PE=1 SV=2	Eif2b5	Q64350	1.59532446	2.968758345	17.6665459	13.2707853	17.191082	16.5853062	19.2036629	18.7345066	19.3018646	19.3487186
1600	Translationally-controlled tumor protein OS=Rattus norvegicus OX=10116 GN=Tpt1 PE=1 SV=1	Tpt1	P63029	3.01477294	2.067279816	17.0010033	18.2512856	18.0511646	18.2543201	19.7127056	20.4537754	19.8915348	19.768877
1601	Translocon-associated protein subunit alpha OS=Rattus norvegicus OX=10116 GN=Ssr1 PE=1 SV=1	Ssr1	A0A0G2K075	1.88266332	1.759676218	15.9718771	17.9167862	16.2639256	17.110817	17.9366169	18.4274178	18.9059982	19.0320778
1602	Translocon-associated protein subunit delta OS=Rattus norvegicus OX=10116 GN=Ssr4 PE=2 SV=1	Ssr4	Q07984	3.26233879	1.748627663	17.5841732	18.4170761	17.475008	17.2652645	19.4491444	19.2485695	19.4577351	19.5805836
1603	Transmembrane emp24 domain-containing protein 10 OS=Rattus norvegicus OX=10116 GN=Tmed10 PE=1 SV=2	Tmed10	Q63584	3.2702615	1.84754467	20.0718021	20.3967571	20.1424389	19.4587936	21.8190403	22.3646336	21.4339924	21.8423042
1604	Transmembrane emp24 domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Tmed2 PE=1 SV=1	Tmed2	Q63524	3.19407973	2.346196651	19.6619606	19.8617764	19.8221512	18.4446316	21.6769886	22.1848526	21.6159477	21.6975174
1605	Transmembrane emp24 domain-containing protein 7 OS=Rattus norvegicus OX=10116 GN=Tmed7 PE=1 SV=1	Tmed7	D3ZTX0	2.52086457	1.67374897	18.9384365	18.76441	19.3686638	18.408308	20.3511772	21.2978058	19.9307899	20.5950413
1606	Transmembrane emp24 domain-containing protein 9 OS=Rattus norvegicus OX=10116 GN=Tmed9 PE=1 SV=1	Tmed9	Q5I0E7	2.83378064	1.720543385	19.102129	19.7363529	19.0985394	18.4575081	20.6162186	21.2889462	20.5369606	20.8345776
1607	Transmembrane emp24 protein transport domain containing 4 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116	Tmed4	G3V6N2	3.29287344	3.374678373	16.02635	16.3323765	14.7406797	14.2767086	18.609417	18.7377338	18.8742943	18.6533833
1608	Transportin 1 OS=Rattus norvegicus OX=10116 GN=Tnpo1 PE=1 SV=3	Tnpo1	F1LQP9	0.70905942	2.130869865	19.7810993	14.4822483	20.9243813	19.6823845	21.477911	20.9966183	20.6599121	20.2591515
1609	Transthyretin OS=Rattus norvegicus OX=10116 GN=Ttr PE=1 SV=1	Ttr	P02767	6.0483915	-4.270005703	25.991581	26.3494339	26.6006165	25.8088589	22.1448021	21.6163044	21.939003	21.9703579
1610	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hadha PE=1 SV=2	Hadha	Q64428	2.88094497	3.915555477	17.4362354	19.1653728	16.6924286	17.7692547	20.3906765	22.5709305	21.8793736	21.8845329
1611	Trifunctional enzyme subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hadhb PE=1 SV=1	Hadhb	Q60587	1.42543445	2.420197487	19.5514107	18.9453583	16.5110283	20.3111057	20.0908508	21.7859154	21.5010509	21.6218758
1612	Trifunctional purine biosynthetic protein adenosine-3 OS=Rattus norvegicus OX=10116 GN=Gart PE=1 SV=1	Gart	G3V918	3.39679917	3.698453903	19.1656342	19.2662067	19.0024357	18.6308441	21.8047447	21.8791618	23.5947227	23.580307
1613	Triggering receptor-expressed on myeloid cells-like 1 OS=Rattus norvegicus OX=10116 GN=Treml1 PE=1 SV=3	Treml1	D3ZYT6	2.96960408	4.882455587	18.2865067	15.3799353	18.3960533	15.5936718	21.7527981	21.5637207	21.8916283	21.9778423
1614	TRIO and F-actin-binding protein OS=Rattus norvegicus OX=10116 GN=Triobp PE=1 SV=1	Triobp	A0A0G2K1P8	0.17134446	0.405161381	18.7947483	16.3452454	16.6278114	14.7041092	16.0070648	17.7221508	17.3182354	17.0451088
1615	Triosephosphate isomerase OS=Rattus norvegicus OX=10116 GN=Tpi1 PE=1 SV=2	Tpi1	P48500	4.35645555	2.582320213	20.9821453	21.9001255	21.6389847	21.051445	23.7264061	24.1620293	24.1184311	23.8951149
1616	Tripartite motif-containing protein 55 OS=Rattus norvegicus OX=10116 GN=Trim55 PE=1 SV=1	Trim55	Q5PQN5	6.11274978	4.57422781	16.7083778	16.4296036	15.7815208	16.4304466	21.0331764	21.0628567	20.6454754	20.9053516
1617	Tripartite motif-containing protein 72 OS=Rattus norvegicus OX=10116 GN=Trim72 PE=1 SV=1	Trim72	A0JPQ4	3.88636805	3.858136892	15.2035694	16.3211117	15.1950712	16.8567677	19.4562073	20.1786957	19.7963924	19.5777721
1618	Tripeptidyl-peptidase 2 OS=Rattus norvegicus OX=10116 GN=Tpp2 PE=2 SV=3	Tpp2	Q64560	3.63855352	2.7975564	17.5300331	17.9350376	17.5373726	17.7438774	19.464241	20.7750816	20.9734631	20.7237606
1619	Triple functional domain protein OS=Rattus norvegicus OX=10116 GN=Trio PE=1 SV=4	Trio	F1M0Z1	0.72315374	0.567908049	16.6953373	16.5045357	16.6823711	15.301816	16.4761829	16.6569767	16.996315	17.3262177
1620	tRNA (guanine(26)-N(2))-dimethyltransferase OS=Rattus norvegicus OX=10116 GN=Trmt1 PE=1 SV=1	Trmt1	A0A140UHW6	0.08245114	0.069444656	18.5681858	18.2561588	17.9446812	18.6171494	18.6321259	18.5033073	18.8638725	17.6646481
1621	tRNA-splicing ligase RtcB homolog OS=Rattus norvegicus OX=10116 GN=Rtcb PE=2 SV=1	Rtcb	Q6AYT3	3.77826981	6.458844423	17.7418499	14.4429159	16.5848675	14.8688526	22.7684517	22.1724663	22.3477154	22.1852303
1622	Tropomodulin-1 OS=Rattus norvegicus OX=10116 GN=Tmod1 PE=1 SV=1	Tmod1	Q6IMZ5	0.61956605	0.656262875	22.1572685	21.2698612	21.2700901	20.730011	22.6653061	22.7700329	21.3284092	21.2885342
1623	Tropomyosin alpha-1 chain OS=Rattus norvegicus OX=10116 GN=Tpm1 PE=1 SV=3	Tpm1	P04692	4.41927726	5.6571455	16.895155	18.094553	16.5748577	17.3470631	23.5676498	23.5403824	21.8814507	22.5507278
1624	Tropomyosin alpha-4 chain OS=Rattus norvegicus OX=10116 GN=Tpm4 PE=1 SV=3	Tpm4	P09495	3.92715055	2.95166254	20.453331	21.0377903	20.6968002	20.544714	24.170372	24.1451263	22.9489269	23.2748604
1625	Troponin I, cardiac muscle OS=Rattus norvegicus OX=10116 GN=Tnni3 PE=1 SV=2	Tnni3	P23693	3.14701623	5.126037836	14.8863773	18.1853218	15.9613466	17.3137894	22.6787357	21.7280941	21.3445911	21.0995655
1626	Troponin I, slow skeletal muscle OS=Rattus norvegicus OX=10116 GN=Tnni1 PE=1 SV=1	Tnni1	A0A096MIZ5	4.00362942	4.86000061	19.5174351	19.4393349	18.9956017	17.3664875	24.1897774	23.3627758	23.4603424	23.745966
1627	Troponin T, cardiac muscle OS=Rattus norvegicus OX=10116 GN=Tnnt2 PE=1 SV=2	Tnnt2	P50753	5.62503946	7.80094862	14.3474159	14.9388218	15.6437035	15.9617939	23.7953587	22.6716614	22.6467743	22.9817352
1628	Tryptophan--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Wars PE=1 SV=2	Wars1	Q6P7B0	4.74297022	5.505094051	16.1646042	17.3436642	17.4120789	17.7287273	22.822155	21.810751	22.9462986	23.0902462
1629	TSC22 domain family protein 4 OS=Rattus norvegicus OX=10116 GN=Tsc22d4 PE=1 SV=1	Tsc22d4	Q3B8N7	3.60147369	4.36319828	19.1359196	17.0640793	17.8801918	19.1111698	22.2642479	23.4129677	22.4620438	22.5048943
1630	Tuberin OS=Rattus norvegicus OX=10116 GN=Tsc2 PE=1 SV=1	Tsc2	A0A0G2JSL4	3.17464326	2.449251175	17.0470047	17.8937588	18.4784813	18.5980129	20.3715515	20.7933426	20.5244827	20.1248856
1631	Tubulin alpha-1A chain OS=Rattus norvegicus OX=10116 GN=Tuba1a PE=1 SV=1	Tuba1a	P68370	6.82219934	4.010397434	25.2490711	24.7278919	24.6941738	25.1428986	29.0588436	28.9234428	28.9509945	28.9223442
1632	Tubulin alpha-1B chain OS=Rattus norvegicus OX=10116 GN=Tuba1b PE=1 SV=1	Tuba1b	Q6P9V9	5.21511217	7.574748755	14.3731384	14.9265909	16.1159954	16.37253	23.0583191	23.4149513	23.1125755	22.5014038
1633	Tubulin alpha-1C chain OS=Rattus norvegicus OX=10116 GN=Tuba1c PE=1 SV=1	Tuba1c	Q6AYZ1	6.29533787	5.550355434	19.0737419	18.0891876	18.0905571	18.1117935	23.9545517	23.9521961	23.8143272	23.8456268
1634	Tubulin alpha-4A chain OS=Rattus norvegicus OX=10116 GN=Tuba4a PE=1 SV=1	Tuba4a	Q5XIF6	6.65429872	3.813116074	19.6294785	19.7117081	19.3552914	19.6726761	23.4520531	23.6016312	23.5215931	23.0463409
1635	Tubulin beta chain OS=Rattus norvegicus OX=10116 GN=Tubb1 PE=1 SV=1	Tubb1	M0R8B6	1.1916289	-1.08259201	17.6196709	18.6687641	18.5625439	18.1216984	18.1236343	17.5720272	16.5716782	16.3749695
1636	Tubulin beta chain OS=Rattus norvegicus OX=10116 GN=Tubb4b PE=1 SV=2	Tubb4b	G3V7C6	6.15607362	3.872380733	22.307415	22.27174	21.5879135	21.8146725	25.9436207	25.9264336	25.7460861	25.8551235
1637	Tubulin beta chain OS=Rattus norvegicus OX=10116 GN=Tubb6 PE=1 SV=1	Tubb6	Q4QQV0	2.79671653	1.247231483	23.1667786	23.0606041	22.3117504	23.2096043	24.0991135	24.1310368	24.4498081	24.0577049
1638	Tubulin beta-2A chain OS=Rattus norvegicus OX=10116 GN=Tubb2a PE=1 SV=1	Tubb2a	P85108	5.89277666	3.109897137	22.0230446	21.4376907	21.7859993	21.3535519	24.7072277	24.7094898	24.8909798	24.7321777
1639	Tubulin beta-2B chain OS=Rattus norvegicus OX=10116 GN=Tubb2b PE=1 SV=1	Tubb2b	Q3KRE8	1.20128806	1.279902458	19.1281242	21.3048038	19.3832111	18.9752026	21.1873627	21.2420044	20.8663712	20.6152134
1640	Tubulin beta-5 chain OS=Rattus norvegicus OX=10116 GN=Tubb5 PE=1 SV=1	Tubb5	P69897	7.65066597	4.160122395	25.7249126	25.2873535	25.2803192	25.4564209	29.6238194	29.6768131	29.5706692	29.5181942
1641	Tubulin folding cofactor D OS=Rattus norvegicus OX=10116 GN=Tbcd PE=1 SV=3	Tbcd	F1M1D5	3.3106887	3.911798477	15.9816275	16.7228889	14.748682	14.5476694	19.1332855	19.3025379	20.1484413	19.063797
1642	Tubulin polymerization-promoting protein family member 3 OS=Rattus norvegicus OX=10116 GN=Tppp3 PE=2 SV=1	Tppp3	Q5PPN5	0.39104964	-0.688462734	17.6154289	18.4832458	18.2264061	15.7969103	17.6109486	17.5530548	15.5820246	16.6221123
1643	Tubulin-specific chaperone A OS=Rattus norvegicus OX=10116 GN=Tbca PE=1 SV=1	Tbca	Q6PEC1	0.26954981	1.0094347	22.7198582	17.6985931	16.6418152	16.436533	20.7495098	18.8765736	19.0832291	18.8252258
1644	Tubulin-specific chaperone E OS=Rattus norvegicus OX=10116 GN=Tbce PE=1 SV=1	Tbce	A0A0G2K191	3.63176864	2.646896362	18.1338673	17.2096004	18.4135418	17.6056995	19.9211674	20.8118515	20.7784119	20.4388638
1645	Tumor protein D52 OS=Rattus norvegicus OX=10116 GN=Tpd52 PE=1 SV=1	Tpd52	A0A0G2K865	2.1838606	5.157339334	17.2154694	17.9750519	16.7665672	12.3751154	21.4447975	21.1498413	21.4058228	20.9610996

1646	Tumor protein D54 OS=Rattus norvegicus OX=10116 GN=Tpd52l2 PE=1 SV=1	Tpd52l2	Q6PCT3	4.60427147	3.859615326	20.2500992	18.649662	19.4618168	19.571619	23.1869793	23.436079	23.4263783	23.3222218
1647	Tumor susceptibility gene 101 protein OS=Rattus norvegicus OX=10116 GN=Tsg101 PE=1 SV=1	Tsg101	Q6IRE4	5.03149965	6.017547131	16.5664635	15.5771952	14.5083532	15.1824989	21.6860371	21.5389748	21.3621159	21.3175716
1648	Type II keratin Kb15 OS=Rattus norvegicus OX=10116 GN=Kb15 PE=3 SV=1	Kb15	A0A0G2JVA8	2.02312307	-1.482485294	23.8509388	24.0611458	22.9710598	24.0274487	22.7544613	22.1437378	22.6459236	21.4365292
1649	Tyrosine-protein phosphatase non-receptor type 11 OS=Rattus norvegicus OX=10116 GN=Ptpn11 PE=1 SV=4	Ptpn11	P41499	5.02783592	7.345947981	15.7507458	14.1000319	13.5968304	15.5241241	21.9858627	22.1291714	22.3209724	21.9195175
1650	Tyrosine-protein phosphatase non-receptor type OS=Rattus norvegicus OX=10116 GN=Ptpn21 PE=1 SV=1	Ptpn21	A0A0G2JTB7	0.09915918	0.291901588	18.5312748	17.4286289	13.9599686	17.9752522	17.9134827	17.7269821	16.6346283	16.7876377
1651	Tyrosine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Yars PE=1 SV=1	Yars1	A0A0H2UHG0	4.7338647	4.593044996	15.432723	15.0582418	16.4354401	14.762536	20.1347942	19.7416954	20.1449432	20.0396881
1652	U2 snRNP auxiliary factor large subunit OS=Rattus norvegicus OX=10116 GN=U2af2 PE=1 SV=2	U2af2	F2Z3T9	3.21892826	4.297362328	15.7137394	14.660737	14.5345984	13.587698	20.2276936	18.8464279	17.8481007	18.7639999
1653	Ubiquilin 4 OS=Rattus norvegicus OX=10116 GN=Ubqln4 PE=1 SV=1	Ubqln4	D4A3P1	4.01842803	2.637015343	19.0639954	18.2177792	18.7692966	18.3378315	21.817379	20.8066902	21.1939392	21.1189556
1654	Ubiquitin carboxyl-terminal hydrolase 28 OS=Rattus norvegicus OX=10116 GN=Usp28 PE=1 SV=1	Usp28	A0A140TAA0	2.10802386	2.48951292	15.507906	16.7005234	15.3247347	14.2804823	18.1016808	18.4313087	18.4605103	16.7781982
1655	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus OX=10116 GN=Uchl5 PE=1 SV=1	Uchl5	Q5HZY3	3.09443582	3.098692656	15.7294407	16.5785122	14.8795919	15.4914818	19.502533	18.1194897	19.2448025	18.2069721
1656	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus OX=10116 GN=Usp13 PE=2 SV=2	Usp13	D3ZDI9	3.50690712	4.333773851	15.1131773	15.5615501	16.0838203	17.5372982	20.9582577	19.7341805	20.5612907	20.3772125
1657	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus OX=10116 GN=Usp5 PE=1 SV=1	Usp5	D3ZVQ0	4.06603957	3.014353275	20.5567284	20.9789371	21.349884	20.3218632	24.353157	23.2965775	23.9971867	23.6179047
1658	Ubiquitin recognition factor in ER-associated degradation protein 1 OS=Rattus norvegicus OX=10116 GN=Ufd1 PE=1 SV=1	Ufd1	Q9ES53	2.21228828	1.723861217	17.633791	16.2083569	17.7625389	17.990799	19.0681324	18.8572216	19.2163296	19.349247
1659	Ubiquitin specific protease 14 OS=Rattus norvegicus OX=10116 GN=Usp14 PE=1 SV=1	Usp14	Q5U2N2	3.31432589	4.004240513	16.6899338	17.1065636	16.7288494	18.8200893	21.3957386	20.6381664	22.1007748	21.2277184
1660	Ubiquitin-40S ribosomal protein S27a OS=Rattus norvegicus OX=10116 GN=Rps27a PE=1 SV=2	Rps27a	P62982	2.54319314	1.234502792	21.6064377	22.7541771	21.9221191	22.2822285	23.510437	23.450552	23.2295818	23.3124027
1661	Ubiquitin-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Ubap2 PE=1 SV=1	Ubap2	A0A0U1RRQ3	0.24980214	0.155108929	22.1038914	22.0156498	22.3681259	22.6533833	23.0642834	22.1951427	22.2428417	22.2592182
1662	Ubiquitin-conjugating enzyme E2 D2 OS=Rattus norvegicus OX=10116 GN=Ube2d2 PE=1 SV=1	Ube2d2	P62839	4.79300893	2.30125618	19.0570564	19.6508064	19.5217953	19.282053	21.8911171	21.4345913	21.9132481	21.4777794
1663	Ubiquitin-conjugating enzyme E2 N OS=Rattus norvegicus OX=10116 GN=Ube2n PE=1 SV=1	Ube2n	Q9EQX9	4.50201555	5.091310501	19.3662529	17.6229496	18.8988762	19.2067032	24.4501305	23.3251038	23.8630371	23.8217525
1664	Ubiquitin-conjugating enzyme E2 V1 OS=Rattus norvegicus OX=10116 GN=LOC100912618 PE=1 SV=1	Ube2v1	D3ZFY8	4.6698397	2.520213604	20.2317638	19.6963024	20.1149693	20.3155441	22.961935	22.2026825	22.7398701	22.5349464
1665	Ubiquitin-conjugating enzyme E2 Z OS=Rattus norvegicus OX=10116 GN=Ube2z PE=1 SV=2	Ube2z	Q3B7D1	0.32296989	-0.696223259	22.5192242	22.8512192	22.8254051	19.0943527	21.0194206	21.0290375	21.273922	21.1829281
1666	Ubiquitin-conjugating enzyme E2M OS=Rattus norvegicus OX=10116 GN=Ube2m PE=1 SV=1	Ube2m	D3ZNQ6	3.98216547	3.48909235	18.6175652	18.465538	18.8378906	17.7497158	22.6962376	21.2894478	21.5832329	22.0581608
1667	Ubiquitin-conjugating enzyme E2O OS=Rattus norvegicus OX=10116 GN=Ube2o PE=1 SV=2	Ube2o	F1M403	2.45663208	4.902808189	16.6989193	18.3905754	18.4715786	14.0065498	22.1529522	21.5624924	21.6061745	21.8572369
1668	Ubiquitin-like modifier-activating enzyme 1 OS=Rattus norvegicus OX=10116 GN=Uba1 PE=1 SV=1	Uba1	Q5U300	5.32647319	4.83700037	19.2292767	20.1583576	20.1460361	19.9920197	25.1742344	24.1042213	24.793047	24.8021889
1669	Ubiquitin-like modifier-activating enzyme 5 OS=Rattus norvegicus OX=10116 GN=Uba5 PE=1 SV=1	Uba5	Q5M7A4	2.71401826	3.155269384	17.476202	18.075285	15.502841	17.6000462	20.557972	19.7290459	20.4697933	20.5186405
1670	Ubiquitin-like modifier-activating enzyme ATG7 OS=Rattus norvegicus OX=10116 GN=Atg7 PE=2 SV=1	Atg7	Q641Y5	0.71691857	-1.33243227	19.2889557	20.2921791	17.1986656	17.6227589	16.2325001	18.4796104	16.4579678	17.9027519
1671	Ubiquitin-like protein 4A OS=Rattus norvegicus OX=10116 GN=Ubl4a PE=2 SV=1	Ubl4a	B2GV38	2.40369579	4.522334814	18.4766636	18.0679359	18.3262882	14.3746443	22.1580715	21.361845	21.9304218	21.8845329
1672	Ubiquitin-specific peptidase 47 OS=Rattus norvegicus OX=10116 GN=Usp47 PE=1 SV=1	Usp47	A0A0G2JUX4	3.68921915	2.53953886	17.0158558	17.8898563	18.3033123	17.5759087	20.5648422	19.804224	20.1679726	20.4060497
1673	UDP-glucose 6-dehydrogenase OS=Rattus norvegicus OX=10116 GN=Ugdh PE=1 SV=1	Ugdh	G3V6C4	3.18573225	1.72449255	18.9456463	18.1195297	18.4967651	18.2856789	20.376009	19.5975933	20.3183498	20.4536381
1674	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1 OS=Rattus norvegicus OX=10116 GN=Uap1l1 PE=1 SV=1	Uap1l1	B5DEH4	3.74066658	2.214234829	16.416584	16.3495426	17.214447	16.8450203	19.3579197	18.4926186	18.8173523	19.0146427
1675	UHRF1-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Uhrf1bp1 PE=1 SV=3	Uhrf1bp1	D3ZMR2	1.94510722	2.50703311	16.1005783	16.3815117	14.1550646	16.3916798	18.905407	18.7277031	18.4542313	16.9696255
1676	UMP-CMP kinase OS=Rattus norvegicus OX=10116 GN=Cmpk1 PE=1 SV=1	Cmpk1	A0A0G2JSJ2	3.88841987	3.314414024	20.2163887	18.6801186	18.7518444	19.3362503	22.3439693	22.3941307	22.9626522	22.5415058
1677	Unc-119 lipid-binding chaperone B OS=Rattus norvegicus OX=10116 GN=Mlec PE=1 SV=1	Unc119b	A0A0G2K121	3.80647471	-2.272502899	22.7705555	22.1531124	23.0965672	22.9534016	20.6680565	20.2613583	20.1031971	20.8510132
1678	Unc-45 myosin chaperone B OS=Rattus norvegicus OX=10116 GN=Unc45b PE=4 SV=1	Unc45b	A0A096MJB5	5.60500877	3.745814323	22.1443501	22.0616627	21.9709702	21.5174675	25.9626331	25.2085953	25.8594303	25.647049
1679	Uncharacterized protein (Fragment) OS=Rattus norvegicus OX=10116 GN=Gigyf2 PE=1 SV=1	Gigyf2	A0A096MJI4	1.058486	-2.314177275	18.7896252	20.2118797	17.3016167	17.3705139	15.3441334	13.9638624	17.9857178	17.1232128
1680	Uncharacterized protein (Fragment) OS=Rattus norvegicus OX=10116 PE=4 SV=1	A0A0G2K4H3_RAT	A0A0G2K4H3	0.66711185	0.516106606	17.7986488	17.4092617	17.3651695	16.8213463	18.6376362	17.1509914	17.6450939	18.0251312
1681	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=Cep170 PE=1 SV=1	Cep170	A0A0G2K315	4.39578538	-2.008429527	22.6848164	22.693119	23.192482	23.0414829	21.2246037	20.8393154	20.5550957	20.9591675
1682	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=Cfhr2 PE=1 SV=3	Cfhr2	F1LWS4	2.51100643	-1.981272221	21.1105785	19.5591221	21.022995	21.1379147	18.4952049	19.1836624	18.6941433	18.5325108
1683	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=LOC690813 PE=1 SV=2	LOC690813	F1M1R0	0.91158781	-1.309712887	18.6858463	17.557148	19.1874886	20.0740986	16.2100277	17.4524727	18.0394154	18.5638142
1684	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=Scgb2b2 PE=4 SV=3	Scgb2b2	F1LSA5	4.15929745	-3.398929596	18.679039	19.6367149	19.4401531	18.2207546	15.2554426	15.6145964	15.7601776	15.7507267
1685	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	A0A0G2JXP0_RAT	A0A0G2JXP0	3.61412154	-4.149447918	21.1073608	20.97645	20.6566448	19.3995914	16.7654667	15.285574	16.7064934	16.7847214
1686	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	A0A0G2JY70_RAT	A0A0G2JY70	5.57608413	4.98576498	18.7115612	17.9092159	18.1336632	17.3866768	22.7151413	23.0809631	23.1147079	23.1733646
1687	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	A0A0G2K0N6_RAT	A0A0G2K0N6	1.34216846	-1.465534449	18.2589111	17.0013256	16.25387	17.3605595	14.8951206	15.2973909	16.1086712	16.7113457
1688	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	A0A0G2K0U9_RAT	A0A0G2K0U9	2.85309564	3.119940281	16.4189434	13.9457064	15.9939699	15.8967457	18.8210258	18.4150238	18.7826996	18.7163773
1689	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	A0A0G2K7I1_RAT	A0A0G2K7I1	0.06184242	-0.242392778	14.4875584	14.3521547	17.0574303	19.4397392	14.7762728	17.6694584	15.1190386	16.8025417
1690	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	D3ZQR5_RAT	D3ZQR5	2.14224272	-1.895699263	18.5792255	18.0817413	19.3515453	17.4921284	16.2468548	17.1872425	16.5463505	15.9413958
1691	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	D4A8Y1_RAT	D4A8Y1	2.73801984	2.762305021	15.7496843	16.1440353	17.6383247	16.989563	19.7048874	18.8035412	20.0872307	18.9751682
1692	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	M0R9U2_RAT	M0R9U2	1.22341265	0.736653805	19.9045715	18.9466534	20.2651234	19.2657738	20.0884476	20.6074905	20.2673798	20.3654194
1693	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	M0RA79_RAT	M0RA79	2.70752744	-2.604149818	19.9987621	19.5131931	20.7749348	21.0008297	17.7609692	18.3193932	18.0957851	16.694973
1694	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	M0RCC9_RAT	M0RCC9	0.01608714	0.036904335	16.3833427	17.5912952	16.3869267	14.0133734	15.9505444	15.9715376	16.735878	15.8645954
1695	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	D3ZZ08_RAT	D3ZZ08	1.948267	-2.755284548	19.5057449	19.008564	19.8875999	19.3151493	15.7032032	18.8658981	15.8378801	16.2889385
1696	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	F1LTN6_RAT	F1LTN6	4.95281079	-4.005538464	24.869627	25.5755424	25.216713	24.3728714	21.275362	21.2779522	20.7202969	20.7389889
1697	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	F1M3U4_RAT	F1M3U4	0.03932107	0.100329399	17.9311085	21.4778748	17.8462486	19.1485157	18.9879513	18.5767612	19.713192	19.5271606
1698	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	M0R4Z4_RAT	M0R4Z4	0.32746419	-0.414763451	17.2187977	18.9947357	17.2224445	16.7093067	17.6342983	17.2294979	16.7688789	16.8535557
1699	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	Crybg3	M0RDY6	6.07582678	3.761772633	18.3153877	18.7560024	19.0366421	18.8449459	22.6381416	22.2054901	22.5971584	22.5592785
1700	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	Fam114a2	D3ZC89	2.54066316	1.747261047	21.2401676	20.8600273	21.218298	22.3164234	23.4085579	22.6335354	23.2708569	23.3110104
1701	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	D3ZPL2_RAT	D3ZPL2	4.67946306	-4.642578125	20.2869091	20.9595661	21.0770111	20.0483322	15.6218767	16.5695324	16.3159943	15.2941027
1702	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	Fam98b	D4AE02	0.09659599	-0.099479198	18.0783939	17.8629246	17.8612862	17.8420773	18.8211498	17.4584217	17.8751411	17.0920525
1703	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	Ighm	F1LM30	1.256647	-2.9545784	17.7501659	21.4924183	19.7075214	16.2175884	16.7606277	14.8030758	16.5443249	15.2413521
1704	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	Hspg2	F1LTJ5	5.21727111	3.427815914	17.2063484	16.798027	16.4029808	17.1836128	20.3393211	20.1289196	20.1346912	20.6993008
1705	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	F1LX60_RAT	F1LX60	2.03041674	-1.799075127	16.8524952	17.5340309	17.5394459	16.5823746	14.7268391	15.4567642	14.6867161	16.4417267
1706	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	F1M269_RAT	F1M269	3.89687837	3.620896816	16.8253021	16.6255054	16.7552834	18.0339832	20.8795052	19.9248562	21.0677509	20.8515491

1707	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	Pkp2	F1M7L9	1.99143752	1.786740303	17.5258808	17.2297096	17.4605541	16.0711479	19.220396	19.539835	18.7175846	17.9564381
1708	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	G3V9J1_RAT	G3V9J1	2.27459851	-1.99835825	18.9623203	18.3297195	19.2419262	19.7382965	17.9298229	16.2613411	16.7208138	17.3668518
1709	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	LOC108349792	A0A0G2K3I6	2.74666703	4.071244717	21.1886978	20.4193478	20.6968193	17.8878937	23.8380642	23.7165833	24.5642414	24.3588486
1710	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	RGD1561333	D4A6W6	4.7439443	5.52176857	18.8270664	17.4831848	17.1128864	17.7702084	22.5854988	23.782135	23.5569515	23.355835
1711	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	Eno1-ps1	M0R5J4	2.09421806	1.394604206	23.9620972	24.1510296	24.7826138	24.7215881	24.9603767	26.0311909	26.3207779	25.8834
1712	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=3	LOC100362298	D3ZM33	4.72439375	4.697120667	20.3797665	19.740509	19.8807964	19.2142601	23.6483307	25.0833817	24.6502628	24.6218395
1713	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	A0A0G2K3S3_RAT	A0A0G2K3S3	5.40040505	-4.791248322	21.5114288	21.6309528	21.5452023	20.8542271	17.256525	16.5538864	16.0873928	16.4790134
1714	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	A0A0G2K613_RAT	A0A0G2K613	3.3575412	3.317065716	19.8005943	19.763092	20.481657	18.4466076	23.5816669	22.6605854	22.7969551	22.7210064
1715	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	D3ZJD3_RAT	D3ZJD3	3.81926805	6.208295107	18.2980042	17.9206581	17.3765926	15.2072191	22.6942806	23.8969078	23.5053787	23.5390873
1716	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	D3ZPN7_RAT	D3ZPN7	3.13355493	2.808564663	20.4693089	19.2674465	19.9886398	19.2640095	21.6346931	23.2258568	22.6850643	22.6780491
1717	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	M0R5W6_RAT	M0R5W6	0.22706177	-0.545508146	16.9225082	14.5163479	18.0948944	17.4120197	15.0080757	15.4533262	16.8759212	17.4264145
1718	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	M0RBP7_RAT	M0RBP7	0.85297759	-0.190316677	19.2533588	19.2518501	19.4493771	19.1635246	18.8326912	19.1746407	19.2725601	19.076952
1719	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	Ighm	F1LPQ6	3.91307718	-2.364390373	21.411293	22.2875252	21.2591305	21.4749489	19.467556	18.8374729	19.3083019	19.3620052
1720	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	F1LVL4_RAT	F1LVL4	2.73911119	-4.651106596	21.0703278	21.2204857	20.5553932	20.5374336	16.5219002	15.0066633	14.7586231	18.4920273
1721	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	Zfp341	F7ETL6	1.4408872	2.540670872	13.0406036	16.7516251	15.4726906	16.8265514	18.6890373	17.9202766	17.1770382	18.467802
1722	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	M0RAZ1_RAT	M0RAZ1	0.1853771	0.204710484	17.2768764	17.2286339	18.4863605	18.5217857	18.5102272	17.4153423	18.1095371	18.2973919
1723	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=3	LOC365839	F1M7K9	4.02739739	2.795096159	15.0237074	15.8053513	15.2823124	14.4274426	18.0857315	17.6266422	17.9919853	18.0148392
1724	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=3	F1M861_RAT	F1M861	0.35816494	-0.451579571	18.5287991	18.6591454	18.0507851	16.628727	18.1752033	17.7438164	17.2685585	16.87356
1725	Unconventional myosin-Ic OS=Rattus norvegicus OX=10116 GN=Myo1c PE=1 SV=2	Myo1c	Q63355	4.68099235	3.392003059	18.2291355	19.3460941	18.940052	19.3208389	22.1364613	22.5597763	22.1750011	22.5328941
1726	Unconventional myosin-Ie OS=Rattus norvegicus OX=10116 GN=Myo1e PE=1 SV=1	Myo1e	Q63356	2.84319921	3.43991971	16.5045338	14.0514078	15.7014017	14.3678865	18.6752739	19.2174225	18.2720165	18.2201958
1727	UPF1, RNA helicase and ATPase OS=Rattus norvegicus OX=10116 GN=Upf1 PE=1 SV=1	Upf1	A0A0U1RS25	2.23153991	4.665978909	19.1535664	18.7526035	14.5051384	18.9145832	22.7855511	22.5117092	22.5032845	22.1892624
1728	Up-regulated during skeletal muscle growth protein 5 OS=Rattus norvegicus OX=10116 GN=Atp5md PE=1 SV=1	Atp5mk	Q9JJW3	3.75175424	3.090051174	18.3368111	18.9417534	17.7703495	17.9076538	20.5818157	21.6888485	21.291502	21.7546062
1729	Uroporphyrinogen decarboxylase OS=Rattus norvegicus OX=10116 GN=Urod PE=1 SV=1	Urod	B0BN55	1.03739417	1.027359009	14.6025553	16.2175388	16.640831	15.1714563	17.0632095	16.2493534	17.0190678	16.4101868
1730	Uteroglobin OS=Rattus norvegicus OX=10116 GN=Scgb1a1 PE=1 SV=2	Scgb1a1	P17559	3.44830729	-4.976519585	21.2538013	21.275135	21.6366577	21.1372776	16.4252758	15.4095583	18.2455425	15.3164167
1731	UTP--glucose-1-phosphate uridylyltransferase OS=Rattus norvegicus OX=10116 GN=Ugp2 PE=1 SV=1	Ugp2	Q4V8I9	4.28379791	2.391450405	20.0232754	19.8445377	19.8829823	19.2869854	22.5427017	21.7188549	22.2191734	22.1228523
1732	UV excision repair protein RAD23 homolog B OS=Rattus norvegicus OX=10116 GN=Rad23b PE=1 SV=1	Rad23b	Q4KMA2	1.70288819	-1.24812746	23.7135372	23.0089741	23.241087	21.9184322	22.0355053	21.5036697	21.6635723	21.6867733
1733	Vacuolar protein sorting 13 homolog C OS=Rattus norvegicus OX=10116 GN=Vps13c PE=1 SV=2	Vps13c	D4A4K4	2.31062017	1.273492813	21.0799789	21.4560299	21.0479279	22.2813301	22.7397404	22.8800697	22.5790062	22.7604218
1734	Vacuolar protein sorting 4 homolog B OS=Rattus norvegicus OX=10116 GN=Vps4b PE=1 SV=1	Vps4b	Q4KLL7	4.4179635	3.189666748	19.2367573	18.7130184	18.1215076	18.5700951	21.3911514	21.7397327	22.2712631	21.9978981
1735	Vacuolar protein sorting-associated protein 28 homolog OS=Rattus norvegicus OX=10116 GN=Vps28 PE=1 SV=1	Vps28	A0A0H2UHM0	1.76338075	1.647626877	21.0259953	19.1726627	19.6063461	21.1237602	22.1753368	21.8035583	21.8344727	21.705904
1736	Vacuolar protein sorting-associated protein 29 OS=Rattus norvegicus OX=10116 GN=Vps29 PE=1 SV=1	Vps29	A0A0G2JTS3	0.69079253	1.477856636	17.9039078	17.0927658	17.6394444	14.856144	16.1198616	19.2581062	19.4862919	18.5394287
1737	Vacuolar protein sorting-associated protein 35 OS=Rattus norvegicus OX=10116 GN=Vps35 PE=1 SV=1	Vps35	G3V8A5	1.17603904	2.903928518	19.1317101	16.4321823	14.5541296	13.4413853	19.1377811	17.6943417	19.3075695	19.035429
1738	Vacuolar protein sorting-associated protein 45 OS=Rattus norvegicus OX=10116 GN=Vps45 PE=1 SV=1	Vps45	O08700	0.92128364	-0.489758492	19.7447777	20.7473488	20.3709965	20.5160332	19.8368435	20.1773167	19.9977074	19.4082546
1739	Vacuolar protein sorting-associated protein 4A OS=Rattus norvegicus OX=10116 GN=Vps4a PE=1 SV=1	Vps4a	F7F1Y3	4.86469787	1.239253044	19.9518509	19.6820602	20.0973282	19.9857273	21.123745	21.2403545	21.229208	21.0806713
1740	Valine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Vars PE=2 SV=2	Vars1	Q04462	2.72764473	4.668142319	16.7374477	13.9756584	17.555357	17.7622566	21.5615387	20.866169	21.0644207	21.2111607
1741	Vanin 1 OS=Rattus norvegicus OX=10116 GN=Vnn1 PE=1 SV=1	Vnn1	Q4KLZ0	4.43548886	4.865496397	15.0966578	15.0668573	15.7889585	16.9608994	20.6592693	20.7650471	20.4560204	20.4950218
1742	Vasodilator-stimulated phosphoprotein OS=Rattus norvegicus OX=10116 GN=Vasp PE=1 SV=1	Vasp	A0A0G2K9C0	3.62968164	6.462329865	15.1501732	14.952466	17.7644272	13.9631033	22.0458908	22.1803913	22.0268784	21.4263287
1743	Versican core protein (Fragments) OS=Rattus norvegicus OX=10116 GN=Vcan PE=2 SV=2	Vcan	Q9ERB4	2.51603466	1.442383289	19.7042961	19.5042591	18.4346581	19.4019928	20.7133465	20.4181309	20.9202194	20.7630424
1744	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acadvl PE=1 SV=1	Acadvl	P45953	2.98405089	2.932025433	16.2245502	17.2494164	15.5280418	16.1869202	18.4899197	20.0853786	18.902298	19.4394341
1745	Very low-density lipoprotein receptor OS=Rattus norvegicus OX=10116 GN=Vldlr PE=4 SV=1	Vldlr	F1LPV2	1.2999177	2.033451319	15.7389421	16.024147	16.2788219	13.6301069	15.8138113	18.1910095	18.2610378	17.5399647
1746	Vesicle transport through interaction with t-SNAREs homolog 1B OS=Rattus norvegicus OX=10116 GN=Vti1b PE=1 SV=2	Vti1b	P58200	2.20766162	4.729885101	16.4414444	15.7256708	17.2063179	12.0490007	20.2295933	20.2211037	19.7974892	20.0937881
1747	Vesicle-associated membrane protein 2 OS=Rattus norvegicus OX=10116 GN=Vamp2 PE=1 SV=2	Vamp2	P63045	4.45882343	3.597121954	17.1535568	15.8859377	16.3598442	17.1741753	20.4376621	20.3467083	20.1475182	20.0301132
1748	Vesicle-associated membrane protein 3 OS=Rattus norvegicus OX=10116 GN=Vamp3 PE=1 SV=1	Vamp3	P63025	5.15304424	2.159743309	20.3425159	19.9951153	20.1845913	20.5673714	22.6134396	22.5531406	22.2689743	22.2930126
1749	Vesicle-associated membrane protein 8 OS=Rattus norvegicus OX=10116 GN=Vamp8 PE=1 SV=1	Vamp8	Q9WUF4	2.20337078	2.282830238	17.6734848	18.9108486	16.4014969	18.1238518	19.8733501	20.5975266	19.8541107	19.9160156
1750	Vesicle-associated membrane protein-associated protein A OS=Rattus norvegicus OX=10116 GN=Vapa PE=1 SV=3	Vapa	Q9Z270	1.90969063	5.042802095	18.9466209	18.8360634	15.1344652	13.24403	21.2147961	22.1193314	21.2787533	21.7195072
1751	Vesicle-associated membrane protein-associated protein B OS=Rattus norvegicus OX=10116 GN=Vapb PE=1 SV=3	Vapb	Q9Z269	0.74631254	1.816495657	18.0335064	18.6506424	19.1252346	14.1579142	19.3360558	20.1268864	18.2969704	19.4733677
1752	Vesicle-fusing ATPase OS=Rattus norvegicus OX=10116 GN=Nsf PE=1 SV=1	Nsf	A0A0G2K6U1	2.83712412	3.01406002	18.0552559	15.9166336	16.585392	16.2846317	20.4988537	19.4470158	19.2394352	19.7128487
1753	Vesicle-trafficking protein SEC22b OS=Rattus norvegicus OX=10116 GN=Sec22b PE=1 SV=3	Sec22b	Q4KM74	3.7176777	2.089174747	19.5492477	19.2038631	18.8339596	18.4569397	21.0639362	21.3726177	20.8553085	21.1088467
1754	Vimentin OS=Rattus norvegicus OX=10116 GN=Vim PE=1 SV=1	Vim	G3V8C3	4.86230665	3.140574932	19.6063728	19.8661327	19.4322262	19.8449173	22.9579182	23.3843174	22.6030159	22.3666973
1755	Vinculin OS=Rattus norvegicus OX=10116 GN=Vcl PE=1 SV=1	Vcl	A0A0G2K8V2	6.93285888	3.022370338	22.7054062	22.7514458	22.7393703	22.5848045	25.879818	25.4328098	25.7840595	25.7738209
1756	Vitronectin OS=Rattus norvegicus OX=10116 GN=Vtn PE=1 SV=1	Vtn	Q3KR94	4.44723672	-2.733194351	25.1312313	25.2538548	25.154892	25.3702888	22.3481617	23.2227669	22.2080002	22.1985607
1757	Voltage-dependent anion-selective channel protein 1 OS=Rattus norvegicus OX=10116 GN=Vdac1 PE=1 SV=4	Vdac1	Q9Z2L0	3.70894063	2.78425312	21.5944328	22.6260853	21.3932343	21.6159706	24.0927448	25.0659657	24.4723244	24.7357006
1758	Voltage-dependent anion-selective channel protein 2 OS=Rattus norvegicus OX=10116 GN=Vdac2 PE=1 SV=2	Vdac2	P81155	4.10673816	1.995258331	21.840847	21.6168957	21.4649734	21.5745697	23.1158714	24.0670261	23.630003	23.6654186
1759	Voltage-dependent anion-selective channel protein 3 OS=Rattus norvegicus OX=10116 GN=Vdac3 PE=1 SV=1	Vdac3	A0A0G2JSR0	4.56038754	3.480305195	18.5731239	19.3572159	18.1230984	18.1779194	21.8310108	22.2584934	21.8624477	22.2006264
1760	Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Rattus norvegicus OX=10116 GN=Cacna2d1 PE=1 SV=1	Cacna2d1	A0A0G2K7E5	0.07165051	-0.063981533	19.011322	19.4691696	19.4815998	19.6380081	19.292572	20.1494198	18.7991505	19.1030312
1761	von Willebrand factor OS=Rattus norvegicus OX=10116 GN=Vwf PE=1 SV=3	Vwf	F1M957	1.68557606	-2.130311489	24.8366909	24.652647	22.4488144	22.5684528	21.1089134	21.3945179	21.3562279	22.1257
1762	V-type proton ATPase 116 kDa subunit a isoform 1 OS=Rattus norvegicus OX=10116 GN=Atp6v0a1 PE=2 SV=1	Atp6v0a1	P25286	3.90358638	3.030369759	16.3737507	16.3642559	17.142807	17.4336052	20.0161095	20.3519917	19.7328472	19.3349495
1763	V-type proton ATPase subunit B, brain isoform OS=Rattus norvegicus OX=10116 GN=Atp6v1b2 PE=1 SV=1	Atp6v1b2	P62815	3.77824872	5.685000658	17.4311218	17.4378185	16.9628887	14.8163557	21.5330276	22.4197655	22.7767487	22.6586456
1764	V-type proton ATPase subunit G OS=Rattus norvegicus OX=10116 GN=Atp6v1g1 PE=1 SV=1	Atp6v1g1	B2GUV5	2.56044341	3.347278595	16.4354668	16.8023872	16.6615334	13.992815	19.6826286	18.9006653	19.4663639	19.2316589
1765	V-type proton ATPase subunit OS=Rattus norvegicus OX=10116 GN=Atp6v0d1 PE=1 SV=1	Atp6v0d1	Q5M7T6	3.35437003	2.616240501	18.494091	17.9084263	17.8277683	16.9347229	20.4700165	20.9244709	20.2213173	20.0141659
1766	WD repeat domain 37 OS=Rattus norvegicus OX=10116 GN=Wdr37 PE=1 SV=3	Wdr37	D3ZQ02	3.89111916	2.996830463	16.0287571	15.8009396	16.9473782	16.7815247	19.8096523	18.8762321	19.2824211	19.5776157
1767	WD repeat-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Wdr1 PE=1 SV=3	Wdr1	Q5RKI0	1.65347666	2.735188007	20.8863907	21.4550591	21.1914291	21.0182228	21.2198505	24.7164001	24.8649426	24.6906605

1768	WD repeat-containing protein 91 OS=Rattus norvegicus OX=10116 GN=Wdr91 PE=2 SV=1	Wdr91	B2RYI0	0.20714967	-0.370056629	17.6747208	19.6885834	16.9514656	16.975193	17.5810547	17.6625214	17.9693813	16.5967789
1769	Xin actin-binding repeat containing 1 OS=Rattus norvegicus OX=10116 GN=Xirp1 PE=1 SV=2	Xirp1	D4ABA9	5.5715119	5.884168625	16.5700912	17.9764614	17.9218998	17.2582817	23.4644909	23.5216599	23.1971893	23.0800686
1770	X-prolyl aminopeptidase (Aminopeptidase P) 1, soluble, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Xpnpep1 PE=	Xpnpep1	A0A0G2JV31	2.29472552	2.983812809	16.0702057	18.5529594	17.2490711	18.0343933	19.3914986	20.7028236	21.4763355	20.2712231
1771	Zinc finger FYVE-type-containing 1 OS=Rattus norvegicus OX=10116 GN=Zfyve1 PE=1 SV=1	Zfyve1	D4A3T4	3.35250263	3.848088026	17.1046619	17.2133083	15.3122149	17.4487953	21.3793545	20.2438469	20.398447	20.4496841
1772	Zinc finger FYVE-type-containing 16 OS=Rattus norvegicus OX=10116 GN=Zfyve16 PE=1 SV=2	Zfyve16	D4ADF6	1.3878025	2.498656034	17.1771145	16.3016949	13.921382	18.4821301	19.0131741	18.9905548	19.0945053	18.7787113
1773	Zinc finger, C2HC-type-containing 1A OS=Rattus norvegicus OX=10116 GN=Zc2hc1a PE=1 SV=1	Zc2hc1a	A0A0G2K782	3.10701455	3.726629734	15.317749	15.1246939	15.6995792	13.8034964	17.4351196	19.2287312	19.2491474	18.9390392
1774	ZW10 interactor OS=Rattus norvegicus OX=10116 GN=Zwint PE=1 SV=1	Zwint	Q8VIL3	1.37577075	0.883261681	20.1495552	19.6200428	19.2957268	19.1920242	21.2384701	20.1108856	20.3054237	20.1356163
1775	Zyxin OS=Rattus norvegicus OX=10116 GN=Zyx PE=1 SV=1	Zyx	D4A7U1	4.40296555	2.163104057	21.8599701	21.6635609	21.8988991	21.3177738	24.2799244	23.5618038	23.793478	23.7574139

Table S3. Top 100 EV proteins identified in Vesiclepedia and ExoCarta databases vs. Evtrap.

Vesiclepedia ***(accessed 06/04/2022)***	**ExoCarta** ***(accessed 06/04/2022)***	**EVtrap (cardiac, 3/4 samples)**
PDCD6IP	CD9	GBE1
GAPDH	PDCD6IP	DECR1
HSPA8	HSPA8	BPNT1
ACTB	GAPDH	HMGCS1
ANXA2	ACTB	HACD2
CD9	ANXA2	OXCT1
PKM	CD63	PAPSS1
HSP90AA1	SDCBP	PDPK1
ENO1	ENO1	LOC100362366
ANXA5	HSP90AA1	A0A0G2JY70_RAT
HSP90AB1	TSG101	LOC100365839
CD63	PKM	NT5E
YWHAZ	LDHA	ATIC
YWHAE	EEF1A1	HMCES
EEF1A1	YWHAZ	NT5C1A
PGK1	PGK1	NT5C2
CLTC	EEF2	OPLAH
PPIA	ALDOA	LOC100360491
SDCBP	HSP90AB1	D3ZPN7_RAT
ALDOA	ANXA5	D3ZJD3_RAT
EEF2	FASN	LOC108349606
ALB	YWHAE	PGLS
TPI1	CLTC	ABHD4
VCP	CD81	ABI1
CFL1	ALB	ABR
MSN	VCP	ABRACL
ATP1A1	TPI1	ABRAXAS2
PRDX1	PPIA	ACAT1
MYH9	MSN	ACAA1A
EZR	CFL1	ACAA2
CD81	PRDX1	ACACA
ANXA6	PFN1	ACACB
FLOT1	RAP1B	ACP1
YWHAB	ITGB1	ANP32A
LDHB	HSPA5	ANP32E
SLC3A2	SLC3A2	ARMT1
GNB1	HIST1H4A	ACO1
PFN1	GNB2	ACO2
TSG101	ATP1A1	ACTR10
YWHAQ	YWHAQ	ACTR1A
GNAI2	FLOT1	ACTR1B
CLIC1	FLNA	ACTR2
ANXA1	CLIC1	ARPC1A
ITGB1	CCT2	ARPC2
LDHA	CDC42	ARPC3
FASN	YWHAG	ARPC4
CDC42	A2M	ARPC5
RAP1B	TUBA1B	ARPC5L-PS1
CCT2	RAC1	ACTR3
YWHAG	LGALS3BP	ACTA1
GNB2	HSPA1A	ACTC1
ACTN4	GNAI2	ACTB
RAB5C	ANXA1	ACTG1
C3	RHOA	ACTN2
RAB10	MFGE8	ACTN4
HIST1H4A	PRDX2	ARPIN
KRT1	GDI2	AHSA1
FN1	EHD4	AHSA2
AHCY	ACTN4	ACBD6
A2M	YWHAB	ACADM
BSG	RAB7A	ACADL
ACTN1	LDHB	ACADVL
ANXA7	GNAS	ACSL1
ACLY	RAB5C	ACSS2
HIST1H4B	ARF1	ACOT1
GDI2	ANXA6	ACOT11
FLNA	ANXA11	ACOT2
UBA1	ACTG1	APPL1
GNAS	KPNB1	AP1B1
GSN	EZR	AP1M1
CCT4	ANXA4	AP2A1
RAN	ACLY	AP2A2
PRDX2	TUBA1C	AP2B1
RHOA	TFRC	AP2M1
CCT3	RAB14	AP3B1
RAC1	HIST2H4A	AP3D1
LGALS3BP	GNB1	AP3M1
TCP1	THBS1	AP3S1
KRT10	RAN	AP3S2
CAP1	RAB5A	AP1S1
RAB7A	PTGFRN	ADD1
TUBB4B	CCT5	APRT
HSPA5	CCT3	ADK
IQGAP1	AHCY	AMPD1
GPI	UBA1	AHCY
RALA	RAB5B	AK1

KPNB1	RAB1A	ADSL
HIST1H4I	LAMP2	ADSS1
TFRC	ITGA6	ADSS
EIF4A1	HIST1H4B	ADGRE5
HIST4H4	BSG	ADGRF5
CCT8	YWHAH	APMAP
TLN1	TUBA1A	ARFGEF1
HIST1H4K	TKT	ARL3
HIST1H4H	TCP1	ADPGK
CCT6A	STOM	ARF1
ANXA11	SLC16A1	ARF2
HIST1H4J	RAB8A	ARF4
HIST1H4F	MYH9	ARF5
HIST1H4D	MVP	ARF6
		ARFGAP1
		ARFGAP2
		ARFGAP3
		ARFIP1
		ARL1
		ARL6IP5
		ARL8B
		ADPRHL1
		ART3
		ART4
		ADRM1
		AFM
		AHNAK
		AKAP1
		AKAP12
		AKAP13
		AKAP2
		AKT1
		AKT1S1
		ANPEP
		AARS1
		AARSD1
		ALB
		ALB
		ADH1
		ADH4
		ALDH1A2
		ALDH16A1
		ALDH2
		ALDH3A2
		ALDH6A1
		ALDH7A1
		ALDH9A1
		AKR1A1
		AKR1B1
		AKR7A2
		ALDOA
		AGPS
		AIF1L
		AAGAB
		ATAT1
		LOC297568
		LOC297568
		AMBP
		AZGP1
		AHSG
		A2M
		AFP
		AFP
		ALPK2
		ALPK3
		AIMP1
		AIMP2
		ACY1
		AASDHPPT
		NPEPPS
		NPEPL1
		AGL
		APCS
		ANAPC1
		ANAPC7
		AAMP
		ANGPTL6
		AGT
		ANK1
		ANKFY1
		ANKLE1
		ANKS1A
		ANKRD17
		ANXA1
		ANXA11
		ANXA2
		ANXA3
		ANXA4

		ANXA5
		ANXA6
		ANXA7
		ATOX1
		AAK1
		APIP
		APOA1
		APOA2
		APOA4
		APOA5
		APOBEC2
		APOB
		APOC1
		APOC2
		APOC3
		APOC4
		APOD
		APOE
		APOF
		APOH
		APOM
		APON
		AIFM1
		API5
		AQP1
		ARAF
		ARCN1
		AGFG1
		AGFG2
		ASAP2
		ARG1
		RNPEP
		ATE1
		RARS1
		AGO2
		ARIH1
		ARMC6
		ARMC8
		AS3MT
		AIP
		NARS1
		ASPH
		DNPEP
		DARS1
		ASPN
		ASPSCR1
		ATXN10
		ATXN2
		ATXN2L
		ABCD3
		ABCE1
		ABCF1
		ABCF2
		ABCF3
		ACLY
		MT-ATP8
		ATP5F1A
		ATP5F1B
		ATP5F1D
		ATP5F1E
		ATP5F1C
		ATP5ME
		ATP5MF
		ATP5MG
		ATP5MK
		ATPAF1
		ATP5PD
		ATP5PF
		ATP5PO
		ATP5PB
		ATP6V0A1
		ATP6V0D1
		ATP6V1A
		ATP6V1B2
		ATP6V1C1
		ATP6V1D
		ATP6V1E1
		ATP6V1F
		ATP6V1G1
		ATP6V1H
		ATP1A1
		ATP1A3
		ATP1B1
		ATP1B3
		ATP2B4
		ATP2A1
		ATP2A2
		ATRN

		ATG3
		ATG5
		ATG7
		BIRC6
		BANF1
		BAG2
		BAG3
		BAG5
		BAG6
		BCAM
		BZW1
		BZW2
		BTF3
		BTF3L4
		BSG
		BCAR1
		BCAP29
		BCAP31
		BAX
		B4GALT1
		B2M
		BLVRA
		BLVRA
		BLVRB
		BLOC1S2
		BTD
		BLMH
		BVES
		BPIFA2F
		BPIFB1
		BASP1
		BASP1
		BRCC3
		BRK1
		BABAM1
		BABAM2
		BROX
		BSDC1
		BTBD1
		BUB3
		CDH1
		CDH11
		CDH13
		CDH15
		CDH2
		CDH5
		CALCOCO1
		CARHSP1
		CACNA2D1
		CAMK1
		CAMK2B
		CAMK2D
		CAMK2G
		CAMKK2
		CACYBP
		CALD1
		CALM3
		CAMSAP1
		CANX
		CAPN1
		CAPN2
		CAPNS1
		CAST
		CNN1
		CNN2
		CNN3
		CALR
		CASQ1
		CASQ2
		CALU
		CTIF
		CAPZA1
		CAPZA2
		CAPZB
		CARMIL1
		CAD
		CAR1
		CAR2
		CBR1
		LOC100360601
		CPA4
		CPB2
		CPD
		CPN1
		CPN2
		CPQ
		CPT1A
		CPT1B

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		CSN2
		CSNK2A1
		CASKIN2
		CASP14
		CASP3
		CAT
		COMTD1
		COMT
		CTNNA1
		CTNNB1
		CTNND1
		CAMP
		CTSA
		CTSB
		CTSD
		CTSH
		CAVIN1
		CAVIN2
		CAVIN3
		CAVIN4
		CAV1
		CAV3
		CNBP
		CNOT9
		CNOT1
		CNOT2
		CNOT3
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		CD47
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		CD99
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		CDC42EP2
		CDC42EP3
		CDC42EP4
		CISD1
		CISD2
		CCAR2
		CAPRIN1
		CDC37
		CDC37L1
		CDC42
		CDC42
		CGREF1
		CEP170
		CEP350
		CDR2L
		CP
		CCT2
		CCT3
		CCT4
		CCT5
		CCT6A
		CCT7
		CCT8
		CHMP2A
		CHMP3
		CHMP6
		CHMP7
		CLIC1
		CLIC4
		CHKB
		CHRNG
		CSPG4
		CHMP4BL1
		CBX3
		CSE1L
		CROCC
		CS
		CLTC
		CLINT1
		CLINT1
		CLTA
		CLTB
		CPSF1
		CPSF6
		CSTF2T
		CLUH

		CLU
		CARM1
		COTL1
		F2
		F9
		F5
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		F11
		F12
		F13A1
		F13B
		CBWD1
		COASY
		CFL1
		CFL2
		A0A0G2KA35_RAT
		CCDC88A
		CCDC141
		CCDC43
		CCDC47
		CCDC6
		CCDC8
		CCDC91
		CHCHD3
		CSDE1
		COLGALT1
		COL1A1
		COL1A2
		COL4A2
		COL6A1
		COL11A1
		COL12A1
		COL14A1
		COLEC11
		COLEC12
		CSF1R
		COMMD10
		COMMD3
		COMMD6
		COMMD9
		CSAP1
		C1QA
		C1QB
		C1QBP
		C1QC
		C1R
		C1S
		C2
		C3
		C4A
		C6
		C7
		C8A
		C8B
		C8G
		C9
		C4BPA
		CFB
		CFH
		CFHR2
		LOC100361907
		CFI
		CFP
		COG7
		COPS2
		COPS3
		COPS4
		COPS5
		COPS6
		COPS7A
		COPS7B
		COPS8
		COPA
		COPB1
		COPB2
		COPB2
		COPE
		COPG2
		COPZ1
		COPZ2
		CCS
		COBLL1
		CNIH4
		CORO7
		CTTN
		CRP
		CKB
		CKM

		CRTC2
		CRTC3
		CRKL
		CRK
		CRYBG3
		CRYBG3
		CRYAB
		CTBP1
		CSK
		CTPS1
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		CLEC3B
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		CELF2
		CUL2
		CUL3
		CUL4A
		CUL5
		CUL7
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		CAND2
		CXADR
		CAP1
		CAP2
		GAK
		CDK1
		CDK16
		CDK4
		CDK5
		CYRIA
		CYRIB
		CSTB
		CST3
		F1M861_RAT
		CSRP3
		CSRP1
		CHORDC1
		CRIP1
		CRIP2
		CMPK1
		CYB5R3
		CYB5A
		COX20
		MT-CO2
		COX4I1
		COX5A
		COX5B
		COX6B1
		COX6C
		COX7A2L
		COX7A2
		COX7B
		COX7C
		CYC1
		POR
		CYGB
		CIAPIN1
		CYFIP1
		CLASP1
		CLASP2
		CKAP5
		CKAP4
		CIAO1
		CIAO2B
		CIAO3
		DAB2
		DAB2IP
		DDB1
		DAZAP1
		DCAF7
		DCAF8
		DDT
		DDX1
		DDX17
		DDX19A
		DDX3X
		DDX5
		DDX6
		DHX15
		DCP1A
		DOCK7
		DAD1
		DEK
		DLK1
		DTX4
		DENND4C
		DENND5A
		DENND5B

		DOHH
		DERA
		DTYMK
		DUT
		DES
		DSC1
		DSG1
		DSP
		DSTN
		DRG1
		DRG2
		DDX39B
		DGKZ
		DIAPH1
		DBI
		DKK3
		DHFR
		DLD
		DLAT
		DLST
		DPYSL2
		DPYSL3
		DDAH1
		DDAH2
		DPP3
		DPP4
		DPH6
		DIP2B
		DVL2
		DVL3
		DLGAP5
		DDI2
		DFFA
		POLE3
		DNAJA1
		DNAJA2
		DNAJA4
		DNAJB1
		DNAJB11
		DNAJB4
		DNAJB5
		DNAJB6
		DNAJC13
		DNAJC5
		DNAJC7
		DNAJC8
		DNAJC9
		DDOST
		DPM1
		DBN1
		DBNL
		DUSP3
		DYRK1A
		DYM
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		DCTN2
		DCTN3
		DCTN4
		DNM1L
		DNM2
		DNM3
		DNAAF4
		DYNC1H1
		DYNC1I2
		DYNC1LI1
		DYNLL1
		DYNLL2
		DYNLRB1
		DYNLT1
		DYNC1LI2
		DST
		EEA1
		ECPAS
		ENTPD1
		EFHD2
		EHBP1
		EHBP1L1
		EHD1
		EHD2
		EHD3
		EHD4
		EMILIN1
		ELN
		ELAVL1
		ETFDH
		ETFA
		ETFB
		ERC1

		EFL1
		ELP1
		ELP2
		ELP3
		ELOB
		ELOC
		EML4
		EMB
		ENAH
		ENAH
		EVL
		ENG
		EMCN
		ERMP1
		ERO1A
		ERP29
		ERP44
		ERGIC1
		ECE1
		EDC3
		EDC4
		ENO1-PS1
		ENO2
		ENO3
		ECI2
		ECH1
		ECHS1
		ECI3
		EFNB1
		EPS15
		EPS15L1
		EGFR
		EPM2AIP1
		EPHX2
		EPN1
		ERLIN2
		EMC1
		EMC2
		EMC8
		ERCC6L
		EPB41
		EPB41L1
		EPB41L2
		EPB41L3
		EPB42
		EEFSEC
		EEF1A1
		EEF1A2
		EEF1B2
		EEF1D
		EEF1E1
		EEF1G
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		EIF1
		EIF2S1
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		EIF2S3
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		EIF2B4
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		EIF4G2
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		EIF4A2
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		EIF4B
		EIF4EBP1
		EIF4EBP2
		EIF4E
		EIF4H
		EIF5A
		EIF5B
		EIF6
		ETF1

		EWSR1
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		EXOC4
		EXOC7
		EXOC8
		XPO1
		XPO5
		XPO7
		EYA3
		EZR
		F11R
		FAM114A1
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		FAM120A
		FAM168A
		FAM210A
		FAM98A
		FAM98B
		FUBP1
		FUBP3
		FAF1
		FADD
		FSCN1
		FABP3
		FABP4
		FABP5
		FASN
		FAU
		FBXO21
		FBXO30
		FBXO40
		FCGBP
		FCHO2
		FEM1A
		FERMT2
		FERMT3
		FTH1
		FETUB
		FHIP1B
		FBN1
		FBN2
		FGA
		FGB
		FGG
		FGL2
		FN1
		FN1
		FBLN1
		FBLN1
		FBLN2
		FBLN5
		FCNA
		FILIP1
		FLNA
		FLNB
		FBLIM1
		FLNC
		FIS1
		FKBP10
		FKBP1A
		FKBP2
		FKBP3
		FKBP4
		FKBP8
		FLAD1
		FLII
		FXR1
		FXR2
		FMR1
		FLCN
		FNBP1
		FMNL3
		FHL1
		FHL2
		FRYL
		FRY
		FCSK
		FH
		FUS
		FXYD1
		FYCO1
		GPS1
		GNA11
		GNAI2
		GNAI3
		GNAO1
		GNAQ
		GNB1

		GNB2
		GNB4
		GNG10
		GNG12
		GNG2
		GNG5
		GSPT1
		G3BP1
		G3BP2
		GALK1
		GALK2
		LGALS1
		GJA1
		GC
		GCN1
		GDI1
		GDI2
		GFUS
		GMPPA
		GSN
		GEMIN5
		GRCC10
		GTF2F1
		GPHN
		GIT1
		GIT2
		GLIPR2
		GMFB
		GPI
		GANAB
		GCLM
		GLUD1
		GOT1
		GOT2
		GATD3A
		GFPT1
		QRICH1
		QARS1
		ENPEP
		EPRS
		GLRX3
		GLRX
		GPX1
		GPX3
		GPX4
		GSTP1
		GSTZ1
		GSTM5
		GSTM7
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		E9PTV9_RAT
		M0R660_RAT
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		GPD1L
		PYGB
		PYGB
		PYGM
		GYS1
		GSK3B
		GYG1
		GYPC
		GP2
		GPLD1
		GLO1
		GPC4
		GNAS
		GNAS
		GGA1
		GGA2
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		VAPB
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		VASP
		VCAN
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		VTA1
		VTI1B
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		VAMP8
		VBP1
		VIM
		VCL
		VTN
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		VDAC3
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		ITGB3
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		LTA4H

Table S4. GO terms for cellular component of proteins from cardiac EVs isolated by EVtrap.

Analysis Type:	PANTHER Overrepresentation Test (Released 20220202)						
Annotation Version and Release Date:	GO Ontology database DOI: 10.5281/zenodo.5725227 Released 2020-11-01						
Analyzed List:	upload_1 (Rattus norvegicus)						
Reference List:	Rattus norvegicus (all genes in database)						
Test Type:	FISHER						
Correction:	FDR						
GO cellular component complete	**Rattus norvegicus - REFLIST (21585)**	**upload_1 (2546)**	**upload_1 (expected)**	**upload_1 (over/under)**	**upload_1 (fold Enrichment)**	**upload_1 (raw P-value)**	**upload_1 (FDR)**
cellular_component (GO:0005575)	18939	2464	2233.9	+	1.1	2.14E-54	3.31E-52
cellular anatomical entity (GO:0110165)	18742	2445	2210.66	+	1.11	1.19E-51	1.60E-49
intracellular anatomical structure (GO:0005622)	13803	2251	1628.1	+	1.38	6.10E-158	6.14E-155
cytoplasm (GO:0005737)	10986	2085	1295.82	+	1.61	1.20E-210	2.42E-207
organelle (GO:0043226)	12499	1992	1474.29	+	1.35	1.39E-93	4.65E-91
intracellular organelle (GO:0043229)	12168	1967	1435.24	+	1.37	4.87E-97	2.45E-94
membrane-bounded organelle (GO:0043227)	11264	1751	1328.61	+	1.32	2.39E-58	4.81E-56
intracellular membrane-bounded organelle (GO:0043231)	10817	1719	1275.89	+	1.35	2.57E-63	7.39E-61
protein-containing complex (GO:0032991)	5722	1198	674.92	+	1.78	3.70E-96	1.49E-93
membrane (GO:0016020)	9463	1192	1116.18	+	1.07	4.39E-03	2.33E-02
nucleus (GO:0005634)	6777	1081	799.36	+	1.35	2.42E-28	1.52E-26
cytosol (GO:0005829)	4027	1057	474.99	+	2.23	1.30E-136	8.74E-134
intracellular non-membrane-bounded organelle (GO:0043232)	4560	888	537.86	+	1.65	7.99E-51	1.01E-48
non-membrane-bounded organelle (GO:0043228)	4560	888	537.86	+	1.65	7.99E-51	9.47E-49
endomembrane system (GO:0012505)	3916	754	461.9	+	1.63	8.40E-40	7.36E-38
organelle lumen (GO:0043233)	4258	705	502.24	+	1.4	8.79E-20	3.62E-18
membrane-enclosed lumen (GO:0031974)	4258	705	502.24	+	1.4	8.79E-20	3.54E-18
intracellular organelle lumen (GO:0070013)	4257	704	502.12	+	1.4	1.39E-19	5.47E-18
nuclear lumen (GO:0031981)	3817	620	450.22	+	1.38	1.90E-15	5.55E-14
organelle membrane (GO:0031090)	2837	567	334.63	+	1.69	3.68E-32	2.65E-30
cell junction (GO:0030054)	2131	548	251.36	+	2.18	9.18E-59	2.06E-56
nucleoplasm (GO:0005654)	3394	544	400.33	+	1.36	1.80E-12	3.66E-11
cell projection (GO:0042995)	2529	527	298.3	+	1.77	1.26E-33	9.39E-32
cytoskeleton (GO:0005856)	2124	518	250.53	+	2.07	2.42E-49	2.71E-47
plasma membrane bounded cell projection (GO:0120025)	2451	509	289.1	+	1.76	5.78E-32	4.02E-30
vesicle (GO:0031982)	2044	486	241.09	+	2.02	2.15E-43	1.97E-41
intracellular vesicle (GO:0097708)	1903	448	224.46	+	2	1.05E-38	8.49E-37
cytoplasmic vesicle (GO:0031410)	1898	447	223.87	+	2	9.58E-39	8.05E-37
synapse (GO:0045202)	1535	413	181.06	+	2.28	3.52E-47	3.74E-45
intrinsic component of membrane (GO:0031224)	6319	383	745.34	-	0.51	1.32E-57	2.42E-55
supramolecular complex (GO:0099080)	1219	377	143.78	+	2.62	5.29E-55	8.88E-53
extracellular region (GO:0005576)	2359	370	278.25	+	1.33	1.38E-07	1.72E-06
neuron projection (GO:0043005)	1652	365	194.86	+	1.87	1.28E-26	7.58E-25
integral component of membrane (GO:0016021)	6174	358	728.24	-	0.49	1.73E-61	4.35E-59
bounding membrane of organelle (GO:0098588)	1487	351	175.4	+	2	3.80E-30	2.47E-28
mitochondrion (GO:0005739)	1619	334	190.96	+	1.75	4.27E-20	1.83E-18
endoplasmic reticulum (GO:0005783)	1701	319	200.64	+	1.59	3.74E-14	9.91E-13
extracellular space (GO:0005615)	1776	315	209.48	+	1.5	2.17E-11	3.95E-10
catalytic complex (GO:1902494)	1504	307	177.4	+	1.73	6.82E-18	2.22E-16
supramolecular polymer (GO:0099081)	904	294	106.63	+	2.76	8.23E-46	7.90E-44
supramolecular fiber (GO:0099512)	896	293	105.69	+	2.77	3.75E-46	3.77E-44
membrane protein complex (GO:0098796)	1194	281	140.84	+	2	8.21E-24	4.24E-22
Golgi apparatus (GO:0005794)	1396	277	164.66	+	1.68	8.02E-15	2.28E-13
microtubule cytoskeleton (GO:0015630)	1272	274	150.04	+	1.83	1.24E-18	4.62E-17
envelope (GO:0031975)	1107	247	130.57	+	1.89	2.22E-18	7.97E-17

organelle envelope (GO:0031967)	1107	247	130.57	+	1.89	2.22E-18	7.83E-17
plasma membrane region (GO:0098590)	1324	243	156.17	+	1.56	4.43E-10	6.92E-09
perinuclear region of cytoplasm (GO:0048471)	754	240	88.94	+	2.7	4.41E-36	3.42E-34
somatodendritic compartment (GO:0036477)	1132	228	133.52	+	1.71	6.76E-13	1.48E-11
organelle subcompartment (GO:0031984)	1227	214	144.73	+	1.48	1.66E-07	2.06E-06
vesicle membrane (GO:0012506)	765	210	90.23	+	2.33	1.58E-24	8.37E-23
endosome (GO:0005768)	863	206	101.79	+	2.02	4.21E-18	1.44E-16
axon (GO:0030424)	838	204	98.84	+	2.06	9.63E-19	3.66E-17
cytoplasmic vesicle membrane (GO:0030659)	739	203	87.17	+	2.33	8.44E-24	4.25E-22
ribonucleoprotein complex (GO:1990904)	1036	200	122.2	+	1.64	5.11E-10	7.91E-09
postsynapse (GO:0098794)	776	199	91.53	+	2.17	2.08E-20	9.31E-19
polymeric cytoskeletal fiber (GO:0099513)	671	193	79.15	+	2.44	1.44E-24	7.82E-23
cell body (GO:0044297)	854	193	100.73	+	1.92	6.07E-15	1.75E-13
anchoring junction (GO:0070161)	661	184	77.97	+	2.36	3.84E-22	1.80E-20
actin cytoskeleton (GO:0015629)	498	177	58.74	+	3.01	2.47E-31	1.66E-29
intracellular protein-containing complex (GO:0140535)	755	168	89.05	+	1.89	1.08E-12	2.27E-11
secretory vesicle (GO:0099503)	657	163	77.49	+	2.1	8.75E-16	2.63E-14
neuronal cell body (GO:0043025)	759	162	89.53	+	1.81	5.14E-11	9.08E-10
dendrite (GO:0030425)	808	162	95.31	+	1.7	2.52E-09	3.60E-08
dendritic tree (GO:0097447)	810	162	95.54	+	1.7	3.57E-09	5.03E-08
presynapse (GO:0098793)	672	160	79.26	+	2.02	3.82E-14	9.99E-13
cell surface (GO:0009986)	1082	160	127.62	+	1.25	7.84E-03	3.94E-02
nuclear outer membrane-endoplasmic reticulum membrane network (GO:0042175)	960	159	113.23	+	1.4	9.73E-05	7.84E-04
microtubule organizing center (GO:0005815)	785	158	92.59	+	1.71	3.03E-09	4.30E-08
mitochondrial envelope (GO:0005740)	675	154	79.62	+	1.93	1.93E-12	3.90E-11
endoplasmic reticulum subcompartment (GO:0098827)	942	154	111.11	+	1.39	1.92E-04	1.47E-03
endoplasmic reticulum membrane (GO:0005789)	932	151	109.93	+	1.37	3.21E-04	2.31E-03
cell leading edge (GO:0031252)	434	144	51.19	+	2.81	2.51E-23	1.23E-21
mitochondrial membrane (GO:0031966)	621	144	73.25	+	1.97	3.54E-12	6.99E-11
side of membrane (GO:0098552)	784	138	92.47	+	1.49	2.39E-05	2.20E-04
cell-cell junction (GO:0005911)	522	132	61.57	+	2.14	2.03E-13	4.86E-12
glutamatergic synapse (GO:0098978)	515	130	60.75	+	2.14	3.79E-13	8.68E-12
centrosome (GO:0005813)	617	125	72.78	+	1.72	1.08E-07	1.38E-06
transport vesicle (GO:0030133)	419	120	49.42	+	2.43	1.43E-15	4.22E-14
neuron to neuron synapse (GO:0098984)	456	119	53.79	+	2.21	5.76E-13	1.28E-11
postsynaptic specialization (GO:0099572)	458	118	54.02	+	2.18	1.13E-12	2.34E-11
vacuole (GO:0005773)	586	118	69.12	+	1.71	3.79E-07	4.44E-06
postsynaptic density (GO:0014069)	422	117	49.78	+	2.35	2.74E-14	7.36E-13
asymmetric synapse (GO:0032279)	428	117	50.48	+	2.32	6.98E-14	1.76E-12
cell cortex (GO:0005938)	332	115	39.16	+	2.94	5.27E-20	2.21E-18
distal axon (GO:0150034)	440	114	51.9	+	2.2	1.98E-12	3.95E-11
contractile fiber (GO:0043292)	238	111	28.07	+	3.95	1.27E-27	7.73E-26
microtubule (GO:0005874)	401	108	47.3	+	2.28	1.02E-12	2.16E-11
myofibril (GO:0030016)	228	106	26.89	+	3.94	2.39E-26	1.38E-24
membrane raft (GO:0045121)	406	106	47.89	+	2.21	9.66E-12	1.82E-10
membrane microdomain (GO:0098857)	407	106	48.01	+	2.21	1.03E-11	1.93E-10
early endosome (GO:0005769)	345	99	40.69	+	2.43	3.98E-13	9.01E-12
endosome membrane (GO:0010008)	361	99	42.58	+	2.32	3.70E-12	7.18E-11
organelle inner membrane (GO:0019866)	453	99	53.43	+	1.85	1.16E-07	1.47E-06
nuclear envelope (GO:0005635)	453	98	53.43	+	1.83	2.35E-07	2.90E-06
sarcomere (GO:0030017)	202	97	23.83	+	4.07	5.06E-25	2.83E-23
apical part of cell (GO:0045177)	495	95	58.39	+	1.63	3.13E-05	2.77E-04
mitochondrial inner membrane (GO:0005743)	395	94	46.59	+	2.02	1.02E-08	1.39E-07
exocytic vesicle (GO:0070382)	303	92	35.74	+	2.57	2.76E-13	6.54E-12

secretory granule (GO:0030141)	416	92	49.07	+	1.87	2.43E-07	2.99E-06
lytic vacuole (GO:0000323)	484	92	57.09	+	1.61	4.81E-05	4.17E-04
lysosome (GO:0005764)	484	92	57.09	+	1.61	4.81E-05	4.16E-04
ribosome (GO:0005840)	533	92	62.87	+	1.46	9.49E-04	6.23E-03
intrinsic component of plasma membrane (GO:0031226)	1441	92	169.97	-	0.54	1.69E-10	2.84E-09
coated vesicle (GO:0030135)	211	91	24.89	+	3.66	4.63E-21	2.12E-19
spindle (GO:0005819)	373	91	44	+	2.07	6.37E-09	8.79E-08
plasma membrane protein complex (GO:0098797)	547	89	64.52	+	1.38	5.89E-03	3.07E-02
ribonucleoprotein granule (GO:0035770)	255	85	30.08	+	2.83	2.18E-14	6.01E-13
Golgi membrane (GO:0000139)	422	84	49.78	+	1.69	2.72E-05	2.45E-04
cell-substrate junction (GO:0030055)	195	83	23	+	3.61	4.71E-19	1.83E-17
extrinsic component of membrane (GO:0019898)	342	83	40.34	+	2.06	2.68E-08	3.55E-07
lamellipodium (GO:0030027)	195	82	23	+	3.57	1.37E-18	5.01E-17
cytoplasmic ribonucleoprotein granule (GO:0036464)	237	82	27.95	+	2.93	1.16E-14	3.24E-13
mitochondrial protein-containing complex (GO:0098798)	300	82	35.39	+	2.32	3.87E-10	6.09E-09
Unclassified (UNCLASSIFIED)	2646	82	312.1	-	0.26	2.14E-54	3.07E-52
integral component of plasma membrane (GO:0005887)	1355	81	159.83	-	0.51	2.34E-11	4.21E-10
focal adhesion (GO:0005925)	183	78	21.59	+	3.61	5.14E-18	1.72E-16
endocytic vesicle (GO:0030139)	198	77	23.35	+	3.3	4.82E-16	1.47E-14
late endosome (GO:0005770)	261	75	30.79	+	2.44	2.76E-10	4.56E-09
synaptic vesicle (GO:0008021)	261	74	30.79	+	2.4	8.07E-10	1.24E-08
extracellular matrix (GO:0031012)	410	74	48.36	+	1.53	1.24E-03	7.82E-03
external encapsulating structure (GO:0030312)	412	74	48.6	+	1.52	1.28E-03	7.98E-03
cytosolic ribosome (GO:0022626)	388	73	45.77	+	1.6	4.06E-04	2.88E-03
apical plasma membrane (GO:0016324)	392	72	46.24	+	1.56	9.75E-04	6.38E-03
cytoplasmic side of membrane (GO:0098562)	217	70	25.6	+	2.73	2.04E-11	3.73E-10
Golgi apparatus subcompartment (GO:0098791)	324	69	38.22	+	1.81	2.12E-05	1.97E-04
cell projection membrane (GO:0031253)	346	69	40.81	+	1.69	1.38E-04	1.07E-03
I band (GO:0031674)	142	68	16.75	+	4.06	6.70E-18	2.21E-16
site of polarized growth (GO:0030427)	233	68	27.48	+	2.47	1.11E-09	1.67E-08
peptidase complex (GO:1905368)	131	66	15.45	+	4.27	2.80E-18	9.74E-17
ruffle (GO:0001726)	174	66	20.52	+	3.22	1.50E-13	3.64E-12
endopeptidase complex (GO:1905369)	100	65	11.8	+	5.51	2.45E-22	1.17E-20
Z disc (GO:0030018)	131	64	15.45	+	4.14	2.93E-17	9.36E-16
inner mitochondrial membrane protein complex (GO:0098800)	161	64	18.99	+	3.37	6.37E-14	1.62E-12
growth cone (GO:0030426)	226	64	26.66	+	2.4	1.12E-08	1.52E-07
collagen-containing extracellular matrix (GO:0062023)	245	62	28.9	+	2.15	4.88E-07	5.65E-06
vacuolar membrane (GO:0005774)	269	62	31.73	+	1.95	7.86E-06	8.04E-05
transport vesicle membrane (GO:0030658)	194	61	22.88	+	2.67	8.31E-10	1.26E-08
neuron projection terminus (GO:0044306)	256	61	30.2	+	2.02	3.25E-06	3.54E-05
cytoplasmic region (GO:0099568)	283	61	33.38	+	1.83	5.89E-05	5.03E-04
midbody (GO:0030496)	184	60	21.7	+	2.76	3.17E-10	5.03E-09
actin-based cell projection (GO:0098858)	234	60	27.6	+	2.17	4.79E-07	5.57E-06
sarcolemma (GO:0042383)	175	59	20.64	+	2.86	1.39E-10	2.37E-09
basal part of cell (GO:0045178)	319	58	37.63	+	1.54	3.88E-03	2.11E-02
mitochondrial matrix (GO:0005759)	321	58	37.86	+	1.53	3.99E-03	2.16E-02
axon terminus (GO:0043679)	232	57	27.36	+	2.08	2.92E-06	3.20E-05
neuron spine (GO:0044309)	231	56	27.25	+	2.06	6.39E-06	6.67E-05
oxidoreductase complex (GO:1990204)	134	55	15.81	+	3.48	1.32E-12	2.72E-11
extrinsic component of plasma membrane (GO:0019897)	190	55	22.41	+	2.45	5.16E-08	6.70E-07
dendritic spine (GO:0043197)	228	54	26.89	+	2.01	1.42E-05	1.38E-04
cortical cytoskeleton (GO:0030863)	121	53	14.27	+	3.71	4.59E-13	1.03E-11
melanosome (GO:0042470)	93	52	10.97	+	4.74	4.13E-16	1.30E-14
pigment granule (GO:0048770)	93	52	10.97	+	4.74	4.13E-16	1.28E-14

actin filament (GO:0005884)	130	52	15.33	+	3.39	1.16E-11	2.14E-10
cytoplasmic side of plasma membrane (GO:0009898)	180	52	21.23	+	2.45	1.32E-07	1.66E-06
proteasome complex (GO:0000502)	66	51	7.78	+	6.55	3.91E-20	1.71E-18
trans-Golgi network (GO:0005802)	226	51	26.66	+	1.91	7.19E-05	6.01E-04
coated vesicle membrane (GO:0030662)	94	49	11.09	+	4.42	2.26E-14	6.15E-13
plasma membrane bounded cell projection cytoplasm (GO:0032838)	242	49	28.54	+	1.72	1.01E-03	6.49E-03
actin filament bundle (GO:0032432)	92	48	10.85	+	4.42	4.04E-14	1.04E-12
membrane coat (GO:0030117)	94	48	11.09	+	4.33	7.47E-14	1.86E-12
coated membrane (GO:0048475)	94	48	11.09	+	4.33	7.47E-14	1.84E-12
clathrin-coated vesicle (GO:0030136)	119	47	14.04	+	3.35	1.56E-10	2.64E-09
actomyosin (GO:0042641)	91	46	10.73	+	4.29	3.24E-13	7.50E-12
respiratory chain complex (GO:0098803)	102	46	12.03	+	3.82	7.17E-12	1.38E-10
mitochondrial respirasome (GO:0005746)	102	46	12.03	+	3.82	7.17E-12	1.36E-10
respirasome (GO:0070469)	108	46	12.74	+	3.61	3.31E-11	5.91E-10
intermediate filament cytoskeleton (GO:0045111)	181	46	21.35	+	2.15	1.64E-05	1.57E-04
lytic vacuole membrane (GO:0098852)	211	45	24.89	+	1.81	6.54E-04	4.50E-03
lysosomal membrane (GO:0005765)	211	45	24.89	+	1.81	6.54E-04	4.48E-03
polysome (GO:0005844)	83	44	9.79	+	4.49	3.03E-13	7.09E-12
phagocytic vesicle (GO:0045335)	107	44	12.62	+	3.49	2.15E-10	3.58E-09
outer membrane (GO:0019867)	198	44	23.35	+	1.88	3.09E-04	2.26E-03
organelle outer membrane (GO:0031968)	198	44	23.35	+	1.88	3.09E-04	2.25E-03
cluster of actin-based cell projections (GO:0098862)	201	44	23.71	+	1.86	4.88E-04	3.42E-03
contractile actin filament bundle (GO:0097517)	83	43	9.79	+	4.39	1.01E-12	2.19E-11
stress fiber (GO:0001725)	83	43	9.79	+	4.39	1.01E-12	2.17E-11
recycling endosome (GO:0055037)	179	43	21.11	+	2.04	9.65E-05	7.81E-04
adherens junction (GO:0005912)	153	42	18.05	+	2.33	6.01E-06	6.31E-05
filopodium (GO:0030175)	108	41	12.74	+	3.22	5.67E-09	7.87E-08
extracellular exosome (GO:0070062)	87	40	10.26	+	3.9	1.04E-10	1.80E-09
extracellular vesicle (GO:1903561)	97	40	11.44	+	3.5	1.31E-09	1.94E-08
extracellular organelle (GO:0043230)	99	40	11.68	+	3.43	2.10E-09	3.06E-08
extracellular membrane-bounded organelle (GO:0065010)	99	40	11.68	+	3.43	2.10E-09	3.04E-08
rough endoplasmic reticulum (GO:0005791)	123	40	14.51	+	2.76	2.74E-07	3.30E-06
mitochondrial outer membrane (GO:0005741)	171	40	20.17	+	1.98	2.61E-04	1.93E-03
leading edge membrane (GO:0031256)	179	40	21.11	+	1.89	5.40E-04	3.78E-03
perikaryon (GO:0043204)	199	40	23.47	+	1.7	2.95E-03	1.68E-02
cytoplasmic stress granule (GO:0010494)	78	38	9.2	+	4.13	8.30E-11	1.44E-09
plasma membrane raft (GO:0044853)	139	38	16.4	+	2.32	1.99E-05	1.86E-04
Golgi-associated vesicle (GO:0005798)	96	37	11.32	+	3.27	2.25E-08	3.00E-07
early endosome membrane (GO:0031901)	125	37	14.74	+	2.51	7.26E-06	7.47E-05
exocytic vesicle membrane (GO:0099501)	134	37	15.81	+	2.34	2.45E-05	2.23E-04
synaptic vesicle membrane (GO:0030672)	134	37	15.81	+	2.34	2.45E-05	2.22E-04
brush border (GO:0005903)	137	37	16.16	+	2.29	3.08E-05	2.75E-04
neuron projection cytoplasm (GO:0120111)	108	36	12.74	+	2.83	7.30E-07	8.18E-06
intermediate filament (GO:0005882)	142	36	16.75	+	2.15	1.18E-04	9.29E-04
vesicle coat (GO:0030120)	57	35	6.72	+	5.21	3.60E-12	7.05E-11
cell-cell contact zone (GO:0044291)	86	35	10.14	+	3.45	1.80E-08	2.43E-07
cortical actin cytoskeleton (GO:0030864)	88	35	10.38	+	3.37	2.85E-08	3.73E-07
terminal bouton (GO:0043195)	131	35	15.45	+	2.27	6.16E-05	5.20E-04
small ribosomal subunit (GO:0015935)	168	35	19.82	+	1.77	3.79E-03	2.06E-02
transcription regulator complex (GO:0005667)	485	35	57.21	-	0.61	3.03E-03	1.71E-02
late endosome membrane (GO:0031902)	120	34	14.15	+	2.4	2.92E-05	2.62E-04
endoplasmic reticulum protein-containing complex (GO:0140534)	130	34	15.33	+	2.22	1.04E-04	8.28E-04
microbody (GO:0042579)	149	34	17.57	+	1.93	9.89E-04	6.43E-03
peroxisome (GO:0005777)	149	34	17.57	+	1.93	9.89E-04	6.41E-03

spindle pole (GO:0000922)	155	34	18.28	+	1.86	1.82E-03	1.11E-02
mitotic spindle (GO:0072686)	162	34	19.11	+	1.78	3.34E-03	1.87E-02
clathrin-coated pit (GO:0005905)	67	33	7.9	+	4.18	1.15E-09	1.71E-08
sarcoplasm (GO:0016528)	79	33	9.32	+	3.54	2.77E-08	3.65E-07
cytosolic small ribosomal subunit (GO:0022627)	133	33	15.69	+	2.1	3.20E-04	2.32E-03
endoplasmic reticulum-Golgi intermediate compartment (GO:0005793)	94	32	11.09	+	2.89	2.55E-06	2.81E-05
caveola (GO:0005901)	104	32	12.27	+	2.61	1.44E-05	1.40E-04
Schaffer collateral - CA1 synapse (GO:0098685)	116	32	13.68	+	2.34	7.20E-05	6.00E-04
intercalated disc (GO:0014704)	63	31	7.43	+	4.17	3.69E-09	5.16E-08
condensed chromosome, centromeric region (GO:0000779)	138	31	16.28	+	1.9	2.27E-03	1.33E-02
lipid droplet (GO:0005811)	101	30	11.91	+	2.52	4.01E-05	3.52E-04
extrinsic component of cytoplasmic side of plasma membrane (GO:0031234)	108	30	12.74	+	2.36	1.22E-04	9.58E-04
nuclear periphery (GO:0034399)	121	30	14.27	+	2.1	7.23E-04	4.86E-03
COPII-coated ER to Golgi transport vesicle (GO:0030134)	61	29	7.2	+	4.03	2.10E-08	2.83E-07
sarcoplasmic reticulum (GO:0016529)	67	29	7.9	+	3.67	1.04E-07	1.33E-06
P-body (GO:0000932)	84	29	9.91	+	2.93	4.28E-06	4.59E-05
ruffle membrane (GO:0032587)	85	29	10.03	+	2.89	8.10E-06	8.24E-05
kinetochore (GO:0000776)	129	29	15.22	+	1.91	2.66E-03	1.52E-02
respiratory chain complex I (GO:0045271)	63	27	7.43	+	3.63	3.30E-07	3.96E-06
NADH dehydrogenase complex (GO:0030964)	63	27	7.43	+	3.63	3.30E-07	3.94E-06
mitochondrial respiratory chain complex I (GO:0005747)	63	27	7.43	+	3.63	3.30E-07	3.91E-06
nuclear matrix (GO:0016363)	99	27	11.68	+	2.31	3.54E-04	2.53E-03
basement membrane (GO:0005604)	114	27	13.45	+	2.01	2.16E-03	1.28E-02
axon cytoplasm (GO:1904115)	66	26	7.78	+	3.34	1.92E-06	2.12E-05
neuromuscular junction (GO:0031594)	98	26	11.56	+	2.25	5.91E-04	4.10E-03
receptor complex (GO:0043235)	406	26	47.89	-	0.54	1.16E-03	7.37E-03
protein-lipid complex (GO:0032994)	34	25	4.01	+	6.23	2.86E-10	4.68E-09
chaperone complex (GO:0101031)	34	25	4.01	+	6.23	2.86E-10	4.65E-09
A band (GO:0031672)	39	25	4.6	+	5.43	2.24E-09	3.22E-08
cell division site (GO:0032153)	70	25	8.26	+	3.03	1.20E-05	1.18E-04
microvillus (GO:0005902)	100	25	11.8	+	2.12	1.79E-03	1.09E-02
lipoprotein particle (GO:1990777)	31	24	3.66	+	6.56	3.10E-10	4.99E-09
plasma lipoprotein particle (GO:0034358)	31	24	3.66	+	6.56	3.10E-10	4.95E-09
proton-transporting two-sector ATPase complex (GO:0016469)	53	24	6.25	+	3.84	6.76E-07	7.65E-06
intrinsic component of synaptic vesicle membrane (GO:0098563)	67	24	7.9	+	3.04	1.71E-05	1.63E-04
secretory granule membrane (GO:0030667)	97	24	11.44	+	2.1	2.52E-03	1.45E-02
autophagosome (GO:0005776)	104	24	12.27	+	1.96	5.43E-03	2.86E-02
proteasome accessory complex (GO:0022624)	25	23	2.95	+	7.8	6.96E-11	1.22E-09
polysomal ribosome (GO:0042788)	41	23	4.84	+	4.76	6.14E-08	7.94E-07
clathrin coat (GO:0030118)	49	23	5.78	+	3.98	7.06E-07	7.94E-06
endocytic vesicle membrane (GO:0030666)	50	23	5.9	+	3.9	9.28E-07	1.03E-05
recycling endosome membrane (GO:0055038)	72	23	8.49	+	2.71	1.32E-04	1.04E-03
myosin complex (GO:0016459)	52	22	6.13	+	3.59	4.67E-06	4.95E-05
inclusion body (GO:0016234)	80	22	9.44	+	2.33	9.86E-04	6.43E-03
endoplasmic reticulum lumen (GO:0005788)	84	22	9.91	+	2.22	2.09E-03	1.24E-02
high-density lipoprotein particle (GO:0034364)	25	21	2.95	+	7.12	1.44E-09	2.12E-08
multivesicular body (GO:0005771)	59	21	6.96	+	3.02	6.05E-05	5.12E-04
lateral plasma membrane (GO:0016328)	73	21	8.61	+	2.44	1.01E-03	6.49E-03
spindle microtubule (GO:0005876)	78	21	9.2	+	2.28	1.56E-03	9.65E-03
proteasome regulatory particle (GO:0005838)	21	20	2.48	+	8.07	8.13E-10	1.24E-08
COPI-coated vesicle (GO:0030137)	34	20	4.01	+	4.99	2.50E-07	3.05E-06
clathrin-coated vesicle membrane (GO:0030665)	45	20	5.31	+	3.77	7.03E-06	7.30E-05
T-tubule (GO:0030315)	71	20	8.37	+	2.39	1.56E-03	9.67E-03
nuclear pore (GO:0005643)	72	20	8.49	+	2.36	1.69E-03	1.04E-02

podosome (GO:0002102)	33	19	3.89	+	4.88	6.35E-07	7.23E-06
Golgi-associated vesicle membrane (GO:0030660)	46	19	5.43	+	3.5	2.67E-05	2.41E-04
myelin sheath (GO:0043209)	67	19	7.9	+	2.4	2.12E-03	1.26E-02
COP9 signalosome (GO:0008180)	27	18	3.18	+	5.65	2.56E-07	3.11E-06
ER to Golgi transport vesicle membrane (GO:0012507)	29	18	3.42	+	5.26	5.54E-07	6.38E-06
cytochrome complex (GO:0070069)	39	18	4.6	+	3.91	1.34E-05	1.31E-04
rough endoplasmic reticulum membrane (GO:0030867)	47	18	5.54	+	3.25	9.43E-05	7.66E-04
cleavage furrow (GO:0032154)	48	18	5.66	+	3.18	1.17E-04	9.28E-04
keratin filament (GO:0045095)	72	18	8.49	+	2.12	8.50E-03	4.22E-02
filamentous actin (GO:0031941)	37	17	4.36	+	3.9	2.42E-05	2.21E-04
smooth endoplasmic reticulum (GO:0005790)	39	17	4.6	+	3.7	4.09E-05	3.57E-04
cytosolic region (GO:0099522)	45	17	5.31	+	3.2	1.67E-04	1.28E-03
SNARE complex (GO:0031201)	48	17	5.66	+	3	3.10E-04	2.26E-03
pore complex (GO:0046930)	36	16	4.25	+	3.77	5.70E-05	4.89E-04
collagen trimer (GO:0005581)	59	16	6.96	+	2.3	6.82E-03	3.47E-02
very-low-density lipoprotein particle (GO:0034361)	18	15	2.12	+	7.07	3.49E-07	4.11E-06
triglyceride-rich plasma lipoprotein particle (GO:0034385)	19	15	2.24	+	6.69	5.63E-07	6.45E-06
ESCRT complex (GO:0036452)	26	15	3.07	+	4.89	9.39E-06	9.46E-05
endoplasmic reticulum exit site (GO:0070971)	27	15	3.18	+	4.71	1.32E-05	1.30E-04
cytoplasmic side of endoplasmic reticulum membrane (GO:0098554)	28	15	3.3	+	4.54	1.83E-05	1.73E-04
cytoplasmic side of rough endoplasmic reticulum membrane (GO:0098556)	20	14	2.36	+	5.93	3.67E-06	3.97E-05
proteasome core complex (GO:0005839)	21	14	2.48	+	5.65	5.52E-06	5.82E-05
mitochondrial proton-transporting ATP synthase complex (GO:0005753)	22	14	2.59	+	5.4	8.15E-06	8.26E-05
proton-transporting ATP synthase complex (GO:0045259)	23	14	2.71	+	5.16	1.18E-05	1.18E-04
clathrin vesicle coat (GO:0030125)	28	14	3.3	+	4.24	6.17E-05	5.18E-04
sarcoplasmic reticulum membrane (GO:0033017)	31	14	3.66	+	3.83	1.44E-04	1.11E-03
phagocytic vesicle membrane (GO:0030670)	34	14	4.01	+	3.49	3.06E-04	2.25E-03
GTPase complex (GO:1905360)	37	14	4.36	+	3.21	6.07E-04	4.19E-03
AP-type membrane coat adaptor complex (GO:0030119)	38	14	4.48	+	3.12	7.50E-04	5.02E-03
autophagosome membrane (GO:0000421)	44	14	5.19	+	2.7	3.89E-03	2.11E-02
protein serine/threonine phosphatase complex (GO:0008287)	50	14	5.9	+	2.37	6.88E-03	3.49E-02
phosphatase complex (GO:1903293)	51	14	6.02	+	2.33	7.73E-03	3.90E-02
proton-transporting two-sector ATPase complex, catalytic domain (GO:0033178)	20	13	2.36	+	5.51	1.45E-05	1.40E-04
translation preinitiation complex (GO:0070993)	21	13	2.48	+	5.25	2.13E-05	1.97E-04
mitochondrial respiratory chain complex IV (GO:0005751)	24	13	2.83	+	4.59	6.03E-05	5.13E-04
respiratory chain complex IV (GO:0045277)	27	13	3.18	+	4.08	1.50E-04	1.16E-03
postsynaptic cytosol (GO:0099524)	30	13	3.54	+	3.67	3.38E-04	2.42E-03
trans-Golgi network transport vesicle (GO:0030140)	32	13	3.77	+	3.44	5.52E-04	3.85E-03
heterotrimeric G-protein complex (GO:0005834)	35	13	4.13	+	3.15	1.08E-03	6.88E-03
postsynaptic specialization, intracellular component (GO:0099091)	38	13	4.48	+	2.9	1.97E-03	1.19E-02
mitochondrial nucleoid (GO:0042645)	46	13	5.43	+	2.4	8.95E-03	4.42E-02
nucleoid (GO:0009295)	46	13	5.43	+	2.4	8.95E-03	4.41E-02
eukaryotic 48S preinitiation complex (GO:0033290)	14	12	1.65	+	7.27	4.33E-06	4.62E-05
COPII vesicle coat (GO:0030127)	15	12	1.77	+	6.78	7.05E-06	7.28E-05
myosin II complex (GO:0016460)	16	12	1.89	+	6.36	1.11E-05	1.12E-04
eukaryotic translation initiation factor 3 complex (GO:0005852)	16	12	1.89	+	6.36	1.11E-05	1.11E-04
clathrin coat of coated pit (GO:0030132)	17	12	2.01	+	5.98	1.72E-05	1.63E-04
anchored component of synaptic vesicle membrane (GO:0098993)	19	12	2.24	+	5.35	3.82E-05	3.36E-04
eukaryotic 43S preinitiation complex (GO:0016282)	20	12	2.36	+	5.09	5.53E-05	4.76E-04
COPI-coated vesicle membrane (GO:0030663)	21	12	2.48	+	4.84	7.86E-05	6.52E-04
platelet alpha granule (GO:0031091)	21	12	2.48	+	4.84	7.86E-05	6.49E-04
clathrin-coated endocytic vesicle (GO:0045334)	25	12	2.95	+	4.07	2.75E-04	2.03E-03
postsynaptic density, intracellular component (GO:0099092)	32	12	3.77	+	3.18	1.56E-03	9.67E-03
proteasome regulatory particle, base subcomplex (GO:0008540)	11	11	1.3	+	8.48	4.11E-06	4.43E-05

fascia adherens (GO:0005916)	14	11	1.65	+	6.66	1.92E-05	1.81E-04
serine-type peptidase complex (GO:1905286)	18	11	2.12	+	5.18	1.00E-04	8.03E-04
serine-type endopeptidase complex (GO:1905370)	18	11	2.12	+	5.18	1.00E-04	8.00E-04
retromer complex (GO:0030904)	19	11	2.24	+	4.91	1.43E-04	1.11E-03
M band (GO:0031430)	22	11	2.59	+	4.24	3.76E-04	2.68E-03
clathrin adaptor complex (GO:0030131)	25	11	2.95	+	3.73	8.66E-04	5.74E-03
Flemming body (GO:0090543)	29	11	3.42	+	3.22	2.24E-03	1.32E-02
ion channel complex (GO:0034702)	281	11	33.14	-	0.33	3.11E-05	2.76E-04
chylomicron (GO:0042627)	11	10	1.3	+	7.71	1.98E-05	1.85E-04
myosin filament (GO:0032982)	14	10	1.65	+	6.06	8.16E-05	6.71E-04
postsynaptic cytoskeleton (GO:0099571)	20	10	2.36	+	4.24	6.91E-04	4.72E-03
myofilament (GO:0036379)	22	10	2.59	+	3.85	1.22E-03	7.72E-03
apicolateral plasma membrane (GO:0016327)	24	10	2.83	+	3.53	2.03E-03	1.22E-02
proton-transporting two-sector ATPase complex, proton-transporting domain (GO:0033177)	25	10	2.95	+	3.39	2.58E-03	1.48E-02
zymogen granule (GO:0042588)	26	10	3.07	+	3.26	3.24E-03	1.82E-02
cytoplasmic dynein complex (GO:0005868)	27	10	3.18	+	3.14	4.03E-03	2.17E-02
proton-transporting V-type ATPase complex (GO:0033176)	29	10	3.42	+	2.92	6.05E-03	3.13E-02
catenin complex (GO:0016342)	30	10	3.54	+	2.83	7.33E-03	3.71E-02
nucleotide-activated protein kinase complex (GO:0031588)	11	9	1.3	+	6.94	9.05E-05	7.39E-04
presynaptic endocytic zone (GO:0098833)	13	9	1.53	+	5.87	2.20E-04	1.68E-03
aminoacyl-tRNA synthetase multienzyme complex (GO:0017101)	13	9	1.53	+	5.87	2.20E-04	1.68E-03
zona pellucida receptor complex (GO:0002199)	13	9	1.53	+	5.87	2.20E-04	1.67E-03
COPI vesicle coat (GO:0030126)	14	9	1.65	+	5.45	3.28E-04	2.36E-03
vacuolar proton-transporting V-type ATPase complex (GO:0016471)	20	9	2.36	+	3.82	2.24E-03	1.32E-02
costamere (GO:0043034)	20	9	2.36	+	3.82	2.24E-03	1.32E-02
microbody lumen (GO:0031907)	22	9	2.59	+	3.47	3.72E-03	2.04E-02
peroxisomal matrix (GO:0005782)	22	9	2.59	+	3.47	3.72E-03	2.03E-02
sperm head (GO:0061827)	26	9	3.07	+	2.93	8.86E-03	4.38E-02
eukaryotic translation initiation factor 3 complex, eIF3m (GO:0071541)	8	8	0.94	+	8.48	8.95E-05	7.33E-04
chaperonin-containing T-complex (GO:0005832)	10	8	1.18	+	6.78	2.51E-04	1.89E-03
endoplasmic reticulum chaperone complex (GO:0034663)	12	8	1.42	+	5.65	5.95E-04	4.12E-03
mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) (GO:0000276)	13	8	1.53	+	5.22	8.73E-04	5.77E-03
insulin-responsive compartment (GO:0032593)	13	8	1.53	+	5.22	8.73E-04	5.75E-03
postsynaptic actin cytoskeleton (GO:0098871)	14	8	1.65	+	4.84	1.25E-03	7.82E-03
clathrin-coated endocytic vesicle membrane (GO:0030669)	14	8	1.65	+	4.84	1.25E-03	7.79E-03
proton-transporting ATP synthase complex, coupling factor F(o) (GO:0045263)	15	8	1.77	+	4.52	1.73E-03	1.06E-02
kinetochore microtubule (GO:0005828)	15	8	1.77	+	4.52	1.73E-03	1.06E-02
messenger ribonucleoprotein complex (GO:1990124)	16	8	1.89	+	4.24	2.36E-03	1.36E-02
tricarboxylic acid cycle enzyme complex (GO:0045239)	17	8	2.01	+	3.99	3.16E-03	1.78E-02
striated muscle thin filament (GO:0005865)	19	8	2.24	+	3.57	5.35E-03	2.83E-02
cation channel complex (GO:0034703)	212	8	25.01	-	0.32	2.41E-04	1.82E-03
cytosolic proteasome complex (GO:0031597)	7	7	0.83	+	8.48	2.53E-04	1.90E-03
membrane attack complex (GO:0005579)	7	7	0.83	+	8.48	2.53E-04	1.89E-03
spherical high-density lipoprotein particle (GO:0034366)	7	7	0.83	+	8.48	2.53E-04	1.88E-03
proteasome core complex, alpha-subunit complex (GO:0019773)	8	7	0.94	+	7.42	4.31E-04	3.05E-03
proteasome regulatory particle, lid subcomplex (GO:0008541)	8	7	0.94	+	7.42	4.31E-04	3.04E-03
presynaptic endocytic zone membrane (GO:0098835)	9	7	1.06	+	6.59	6.97E-04	4.74E-03
Arp2/3 protein complex (GO:0005885)	9	7	1.06	+	6.59	6.97E-04	4.73E-03
cardiac myofibril (GO:0097512)	9	7	1.06	+	6.59	6.97E-04	4.71E-03
blood microparticle (GO:0072562)	10	7	1.18	+	5.93	1.08E-03	6.91E-03
low-density lipoprotein particle (GO:0034362)	10	7	1.18	+	5.93	1.08E-03	6.89E-03
haptoglobin-hemoglobin complex (GO:0031838)	11	7	1.3	+	5.4	1.60E-03	9.88E-03
proton-transporting V-type ATPase, V1 domain (GO:0033180)	12	7	1.42	+	4.95	2.31E-03	1.35E-02
respiratory chain complex III (GO:0045275)	12	7	1.42	+	4.95	2.31E-03	1.34E-02

nucleocytoplasmic transport complex (GO:0031074)	12	7	1.42	+	4.95	2.31E-03	1.34E-02
mitochondrial respiratory chain complex III (GO:0005750)	12	7	1.42	+	4.95	2.31E-03	1.34E-02
proteasome core complex, beta-subunit complex (GO:0019774)	13	7	1.53	+	4.57	3.23E-03	1.82E-02
pseudopodium (GO:0031143)	13	7	1.53	+	4.57	3.23E-03	1.81E-02
cell pole (GO:0060187)	14	7	1.65	+	4.24	4.41E-03	2.34E-02
RISC complex (GO:0016442)	15	7	1.77	+	3.96	5.89E-03	3.06E-02
RNAi effector complex (GO:0031332)	15	7	1.77	+	3.96	5.89E-03	3.05E-02
lamellipodium membrane (GO:0031258)	16	7	1.89	+	3.71	7.71E-03	3.89E-02
fibrinogen complex (GO:0005577)	6	6	0.71	+	8.48	7.21E-04	4.86E-03
proton-transporting ATP synthase complex, catalytic core F(1) (GO:0045261)	7	6	0.83	+	7.27	1.22E-03	7.71E-03
vacuolar proton-transporting V-type ATPase, V1 domain (GO:0000221)	8	6	0.94	+	6.36	1.94E-03	1.18E-02
glycogen granule (GO:0042587)	8	6	0.94	+	6.36	1.94E-03	1.17E-02
cAMP-dependent protein kinase complex (GO:0005952)	9	6	1.06	+	5.65	2.95E-03	1.69E-02
MCM complex (GO:0042555)	9	6	1.06	+	5.65	2.95E-03	1.68E-02
ESCRT III complex (GO:0000815)	10	6	1.18	+	5.09	4.31E-03	2.32E-02
AP-2 adaptor complex (GO:0030122)	10	6	1.18	+	5.09	4.31E-03	2.31E-02
hemoglobin complex (GO:0005833)	10	6	1.18	+	5.09	4.31E-03	2.30E-02
cell tip (GO:0051286)	10	6	1.18	+	5.09	4.31E-03	2.30E-02
ESCRT I complex (GO:0000813)	11	6	1.3	+	4.62	6.07E-03	3.13E-02
clathrin coat of endocytic vesicle (GO:0030128)	11	6	1.3	+	4.62	6.07E-03	3.12E-02
CMG complex (GO:0071162)	11	6	1.3	+	4.62	6.07E-03	3.11E-02
DNA replication preinitiation complex (GO:0031261)	12	6	1.42	+	4.24	8.30E-03	4.15E-02
clathrin coat of trans-Golgi network vesicle (GO:0030130)	12	6	1.42	+	4.24	8.30E-03	4.14E-02
extrinsic component of endosome membrane (GO:0031313)	12	6	1.42	+	4.24	8.30E-03	4.13E-02
mCRD-mediated mRNA stability complex (GO:0106002)	5	5	0.59	+	8.48	2.08E-03	1.24E-02
mitochondrial proton-transporting ATP synthase complex, catalytic sector F(1) (GO:0000275)	6	5	0.71	+	7.07	3.48E-03	1.94E-02
prefoldin complex (GO:0016272)	6	5	0.71	+	7.07	3.48E-03	1.93E-02
sarcoplasmic reticulum lumen (GO:0033018)	6	5	0.71	+	7.07	3.48E-03	1.93E-02
eukaryotic translation initiation factor 2B complex (GO:0005851)	6	5	0.71	+	7.07	3.48E-03	1.92E-02
intermediate-density lipoprotein particle (GO:0034363)	6	5	0.71	+	7.07	3.48E-03	1.92E-02
CRD-mediated mRNA stability complex (GO:0070937)	6	5	0.71	+	7.07	3.48E-03	1.91E-02
spectrin (GO:0008091)	7	5	0.83	+	6.06	5.46E-03	2.87E-02
mitochondrial pyruvate dehydrogenase complex (GO:0005967)	7	5	0.83	+	6.06	5.46E-03	2.86E-02
VCP-NPL4-UFD1 AAA ATPase complex (GO:0034098)	7	5	0.83	+	6.06	5.46E-03	2.86E-02
basal cortex (GO:0045180)	7	5	0.83	+	6.06	5.46E-03	2.85E-02
pyruvate dehydrogenase complex (GO:0045254)	8	5	0.94	+	5.3	8.10E-03	4.06E-02
FAR/SIN/STRIPAK complex (GO:0090443)	4	4	0.47	+	8.48	6.10E-03	3.12E-02
GAIT complex (GO:0097452)	4	4	0.47	+	8.48	6.10E-03	3.11E-02
tubular endosome (GO:0097422)	5	4	0.59	+	6.78	1.01E-02	4.95E-02
BRISC complex (GO:0070552)	5	4	0.59	+	6.78	1.01E-02	4.94E-02
ER membrane insertion complex (GO:0072379)	5	4	0.59	+	6.78	1.01E-02	4.92E-02
CIA complex (GO:0097361)	5	4	0.59	+	6.78	1.01E-02	4.91E-02
MMXD complex (GO:0071817)	5	4	0.59	+	6.78	1.01E-02	4.90E-02
dendritic filopodium (GO:1902737)	5	4	0.59	+	6.78	1.01E-02	4.89E-02
organellar ribosome (GO:0000313)	88	1	10.38	-	0.1	8.63E-04	5.76E-03
mitochondrial ribosome (GO:0005761)	88	1	10.38	-	0.1	8.63E-04	5.74E-03

Table S5. GO terms for molecular function of proteins from cardiac EVs isolated by EVtrap.

Analysis Type:	PANTHER Overrepresentation Test (Released 20220202)						
Annotation Version and Release Date:	GO Ontology database DOI: 10.5281/zenodo.5725227 Released 2020-11-01						
Analyzed List:	upload_1 (Rattus norvegicus)						
Reference List:	Rattus norvegicus (all genes in database)						
Test Type:	FISHER						
Correction:	FDR						
GO molecular function complete	**Rattus norvegicus - REFLIST (21585)**	**upload_1 (2546)**	**upload_1 (expected)**	**upload_1 (over/under)**	**upload_1 (fold Enrichment)**	**upload_1 (raw P-value)**	**upload_1 (FDR)**
molecular_function (GO:0003674)	17083	2315	2014.98	+	1.15	7.2E-53	3.46E-50
binding (GO:0005488)	12729	2042	1501.41	+	1.36	2.93E-104	7.03E-101
protein binding (GO:0005515)	7540	1510	889.36	+	1.7	6.12E-123	2.94E-119
catalytic activity (GO:0003824)	5484	927	646.85	+	1.43	8.86E-31	1.64E-28
ion binding (GO:0043167)	5052	918	595.89	+	1.54	1.78E-41	5.02E-39
organic cyclic compound binding (GO:0097159)	5373	855	633.76	+	1.35	2.36E-20	2.36E-18
heterocyclic compound binding (GO:1901363)	5312	834	626.56	+	1.33	3.19E-18	2.84E-16
enzyme binding (GO:0019899)	2188	593	258.08	+	2.3	1.81E-71	1.73E-68
small molecule binding (GO:0036094)	2391	561	282.02	+	1.99	2.49E-49	9.97E-47
cation binding (GO:0043169)	3389	554	399.74	+	1.39	4.07E-14	2.92E-12
metal ion binding (GO:0046872)	3293	533	388.42	+	1.37	7.95E-13	5.46E-11
identical protein binding (GO:0042802)	2218	514	261.62	+	1.96	2.12E-43	6.79E-41
anion binding (GO:0043168)	2291	511	270.23	+	1.89	4.43E-39	1.06E-36
carbohydrate derivative binding (GO:0097367)	2117	495	249.7	+	1.98	2.02E-42	6.05E-40
nucleoside phosphate binding (GO:1901265)	2036	490	240.15	+	2.04	5.24E-45	1.94E-42
nucleotide binding (GO:0000166)	2036	490	240.15	+	2.04	5.24E-45	1.8E-42
protein-containing complex binding (GO:0044877)	1528	459	180.23	+	2.55	1.18E-64	7.06E-62
purine nucleotide binding (GO:0017076)	1787	432	210.78	+	2.05	1.17E-39	2.95E-37
ribonucleotide binding (GO:0032553)	1791	430	211.25	+	2.04	8.63E-39	1.97E-36
purine ribonucleotide binding (GO:0032555)	1772	425	209.01	+	2.03	2.83E-38	6.17E-36
purine ribonucleoside triphosphate binding (GO:0035639)	1694	404	199.81	+	2.02	8.81E-36	1.84E-33
hydrolase activity (GO:0016787)	2212	395	260.91	+	1.51	1.11E-14	8.17E-13
molecular function regulator (GO:0098772)	1818	359	214.44	+	1.67	6.92E-19	6.52E-17
catalytic activity, acting on a protein (GO:0140096)	2222	358	262.09	+	1.37	2.05E-08	0.000000994
adenyl nucleotide binding (GO:0030554)	1448	330	170.79	+	1.93	5.2E-26	8.06E-24
adenyl ribonucleotide binding (GO:0032559)	1435	323	169.26	+	1.91	1.35E-24	1.97E-22
transferase activity (GO:0016740)	2213	317	261.03	+	1.21	0.000796	0.0162
ATP binding (GO:0005524)	1368	303	161.36	+	1.88	3.75E-22	4.74E-20
cytoskeletal protein binding (GO:0008092)	992	298	117.01	+	2.55	4.98E-41	1.33E-38
RNA binding (GO:0003723)	1251	284	147.56	+	1.92	5.21E-22	6.25E-20
enzyme regulator activity (GO:0030234)	1143	278	134.82	+	2.06	1.88E-25	2.82E-23
signaling receptor binding (GO:0005102)	1614	261	190.37	+	1.37	0.00000206	0.0000793
Unclassified (UNCLASSIFIED)	4502	231	531.02	-	0.44	7.2E-53	3.15E-50
kinase binding (GO:0019900)	833	227	98.25	+	2.31	3.23E-26	5.35E-24
protein kinase binding (GO:0019901)	745	204	87.87	+	2.32	7.88E-24	1.08E-21
protein domain specific binding (GO:0019904)	800	196	94.36	+	2.08	2.91E-18	2.64E-16
protein dimerization activity (GO:0046983)	999	194	117.83	+	1.65	6.56E-10	3.42E-08
structural molecule activity (GO:0005198)	793	183	93.54	+	1.96	5.9E-15	4.57E-13
lipid binding (GO:0008289)	787	181	92.83	+	1.95	1.1E-14	8.22E-13
oxidoreductase activity (GO:0016491)	779	167	91.88	+	1.82	2.05E-11	1.15E-09
transferase activity, transferring phosphorus-containing groups (GO:0016772)	904	160	106.63	+	1.5	0.000004	0.000147
pyrophosphatase activity (GO:0016462)	531	157	62.63	+	2.51	3.86E-21	4.21E-19
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides (GO:0016818)	536	157	63.22	+	2.48	1.01E-20	1.07E-18
hydrolase activity, acting on acid anhydrides (GO:0016817)	536	157	63.22	+	2.48	1.01E-20	1.05E-18
protein homodimerization activity (GO:0042803)	697	155	82.21	+	1.89	8.84E-12	5.37E-10
actin binding (GO:0003779)	421	151	49.66	+	3.04	2.93E-27	5.02E-25
nucleoside-triphosphatase activity (GO:0017111)	476	149	56.15	+	2.65	4.51E-22	5.56E-20
DNA binding (GO:0003677)	2108	141	248.64	-	0.57	1.99E-13	1.4E-11
calcium ion binding (GO:0005509)	667	137	78.67	+	1.74	1.21E-08	0.000000598

kinase activity (GO:0016301)	764	136	90.12	+	1.51	0.0000151	0.0005
phospholipid binding (GO:0005543)	473	119	55.79	+	2.13	3.69E-12	2.33E-10
enzyme activator activity (GO:0008047)	462	118	54.49	+	2.17	2.11E-12	1.37E-10
mRNA binding (GO:0003729)	346	117	40.81	+	2.87	1.35E-19	1.32E-17
guanyl ribonucleotide binding (GO:0032561)	384	116	45.29	+	2.56	1.74E-16	1.49E-14
guanyl nucleotide binding (GO:0019001)	385	116	45.41	+	2.55	1.97E-16	1.66E-14
phosphotransferase activity, alcohol group as acceptor (GO:0016773)	674	116	79.5	+	1.46	0.000249	0.00608
GTP binding (GO:0005525)	360	113	42.46	+	2.66	4.2E-17	3.67E-15
molecular adaptor activity (GO:0060090)	355	108	41.87	+	2.58	1.25E-15	9.99E-14
peptidase activity (GO:0008233)	641	104	75.61	+	1.38	0.00294	0.0496
ATP-dependent activity (GO:0140657)	501	103	59.09	+	1.74	0.000000831	0.0000338
GTPase binding (GO:0051020)	309	101	36.45	+	2.77	2.22E-16	1.84E-14
enzyme inhibitor activity (GO:0004857)	384	101	45.29	+	2.23	2.17E-11	1.2E-09
protein kinase activity (GO:0004672)	564	98	66.53	+	1.47	0.000519	0.0116
GTPase activity (GO:0003924)	302	96	35.62	+	2.69	5.57E-15	4.39E-13
amide binding (GO:0033218)	433	96	51.07	+	1.88	0.00000013	0.00000588
ubiquitin-like protein ligase binding (GO:0044389)	331	95	39.04	+	2.43	1.33E-12	8.89E-11
transcription regulator activity (GO:0140110)	1650	92	194.62	-	0.47	9.6E-16	7.82E-14
actin filament binding (GO:0051015)	221	90	26.07	+	3.45	1.51E-19	1.45E-17
GTPase regulator activity (GO:0030695)	426	90	50.25	+	1.79	0.00000204	0.0000802
nucleoside-triphosphatase regulator activity (GO:0060589)	426	90	50.25	+	1.79	0.00000204	0.0000795
ubiquitin protein ligase binding (GO:0031625)	312	89	36.8	+	2.42	1.04E-11	6.18E-10
small GTPase binding (GO:0031267)	271	88	31.97	+	2.75	2.77E-14	2.01E-12
protein-macromolecule adaptor activity (GO:0030674)	286	86	33.73	+	2.55	1.7E-12	1.12E-10
cell adhesion molecule binding (GO:0050839)	292	85	34.44	+	2.47	1.38E-11	7.92E-10
protein serine/threonine kinase activity (GO:0004674)	413	85	48.71	+	1.74	0.00000833	0.000286
tubulin binding (GO:0015631)	384	82	45.29	+	1.81	0.000004	0.000146
phosphatase binding (GO:0019902)	232	71	27.36	+	2.59	8.6E-11	4.64E-09
peptide binding (GO:0042277)	355	71	41.87	+	1.7	0.000119	0.00336
translation regulator activity (GO:0045182)	141	69	16.63	+	4.15	1.58E-18	1.46E-16
protein C-terminus binding (GO:0008022)	228	67	26.89	+	2.49	1.29E-09	6.65E-08
phosphatidylinositol binding (GO:0035091)	280	66	33.03	+	2	0.00000219	0.0000837
protein serine kinase activity (GO:0106310)	243	64	28.66	+	2.23	9.73E-08	0.00000449
peptidase regulator activity (GO:0061134)	247	64	29.13	+	2.2	0.000000196	0.00000855
sequence-specific DNA binding (GO:0043565)	1468	64	173.15	-	0.37	1.45E-20	1.48E-18
ribonucleoprotein complex binding (GO:0043021)	173	62	20.41	+	3.04	9.44E-12	5.67E-10
double-stranded DNA binding (GO:0003690)	1462	62	172.45	-	0.36	3.25E-21	3.63E-19
protein phosphatase binding (GO:0019903)	184	61	21.7	+	2.81	1.51E-10	7.96E-09
magnesium ion binding (GO:0000287)	220	59	25.95	+	2.27	0.000000198	0.00000859
sulfur compound binding (GO:1901681)	260	59	30.67	+	1.92	0.0000196	0.000639
heat shock protein binding (GO:0031072)	150	58	17.69	+	3.28	2.35E-12	1.5E-10
ligase activity (GO:0016874)	173	55	20.41	+	2.7	3.41E-09	0.000000172
endopeptidase regulator activity (GO:0061135)	221	55	26.07	+	2.11	0.00000408	0.000147
carbohydrate binding (GO:0030246)	262	55	30.9	+	1.78	0.000209	0.00523
translation regulator activity, nucleic acid binding (GO:0090079)	110	54	12.97	+	4.16	7.44E-15	5.67E-13
ATP hydrolysis activity (GO:0016887)	170	53	20.05	+	2.64	1.59E-08	0.000000779
GTPase activator activity (GO:0005096)	217	53	25.6	+	2.07	0.00000865	0.000295
microtubule binding (GO:0008017)	273	53	32.2	+	1.65	0.00141	0.0263
sequence-specific double-stranded DNA binding (GO:1990837)	1374	53	162.07	-	0.33	2.5E-22	3.24E-20
calmodulin binding (GO:0005516)	177	51	20.88	+	2.44	0.000000188	0.00000827
transcription regulatory region nucleic acid binding (GO:0001067)	1329	51	156.76	-	0.33	8.26E-22	9.45E-20
endopeptidase inhibitor activity (GO:0004866)	207	50	24.42	+	2.05	0.0000216	0.0007
peptidase inhibitor activity (GO:0030414)	212	50	25.01	+	2	0.0000412	0.0013
integrin binding (GO:0005178)	147	49	17.34	+	2.83	6.79E-09	0.00000034
chaperone binding (GO:0051087)	112	48	13.21	+	3.63	1.05E-11	6.16E-10
transcription cis-regulatory region binding (GO:0000976)	1324	48	156.17	-	0.31	3.99E-23	5.32E-21
molecular transducer activity (GO:0060089)	2437	48	287.45	-	0.17	2.43E-68	1.94E-65

signaling receptor activity (GO:0038023)	2437	48	287.45	-	0.17	2.43E-68	1.66E-65
kinase regulator activity (GO:0019207)	226	47	26.66	+	1.76	0.000703	0.0147
translation factor activity, RNA binding (GO:0008135)	93	46	10.97	+	4.19	5.87E-13	4.08E-11
glycosaminoglycan binding (GO:0005539)	216	45	25.48	+	1.77	0.00107	0.0211
unfolded protein binding (GO:0051082)	94	44	11.09	+	3.97	7.79E-12	4.86E-10
protease binding (GO:0002020)	148	44	17.46	+	2.52	0.000000669	0.0000277
mRNA 3'-UTR binding (GO:0003730)	96	42	11.32	+	3.71	1.22E-10	6.49E-09
protein N-terminus binding (GO:0047485)	131	41	15.45	+	2.65	0.000000524	0.0000221
isomerase activity (GO:0016853)	168	41	19.82	+	2.07	0.0000946	0.00277
phosphatidylinositol phosphate binding (GO:1901981)	186	41	21.94	+	1.87	0.000666	0.0145
molecular carrier activity (GO:0140104)	72	40	8.49	+	4.71	1.17E-12	7.89E-11
protein kinase regulator activity (GO:0019887)	193	40	22.76	+	1.76	0.0018	0.0322
GDP binding (GO:0019003)	79	39	9.32	+	4.19	3.46E-11	1.89E-09
transmembrane transporter binding (GO:0044325)	149	39	17.57	+	2.22	0.0000365	0.00117
ubiquitin-like protein binding (GO:0032182)	117	38	13.8	+	2.75	0.000000559	0.0000233
primary active transmembrane transporter activity (GO:0015399)	153	37	18.05	+	2.05	0.000208	0.00523
structural constituent of cytoskeleton (GO:0005200)	63	36	7.43	+	4.84	8.41E-12	5.18E-10
ubiquitin binding (GO:0043130)	96	36	11.32	+	3.18	6.04E-08	0.00000285
antioxidant activity (GO:0016209)	88	35	10.38	+	3.37	2.85E-08	0.00000136
ATPase binding (GO:0051117)	99	35	11.68	+	3	0.00000029	0.0000124
SNARE binding (GO:0000149)	121	35	14.27	+	2.45	0.0000172	0.000567
single-stranded DNA binding (GO:0003697)	127	35	14.98	+	2.34	0.0000471	0.00145
signaling receptor regulator activity (GO:0030545)	509	34	60.04	-	0.57	0.000658	0.0144
proton transmembrane transporter activity (GO:0015078)	109	33	12.86	+	2.57	0.0000121	0.000404
calcium-dependent protein binding (GO:0048306)	94	32	11.09	+	2.89	0.00000255	0.0000965
signaling receptor activator activity (GO:0030546)	473	32	55.79	-	0.57	0.00123	0.0238
RNA polymerase II transcription regulatory region sequence-specific DNA binding (GO:0000977)	1227	32	144.73	-	0.22	2.27E-28	4.05E-26
transmembrane signaling receptor activity (GO:0004888)	2249	32	265.27	-	0.12	4.03E-73	4.84E-70
translation initiation factor activity (GO:0003743)	60	31	7.08	+	4.38	1.5E-09	7.67E-08
ribosome binding (GO:0043022)	73	30	8.61	+	3.48	0.000000155	0.00000695
SH3 domain binding (GO:0017124)	111	30	13.09	+	2.29	0.00016	0.00421
single-stranded RNA binding (GO:0003727)	123	30	14.51	+	2.07	0.000808	0.0163
receptor ligand activity (GO:0048018)	464	30	54.73	-	0.55	0.00063	0.0138
electron transfer activity (GO:0009055)	61	29	7.2	+	4.03	0.000000021	0.00000101
cytoskeletal motor activity (GO:0003774)	104	29	12.27	+	2.36	0.000161	0.00422
cis-regulatory region sequence-specific DNA binding (GO:0000987)	1083	29	127.74	-	0.23	1.4E-24	1.98E-22
NAD binding (GO:0051287)	69	28	8.14	+	3.44	0.000000487	0.0000207
exopeptidase activity (GO:0008238)	97	28	11.44	+	2.45	0.000103	0.003
phosphatase regulator activity (GO:0019208)	97	27	11.44	+	2.36	0.000313	0.00748
protein serine/threonine/tyrosine kinase activity (GO:0004712)	99	27	11.68	+	2.31	0.000354	0.00834
metal ion transmembrane transporter activity (GO:0046873)	424	27	50.01	-	0.54	0.00084	0.0169
monosaccharide binding (GO:0048029)	86	26	10.14	+	2.56	0.000137	0.00377
steroid binding (GO:0005496)	101	26	11.91	+	2.18	0.00116	0.0226
protein kinase C binding (GO:0005080)	60	25	7.08	+	3.53	0.00000134	0.0000532
myosin binding (GO:0017022)	74	25	8.73	+	2.86	0.0000415	0.0013
scaffold protein binding (GO:0097110)	85	25	10.03	+	2.49	0.000228	0.00562
rRNA binding (GO:0019843)	88	25	10.38	+	2.41	0.000303	0.00727
RNA polymerase II cis-regulatory region sequence-specific DNA binding (GO:0000978)	1059	25	124.91	-	0.2	3.44E-26	5.52E-24
oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor (GO:0016620)	65	24	7.67	+	3.13	0.0000114	0.000384
oxidoreductase activity, acting on the aldehyde or oxo group of donors (GO:0016903)	76	24	8.96	+	2.68	0.000103	0.00299
oxidoreductase activity, acting on peroxide as acceptor (GO:0016684)	56	23	6.61	+	3.48	0.00000424	0.000152
double-stranded RNA binding (GO:0003725)	77	23	9.08	+	2.53	0.000258	0.00626
protein folding chaperone (GO:0044183)	45	22	5.31	+	4.14	0.000000721	0.0000296
peroxidase activity (GO:0004601)	52	22	6.13	+	3.59	0.00000467	0.000166
Hsp70 protein binding (GO:0030544)	52	22	6.13	+	3.59	0.00000467	0.000165
clathrin binding (GO:0030276)	68	22	8.02	+	2.74	0.000172	0.00448
oxidoreductase activity, acting on NAD(P)H (GO:0016651)	69	22	8.14	+	2.7	0.000192	0.00497

signaling adaptor activity (GO:0035591)	70	22	8.26	+	2.66	0.000217	0.00536
syntaxin binding (GO:0019905)	79	22	9.32	+	2.36	0.000892	0.0178
alcohol binding (GO:0043178)	86	22	10.14	+	2.17	0.00238	0.0406
ADP binding (GO:0043531)	43	21	5.07	+	4.14	0.0000013	0.000052
Hsp90 protein binding (GO:0051879)	49	21	5.78	+	3.63	0.00000652	0.000227
extracellular matrix binding (GO:0050840)	61	21	7.2	+	2.92	0.0000893	0.00265
collagen binding (GO:0005518)	69	21	8.14	+	2.58	0.000405	0.00936
DNA-binding transcription factor activity (GO:0003700)	1212	21	142.96	-	0.15	1.42E-35	2.84E-33
nucleocytoplasmic carrier activity (GO:0140142)	31	20	3.66	+	5.47	8.25E-08	0.00000385
protein kinase A binding (GO:0051018)	54	20	6.37	+	3.14	0.0000575	0.00176
polyubiquitin modification-dependent protein binding (GO:0031593)	55	20	6.49	+	3.08	0.0000707	0.00212
metalloexopeptidase activity (GO:0008235)	66	20	7.78	+	2.57	0.000585	0.013
DNA-binding transcription factor activity, RNA polymerase II-specific (GO:0000981)	1164	20	137.3	-	0.15	2.02E-34	3.88E-32
metal cluster binding (GO:0051540)	61	19	7.2	+	2.64	0.000667	0.0144
iron-sulfur cluster binding (GO:0051536)	61	19	7.2	+	2.64	0.000667	0.0144
aminopeptidase activity (GO:0004177)	34	18	4.01	+	4.49	0.00000309	0.000115
translation initiation factor binding (GO:0031369)	37	18	4.36	+	4.12	0.00000764	0.000264
signal sequence binding (GO:0005048)	45	18	5.31	+	3.39	0.0000602	0.00182
ATPase-coupled cation transmembrane transporter activity (GO:0019829)	48	18	5.66	+	3.18	0.000117	0.00331
sterol binding (GO:0032934)	56	18	6.61	+	2.73	0.000804	0.0163
G protein activity (GO:0003925)	29	17	3.42	+	4.97	0.00000205	0.0000792
lipoprotein particle receptor binding (GO:0070325)	30	17	3.54	+	4.8	0.00000289	0.000108
mRNA 5'-UTR binding (GO:0048027)	32	17	3.77	+	4.5	0.00000558	0.000196
oxidoreduction-driven active transmembrane transporter activity (GO:0015453)	39	17	4.6	+	3.7	0.0000409	0.0013
oxidoreductase activity, acting on a sulfur group of donors (GO:0016667)	55	17	6.49	+	2.62	0.00143	0.0264
oxidoreductase activity, acting on the CH-CH group of donors (GO:0016627)	58	17	6.84	+	2.48	0.00201	0.0352
fatty acid binding (GO:0005504)	59	17	6.96	+	2.44	0.00228	0.0395
disordered domain specific binding (GO:0097718)	39	16	4.6	+	3.48	0.00012	0.00336
quaternary ammonium group binding (GO:0050997)	42	16	4.95	+	3.23	0.000238	0.00584
gated channel activity (GO:0022836)	334	16	39.4	-	0.41	0.0000717	0.00214
poly-purine tract binding (GO:0070717)	31	15	3.66	+	4.1	0.0000454	0.00141
SNAP receptor activity (GO:0005484)	37	15	4.36	+	3.44	0.000216	0.00538
protein phosphatase 2A binding (GO:0051721)	41	15	4.84	+	3.1	0.000522	0.0116
beta-tubulin binding (GO:0048487)	43	15	5.07	+	2.96	0.000781	0.016
cholesterol binding (GO:0015485)	46	15	5.43	+	2.76	0.00137	0.026
ligase activity, forming carbon-oxygen bonds (GO:0016875)	46	15	5.43	+	2.76	0.00137	0.0258
aminoacyl-tRNA ligase activity (GO:0004812)	46	15	5.43	+	2.76	0.00137	0.0257
proton-transporting ATP synthase activity, rotational mechanism (GO:0046933)	17	14	2.01	+	6.98	0.000000949	0.0000383
nuclear import signal receptor activity (GO:0061608)	20	14	2.36	+	5.93	0.00000367	0.000135
proton channel activity (GO:0015252)	23	14	2.71	+	5.16	0.0000118	0.000398
phosphatidylcholine binding (GO:0031210)	30	14	3.54	+	3.96	0.000109	0.00315
protein-lipid complex binding (GO:0071814)	31	14	3.66	+	3.83	0.000144	0.0039
lipoprotein particle binding (GO:0071813)	31	14	3.66	+	3.83	0.000144	0.00388
microfilament motor activity (GO:0000146)	31	14	3.66	+	3.83	0.000144	0.00385
poly-pyrimidine tract binding (GO:0008187)	31	14	3.66	+	3.83	0.000144	0.00383
peptidase activator activity (GO:0016504)	36	14	4.25	+	3.3	0.000487	0.011
4 iron, 4 sulfur cluster binding (GO:0051539)	36	14	4.25	+	3.3	0.000487	0.011
pre-mRNA binding (GO:0036002)	37	14	4.36	+	3.21	0.000607	0.0134
molecular function activator activity (GO:0140677)	38	14	4.48	+	3.12	0.00075	0.0154
cis-trans isomerase activity (GO:0016859)	40	14	4.72	+	2.97	0.00113	0.0221
actinin binding (GO:0042805)	41	14	4.84	+	2.89	0.00137	0.0261
disulfide oxidoreductase activity (GO:0015036)	41	14	4.84	+	2.89	0.00137	0.026
tau protein binding (GO:0048156)	22	13	2.59	+	5.01	0.0000306	0.000986
NADH dehydrogenase activity (GO:0003954)	23	13	2.71	+	4.79	0.0000433	0.00135
low-density lipoprotein particle receptor binding (GO:0050750)	26	13	3.07	+	4.24	0.000112	0.00319
actin monomer binding (GO:0003785)	28	13	3.3	+	3.94	0.000199	0.00512
14-3-3 protein binding (GO:0071889)	33	13	3.89	+	3.34	0.000696	0.0147

oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor (GO:0016655)	33	13	3.89	+	3.34	0.000696	0.0147
peptidyl-prolyl cis-trans isomerase activity (GO:0003755)	36	13	4.25	+	3.06	0.00133	0.0255
DNA-binding transcription activator activity, RNA polymerase II-specific (GO:0001228)	485	13	57.21	-	0.23	1.58E-11	8.91E-10
DNA-binding transcription activator activity (GO:0001216)	491	13	57.91	-	0.22	1.14E-11	6.61E-10
translation elongation factor activity (GO:0003746)	22	12	2.59	+	4.62	0.00011	0.00314
metalloaminopeptidase activity (GO:0070006)	23	12	2.71	+	4.42	0.000151	0.00401
complement binding (GO:0001848)	23	12	2.71	+	4.42	0.000151	0.00399
ATPase activator activity (GO:0001671)	24	12	2.83	+	4.24	0.000205	0.00522
poly(A) binding (GO:0008143)	24	12	2.83	+	4.24	0.000205	0.00519
nuclear localization sequence binding (GO:0008139)	26	12	3.07	+	3.91	0.000363	0.00851
poly(U) RNA binding (GO:0008266)	27	12	3.18	+	3.77	0.000475	0.0108
sterol transporter activity (GO:0015248)	33	12	3.89	+	3.08	0.00192	0.034
proteasome binding (GO:0070628)	19	11	2.24	+	4.91	0.000143	0.00393
NADH dehydrogenase (ubiquinone) activity (GO:0008137)	19	11	2.24	+	4.91	0.000143	0.0039
NADH dehydrogenase (quinone) activity (GO:0050136)	20	11	2.36	+	4.66	0.000201	0.00513
GTPase activating protein binding (GO:0032794)	21	11	2.48	+	4.44	0.000277	0.00668
NAD(P)H dehydrogenase (quinone) activity (GO:0003955)	22	11	2.59	+	4.24	0.000376	0.00872
nitric-oxide synthase binding (GO:0050998)	23	11	2.71	+	4.05	0.000503	0.0113
oxygen binding (GO:0019825)	27	11	3.18	+	3.45	0.00142	0.0265
fatty acid derivative binding (GO:1901567)	28	11	3.3	+	3.33	0.0018	0.0322
ankyrin binding (GO:0030506)	21	10	2.48	+	4.04	0.000924	0.0183
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (GO:0016705)	218	10	25.71	-	0.39	0.00108	0.0213
lipase inhibitor activity (GO:0055102)	14	9	1.65	+	5.45	0.000328	0.00777
ATPase-coupled ion transmembrane transporter activity (GO:0042625)	16	9	1.89	+	4.77	0.000675	0.0145
proton-transporting ATPase activity, rotational mechanism (GO:0046961)	16	9	1.89	+	4.77	0.000675	0.0144
ATPase activity, coupled to transmembrane movement of ions, rotational mechanism (GO:0044769)	16	9	1.89	+	4.77	0.000675	0.0143
pyrophosphate hydrolysis-driven proton transmembrane transporter activity (GO:0009678)	18	9	2.12	+	4.24	0.00127	0.0246
clathrin adaptor activity (GO:0035615)	19	9	2.24	+	4.02	0.0017	0.0309
cargo adaptor activity (GO:0140312)	20	9	2.36	+	3.82	0.00224	0.039
structural constituent of muscle (GO:0008307)	21	9	2.48	+	3.63	0.00291	0.0492
oxygen carrier activity (GO:0005344)	13	8	1.53	+	5.22	0.000873	0.0175
1-phosphatidylinositol binding (GO:0005545)	14	8	1.65	+	4.84	0.00125	0.0241
threonine-type endopeptidase activity (GO:0004298)	15	8	1.77	+	4.52	0.00173	0.0313
protein kinase A catalytic subunit binding (GO:0034236)	15	8	1.77	+	4.52	0.00173	0.0312
opsonin binding (GO:0001846)	16	8	1.89	+	4.24	0.00236	0.0408
S100 protein binding (GO:0044548)	16	8	1.89	+	4.24	0.00236	0.0407
sequence-specific mRNA binding (GO:1990825)	16	8	1.89	+	4.24	0.00236	0.0406
RNA cap binding (GO:0000339)	16	8	1.89	+	4.24	0.00236	0.0404
DNA-binding transcription repressor activity, RNA polymerase II-specific (GO:0001227)	300	8	35.39	-	0.23	0.000000179	0.00000795
DNA-binding transcription repressor activity (GO:0001217)	302	8	35.62	-	0.22	0.000000126	0.00000577
G protein-coupled receptor activity (GO:0004930)	1781	8	210.07	-	0.04	2.43E-76	3.89E-73
AMP-activated protein kinase activity (GO:0004679)	8	7	0.94	+	7.42	0.000431	0.00991
GDP-dissociation inhibitor binding (GO:0051021)	8	7	0.94	+	7.42	0.000431	0.00986
peroxiredoxin activity (GO:0051920)	9	7	1.06	+	6.59	0.000697	0.0146
ubiquitin-like modifier activating enzyme activity (GO:0008641)	11	7	1.3	+	5.4	0.0016	0.0293
profilin binding (GO:0005522)	11	7	1.3	+	5.4	0.0016	0.0292
cytokine activity (GO:0005125)	197	7	23.24	-	0.3	0.000324	0.0077
RNA strand annealing activity (GO:0033592)	6	6	0.71	+	8.48	0.000721	0.0149
proteasome-activating activity (GO:0036402)	6	6	0.71	+	8.48	0.000721	0.0149
nitric-oxide synthase regulator activity (GO:0030235)	8	6	0.94	+	6.36	0.00194	0.0344
thioredoxin peroxidase activity (GO:0008379)	8	6	0.94	+	6.36	0.00194	0.0342
phosphatidylcholine-sterol O-acyltransferase activator activity (GO:0060228)	5	5	0.59	+	8.48	0.00208	0.0363
voltage-gated cation channel activity (GO:0022843)	145	5	17.1	-	0.29	0.00192	0.0341
G protein-coupled peptide receptor activity (GO:0008528)	147	5	17.34	-	0.29	0.00138	0.0258
peptide receptor activity (GO:0001653)	156	5	18.4	-	0.27	0.000716	0.0149
methylation-dependent protein binding (GO:0140034)	116	3	13.68	-	0.22	0.00154	0.0284
methylated histone binding (GO:0035064)	116	3	13.68	-	0.22	0.00154	0.0283

immune receptor activity (GO:0140375)	132	3	15.57	-	0.19	0.000375	0.00874
cytokine receptor activity (GO:0004896)	95	2	11.21	-	0.18	0.00256	0.0435
potassium channel activity (GO:0005267)	126	2	14.86	-	0.13	0.000134	0.00372
pheromone receptor activity (GO:0016503)	94	0	11.09	-	< 0.01	0.000058	0.00176
steroid hydroxylase activity (GO:0008395)	64	0	7.55	-	< 0.01	0.00158	0.029
odorant binding (GO:0005549)	440	0	51.9	-	< 0.01	6.71E-22	7.87E-20
olfactory receptor activity (GO:0004984)	1208	0	142.49	-	< 0.01	1.54E-60	8.24E-58
voltage-gated potassium channel activity (GO:0005249)	91	0	10.73	-	< 0.01	0.0000911	0.00268

Table S6. GO terms for biological process of proteins from cardiac EVs isolated by EVtrap.

Analysis Type:	PANTHER Overrepresentation Test (Released 20220202)						
Annotation Version and Release Date:	GO Ontology database DOI: 10.5281/zenodo.5725227 Released 2020-11-01						
Analyzed List:	upload_1 (Rattus norvegicus)						
Reference List:	Rattus norvegicus (all genes in database)						
Test Type:	FISHER						
Correction:	FDR						
GO biological process complete	**Rattus norvegicus - REFLIST (21585**	**upload_1 (2546)**	**upload_1 (expected)**	**upload_1 (over/under**	**upload_1 (fold Enrichment**	**upload_1 (raw P-value**	**upload_1 (FDR)**
biological_process (GO:0008150)	18177	2434	2144.02	+	1.14	7.46E-68	5.94E-64
cellular process (GO:0009987)	15611	2222	1841.35	+	1.21	2.51E-67	9.99E-64
biological regulation (GO:0065007)	12849	1739	1515.57	+	1.15	5.01E-18	5.91E-16
regulation of biological process (GO:0050789)	12133	1634	1431.12	+	1.14	1.02E-14	7.44E-13
regulation of cellular process (GO:0050794)	11676	1552	1377.21	+	1.13	4.2E-11	2.12E-09
metabolic process (GO:0008152)	7887	1347	930.29	+	1.45	2.03E-56	3.6E-53
response to stimulus (GO:0050896)	8829	1287	1041.4	+	1.24	2.08E-20	2.89E-18
organic substance metabolic process (GO:0071704)	7433	1241	876.74	+	1.42	1.89E-44	1.12E-41
cellular metabolic process (GO:0044237)	6945	1218	819.18	+	1.49	7.05E-54	8.03E-51
primary metabolic process (GO:0044238)	6836	1149	806.32	+	1.42	9.87E-41	4.25E-38
nitrogen compound metabolic process (GO:0006807)	6306	1081	743.81	+	1.45	8.82E-41	3.9E-38
positive regulation of biological process (GO:0048518)	6361	1079	750.29	+	1.44	9.21E-39	3.41E-36
cellular component organization or biogenesis (GO:0071840)	5336	1052	629.39	+	1.67	1.52E-66	4.85E-63
multicellular organismal process (GO:0032501)	7482	1041	882.52	+	1.18	8.03E-10	3.51E-08
cellular component organization (GO:0016043)	5114	1030	603.21	+	1.71	3.36E-69	5.35E-65
positive regulation of cellular process (GO:0048522)	5879	992	693.44	+	1.43	1.7E-33	4.83E-31
developmental process (GO:0032502)	5777	990	681.41	+	1.45	5.94E-36	1.97E-33
regulation of metabolic process (GO:0019222)	6466	981	762.68	+	1.29	3.13E-18	3.75E-16
cellular response to stimulus (GO:0051716)	7182	961	847.13	+	1.13	0.00000754	0.000171
localization (GO:0051179)	5035	946	593.89	+	1.59	6.61E-49	5.01E-46
macromolecule metabolic process (GO:0043170)	5749	941	678.11	+	1.39	6.93E-27	1.43E-24
negative regulation of biological process (GO:0048519)	5324	924	627.98	+	1.47	1.42E-34	4.19E-32
organonitrogen compound metabolic process (GO:1901564)	4889	922	576.67	+	1.6	8.56E-48	5.68E-45
anatomical structure development (GO:0048856)	5299	919	625.03	+	1.47	2.83E-34	8.19E-32
regulation of macromolecule metabolic process (GO:0060255)	5972	897	704.41	+	1.27	4.49E-15	3.41E-13
regulation of cellular metabolic process (GO:0031323)	5771	887	680.7	+	1.3	2.7E-17	2.84E-15
negative regulation of cellular process (GO:0048523)	4885	854	576.2	+	1.48	3.88E-32	1.03E-29
multicellular organism development (GO:0007275)	4880	848	575.61	+	1.47	5E-31	1.29E-28
regulation of primary metabolic process (GO:0080090)	5574	848	657.47	+	1.29	2.55E-15	2.01E-13
response to chemical (GO:0042221)	5377	828	634.23	+	1.31	4.61E-16	4.04E-14
regulation of nitrogen compound metabolic process (GO:0051171)	5401	815	637.06	+	1.28	8.3E-14	5.58E-12
system development (GO:0048731)	4546	800	536.21	+	1.49	2.01E-30	4.92E-28
regulation of biological quality (GO:0065008)	3945	792	465.32	+	1.7	1.5E-48	1.09E-45
establishment of localization (GO:0051234)	3778	755	445.62	+	1.69	5.25E-45	3.22E-42
cellular macromolecule metabolic process (GO:0044260)	4374	755	515.92	+	1.46	4.03E-26	7.93E-24
transport (GO:0006810)	3617	729	426.63	+	1.71	3E-44	1.71E-41
protein metabolic process (GO:0019538)	3942	719	464.97	+	1.55	6.74E-31	1.7E-28
response to organic substance (GO:0010033)	3303	682	389.6	+	1.75	5.6E-44	3.08E-41
organelle organization (GO:0006996)	3136	676	369.9	+	1.83	2.59E-49	2.06E-46
response to stress (GO:0006950)	3386	675	399.39	+	1.69	4.48E-39	1.7E-36
regulation of response to stimulus (GO:0048583)	3902	661	460.25	+	1.44	1.93E-20	2.7E-18
animal organ development (GO:0048513)	3598	631	424.39	+	1.49	1.47E-22	2.47E-20
regulation of localization (GO:0032879)	2978	620	351.26	+	1.77	2.15E-40	9.02E-38
cellular developmental process (GO:0048869)	3553	619	419.08	+	1.48	1.79E-21	2.71E-19
positive regulation of metabolic process (GO:0009893)	3809	618	449.28	+	1.38	2.78E-15	2.14E-13
regulation of molecular function (GO:0065009)	2972	617	350.55	+	1.76	8.54E-40	3.49E-37

regulation of gene expression (GO:0010468)	4572	614	539.28	+	1.14	0.000757	0.0104
cell differentiation (GO:0030154)	3505	608	413.42	+	1.47	1.19E-20	1.69E-18
cellular protein metabolic process (GO:0044267)	3303	606	389.6	+	1.56	8.98E-26	1.72E-23
signaling (GO:0023052)	5567	589	656.64	-	0.9	0.00363	0.0385
cellular response to chemical stimulus (GO:0070887)	2858	574	337.11	+	1.7	4.55E-33	1.25E-30
cellular localization (GO:0051641)	2326	565	274.36	+	2.06	7.29E-54	7.75E-51
regulation of signaling (GO:0023051)	3352	563	395.38	+	1.42	2.18E-16	1.97E-14
positive regulation of macromolecule metabolic process (GO:0010604)	3493	559	412.01	+	1.36	9.52E-13	5.66E-11
regulation of cell communication (GO:0010646)	3339	558	393.84	+	1.42	7.9E-16	6.69E-14
cellular nitrogen compound metabolic process (GO:0034641)	3080	554	363.29	+	1.52	1.44E-21	2.22E-19
regulation of protein metabolic process (GO:0051246)	2581	552	304.43	+	1.81	3.67E-38	1.27E-35
signal transduction (GO:0007165)	5248	551	619.01	-	0.89	0.00277	0.0312
cellular component biogenesis (GO:0044085)	2513	546	296.41	+	1.84	2.49E-39	9.9E-37
regulation of cellular component organization (GO:0051128)	2417	544	285.09	+	1.91	5.42E-43	2.7E-40
positive regulation of cellular metabolic process (GO:0031325)	3316	538	391.13	+	1.38	3.99E-13	2.48E-11
macromolecule localization (GO:0033036)	2227	537	262.68	+	2.04	4.77E-50	4.23E-47
regulation of biosynthetic process (GO:0009889)	3943	527	465.09	+	1.13	0.00327	0.0355
cellular component assembly (GO:0022607)	2257	518	266.22	+	1.95	8.81E-43	4.25E-40
regulation of cellular protein metabolic process (GO:0032268)	2408	515	284.03	+	1.81	2.76E-35	8.98E-33
negative regulation of metabolic process (GO:0009892)	2973	505	350.67	+	1.44	2.71E-15	2.1E-13
regulation of catalytic activity (GO:0050790)	2263	504	266.93	+	1.89	2.41E-38	8.52E-36
positive regulation of nitrogen compound metabolic process (GO:0051173)	3090	498	364.47	+	1.37	1.12E-11	6.11E-10
regulation of multicellular organismal process (GO:0051239)	2829	483	333.69	+	1.45	6.57E-15	4.89E-13
regulation of signal transduction (GO:0009966)	2897	482	341.71	+	1.41	2.91E-13	1.84E-11
protein localization (GO:0008104)	1835	472	216.44	+	2.18	6.45E-50	5.41E-47
cellular response to organic substance (GO:0071310)	2249	464	265.27	+	1.75	2.36E-28	5.23E-26
response to oxygen-containing compound (GO:1901700)	2046	452	241.33	+	1.87	2.26E-33	6.31E-31
negative regulation of macromolecule metabolic process (GO:0010605)	2754	450	324.84	+	1.39	2.8E-11	1.46E-09
organic cyclic compound metabolic process (GO:1901360)	2717	448	320.48	+	1.4	9.32E-12	5.15E-10
establishment of localization in cell (GO:0051649)	1653	443	194.98	+	2.27	1.73E-50	1.62E-47
response to external stimulus (GO:0009605)	2603	435	307.03	+	1.42	3.96E-12	2.27E-10
regulation of developmental process (GO:0050793)	2554	432	301.25	+	1.43	8.68E-13	5.2E-11
negative regulation of cellular metabolic process (GO:0031324)	2533	431	298.77	+	1.44	4.53E-13	2.81E-11
biosynthetic process (GO:0009058)	2325	427	274.24	+	1.56	1.24E-17	1.39E-15
nervous system development (GO:0007399)	2361	418	278.49	+	1.5	5.62E-15	4.22E-13
organic substance transport (GO:0071702)	1777	416	209.6	+	1.98	3.27E-35	1.04E-32
regulation of transport (GO:0051049)	1965	416	231.78	+	1.79	2.94E-27	6.24E-25
organic substance biosynthetic process (GO:1901576)	2263	416	266.93	+	1.56	2.97E-17	3.01E-15
cellular aromatic compound metabolic process (GO:0006725)	2487	413	293.35	+	1.41	3.47E-11	1.78E-09
catabolic process (GO:0009056)	1822	403	214.91	+	1.88	1.14E-29	2.7E-27
heterocycle metabolic process (GO:0046483)	2424	403	285.92	+	1.41	5.15E-11	2.55E-09
cellular biosynthetic process (GO:0044249)	2202	401	259.73	+	1.54	4.99E-16	4.34E-14
negative regulation of nitrogen compound metabolic process (GO:0051172)	2375	401	280.14	+	1.43	9.21E-12	5.11E-10
macromolecule modification (GO:0043412)	2733	400	322.36	+	1.24	0.0000252	0.000514
response to endogenous stimulus (GO:0009719)	1694	395	199.81	+	1.98	4.92E-33	1.33E-30
positive regulation of response to stimulus (GO:0048584)	2247	392	265.04	+	1.48	3.34E-13	2.09E-11
anatomical structure morphogenesis (GO:0009653)	2283	390	269.29	+	1.45	5.16E-12	2.94E-10
intracellular transport (GO:0046907)	1280	386	150.98	+	2.56	6.2E-54	7.59E-51
cellular protein modification process (GO:0006464)	2540	385	299.6	+	1.29	0.00000195	0.0000501
protein modification process (GO:0036211)	2540	385	299.6	+	1.29	0.00000195	0.00005
nucleobase-containing compound metabolic process (GO:0006139)	2275	383	268.34	+	1.43	4.69E-11	2.36E-09
cellular macromolecule localization (GO:0070727)	1390	376	163.95	+	2.29	3.62E-43	1.86E-40
cellular protein localization (GO:0034613)	1380	375	162.77	+	2.3	1.97E-43	1.05E-40
nitrogen compound transport (GO:0071705)	1425	370	168.08	+	2.2	3.27E-39	1.27E-36

immune system process (GO:0002376)	2122	358	250.29	+	1.43	1.9E-10	8.84E-09
regulation of cell death (GO:0010941)	1730	355	204.06	+	1.74	4E-21	5.96E-19
cellular catabolic process (GO:0044248)	1564	354	184.48	+	1.92	1.86E-27	4.06E-25
organic substance catabolic process (GO:1901575)	1574	351	185.66	+	1.89	3.15E-26	6.28E-24
cell development (GO:0048468)	1829	349	215.73	+	1.62	1.76E-16	1.6E-14
phosphorus metabolic process (GO:0006793)	1794	347	211.61	+	1.64	3.89E-17	3.82E-15
phosphate-containing compound metabolic process (GO:0006796)	1777	345	209.6	+	1.65	2.92E-17	3E-15
establishment of protein localization (GO:0045184)	1138	344	134.23	+	2.56	4.56E-48	3.16E-45
response to nitrogen compound (GO:1901698)	1406	343	165.84	+	2.07	1.32E-31	3.45E-29
gene expression (GO:0010467)	2040	343	240.62	+	1.43	7.04E-10	3.11E-08
small molecule metabolic process (GO:0044281)	1531	334	180.58	+	1.85	1.69E-23	3E-21
vesicle-mediated transport (GO:0016192)	1255	328	148.03	+	2.22	5.61E-35	1.72E-32
regulation of intracellular signal transduction (GO:1902531)	1656	327	195.33	+	1.67	2.93E-17	2.99E-15
tissue development (GO:0009888)	1774	327	209.25	+	1.56	1.08E-13	7.23E-12
response to organonitrogen compound (GO:0010243)	1316	325	155.23	+	2.09	8.15E-31	2.03E-28
protein transport (GO:0015031)	1039	324	122.55	+	2.64	1.54E-47	9.79E-45
protein-containing complex subunit organization (GO:0043933)	1318	321	155.46	+	2.06	1.59E-29	3.72E-27
response to abiotic stimulus (GO:0009628)	1421	320	167.61	+	1.91	2E-24	3.61E-22
positive regulation of molecular function (GO:0044093)	1527	319	180.11	+	1.77	6.1E-20	8.1E-18
cytoskeleton organization (GO:0007010)	1147	317	135.29	+	2.34	1.04E-37	3.54E-35
positive regulation of protein metabolic process (GO:0051247)	1519	316	179.17	+	1.76	2.05E-19	2.66E-17
positive regulation of signaling (GO:0023056)	1801	313	212.43	+	1.47	2.01E-10	9.3E-09
regulation of programmed cell death (GO:0043067)	1555	310	183.42	+	1.69	7.62E-17	7.31E-15
response to organic cyclic compound (GO:0014070)	1323	309	156.05	+	1.98	1.01E-25	1.92E-23
positive regulation of cell communication (GO:0010647)	1794	308	211.61	+	1.46	9.67E-10	4.14E-08
homeostatic process (GO:0042592)	1721	305	203	+	1.5	5.29E-11	2.61E-09
regulation of apoptotic process (GO:0042981)	1526	304	180	+	1.69	1.62E-16	1.49E-14
negative regulation of response to stimulus (GO:0048585)	1637	303	193.09	+	1.57	7.75E-13	4.7E-11
cellular response to stress (GO:0033554)	1567	299	184.83	+	1.62	3.71E-14	2.59E-12
positive regulation of cellular protein metabolic process (GO:0032270)	1435	295	169.26	+	1.74	1.64E-17	1.78E-15
positive regulation of biosynthetic process (GO:0009891)	2064	295	243.45	+	1.21	0.00148	0.0185
regulation of organelle organization (GO:0033043)	1147	292	135.29	+	2.16	2.15E-29	4.96E-27
regulation of protein modification process (GO:0031399)	1564	291	184.48	+	1.58	1.47E-12	8.63E-11
cellular response to oxygen-containing compound (GO:1901701)	1277	289	150.63	+	1.92	2.47E-22	4.05E-20
positive regulation of cellular biosynthetic process (GO:0031328)	2015	288	237.67	+	1.21	0.00169	0.0204
biological process involved in interspecies interaction between organisms (GO:0044419)	1533	285	180.82	+	1.58	2.88E-12	1.67E-10
positive regulation of cellular component organization (GO:0051130)	1166	283	137.53	+	2.06	1.12E-25	2.11E-23
neurogenesis (GO:0022008)	1572	282	185.42	+	1.52	9.43E-11	4.57E-09
cellular nitrogen compound biosynthetic process (GO:0044271)	1272	280	150.04	+	1.87	3.85E-20	5.24E-18
regulation of response to stress (GO:0080134)	1321	279	155.81	+	1.79	6.37E-18	7.41E-16
regulation of phosphate metabolic process (GO:0019220)	1441	278	169.97	+	1.64	1.2E-13	7.98E-12
regulation of phosphorus metabolic process (GO:0051174)	1442	278	170.09	+	1.63	1.24E-13	8.14E-12
protein-containing complex assembly (GO:0065003)	1146	276	135.17	+	2.04	1.22E-24	2.24E-22
organonitrogen compound biosynthetic process (GO:1901566)	1285	276	151.57	+	1.82	1.23E-18	1.5E-16
movement of cell or subcellular component (GO:0006928)	1469	275	173.27	+	1.59	3.5E-12	2.01E-10
response to hormone (GO:0009725)	1084	274	127.86	+	2.14	3.02E-27	6.32E-25
positive regulation of multicellular organismal process (GO:0051240)	1625	274	191.67	+	1.43	3.77E-08	0.00000128
cellular response to endogenous stimulus (GO:0071495)	1265	273	149.21	+	1.83	1.47E-18	1.77E-16
intracellular signal transduction (GO:0035556)	1378	271	162.54	+	1.67	3.86E-14	2.66E-12
positive regulation of signal transduction (GO:0009967)	1579	271	186.25	+	1.46	1.27E-08	0.000000468
negative regulation of protein metabolic process (GO:0051248)	1078	269	127.15	+	2.12	6.27E-26	1.22E-23
regulation of cell population proliferation (GO:0042127)	1746	265	205.94	+	1.29	0.000108	0.0019
system process (GO:0003008)	2816	265	332.15	-	0.8	0.000126	0.00218
regulation of catabolic process (GO:0009894)	941	258	110.99	+	2.32	5.02E-30	1.21E-27

positive regulation of transport (GO:0051050)	1096	258	129.28	+	2	8.24E-22	1.31E-19
reproductive process (GO:0022414)	1656	256	195.33	+	1.31	0.0000451	0.000867
reproduction (GO:0000003)	1659	256	195.68	+	1.31	0.0000538	0.00101
negative regulation of molecular function (GO:0044092)	1142	253	134.7	+	1.88	1.43E-18	1.74E-16
proteolysis (GO:0006508)	1255	251	148.03	+	1.7	8.66E-14	5.79E-12
generation of neurons (GO:0048699)	1417	251	167.14	+	1.5	3.89E-09	0.000000154
response to biotic stimulus (GO:0009607)	1442	251	170.09	+	1.48	1.36E-08	0.0000005
regulation of protein localization (GO:0032880)	962	250	113.47	+	2.2	2.92E-26	5.9E-24
regulation of cellular component biogenesis (GO:0044087)	984	250	116.07	+	2.15	4.19E-25	7.76E-23
response to lipid (GO:0033993)	1205	250	142.13	+	1.76	2.78E-15	2.15E-13
regulation of cell differentiation (GO:0045595)	1627	250	191.91	+	1.3	0.0000764	0.00139
negative regulation of cellular protein metabolic process (GO:0032269)	1016	249	119.84	+	2.08	3.46E-23	6.06E-21
positive regulation of developmental process (GO:0051094)	1454	248	171.5	+	1.45	9.43E-08	0.00000304
response to other organism (GO:0051707)	1398	247	164.9	+	1.5	6.57E-09	0.000000251
response to external biotic stimulus (GO:0043207)	1402	247	165.37	+	1.49	7.02E-09	0.000000266
regulation of hydrolase activity (GO:0051336)	1023	243	120.67	+	2.01	4.25E-21	6.27E-19
negative regulation of cell death (GO:0060548)	1116	243	131.63	+	1.85	4.62E-17	4.52E-15
regulation of cellular localization (GO:0060341)	899	242	106.04	+	2.28	2.67E-27	5.75E-25
regulation of cellular component movement (GO:0051270)	1115	241	131.52	+	1.83	1.38E-16	1.28E-14
regulation of phosphorylation (GO:0042325)	1291	241	152.28	+	1.58	1.23E-10	5.83E-09
negative regulation of cell communication (GO:0010648)	1376	241	162.3	+	1.48	1.77E-08	0.000000635
negative regulation of signaling (GO:0023057)	1379	241	162.66	+	1.48	2.28E-08	0.000000807
positive regulation of gene expression (GO:0010628)	1211	233	142.84	+	1.63	1.96E-11	1.05E-09
macromolecule biosynthetic process (GO:0009059)	1367	232	161.24	+	1.44	0.000000321	0.00000955
regulation of immune system process (GO:0002682)	1479	232	174.45	+	1.33	0.0000514	0.000975
cell projection organization (GO:0030030)	1196	230	141.07	+	1.63	2.77E-11	1.45E-09
cellular macromolecule biosynthetic process (GO:0034645)	1353	230	159.59	+	1.44	0.00000035	0.0000104
regulation of locomotion (GO:0040012)	1082	229	127.62	+	1.79	6.8E-15	5.04E-13
regulation of multicellular organismal development (GO:2000026)	1462	229	172.45	+	1.33	0.0000563	0.00105
organonitrogen compound catabolic process (GO:1901565)	1019	228	120.19	+	1.9	3.73E-17	3.72E-15
positive regulation of catalytic activity (GO:0043085)	1121	227	132.22	+	1.72	5.33E-13	3.28E-11
intracellular protein transport (GO:0006886)	653	226	77.02	+	2.93	2.19E-38	7.93E-36
negative regulation of signal transduction (GO:0009968)	1247	225	147.09	+	1.53	6.57E-09	0.000000251
regulation of anatomical structure morphogenesis (GO:0022603)	983	224	115.95	+	1.93	1.17E-17	1.31E-15
regulation of cell motility (GO:2000145)	1034	221	121.96	+	1.81	8.41E-15	6.15E-13
chemical homeostasis (GO:0048878)	1248	221	147.2	+	1.5	3.82E-08	0.0000013
regulation of cellular catabolic process (GO:0031329)	788	220	92.95	+	2.37	1.56E-26	3.19E-24
central nervous system development (GO:0007417)	1195	220	140.95	+	1.56	2.52E-09	0.000000102
plasma membrane bounded cell projection organization (GO:0120036)	1156	216	136.35	+	1.58	1.11E-09	4.69E-08
macromolecule catabolic process (GO:0009057)	917	214	108.16	+	1.98	9.05E-18	1.03E-15
locomotion (GO:0040011)	1247	214	147.09	+	1.45	0.000000505	0.0000145
cellular amide metabolic process (GO:0043603)	880	213	103.8	+	2.05	2.43E-19	3.1E-17
defense response (GO:0006952)	1263	211	148.97	+	1.42	0.00000331	0.0000815
regulation of cell migration (GO:0030334)	977	210	115.24	+	1.82	2.44E-14	1.73E-12
negative regulation of programmed cell death (GO:0043069)	989	210	116.65	+	1.8	6.99E-14	4.72E-12
circulatory system development (GO:0072359)	956	209	112.76	+	1.85	6.4E-15	4.79E-13
regulation of protein phosphorylation (GO:0001932)	1138	209	134.23	+	1.56	7.58E-09	0.000000286
regulation of transcription by RNA polymerase II (GO:0006357)	2393	209	282.26	-	0.74	0.0000058	0.000136
actin filament-based process (GO:0030029)	590	205	69.59	+	2.95	3.54E-35	1.11E-32
response to inorganic substance (GO:0010035)	767	205	90.47	+	2.27	7.9E-23	1.35E-20
negative regulation of apoptotic process (GO:0043066)	967	205	114.06	+	1.8	1.67E-13	1.08E-11
organic acid metabolic process (GO:0006082)	872	202	102.85	+	1.96	1.25E-16	1.18E-14
positive regulation of intracellular signal transduction (GO:1902533)	1027	201	121.14	+	1.66	1.75E-10	8.25E-09
cellular protein-containing complex assembly (GO:0034622)	781	199	92.12	+	2.16	4.35E-20	5.82E-18

membrane organization (GO:0061024)	762	198	89.88	+	2.2	6.5E-21	9.49E-19
oxoacid metabolic process (GO:0043436)	844	197	99.55	+	1.98	1.6E-16	1.48E-14
negative regulation of catalytic activity (GO:0043086)	768	196	90.59	+	2.16	6.17E-20	8.13E-18
carboxylic acid metabolic process (GO:0019752)	828	196	97.66	+	2.01	5.66E-17	5.5E-15
actin cytoskeleton organization (GO:0030036)	537	193	63.34	+	3.05	9.38E-35	2.82E-32
regulation of proteolysis (GO:0030162)	787	193	92.83	+	2.08	4.3E-18	5.12E-16
negative regulation of multicellular organismal process (GO:0051241)	1111	191	131.04	+	1.46	0.00000207	0.0000529
neuron differentiation (GO:0030182)	1140	191	134.47	+	1.42	0.00000812	0.000183
cellular response to nitrogen compound (GO:1901699)	780	190	92	+	2.07	1.93E-17	2.05E-15
immune response (GO:0006955)	1259	190	148.5	+	1.28	0.00147	0.0184
cellular macromolecule catabolic process (GO:0044265)	819	189	96.6	+	1.96	1.87E-15	1.5E-13
localization of cell (GO:0051674)	1045	188	123.26	+	1.53	0.00000019	0.00000586
cell motility (GO:0048870)	1045	188	123.26	+	1.53	0.00000019	0.00000585
epithelium development (GO:0060429)	1121	186	132.22	+	1.41	0.0000195	0.000413
negative regulation of cellular component organization (GO:0051129)	716	185	84.45	+	2.19	2.35E-19	3.02E-17
head development (GO:0060322)	993	185	117.13	+	1.58	2.53E-08	0.00000089
response to cytokine (GO:0034097)	936	184	110.4	+	1.67	7.19E-10	3.17E-08
organophosphate metabolic process (GO:0019637)	812	180	95.78	+	1.88	1.95E-13	1.26E-11
protein localization to organelle (GO:0033365)	690	179	81.39	+	2.2	7.13E-19	8.94E-17
regulation of cell projection organization (GO:0031344)	763	179	90	+	1.99	3.04E-15	2.33E-13
positive regulation of protein modification process (GO:0031401)	1030	179	121.49	+	1.47	0.00000234	0.0000593
regulation of vesicle-mediated transport (GO:0060627)	629	178	74.19	+	2.4	4.28E-22	6.89E-20
regulation of response to external stimulus (GO:0032101)	933	177	110.05	+	1.61	1.77E-08	0.000000635
brain development (GO:0007420)	940	177	110.88	+	1.6	2.63E-08	0.000000923
multi-organism reproductive process (GO:0044703)	1140	176	134.47	+	1.31	0.000878	0.0118
supramolecular fiber organization (GO:0097435)	520	175	61.34	+	2.85	9.1E-29	2.07E-26
protein catabolic process (GO:0030163)	706	175	83.27	+	2.1	7.6E-17	7.34E-15
regulation of plasma membrane bounded cell projection organization (GO:0120035)	745	175	87.87	+	1.99	5.61E-15	4.24E-13
cell migration (GO:0016477)	890	175	104.98	+	1.67	1.93E-09	7.96E-08
cellular response to organonitrogen compound (GO:0071417)	710	174	83.75	+	2.08	2.31E-16	2.08E-14
cell cycle (GO:0007049)	853	174	100.61	+	1.73	1.84E-10	8.57E-09
anatomical structure formation involved in morphogenesis (GO:0048646)	947	174	111.7	+	1.56	0.000000151	0.00000471
phosphorylation (GO:0016310)	957	174	112.88	+	1.54	0.000000291	0.00000873
carbohydrate derivative metabolic process (GO:1901135)	881	173	103.92	+	1.66	2.96E-09	0.000000119
neuron development (GO:0048666)	917	173	108.16	+	1.6	3.27E-08	0.00000112
regulation of cell cycle (GO:0051726)	1028	173	121.25	+	1.43	0.0000211	0.000441
peptide metabolic process (GO:0006518)	633	172	74.66	+	2.3	7.93E-20	1.04E-17
lipid metabolic process (GO:0006629)	1152	172	135.88	+	1.27	0.00371	0.0392
regulation of transferase activity (GO:0051338)	869	170	102.5	+	1.66	4.5E-09	0.000000176
negative regulation of gene expression (GO:0010629)	916	170	108.04	+	1.57	0.000000127	0.00000402
positive regulation of phosphorus metabolic process (GO:0010562)	941	170	110.99	+	1.53	0.000000522	0.0000149
positive regulation of phosphate metabolic process (GO:0045937)	941	170	110.99	+	1.53	0.000000522	0.0000149
tube development (GO:0035295)	978	170	115.36	+	1.47	0.00000438	0.000105
developmental process involved in reproduction (GO:0003006)	1111	168	131.04	+	1.28	0.00272	0.0307
response to xenobiotic stimulus (GO:0009410)	694	167	81.86	+	2.04	4.26E-15	3.24E-13
regulation of cytoskeleton organization (GO:0051493)	539	165	63.58	+	2.6	1.64E-23	2.94E-21
cellular homeostasis (GO:0019725)	931	165	109.81	+	1.5	0.0000021	0.0000533
positive regulation of cell population proliferation (GO:0008284)	1028	164	121.25	+	1.35	0.00034	0.00518
cell death (GO:0008219)	797	161	94.01	+	1.71	1.97E-09	8.12E-08
cellular response to cytokine stimulus (GO:0071345)	799	160	94.24	+	1.7	3.92E-09	0.000000155
positive regulation of cellular component movement (GO:0051272)	629	159	74.19	+	2.14	5.92E-16	5.12E-14
positive regulation of locomotion (GO:0040017)	631	159	74.43	+	2.14	6.6E-16	5.68E-14
response to peptide (GO:1901652)	630	158	74.31	+	2.13	1.06E-15	8.82E-14
amide biosynthetic process (GO:0043604)	605	157	71.36	+	2.2	1.1E-16	1.05E-14

cellular protein catabolic process (GO:0044257)	647	157	76.32	+	2.06	1.44E-14	1.04E-12
neuron projection development (GO:0031175)	744	156	87.76	+	1.78	3.11E-10	1.41E-08
regulation of cell adhesion (GO:0030155)	774	156	91.3	+	1.71	4.45E-09	0.000000175
positive regulation of cell motility (GO:2000147)	612	155	72.19	+	2.15	1.1E-15	9.16E-14
positive regulation of cell differentiation (GO:0045597)	950	155	112.05	+	1.38	0.000202	0.00329
response to wounding (GO:0009611)	489	154	57.68	+	2.67	5.56E-23	9.63E-21
programmed cell death (GO:0012501)	757	154	89.29	+	1.72	3.09E-09	0.000000124
microtubule-based process (GO:0007017)	785	154	92.59	+	1.66	2.66E-08	0.00000093
negative regulation of developmental process (GO:0051093)	979	154	115.48	+	1.33	0.00105	0.0139
cell morphogenesis (GO:0000902)	764	153	90.12	+	1.7	7.19E-09	0.000000272
biological adhesion (GO:0022610)	811	153	95.66	+	1.6	0.000000242	0.00000731
apoptotic process (GO:0006915)	718	152	84.69	+	1.79	3.17E-10	1.43E-08
organelle assembly (GO:0070925)	756	152	89.17	+	1.7	8.04E-09	0.000000301
cell cycle process (GO:0022402)	771	152	90.94	+	1.67	2.09E-08	0.000000738
cell adhesion (GO:0007155)	800	152	94.36	+	1.61	0.000000157	0.00000487
proteolysis involved in cellular protein catabolic process (GO:0051603)	618	151	72.89	+	2.07	3.82E-14	2.64E-12
positive regulation of immune system process (GO:0002684)	959	151	113.12	+	1.33	0.00112	0.0147
organelle localization (GO:0051640)	489	150	57.68	+	2.6	1.56E-21	2.38E-19
positive regulation of cell migration (GO:0030335)	585	150	69	+	2.17	1.27E-15	1.04E-13
organic cyclic compound biosynthetic process (GO:1901362)	810	150	95.54	+	1.57	0.000000734	0.0000203
regulation of establishment of protein localization (GO:0070201)	610	149	71.95	+	2.07	4.48E-14	3.06E-12
defense response to other organism (GO:0098542)	893	149	105.33	+	1.41	0.000107	0.00189
regulation of cellular response to stress (GO:0080135)	694	148	81.86	+	1.81	3.48E-10	1.56E-08
regulation of secretion (GO:0051046)	786	148	92.71	+	1.6	0.000000385	0.0000114
positive regulation of phosphorylation (GO:0042327)	853	148	100.61	+	1.47	0.0000198	0.000417
posttranscriptional regulation of gene expression (GO:0010608)	486	147	57.32	+	2.56	1.33E-20	1.88E-18
regulation of anatomical structure size (GO:0090066)	570	147	67.23	+	2.19	1.6E-15	1.3E-13
heart development (GO:0007507)	621	147	73.25	+	2.01	6.17E-13	3.76E-11
regulation of immune response (GO:0050776)	901	147	106.28	+	1.38	0.000311	0.00479
response to extracellular stimulus (GO:0009991)	750	146	88.46	+	1.65	8.69E-08	0.00000281
nucleobase-containing small molecule metabolic process (GO:0055086)	475	145	56.03	+	2.59	1.09E-20	1.56E-18
positive regulation of protein localization (GO:1903829)	517	143	60.98	+	2.34	2.8E-17	2.93E-15
muscle structure development (GO:0061061)	517	143	60.98	+	2.34	2.8E-17	2.91E-15
cellular component morphogenesis (GO:0032989)	637	143	75.14	+	1.9	3.14E-11	1.61E-09
cellular lipid metabolic process (GO:0044255)	916	143	108.04	+	1.32	0.0021	0.0247
positive regulation of cellular component biogenesis (GO:0044089)	532	141	62.75	+	2.25	9.49E-16	7.95E-14
response to peptide hormone (GO:0043434)	537	141	63.34	+	2.23	1.98E-15	1.58E-13
response to nutrient levels (GO:0031667)	718	141	84.69	+	1.66	8.91E-08	0.00000288
cellular chemical homeostasis (GO:0055082)	841	141	99.2	+	1.42	0.000159	0.00268
regulation of cellular amide metabolic process (GO:0034248)	438	140	51.66	+	2.71	2.22E-21	3.34E-19
peptide biosynthetic process (GO:0043043)	496	140	58.5	+	2.39	1.87E-17	2E-15
regulation of protein transport (GO:0051223)	584	140	68.88	+	2.03	8.7E-13	5.19E-11
cellular response to hormone stimulus (GO:0032870)	605	140	71.36	+	1.96	1E-11	5.49E-10
generation of precursor metabolites and energy (GO:0006091)	352	139	41.52	+	3.35	1.82E-28	4.09E-26
response to growth factor (GO:0070848)	586	139	69.12	+	2.01	2.17E-12	1.27E-10
cellular response to organic cyclic compound (GO:0071407)	650	139	76.67	+	1.81	1.32E-09	5.56E-08
translation (GO:0006412)	478	138	56.38	+	2.45	5.53E-18	6.48E-16
localization within membrane (GO:0051668)	532	138	62.75	+	2.2	1.12E-14	8.1E-13
regulation of growth (GO:0040008)	688	138	81.15	+	1.7	4.88E-08	0.00000164
regulation of kinase activity (GO:0043549)	755	138	89.05	+	1.55	0.00000379	0.0000924
endomembrane system organization (GO:0010256)	462	137	54.49	+	2.51	1.02E-18	1.26E-16
modification-dependent protein catabolic process (GO:0019941)	538	137	63.46	+	2.16	4.02E-14	2.76E-12
modification-dependent macromolecule catabolic process (GO:0043632)	549	137	64.76	+	2.12	1.21E-13	8.03E-12
positive regulation of catabolic process (GO:0009896)	505	136	59.57	+	2.28	1.5E-15	1.23E-13

mitotic cell cycle (GO:0000278)	561	136	66.17	+	2.06	1.18E-12	6.97E-11
positive regulation of organelle organization (GO:0010638)	519	135	61.22	+	2.21	1.53E-14	1.1E-12
heterocycle biosynthetic process (GO:0018130)	683	135	80.56	+	1.68	0.000000117	0.00000374
regulation of secretion by cell (GO:1903530)	702	135	82.8	+	1.63	0.00000054	0.0000153
regulation of MAPK cascade (GO:0043408)	721	135	85.04	+	1.59	0.00000174	0.0000452
positive regulation of protein phosphorylation (GO:0001934)	771	135	90.94	+	1.48	0.0000337	0.000663
regulation of actin filament-based process (GO:0032970)	406	134	47.89	+	2.8	1.33E-21	2.08E-19
regulation of protein-containing complex assembly (GO:0043254)	418	134	49.3	+	2.72	1.02E-20	1.48E-18
ubiquitin-dependent protein catabolic process (GO:0006511)	524	134	61.81	+	2.17	5.4E-14	3.66E-12
positive regulation of cell death (GO:0010942)	697	133	82.21	+	1.62	0.000000891	0.0000242
regulation of supramolecular fiber organization (GO:1902903)	382	131	45.06	+	2.91	3.68E-22	5.97E-20
aromatic compound biosynthetic process (GO:0019438)	689	131	81.27	+	1.61	0.00000138	0.0000366
ion homeostasis (GO:0050801)	829	131	97.78	+	1.34	0.0022	0.0257
chordate embryonic development (GO:0043009)	811	130	95.66	+	1.36	0.00137	0.0173
embryo development ending in birth or egg hatching (GO:0009792)	827	130	97.55	+	1.33	0.00259	0.0294
nucleoside phosphate metabolic process (GO:0006753)	418	129	49.3	+	2.62	8.77E-19	1.09E-16
cellular response to growth factor stimulus (GO:0071363)	546	129	64.4	+	2	2.14E-11	1.14E-09
regulation of system process (GO:0044057)	648	129	76.43	+	1.69	0.0000002	0.00000613
nucleotide metabolic process (GO:0009117)	408	128	48.12	+	2.66	3.65E-19	4.62E-17
response to oxidative stress (GO:0006979)	453	127	53.43	+	2.38	8.61E-16	7.26E-14
response to metal ion (GO:0010038)	520	127	61.34	+	2.07	4.8E-12	2.74E-10
regulation of neuron projection development (GO:0010975)	555	127	65.46	+	1.94	1.61E-10	7.6E-09
positive regulation of hydrolase activity (GO:0051345)	560	127	66.05	+	1.92	2.82E-10	1.29E-08
regulation of translation (GO:0006417)	380	126	44.82	+	2.81	2.09E-20	2.87E-18
monocarboxylic acid metabolic process (GO:0032787)	532	126	62.75	+	2.01	2.95E-11	1.52E-09
negative regulation of protein modification process (GO:0031400)	528	125	62.28	+	2.01	3.87E-11	1.97E-09
nervous system process (GO:0050877)	2263	123	266.93	-	0.46	1.16E-22	1.96E-20
protein localization to membrane (GO:0072657)	466	122	54.97	+	2.22	2.19E-13	1.39E-11
regulation of cell development (GO:0060284)	597	122	70.42	+	1.73	0.00000013	0.00000411
regulation of cell cycle process (GO:0010564)	669	122	78.91	+	1.55	0.0000162	0.000348
regulation of protein catabolic process (GO:0042176)	399	121	47.06	+	2.57	2.89E-17	2.99E-15
cell junction organization (GO:0034330)	532	121	62.75	+	1.93	5.71E-10	2.53E-08
nucleobase-containing compound biosynthetic process (GO:0034654)	613	121	72.3	+	1.67	0.000000654	0.0000184
cellular response to lipid (GO:0071396)	630	121	74.31	+	1.63	0.0000022	0.0000558
regulation of protein kinase activity (GO:0045859)	634	119	74.78	+	1.59	0.00000735	0.000167
tube morphogenesis (GO:0035239)	698	119	82.33	+	1.45	0.000256	0.00406
negative regulation of transport (GO:0051051)	521	118	61.45	+	1.92	1.28E-09	5.39E-08
regulation of ion transport (GO:0043269)	754	118	88.94	+	1.33	0.00491	0.0494
positive regulation of cellular catabolic process (GO:0031331)	437	117	51.55	+	2.27	1.99E-13	1.28E-11
circulatory system process (GO:0003013)	472	117	55.67	+	2.1	1.41E-11	7.54E-10
endocytosis (GO:0006897)	478	117	56.38	+	2.08	2.9E-11	1.5E-09
gland development (GO:0048732)	614	117	72.42	+	1.62	0.0000041	0.0000994
positive regulation of apoptotic process (GO:0043065)	610	116	71.95	+	1.61	0.00000508	0.00012
positive regulation of programmed cell death (GO:0043068)	621	116	73.25	+	1.58	0.0000106	0.000236
protein phosphorylation (GO:0006468)	716	116	84.45	+	1.37	0.00188	0.0226
regulation of actin cytoskeleton organization (GO:0032956)	359	115	42.34	+	2.72	8.87E-18	1.02E-15
positive regulation of cell projection organization (GO:0031346)	443	115	52.25	+	2.2	1.42E-12	8.35E-11
negative regulation of intracellular signal transduction (GO:1902532)	538	115	63.46	+	1.81	3.15E-08	0.00000108
innate immune response (GO:0045087)	641	115	75.61	+	1.52	0.0000529	0.000997
cell activation (GO:0001775)	653	115	77.02	+	1.49	0.000125	0.00217
purine-containing compound metabolic process (GO:0072521)	357	114	42.11	+	2.71	1.4E-17	1.54E-15
aging (GO:0007568)	464	114	54.73	+	2.08	3.93E-11	1.99E-09
response to oxygen levels (GO:0070482)	479	114	56.5	+	2.02	1.87E-10	8.71E-09
regulation of peptidase activity (GO:0052547)	485	114	57.21	+	1.99	3.6E-10	1.61E-08

regulation of cellular component size (GO:0032535)	400	113	47.18	+	2.4	2.07E-14	1.48E-12
ribose phosphate metabolic process (GO:0019693)	346	112	40.81	+	2.74	9.71E-18	1.1E-15
regulation of body fluid levels (GO:0050878)	396	112	46.71	+	2.4	2.66E-14	1.87E-12
Unclassified (UNCLASSIFIED)	3408	112	401.98	-	0.28	7.46E-68	3.96E-64
blood circulation (GO:0008015)	442	111	52.13	+	2.13	2.29E-11	1.21E-09
negative regulation of phosphorus metabolic process (GO:0010563)	449	111	52.96	+	2.1	5.07E-11	2.53E-09
negative regulation of phosphate metabolic process (GO:0045936)	449	111	52.96	+	2.1	5.07E-11	2.52E-09
wound healing (GO:0042060)	338	110	39.87	+	2.76	1.57E-17	1.71E-15
regulation of intracellular transport (GO:0032386)	366	110	43.17	+	2.55	1.51E-15	1.23E-13
epithelial cell differentiation (GO:0030855)	589	110	69.47	+	1.58	0.0000195	0.000413
regulation of transmembrane transport (GO:0034762)	604	110	71.24	+	1.54	0.0000539	0.00101
mitotic cell cycle process (GO:1903047)	482	109	56.85	+	1.92	5.77E-09	0.000000222
cell morphogenesis involved in differentiation (GO:0000904)	590	109	69.59	+	1.57	0.0000341	0.000671
purine nucleotide metabolic process (GO:0006163)	331	108	39.04	+	2.77	2.98E-17	3.01E-15
regulation of endopeptidase activity (GO:0052548)	462	108	54.49	+	1.98	1.3E-09	5.49E-08
ribonucleotide metabolic process (GO:0009259)	335	107	39.51	+	2.71	1.06E-16	1.01E-14
regulation of defense response (GO:0031347)	604	107	71.24	+	1.5	0.000151	0.00257
microtubule cytoskeleton organization (GO:0000226)	523	106	61.69	+	1.72	0.00000132	0.0000352
cell part morphogenesis (GO:0032990)	539	106	63.58	+	1.67	0.00000352	0.0000865
establishment of organelle localization (GO:0051656)	348	105	41.05	+	2.56	7.24E-15	5.32E-13
response to steroid hormone (GO:0048545)	449	105	52.96	+	1.98	2.65E-09	0.000000107
Golgi vesicle transport (GO:0048193)	263	104	31.02	+	3.35	1.26E-21	1.99E-19
regulation of cell morphogenesis (GO:0022604)	331	103	39.04	+	2.64	1.76E-15	1.41E-13
regulation of apoptotic signaling pathway (GO:2001233)	406	103	47.89	+	2.15	7.11E-11	3.46E-09
organophosphate biosynthetic process (GO:0090407)	445	103	52.49	+	1.96	5.4E-09	0.000000209
purine ribonucleotide metabolic process (GO:0009150)	316	102	37.27	+	2.74	3.79E-16	3.38E-14
establishment of protein localization to organelle (GO:0072594)	327	102	38.57	+	2.64	2.22E-15	1.76E-13
positive regulation of establishment of protein localization (GO:1904951)	364	102	42.93	+	2.38	7.75E-13	4.68E-11
response to decreased oxygen levels (GO:0036293)	438	102	51.66	+	1.97	6.25E-09	0.00000024
positive regulation of cell adhesion (GO:0045785)	477	102	56.26	+	1.81	0.000000219	0.00000668
non-membrane-bounded organelle assembly (GO:0140694)	336	101	39.63	+	2.55	1.97E-14	1.41E-12
negative regulation of hydrolase activity (GO:0051346)	389	101	45.88	+	2.2	4.73E-11	2.37E-09
cell projection morphogenesis (GO:0048858)	512	101	60.39	+	1.67	0.00000531	0.000125
secretion (GO:0046903)	536	101	63.22	+	1.6	0.0000347	0.000681
positive regulation of transferase activity (GO:0051347)	562	101	66.29	+	1.52	0.000148	0.00253
energy derivation by oxidation of organic compounds (GO:0015980)	232	99	27.36	+	3.62	1.56E-22	2.59E-20
regulation of protein stability (GO:0031647)	303	99	35.74	+	2.77	4.55E-16	4E-14
cellular response to peptide (GO:1901653)	389	99	45.88	+	2.16	1.36E-10	6.43E-09
response to hypoxia (GO:0001666)	417	99	49.19	+	2.01	4.28E-09	0.000000168
vasculature development (GO:0001944)	537	99	63.34	+	1.56	0.0000804	0.00146
reproductive structure development (GO:0048608)	555	99	65.46	+	1.51	0.000224	0.00359
reproductive system development (GO:0061458)	560	99	66.05	+	1.5	0.000303	0.00468
muscle cell differentiation (GO:0042692)	291	98	34.32	+	2.86	1.26E-16	1.18E-14
plasma membrane bounded cell projection morphogenesis (GO:0120039)	507	98	59.8	+	1.64	0.0000161	0.000347
negative regulation of proteolysis (GO:0045861)	377	97	44.47	+	2.18	1.82E-10	8.52E-09
blood vessel development (GO:0001568)	504	97	59.45	+	1.63	0.0000206	0.000432
muscle tissue development (GO:0060537)	357	96	42.11	+	2.28	2.22E-11	1.18E-09
positive regulation of proteolysis (GO:0045862)	379	96	44.7	+	2.15	3.37E-10	1.52E-08
regulation of cell growth (GO:0001558)	442	96	52.13	+	1.84	0.000000251	0.00000758
mitochondrion organization (GO:0007005)	449	96	52.96	+	1.81	0.000000448	0.000013
enzyme linked receptor protein signaling pathway (GO:0007167)	578	96	68.18	+	1.41	0.00223	0.0261
positive regulation of immune response (GO:0050778)	584	96	68.88	+	1.39	0.00289	0.0321
regulation of actin filament organization (GO:0110053)	270	95	31.85	+	2.98	3.82E-17	3.78E-15
cellular response to abiotic stimulus (GO:0071214)	379	95	44.7	+	2.13	8.33E-10	3.63E-08

cellular response to environmental stimulus (GO:0104004)	379	95	44.7	+	2.13	8.33E-10	3.62E-08
striated muscle tissue development (GO:0014706)	335	94	39.51	+	2.38	5.39E-12	3.06E-10
positive regulation of protein transport (GO:0051222)	348	94	41.05	+	2.29	3.63E-11	1.85E-09
carbohydrate metabolic process (GO:0005975)	442	94	52.13	+	1.8	0.000000754	0.0000208
neuron projection morphogenesis (GO:0048812)	501	94	59.09	+	1.59	0.0000628	0.00116
actin filament organization (GO:0007015)	268	93	31.61	+	2.94	2.66E-16	2.39E-14
positive regulation of secretion (GO:0051047)	424	93	50.01	+	1.86	0.00000031	0.00000924
cell-cell adhesion (GO:0098609)	471	93	55.56	+	1.67	0.000015	0.000324
mRNA metabolic process (GO:0016071)	513	93	60.51	+	1.54	0.000217	0.0035
vesicle organization (GO:0016050)	262	92	30.9	+	2.98	1.34E-16	1.24E-14
negative regulation of catabolic process (GO:0009895)	319	92	37.63	+	2.45	3.17E-12	1.83E-10
in utero embryonic development (GO:0001701)	518	92	61.1	+	1.51	0.000491	0.00714
ribonucleoprotein complex biogenesis (GO:0022613)	481	91	56.74	+	1.6	0.0000788	0.00143
response to radiation (GO:0009314)	531	91	62.63	+	1.45	0.00145	0.0181
negative regulation of phosphorylation (GO:0042326)	392	90	46.24	+	1.95	7.46E-08	0.00000245
developmental growth (GO:0048589)	481	90	56.74	+	1.59	0.000105	0.00186
growth (GO:0040007)	485	90	57.21	+	1.57	0.000146	0.0025
cell division (GO:0051301)	365	89	43.05	+	2.07	7.31E-09	0.000000276
carbohydrate derivative biosynthetic process (GO:1901137)	492	89	58.03	+	1.53	0.000356	0.00539
proteasomal protein catabolic process (GO:0010498)	362	88	42.7	+	2.06	1.01E-08	0.000000374
cellular response to external stimulus (GO:0071496)	397	88	46.83	+	1.88	0.000000428	0.0000125
positive regulation of MAPK cascade (GO:0043410)	525	88	61.92	+	1.42	0.00269	0.0304
ATP metabolic process (GO:0046034)	225	87	26.54	+	3.28	7.98E-18	9.21E-16
negative regulation of organelle organization (GO:0010639)	345	87	40.69	+	2.14	2.86E-09	0.000000115
response to ketone (GO:1901654)	365	87	43.05	+	2.02	2.74E-08	0.000000952
positive regulation of response to external stimulus (GO:0032103)	440	87	51.9	+	1.68	0.0000283	0.000568
forebrain development (GO:0030900)	490	87	57.8	+	1.51	0.000589	0.00839
striated muscle cell differentiation (GO:0051146)	224	86	26.42	+	3.25	1.74E-17	1.88E-15
positive regulation of cell development (GO:0010720)	375	86	44.23	+	1.94	0.000000143	0.00000447
regulation of metal ion transport (GO:0010959)	448	86	52.84	+	1.63	0.0000624	0.00116
positive regulation of secretion by cell (GO:1903532)	369	85	43.52	+	1.95	0.000000169	0.00000525
regulation of ion transmembrane transport (GO:0034765)	501	85	59.09	+	1.44	0.00265	0.03
response to mechanical stimulus (GO:0009612)	321	84	37.86	+	2.22	1.32E-09	5.55E-08
regulation of cellular protein catabolic process (GO:1903362)	257	83	30.31	+	2.74	1.94E-13	1.26E-11
cellular response to peptide hormone stimulus (GO:0071375)	314	83	37.04	+	2.24	9.61E-10	4.13E-08
small molecule biosynthetic process (GO:0044283)	409	83	48.24	+	1.72	0.0000152	0.000329
protein folding (GO:0006457)	181	82	21.35	+	3.84	3.9E-20	5.26E-18
regeneration (GO:0031099)	276	82	32.55	+	2.52	1.31E-11	7.07E-10
negative regulation of response to external stimulus (GO:0032102)	387	82	45.65	+	1.8	0.00000441	0.000106
response to alcohol (GO:0097305)	412	82	48.6	+	1.69	0.0000312	0.00062
export from cell (GO:0140352)	435	82	51.31	+	1.6	0.00016	0.00268
inflammatory response (GO:0006954)	447	82	52.72	+	1.56	0.000425	0.00629
response to molecule of bacterial origin (GO:0002237)	461	82	54.38	+	1.51	0.000863	0.0117
response to insulin (GO:0032868)	291	81	34.32	+	2.36	2.19E-10	1.01E-08
cellular response to chemical stress (GO:0062197)	317	81	37.39	+	2.17	7.71E-09	0.00000029
response to reactive oxygen species (GO:0000302)	240	80	28.31	+	2.83	1.3E-13	8.55E-12
regulation of mRNA metabolic process (GO:1903311)	298	80	35.15	+	2.28	1.06E-09	4.54E-08
fatty acid metabolic process (GO:0006631)	352	80	41.52	+	1.93	0.000000506	0.0000145
regulation of developmental growth (GO:0048638)	394	80	46.47	+	1.72	0.0000212	0.000442
regulation of binding (GO:0051098)	397	80	46.83	+	1.71	0.0000304	0.000608
response to lipopolysaccharide (GO:0032496)	442	80	52.13	+	1.53	0.000673	0.00941
regulation of neurogenesis (GO:0050767)	444	80	52.37	+	1.53	0.000699	0.0097
organic hydroxy compound metabolic process (GO:1901615)	465	80	54.85	+	1.46	0.00235	0.027
muscle system process (GO:0003012)	271	79	31.97	+	2.47	5.44E-11	2.67E-09

regulation of GTPase activity (GO:0043087)	350	79	41.28	+	1.91	0.000000997	0.0000268
regulation of DNA metabolic process (GO:0051052)	422	79	49.78	+	1.59	0.000295	0.00457
cell morphogenesis involved in neuron differentiation (GO:0048667)	460	79	54.26	+	1.46	0.0028	0.0315
regulation of mitotic cell cycle (GO:0007346)	466	79	54.97	+	1.44	0.00372	0.0391
regulation of cell-substrate adhesion (GO:0010810)	232	78	27.36	+	2.85	1.99E-13	1.27E-11
negative regulation of cellular catabolic process (GO:0031330)	253	78	29.84	+	2.61	7E-12	3.92E-10
response to carbohydrate (GO:0009743)	277	78	32.67	+	2.39	2.73E-10	1.25E-08
regulation of small molecule metabolic process (GO:0062012)	366	78	43.17	+	1.81	0.00000727	0.000166
axon development (GO:0061564)	414	78	48.83	+	1.6	0.00026	0.00412
regulation of protein polymerization (GO:0032271)	206	77	24.3	+	3.17	2.69E-15	2.1E-13
regulation of lipid metabolic process (GO:0019216)	368	77	43.41	+	1.77	0.0000156	0.000335
immune effector process (GO:0002252)	412	77	48.6	+	1.58	0.000338	0.00516
endosomal transport (GO:0016197)	206	76	24.3	+	3.13	7.11E-15	5.24E-13
response to nutrient (GO:0007584)	307	76	36.21	+	2.1	5.35E-08	0.00000179
negative regulation of protein phosphorylation (GO:0001933)	347	76	40.93	+	1.86	0.00000427	0.000103
cellular respiration (GO:0045333)	174	75	20.52	+	3.65	1.37E-17	1.52E-15
synapse organization (GO:0050808)	324	75	38.22	+	1.96	0.000000635	0.0000179
regulation of cation transmembrane transport (GO:1904062)	380	75	44.82	+	1.67	0.000105	0.00186
secretion by cell (GO:0032940)	386	75	45.53	+	1.65	0.00016	0.00269
blood vessel morphogenesis (GO:0048514)	401	75	47.3	+	1.59	0.00038	0.0057
protein localization to cell periphery (GO:1990778)	259	74	30.55	+	2.42	4.38E-10	1.96E-08
small molecule catabolic process (GO:0044282)	328	74	38.69	+	1.91	0.00000169	0.000044
regulation of proteolysis involved in cellular protein catabolic process (GO:1903050)	222	73	26.19	+	2.79	2.57E-12	1.49E-10
sulfur compound metabolic process (GO:0006790)	327	73	38.57	+	1.89	0.00000338	0.000083
rhythmic process (GO:0048511)	336	73	39.63	+	1.84	0.00000675	0.000155
muscle cell development (GO:0055001)	177	72	20.88	+	3.45	6.77E-16	5.77E-14
nucleotide biosynthetic process (GO:0009165)	199	71	23.47	+	3.02	2.75E-13	1.75E-11
nucleoside phosphate biosynthetic process (GO:1901293)	203	71	23.94	+	2.97	4.91E-13	3.03E-11
regulation of muscle system process (GO:0090257)	259	71	30.55	+	2.32	4.22E-09	0.000000167
negative regulation of peptidase activity (GO:0010466)	284	71	33.5	+	2.12	0.000000114	0.00000366
regulation of angiogenesis (GO:0045765)	298	71	35.15	+	2.02	0.000000531	0.0000151
regulation of vasculature development (GO:1901342)	302	71	35.62	+	1.99	0.000000931	0.0000252
positive regulation of growth (GO:0045927)	306	71	36.09	+	1.97	0.00000116	0.0000309
proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)	319	71	37.63	+	1.89	0.00000574	0.000135
response to corticosteroid (GO:0031960)	320	71	37.74	+	1.88	0.00000589	0.000138
regulation of protein serine/threonine kinase activity (GO:0071900)	364	71	42.93	+	1.65	0.000197	0.00322
cardiac muscle tissue development (GO:0048738)	185	70	21.82	+	3.21	3.04E-14	2.13E-12
protein stabilization (GO:0050821)	187	70	22.06	+	3.17	4.64E-14	3.16E-12
nuclear transport (GO:0051169)	232	70	27.36	+	2.56	1.79E-10	8.4E-09
response to toxic substance (GO:0009636)	296	70	34.91	+	2	0.000000776	0.0000214
regulation of epithelial cell proliferation (GO:0050678)	376	70	44.35	+	1.58	0.000771	0.0106
nucleocytoplasmic transport (GO:0006913)	231	69	27.25	+	2.53	4.94E-10	0.000000022
small GTPase mediated signal transduction (GO:0007264)	237	69	27.95	+	2.47	8.75E-10	3.79E-08
regulation of endocytosis (GO:0030100)	237	69	27.95	+	2.47	8.75E-10	3.78E-08
negative regulation of endopeptidase activity (GO:0010951)	279	69	32.91	+	2.1	0.000000234	0.00000712
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	374	69	44.11	+	1.56	0.00099	0.0132
positive regulation of protein kinase activity (GO:0045860)	396	69	46.71	+	1.48	0.00366	0.0388
regulation of neuron death (GO:1901214)	397	69	46.83	+	1.47	0.00372	0.0391
positive regulation of cellular amide metabolic process (GO:0034250)	183	68	21.59	+	3.15	1.41E-13	9.21E-12
ribonucleoprotein complex subunit organization (GO:0071826)	229	68	27.01	+	2.52	7.61E-10	3.34E-08
regulation of intracellular protein transport (GO:0033157)	254	68	29.96	+	2.27	2.31E-08	0.000000814
negative regulation of cellular component movement (GO:0051271)	321	68	37.86	+	1.8	0.0000281	0.000566
aerobic respiration (GO:0009060)	144	67	16.99	+	3.94	3.65E-17	3.66E-15
positive regulation of cytoskeleton organization (GO:0051495)	209	67	24.65	+	2.72	6.8E-11	3.33E-09

positive regulation of intracellular transport (GO:0032388)	217	67	25.6	+	2.62	2.81E-10	1.28E-08
response to temperature stimulus (GO:0009266)	238	67	28.07	+	2.39	5.04E-09	0.000000196
cellular component disassembly (GO:0022411)	264	67	31.14	+	2.15	0.000000176	0.00000546
negative regulation of locomotion (GO:0040013)	348	67	41.05	+	1.63	0.000487	0.0071
positive regulation of protein-containing complex assembly (GO:0031334)	206	66	24.3	+	2.72	9.88E-11	4.75E-09
protein localization to plasma membrane (GO:0072659)	208	66	24.53	+	2.69	1.2E-10	5.72E-09
protein targeting (GO:0006605)	228	66	26.89	+	2.45	2.51E-09	0.000000102
positive regulation of protein catabolic process (GO:0045732)	229	66	27.01	+	2.44	2.82E-09	0.000000114
regulation of microtubule-based process (GO:0032886)	273	66	32.2	+	2.05	0.00000107	0.0000287
multi-multicellular organism process (GO:0044706)	313	66	36.92	+	1.79	0.0000453	0.000869
ribonucleoprotein complex assembly (GO:0022618)	222	65	26.19	+	2.48	2.63E-09	0.000000107
response to monosaccharide (GO:0034284)	239	65	28.19	+	2.31	2.72E-08	0.000000949
cellular response to oxidative stress (GO:0034599)	263	65	31.02	+	2.1	0.000000694	0.0000193
negative regulation of transferase activity (GO:0051348)	266	65	31.38	+	2.07	0.0000008	0.0000219
cellular response to inorganic substance (GO:0071241)	285	65	33.62	+	1.93	0.00000614	0.000143
negative regulation of cell motility (GO:2000146)	313	65	36.92	+	1.76	0.0000904	0.00163
telencephalon development (GO:0021537)	333	65	39.28	+	1.65	0.000372	0.00558
mRNA processing (GO:0006397)	365	65	43.05	+	1.51	0.00324	0.0353
positive regulation of supramolecular fiber organization (GO:1902905)	187	64	22.06	+	2.9	1.4E-11	7.54E-10
regulation of proteasomal protein catabolic process (GO:0061136)	188	64	22.18	+	2.89	1.67E-11	8.92E-10
liver development (GO:0001889)	240	64	28.31	+	2.26	8.02E-08	0.00000261
hepaticobiliary system development (GO:0061008)	243	64	28.66	+	2.23	9.73E-08	0.00000313
organic cyclic compound catabolic process (GO:1901361)	335	64	39.51	+	1.62	0.000703	0.00974
lipid localization (GO:0010876)	348	64	41.05	+	1.56	0.00155	0.0192
negative regulation of supramolecular fiber organization (GO:1902904)	168	63	19.82	+	3.18	7.98E-13	4.8E-11
regulation of epithelial cell migration (GO:0010632)	239	63	28.19	+	2.23	0.000000127	0.00000402
regulation of blood circulation (GO:1903522)	269	63	31.73	+	1.99	0.00000359	0.0000877
response to glucocorticoid (GO:0051384)	292	63	34.44	+	1.83	0.0000368	0.000717
regulation of transporter activity (GO:0032409)	298	63	35.15	+	1.79	0.0000625	0.00115
regulation of ERK1 and ERK2 cascade (GO:0070372)	328	63	38.69	+	1.63	0.00063	0.00889
G protein-coupled receptor signaling pathway (GO:0007186)	2063	63	243.34	-	0.26	1.87E-42	8.77E-40
hemostasis (GO:0007599)	134	62	15.81	+	3.92	6.68E-16	5.73E-14
regulation of actin polymerization or depolymerization (GO:0008064)	160	62	18.87	+	3.29	3.84E-13	2.4E-11
regulation of actin filament length (GO:0030832)	162	62	19.11	+	3.24	5.94E-13	3.64E-11
establishment or maintenance of cell polarity (GO:0007163)	202	62	23.83	+	2.6	1.1E-09	4.66E-08
muscle contraction (GO:0006936)	206	62	24.3	+	2.55	2.45E-09	0.0000001
regulation of exocytosis (GO:0017157)	261	62	30.79	+	2.01	0.00000379	0.0000925
female pregnancy (GO:0007565)	276	62	32.55	+	1.9	0.0000151	0.000327
regulation of response to biotic stimulus (GO:0002831)	337	62	39.75	+	1.56	0.00175	0.0211
positive regulation of nervous system development (GO:0051962)	348	62	41.05	+	1.51	0.00345	0.0371
blood coagulation (GO:0007596)	132	61	15.57	+	3.92	1.2E-15	9.86E-14
coagulation (GO:0050817)	135	61	15.92	+	3.83	2.67E-15	2.1E-13
negative regulation of cellular amide metabolic process (GO:0034249)	187	61	22.06	+	2.77	2.21E-10	1.02E-08
regulation of protein localization to membrane (GO:1905475)	207	61	24.42	+	2.5	5.54E-09	0.000000214
positive regulation of neuron projection development (GO:0010976)	222	61	26.19	+	2.33	4.95E-08	0.00000166
regulation of protein modification by small protein conjugation or removal (GO:1903320)	249	61	29.37	+	2.08	0.00000152	0.00004
positive regulation of DNA metabolic process (GO:0051054)	250	61	29.49	+	2.07	0.00000163	0.0000426
response to estradiol (GO:0032355)	253	61	29.84	+	2.04	0.00000273	0.0000683
cell junction assembly (GO:0034329)	262	61	30.9	+	1.97	0.00000627	0.000146
regulation of autophagy (GO:0010506)	273	61	32.2	+	1.89	0.0000204	0.000429
gliogenesis (GO:0042063)	284	61	33.5	+	1.82	0.0000605	0.00113
activation of immune response (GO:0002253)	314	61	37.04	+	1.65	0.000649	0.00915
alcohol metabolic process (GO:0006066)	317	61	37.39	+	1.63	0.000708	0.0098
positive regulation of cell cycle (GO:0045787)	341	61	40.22	+	1.52	0.00399	0.0417

positive regulation of translation (GO:0045727)	154	60	18.16	+	3.3	7.62E-13	4.63E-11
biological process involved in symbiotic interaction (GO:0044403)	207	60	24.42	+	2.46	1.58E-08	0.000000576
response to endoplasmic reticulum stress (GO:0034976)	221	60	26.07	+	2.3	0.000000125	0.00000396
autophagy (GO:0006914)	234	60	27.6	+	2.17	0.000000479	0.0000138
process utilizing autophagic mechanism (GO:0061919)	234	60	27.6	+	2.17	0.000000479	0.0000138
negative regulation of apoptotic signaling pathway (GO:2001234)	246	60	29.02	+	2.07	0.0000021	0.0000533
regulation of transmembrane transporter activity (GO:0022898)	285	60	33.62	+	1.78	0.0000942	0.00168
negative regulation of cell migration (GO:0030336)	297	60	35.03	+	1.71	0.000336	0.00514
regulation of protein secretion (GO:0050708)	304	60	35.86	+	1.67	0.000534	0.00767
aromatic compound catabolic process (GO:0019439)	305	60	35.98	+	1.67	0.000546	0.00783
lipid transport (GO:0006869)	307	60	36.21	+	1.66	0.000577	0.00823
regulation of response to wounding (GO:1903034)	171	59	20.17	+	2.93	7.06E-11	3.45E-09
regulation of cell projection assembly (GO:0060491)	202	59	23.83	+	2.48	1.27E-08	0.000000467
establishment of protein localization to membrane (GO:0090150)	207	59	24.42	+	2.42	2.94E-08	0.00000101
response to hexose (GO:0009746)	222	59	26.19	+	2.25	0.000000231	0.00000704
positive regulation of neurogenesis (GO:0050769)	290	59	34.21	+	1.72	0.000287	0.00447
RNA splicing (GO:0008380)	294	59	34.68	+	1.7	0.000436	0.00642
positive regulation of ion transport (GO:0043270)	331	59	39.04	+	1.51	0.00458	0.0464
ribose phosphate biosynthetic process (GO:0046390)	158	58	18.64	+	3.11	1.28E-11	6.92E-10
regulation of plasma membrane bounded cell projection assembly (GO:0120032)	199	58	23.47	+	2.47	0.000000018	0.000000644
regulation of cell size (GO:0008361)	226	58	26.66	+	2.18	0.000000789	0.0000216
cellular amino acid metabolic process (GO:0006520)	265	58	31.26	+	1.86	0.0000517	0.000978
muscle organ development (GO:0007517)	284	58	33.5	+	1.73	0.000258	0.00409
actomyosin structure organization (GO:0031032)	112	57	13.21	+	4.31	3.95E-16	3.5E-14
vacuolar transport (GO:0007034)	151	57	17.81	+	3.2	7.84E-12	4.38E-10
response to glucose (GO:0009749)	210	57	24.77	+	2.3	0.000000196	0.00000602
positive regulation of transmembrane transport (GO:0034764)	260	57	30.67	+	1.86	0.0000637	0.00117
cellular nitrogen compound catabolic process (GO:0044270)	286	57	33.73	+	1.69	0.000518	0.00746
cellular response to extracellular stimulus (GO:0031668)	291	57	34.32	+	1.66	0.000781	0.0107
purine-containing compound biosynthetic process (GO:0072522)	152	56	17.93	+	3.12	2.56E-11	1.34E-09
regulation of small GTPase mediated signal transduction (GO:0051056)	236	56	27.84	+	2.01	0.0000123	0.000271
regulation of ion transmembrane transporter activity (GO:0032412)	274	56	32.32	+	1.73	0.000389	0.0058
regulation of calcium ion transport (GO:0051924)	292	56	34.44	+	1.63	0.00145	0.0181
anatomical structure homeostasis (GO:0060249)	301	56	35.5	+	1.58	0.00233	0.0267
positive regulation of cell-substrate adhesion (GO:0010811)	144	55	16.99	+	3.24	1.26E-11	6.85E-10
vesicle localization (GO:0051648)	156	55	18.4	+	2.99	2.01E-10	9.29E-09
negative regulation of cytoskeleton organization (GO:0051494)	165	55	19.46	+	2.83	1.33E-09	5.55E-08
negative regulation of translation (GO:0017148)	165	55	19.46	+	2.83	1.33E-09	5.54E-08
Ras protein signal transduction (GO:0007265)	174	55	20.52	+	2.68	3.97E-09	0.000000157
regulation of lipid localization (GO:1905952)	185	55	21.82	+	2.52	3.07E-08	0.00000106
cellular response to insulin stimulus (GO:0032869)	195	55	23	+	2.39	0.00000012	0.00000381
negative regulation of kinase activity (GO:0033673)	229	55	27.01	+	2.04	0.00000922	0.000207
vascular process in circulatory system (GO:0003018)	240	55	28.31	+	1.94	0.000033	0.000652
positive regulation of GTPase activity (GO:0043547)	258	55	30.43	+	1.81	0.000184	0.00303
regulation of synapse organization (GO:0050807)	262	55	30.9	+	1.78	0.000209	0.00338
regulation of synapse structure or activity (GO:0050803)	270	55	31.85	+	1.73	0.000497	0.00722
lipid catabolic process (GO:0016042)	280	55	33.03	+	1.67	0.00087	0.0118
heterocycle catabolic process (GO:0046700)	284	55	33.5	+	1.64	0.00126	0.0161
homeostasis of number of cells (GO:0048872)	286	55	33.73	+	1.63	0.00134	0.0169
humoral immune response (GO:0006959)	303	55	35.74	+	1.54	0.00415	0.0428
ribonucleotide biosynthetic process (GO:0009260)	150	54	17.69	+	3.05	1.15E-10	5.52E-09
regulation of mRNA catabolic process (GO:0061013)	170	54	20.05	+	2.69	4.87E-09	0.00000019
regulation of organelle assembly (GO:1902115)	211	54	24.89	+	2.17	0.0000025	0.0000629
negative regulation of protein localization (GO:1903828)	227	54	26.78	+	2.02	0.0000134	0.000292

pallium development (GO:0021543)	234	54	27.6	+	1.96	0.0000272	0.000549
regulation of response to DNA damage stimulus (GO:2001020)	243	54	28.66	+	1.88	0.0000814	0.00147
regulation of actin filament polymerization (GO:0030833)	141	53	16.63	+	3.19	4.76E-11	2.38E-09
establishment of vesicle localization (GO:0051650)	144	53	16.99	+	3.12	8.9E-11	4.32E-09
purine nucleotide biosynthetic process (GO:0006164)	145	53	17.1	+	3.1	1.09E-10	5.24E-09
viral process (GO:0016032)	152	53	17.93	+	2.96	5.42E-10	0.000000024
regulation of ubiquitin-dependent protein catabolic process (GO:2000058)	161	53	18.99	+	2.79	3.31E-09	0.000000132
response to hydrogen peroxide (GO:0042542)	170	53	20.05	+	2.64	1.59E-08	0.000000578
protein localization to nucleus (GO:0034504)	189	53	22.29	+	2.38	0.000000242	0.00000732
regulation of protein ubiquitination (GO:0031396)	214	53	25.24	+	2.1	0.00000754	0.00017
negative regulation of cell projection organization (GO:0031345)	222	53	26.19	+	2.02	0.0000166	0.000357
angiogenesis (GO:0001525)	283	53	33.38	+	1.59	0.00301	0.0332
cytoplasmic translation (GO:0002181)	154	52	18.16	+	2.86	1.67E-09	6.91E-08
protein import (GO:0017038)	163	52	19.23	+	2.7	8.61E-09	0.000000321
positive regulation of cell growth (GO:0030307)	194	52	22.88	+	2.27	0.000000995	0.0000268
exocytosis (GO:0006887)	224	52	26.42	+	1.97	0.0000427	0.000827
response to purine-containing compound (GO:0014074)	225	52	26.54	+	1.96	0.000044	0.000849
glucose homeostasis (GO:0042593)	258	52	30.43	+	1.71	0.000747	0.0103
carbohydrate homeostasis (GO:0033500)	260	52	30.67	+	1.7	0.000804	0.011
negative regulation of neuron death (GO:1901215)	263	52	31.02	+	1.68	0.00114	0.0149
endoplasmic reticulum to Golgi vesicle-mediated transport (GO:0006888)	111	51	13.09	+	3.9	3.03E-13	1.91E-11
cytosolic transport (GO:0016482)	135	51	15.92	+	3.2	9.5E-11	4.59E-09
negative regulation of protein-containing complex assembly (GO:0031333)	144	51	16.99	+	3	9.24E-10	3.98E-08
regulation of protein localization to nucleus (GO:1900180)	162	51	19.11	+	2.67	1.64E-08	0.000000593
positive regulation of binding (GO:0051099)	196	51	23.12	+	2.21	0.00000305	0.0000756
response to acid chemical (GO:0001101)	216	51	25.48	+	2	0.0000312	0.00062
cellular response to metal ion (GO:0071248)	247	51	29.13	+	1.75	0.000571	0.00815
regulation of cysteine-type endopeptidase activity (GO:2000116)	250	51	29.49	+	1.73	0.00063	0.00889
response to ethanol (GO:0045471)	251	51	29.61	+	1.72	0.000656	0.00923
leukocyte mediated immunity (GO:0002443)	276	51	32.55	+	1.57	0.00473	0.0477
Golgi organization (GO:0007030)	125	50	14.74	+	3.39	2.86E-11	1.48E-09
regulation of microtubule cytoskeleton organization (GO:0070507)	164	50	19.34	+	2.58	6.24E-08	0.00000207
positive regulation of intracellular protein transport (GO:0090316)	175	50	20.64	+	2.42	0.000000298	0.00000891
regulation of intrinsic apoptotic signaling pathway (GO:2001242)	181	50	21.35	+	2.34	0.000000753	0.0000208
regulation of heart contraction (GO:0008016)	195	50	23	+	2.17	0.00000483	0.000115
carboxylic acid biosynthetic process (GO:0046394)	242	50	28.54	+	1.75	0.000528	0.0076
organic acid biosynthetic process (GO:0016053)	244	50	28.78	+	1.74	0.000749	0.0103
nucleobase-containing compound catabolic process (GO:0034655)	249	50	29.37	+	1.7	0.00117	0.0152
cellular response to nutrient levels (GO:0031669)	253	50	29.84	+	1.68	0.00131	0.0167
extracellular matrix organization (GO:0030198)	270	50	31.85	+	1.57	0.0044	0.0452
purine ribonucleotide biosynthetic process (GO:0009152)	136	49	16.04	+	3.05	8.05E-10	3.52E-08
regulation of cell shape (GO:0008360)	147	49	17.34	+	2.83	6.79E-09	0.000000258
regulation of mRNA stability (GO:0043488)	152	49	17.93	+	2.73	1.98E-08	0.000000705
animal organ regeneration (GO:0031100)	160	49	18.87	+	2.6	8.17E-08	0.00000266
regulation of RNA stability (GO:0043487)	165	49	19.46	+	2.52	0.000000142	0.00000447
regulation of cell junction assembly (GO:1901888)	220	49	25.95	+	1.89	0.000131	0.00226
glial cell differentiation (GO:0010001)	227	49	26.78	+	1.83	0.000245	0.00391
protein maturation (GO:0051604)	249	49	29.37	+	1.67	0.00164	0.02
cardiocyte differentiation (GO:0035051)	134	48	15.81	+	3.04	1.39E-09	0.000000058
receptor-mediated endocytosis (GO:0006898)	150	48	17.69	+	2.71	3.22E-08	0.0000011
cellular response to reactive oxygen species (GO:0034614)	155	48	18.28	+	2.63	0.000000064	0.00000211
positive regulation of epithelial cell migration (GO:0010634)	157	48	18.52	+	2.59	0.000000118	0.00000377
negative regulation of protein kinase activity (GO:0006469)	206	48	24.3	+	1.98	0.0000769	0.0014
carboxylic acid catabolic process (GO:0046395)	209	48	24.65	+	1.95	0.0000869	0.00157

organic acid catabolic process (GO:0016054)	211	48	24.89	+	1.93	0.0000971	0.00173
positive regulation of developmental growth (GO:0048639)	217	48	25.6	+	1.88	0.000177	0.00295
regulation of protein binding (GO:0043393)	218	48	25.71	+	1.87	0.00026	0.00412
epithelial cell development (GO:0002064)	245	48	28.9	+	1.66	0.00207	0.0243
lung development (GO:0030324)	251	48	29.61	+	1.62	0.00316	0.0346
respiratory tube development (GO:0030323)	254	48	29.96	+	1.6	0.00443	0.0452
oxidative phosphorylation (GO:0006119)	106	47	12.5	+	3.76	6.78E-12	3.82E-10
regulation of wound healing (GO:0061041)	128	47	15.1	+	3.11	1.08E-09	4.59E-08
response to heat (GO:0009408)	141	47	16.63	+	2.83	1.38E-08	0.000000507
regulation of Ras protein signal transduction (GO:0046578)	200	47	23.59	+	1.99	0.0000621	0.00115
peptidyl-serine modification (GO:0018209)	216	47	25.48	+	1.84	0.000357	0.0054
regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043281)	223	47	26.3	+	1.79	0.000629	0.00889
regulation of leukocyte migration (GO:0002685)	233	47	27.48	+	1.71	0.0016	0.0196
regulation of protein localization to cell periphery (GO:1904375)	146	46	17.22	+	2.67	8.55E-08	0.00000277
cell-substrate adhesion (GO:0031589)	182	46	21.47	+	2.14	0.0000173	0.00037
cytoskeleton-dependent intracellular transport (GO:0030705)	188	46	22.18	+	2.07	0.0000366	0.000716
cellular response to oxygen levels (GO:0071453)	203	46	23.94	+	1.92	0.00016	0.00269
regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043122)	242	46	28.54	+	1.61	0.00486	0.0488
cardiac muscle cell differentiation (GO:0055007)	105	45	12.38	+	3.63	4.6E-11	2.32E-09
electron transport chain (GO:0022900)	122	45	14.39	+	3.13	2.16E-09	8.87E-08
regulation of protein-containing complex disassembly (GO:0043244)	132	45	15.57	+	2.89	1.78E-08	0.000000637
positive regulation of cellular protein catabolic process (GO:1903364)	152	45	17.93	+	2.51	0.000000521	0.0000149
positive regulation of angiogenesis (GO:0045766)	178	45	21	+	2.14	0.0000229	0.000474
positive regulation of vasculature development (GO:1904018)	178	45	21	+	2.14	0.0000229	0.000474
regulation of smooth muscle cell proliferation (GO:0048660)	183	45	21.59	+	2.08	0.0000315	0.000625
regulation of lipid biosynthetic process (GO:0046890)	194	45	22.88	+	1.97	0.000116	0.00203
regulation of cell morphogenesis involved in differentiation (GO:0010769)	125	44	14.74	+	2.98	1.63E-08	0.000000589
regulation of proteasomal ubiquitin-dependent protein catabolic process (GO:0032434)	131	44	15.45	+	2.85	3.45E-08	0.00000118
regulation of lipid transport (GO:0032368)	155	44	18.28	+	2.41	0.00000204	0.0000521
positive regulation of apoptotic signaling pathway (GO:2001235)	157	44	18.52	+	2.38	0.00000244	0.0000614
regulation of RNA splicing (GO:0043484)	164	44	19.34	+	2.27	0.00000656	0.000152
response to transforming growth factor beta (GO:0071559)	167	44	19.7	+	2.23	0.000013	0.000285
response to amino acid (GO:0043200)	184	44	21.7	+	2.03	0.0000772	0.0014
response to alkaloid (GO:0043279)	186	44	21.94	+	2.01	0.0000873	0.00157
peptidyl-serine phosphorylation (GO:0018105)	190	44	22.41	+	1.96	0.000151	0.00257
response to organophosphorus (GO:0046683)	192	44	22.65	+	1.94	0.000168	0.0028
cellular modified amino acid metabolic process (GO:0006575)	195	44	23	+	1.91	0.000271	0.00426
cellular component assembly involved in morphogenesis (GO:0010927)	113	43	13.33	+	3.23	2.3E-09	0.000000094
import into nucleus (GO:0051170)	117	43	13.8	+	3.12	5.32E-09	0.000000207
cellular response to toxic substance (GO:0097237)	123	43	14.51	+	2.96	2.61E-08	0.000000915
vesicle-mediated transport in synapse (GO:0099003)	144	43	16.99	+	2.53	0.000000871	0.0000237
regulation of extrinsic apoptotic signaling pathway (GO:2001236)	168	43	19.82	+	2.17	0.0000228	0.000474
regulation of endothelial cell migration (GO:0010594)	173	43	20.41	+	2.11	0.0000466	0.000889
maintenance of location (GO:0051235)	183	43	21.59	+	1.99	0.00012	0.00209
placenta development (GO:0001890)	189	43	22.29	+	1.93	0.000228	0.00365
cellular lipid catabolic process (GO:0044242)	189	43	22.29	+	1.93	0.000228	0.00365
ameboidal-type cell migration (GO:0001667)	195	43	23	+	1.87	0.000416	0.00616
positive regulation of peptidase activity (GO:0010952)	196	43	23.12	+	1.86	0.000439	0.00646
microtubule-based transport (GO:0099111)	200	43	23.59	+	1.82	0.000701	0.00973
protein autophosphorylation (GO:0046777)	204	43	24.06	+	1.79	0.00112	0.0146
viral life cycle (GO:0019058)	120	42	14.15	+	2.97	3.83E-08	0.0000013
mitochondrial transport (GO:0006839)	151	42	17.81	+	2.36	0.00000492	0.000117
monosaccharide metabolic process (GO:0005996)	151	42	17.81	+	2.36	0.00000492	0.000117
spindle organization (GO:0007051)	155	42	18.28	+	2.3	0.0000107	0.000238

cellular response to transforming growth factor beta stimulus (GO:0071560)	159	42	18.75	+	2.24	0.0000142	0.000309
positive regulation of protein secretion (GO:0050714)	163	42	19.23	+	2.18	0.0000282	0.000568
regulation of calcium ion transmembrane transport (GO:1903169)	176	42	20.76	+	2.02	0.000133	0.00229
response to calcium ion (GO:0051592)	179	42	21.11	+	1.99	0.000154	0.00262
negative regulation of MAPK cascade (GO:0043409)	188	42	22.18	+	1.89	0.000479	0.00701
cell-cell junction organization (GO:0045216)	189	42	22.29	+	1.88	0.000494	0.00719
regulation of chromosome organization (GO:0033044)	208	42	24.53	+	1.71	0.00249	0.0284
sensory perception (GO:0007600)	1726	42	203.59	-	0.21	4.68E-42	2.13E-39
cellular detoxification (GO:1990748)	111	41	13.09	+	3.13	1.07E-08	0.000000395
lysosomal transport (GO:0007041)	116	41	13.68	+	3	2.91E-08	0.00000101
regulation of phagocytosis (GO:0050764)	123	41	14.51	+	2.83	0.000000119	0.00000379
negative regulation of protein catabolic process (GO:0042177)	124	41	14.63	+	2.8	0.000000139	0.00000437
detoxification (GO:0098754)	128	41	15.1	+	2.72	0.000000389	0.0000114
response to activity (GO:0014823)	142	41	16.75	+	2.45	0.00000271	0.000068
regulation of reactive oxygen species metabolic process (GO:2000377)	163	41	19.23	+	2.13	0.0000479	0.000913
cellular response to ketone (GO:1901655)	164	41	19.34	+	2.12	0.0000518	0.000979
regulation of muscle contraction (GO:0006937)	165	41	19.46	+	2.11	0.0000563	0.00105
heart process (GO:0003015)	106	40	12.5	+	3.2	9.91E-09	0.000000369
protein import into nucleus (GO:0006606)	112	40	13.21	+	3.03	3.39E-08	0.00000116
regulation of actin filament bundle assembly (GO:0032231)	113	40	13.33	+	3	4.13E-08	0.00000139
regulation of protein localization to plasma membrane (GO:1903076)	120	40	14.15	+	2.83	0.000000171	0.00000529
positive regulation of endocytosis (GO:0045807)	126	40	14.86	+	2.69	0.000000615	0.0000173
membrane fusion (GO:0061025)	136	40	16.04	+	2.49	0.00000283	0.0000705
transport along microtubule (GO:0010970)	157	40	18.52	+	2.16	0.0000553	0.00104
organic hydroxy compound transport (GO:0015850)	162	40	19.11	+	2.09	0.0000782	0.00142
negative regulation of neuron projection development (GO:0010977)	168	40	19.82	+	2.02	0.000158	0.00267
regulation of axonogenesis (GO:0050770)	189	40	22.29	+	1.79	0.00155	0.0192
positive regulation of ion transmembrane transport (GO:0034767)	196	40	23.12	+	1.73	0.00265	0.03
regulation of MAP kinase activity (GO:0043405)	198	40	23.35	+	1.71	0.00284	0.0317
regulation of carbohydrate metabolic process (GO:0006109)	204	40	24.06	+	1.66	0.00452	0.046
vesicle budding from membrane (GO:0006900)	59	39	6.96	+	5.6	3.79E-14	2.64E-12
cardiac muscle cell development (GO:0055013)	73	39	8.61	+	4.53	5.54E-12	3.13E-10
cardiac cell development (GO:0055006)	78	39	9.2	+	4.24	2.58E-11	1.35E-09
striated muscle contraction (GO:0006941)	116	39	13.68	+	2.85	0.000000212	0.00000648
proton transmembrane transport (GO:1902600)	120	39	14.15	+	2.76	0.000000391	0.0000114
vesicle-mediated transport to the plasma membrane (GO:0098876)	121	39	14.27	+	2.73	0.000000459	0.0000133
regulation of nucleocytoplasmic transport (GO:0046822)	130	39	15.33	+	2.54	0.00000206	0.0000526
synaptic vesicle cycle (GO:0099504)	133	39	15.69	+	2.49	0.00000405	0.0000985
regulation of generation of precursor metabolites and energy (GO:0043467)	145	39	17.1	+	2.28	0.0000188	0.000399
mitotic nuclear division (GO:0140014)	159	39	18.75	+	2.08	0.000108	0.00191
response to vitamin (GO:0033273)	175	39	20.64	+	1.89	0.000698	0.0097
lipid modification (GO:0030258)	179	39	21.11	+	1.85	0.00117	0.0152
positive regulation of endopeptidase activity (GO:0010950)	181	39	21.35	+	1.83	0.00124	0.016
alpha-amino acid metabolic process (GO:1901605)	187	39	22.06	+	1.77	0.00212	0.0248
cellular response to radiation (GO:0071478)	189	39	22.29	+	1.75	0.00228	0.0265
translational initiation (GO:0006413)	66	38	7.78	+	4.88	1.88E-12	1.1E-10
chaperone-mediated protein folding (GO:0061077)	71	38	8.37	+	4.54	9.91E-12	5.46E-10
nucleoside triphosphate metabolic process (GO:0009141)	95	38	11.21	+	3.39	6.53E-09	0.00000025
respiratory electron transport chain (GO:0022904)	99	38	11.68	+	3.25	1.59E-08	0.000000578
positive regulation of cell morphogenesis involved in differentiation (GO:0010770)	105	38	12.38	+	3.07	5.59E-08	0.00000186
nucleoside diphosphate metabolic process (GO:0009132)	112	38	13.21	+	2.88	0.000000267	0.00000804
protein-containing complex disassembly (GO:0032984)	129	38	15.22	+	2.5	0.00000537	0.000127
regulation of cell-matrix adhesion (GO:0001952)	130	38	15.33	+	2.48	0.00000582	0.000136
hexose metabolic process (GO:0019318)	132	38	15.57	+	2.44	0.00000703	0.000161

cellular oxidant detoxification (GO:0098869)	95	37	11.21	+	3.3	0.000000018	0.000000643
positive regulation of protein localization to nucleus (GO:1900182)	105	37	12.38	+	2.99	0.000000144	0.0000045
cellular response to mechanical stimulus (GO:0071260)	116	37	13.68	+	2.7	0.00000177	0.0000457
regulation of endothelial cell proliferation (GO:0001936)	140	37	16.51	+	2.24	0.0000609	0.00113
RNA localization (GO:0006403)	146	37	17.22	+	2.15	0.0000915	0.00164
cerebral cortex development (GO:0021987)	148	37	17.46	+	2.12	0.000151	0.00257
regulation of mRNA processing (GO:0050684)	149	37	17.57	+	2.11	0.000159	0.00268
macroautophagy (GO:0016236)	149	37	17.57	+	2.11	0.000159	0.00267
cellular carbohydrate metabolic process (GO:0044262)	157	37	18.52	+	2	0.000363	0.00548
regulation of viral process (GO:0050792)	162	37	19.11	+	1.94	0.000666	0.00933
positive regulation of hormone secretion (GO:0046887)	176	37	20.76	+	1.78	0.0023	0.0266
immunoglobulin mediated immune response (GO:0016064)	179	37	21.11	+	1.75	0.0035	0.0374
positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)	180	37	21.23	+	1.74	0.00359	0.0382
nucleobase-containing compound transport (GO:0015931)	181	37	21.35	+	1.73	0.0037	0.0392
blood vessel diameter maintenance (GO:0097746)	181	37	21.35	+	1.73	0.0037	0.0392
regulation of tube diameter (GO:0035296)	181	37	21.35	+	1.73	0.0037	0.0391
cellular response to decreased oxygen levels (GO:0036294)	182	37	21.47	+	1.72	0.00383	0.0402
regulation of tube size (GO:0035150)	182	37	21.47	+	1.72	0.00383	0.0401
negative regulation of ion transport (GO:0043271)	183	37	21.59	+	1.71	0.00398	0.0416
myofibril assembly (GO:0030239)	63	36	7.43	+	4.84	8.41E-12	4.69E-10
striated muscle cell development (GO:0055002)	64	36	7.55	+	4.77	1.18E-11	6.45E-10
heart contraction (GO:0060047)	91	36	10.73	+	3.35	2.03E-08	0.00000072
regulation of protein depolymerization (GO:1901879)	94	36	11.09	+	3.25	3.94E-08	0.00000133
regulation of muscle adaptation (GO:0043502)	108	36	12.74	+	2.83	0.00000073	0.0000203
positive regulation of plasma membrane bounded cell projection assembly (GO:0120034)	113	36	13.33	+	2.7	0.00000157	0.0000411
complement activation (GO:0006956)	129	36	15.22	+	2.37	0.0000198	0.000417
positive regulation of proteolysis involved in cellular protein catabolic process (GO:1903052)	130	36	15.33	+	2.35	0.000033	0.000652
regulation of dephosphorylation (GO:0035303)	132	36	15.57	+	2.31	0.0000372	0.000726
response to interferon-gamma (GO:0034341)	144	36	16.99	+	2.12	0.000202	0.00329
response to cAMP (GO:0051591)	150	36	17.69	+	2.03	0.000287	0.00447
response to UV (GO:0009411)	154	36	18.16	+	1.98	0.000499	0.00724
positive regulation of lipid metabolic process (GO:0045834)	171	36	20.17	+	1.78	0.00285	0.0318
positive regulation of cation transmembrane transport (GO:1904064)	176	36	20.76	+	1.73	0.00462	0.0468
pyruvate metabolic process (GO:0006090)	92	35	10.85	+	3.23	0.000000069	0.00000227
ribonucleoside diphosphate metabolic process (GO:0009185)	92	35	10.85	+	3.23	0.000000069	0.00000227
cytokinesis (GO:0000910)	100	35	11.8	+	2.97	0.000000352	0.0000104
regulation of actomyosin structure organization (GO:0110020)	109	35	12.86	+	2.72	0.00000191	0.0000493
regulation of receptor-mediated endocytosis (GO:0048259)	123	35	14.51	+	2.41	0.0000205	0.00043
establishment of cell polarity (GO:0030010)	125	35	14.74	+	2.37	0.0000251	0.000513
plasma membrane organization (GO:0007009)	134	35	15.81	+	2.21	0.000121	0.00211
dendrite development (GO:0016358)	141	35	16.63	+	2.1	0.000282	0.0044
regulation of cellular ketone metabolic process (GO:0010565)	142	35	16.75	+	2.09	0.000293	0.00456
lipid homeostasis (GO:0055088)	167	35	19.7	+	1.78	0.00369	0.039
negative regulation of protein polymerization (GO:0032272)	77	34	9.08	+	3.74	5.74E-09	0.000000222
positive regulation of protein polymerization (GO:0032273)	96	34	11.32	+	3	0.000000412	0.000012
regulation of mRNA splicing, via spliceosome (GO:0048024)	110	34	12.97	+	2.62	0.00000686	0.000157
organelle fusion (GO:0048284)	113	34	13.33	+	2.55	0.00000944	0.000212
positive regulation of proteasomal protein catabolic process (GO:1901800)	114	34	13.45	+	2.53	0.0000107	0.000237
microtubule cytoskeleton organization involved in mitosis (GO:1902850)	118	34	13.92	+	2.44	0.0000248	0.000508
cellular response to carbohydrate stimulus (GO:0071322)	132	34	15.57	+	2.18	0.000179	0.00296
positive regulation of response to DNA damage stimulus (GO:2001022)	136	34	16.04	+	2.12	0.000229	0.00367
protein-containing complex localization (GO:0031503)	157	34	18.52	+	1.84	0.0028	0.0315
MAPK cascade (GO:0000165)	157	34	18.52	+	1.84	0.0028	0.0314
positive regulation of small molecule metabolic process (GO:0062013)	162	34	19.11	+	1.78	0.00334	0.0362

protein polymerization (GO:0051258)	88	33	10.38	+	3.18	0.000000211	0.00000648
cytoskeleton-dependent cytokinesis (GO:0061640)	97	33	11.44	+	2.88	0.00000174	0.0000452
carbohydrate catabolic process (GO:0016052)	115	33	13.56	+	2.43	0.0000356	0.000697
positive regulation of lipid localization (GO:1905954)	120	33	14.15	+	2.33	0.0000564	0.00105
protein modification by small protein removal (GO:0070646)	150	33	17.69	+	1.87	0.00226	0.0262
monocarboxylic acid biosynthetic process (GO:0072330)	152	33	17.93	+	1.84	0.00246	0.0281
homotypic cell-cell adhesion (GO:0034109)	59	32	6.96	+	4.6	3.25E-10	1.47E-08
response to epidermal growth factor (GO:0070849)	64	32	7.55	+	4.24	1.53E-09	6.36E-08
platelet activation (GO:0030168)	70	32	8.26	+	3.88	8.33E-09	0.000000312
retrograde transport, endosome to Golgi (GO:0042147)	78	32	9.2	+	3.48	6.24E-08	0.00000207
lipid oxidation (GO:0034440)	86	32	10.14	+	3.15	0.000000369	0.0000109
negative regulation of response to wounding (GO:1903035)	87	32	10.26	+	3.12	0.000000454	0.0000132
nucleotide phosphorylation (GO:0046939)	89	32	10.5	+	3.05	0.000000682	0.000019
post-Golgi vesicle-mediated transport (GO:0006892)	90	32	10.62	+	3.01	0.000000832	0.0000227
regulation of stress fiber assembly (GO:0051492)	96	32	11.32	+	2.83	0.00000319	0.0000787
maintenance of protein location (GO:0045185)	100	32	11.8	+	2.71	0.00000561	0.000132
positive regulation of endothelial cell migration (GO:0010595)	110	32	12.97	+	2.47	0.000028	0.000566
postsynapse organization (GO:0099173)	113	32	13.33	+	2.4	0.0000549	0.00103
RNA transport (GO:0050658)	123	32	14.51	+	2.21	0.000188	0.00309
nucleic acid transport (GO:0050657)	123	32	14.51	+	2.21	0.000188	0.00309
establishment of RNA localization (GO:0051236)	125	32	14.74	+	2.17	0.000225	0.00361
regulation of extent of cell growth (GO:0061387)	133	32	15.69	+	2.04	0.000783	0.0107
negative regulation of transmembrane transport (GO:0034763)	139	32	16.4	+	1.95	0.00155	0.0192
fatty acid oxidation (GO:0019395)	81	31	9.55	+	3.24	0.000000341	0.0000101
nucleoside diphosphate phosphorylation (GO:0006165)	86	31	10.14	+	3.06	0.000000969	0.0000262
membrane docking (GO:0022406)	88	31	10.38	+	2.99	0.00000144	0.000038
organelle membrane fusion (GO:0090174)	92	31	10.85	+	2.86	0.00000413	0.0001
negative regulation of protein modification by small protein conjugation or removal (GO:1903321)	97	31	11.44	+	2.71	0.00000804	0.000181
biological process involved in interaction with symbiont (GO:0051702)	101	31	11.91	+	2.6	0.0000209	0.000437
glucose metabolic process (GO:0006006)	102	31	12.03	+	2.58	0.0000228	0.000473
monocarboxylic acid catabolic process (GO:0072329)	103	31	12.15	+	2.55	0.0000251	0.000514
biological process involved in interaction with host (GO:0051701)	103	31	12.15	+	2.55	0.0000251	0.000513
positive regulation of exocytosis (GO:0045921)	108	31	12.74	+	2.43	0.0000694	0.00127
regulation of macroautophagy (GO:0016241)	113	31	13.33	+	2.33	0.000102	0.00182
cellular response to interferon-gamma (GO:0071346)	114	31	13.45	+	2.31	0.000113	0.00198
cell-matrix adhesion (GO:0007160)	122	31	14.39	+	2.15	0.000316	0.00485
positive regulation of mRNA metabolic process (GO:1903313)	122	31	14.39	+	2.15	0.000316	0.00485
regulation of DNA biosynthetic process (GO:2000278)	130	31	15.33	+	2.02	0.00108	0.0142
regulation of sequestering of calcium ion (GO:0051282)	132	31	15.57	+	1.99	0.00119	0.0154
regulation of dendrite development (GO:0050773)	136	31	16.04	+	1.93	0.00211	0.0247
positive regulation of autophagy (GO:0010508)	139	31	16.4	+	1.89	0.00237	0.0272
regulation of peptidyl-serine phosphorylation (GO:0033135)	144	31	16.99	+	1.83	0.0041	0.0426
regulation of substrate adhesion-dependent cell spreading (GO:1900024)	63	30	7.43	+	4.04	1.17E-08	0.000000434
ribonucleoside triphosphate metabolic process (GO:0009199)	69	30	8.14	+	3.69	5.82E-08	0.00000193
purine nucleoside triphosphate metabolic process (GO:0009144)	70	30	8.26	+	3.63	7.48E-08	0.00000245
regulation of cell-substrate junction organization (GO:0150116)	70	30	8.26	+	3.63	7.48E-08	0.00000244
positive regulation of response to wounding (GO:1903036)	77	30	9.08	+	3.3	0.000000387	0.0000114
ATP synthesis coupled electron transport (GO:0042773)	77	30	9.08	+	3.3	0.000000387	0.0000114
purine ribonucleoside diphosphate metabolic process (GO:0009179)	83	30	9.79	+	3.06	0.00000138	0.0000365
purine nucleoside diphosphate metabolic process (GO:0009135)	83	30	9.79	+	3.06	0.00000138	0.0000364
vesicle fusion (GO:0006906)	88	30	10.38	+	2.89	0.0000055	0.00013
positive regulation of phagocytosis (GO:0050766)	90	30	10.62	+	2.83	0.00000674	0.000155
reactive oxygen species metabolic process (GO:0072593)	98	30	11.56	+	2.6	0.0000304	0.000608
negative regulation of mRNA metabolic process (GO:1903312)	98	30	11.56	+	2.6	0.0000304	0.000608

regulation of microtubule polymerization or depolymerization (GO:0031110)	99	30	11.68	+	2.57	0.000033	0.000652
regulation of smooth muscle cell migration (GO:0014910)	101	30	11.91	+	2.52	0.0000401	0.00078
receptor metabolic process (GO:0043112)	103	30	12.15	+	2.47	0.0000504	0.000958
humoral immune response mediated by circulating immunoglobulin (GO:0002455)	119	30	14.04	+	2.14	0.000442	0.0065
positive regulation of mitotic cell cycle (GO:0045931)	128	30	15.1	+	1.99	0.00156	0.0193
sister chromatid segregation (GO:0000819)	131	30	15.45	+	1.94	0.00182	0.0219
cell-cell junction assembly (GO:0007043)	133	30	15.69	+	1.91	0.00287	0.032
positive regulation of transporter activity (GO:0032411)	135	30	15.92	+	1.88	0.00309	0.034
regulated exocytosis (GO:0045055)	136	30	16.04	+	1.87	0.00322	0.0352
cellular glucose homeostasis (GO:0001678)	138	30	16.28	+	1.84	0.00357	0.038
nucleoside triphosphate biosynthetic process (GO:0009142)	64	29	7.55	+	3.84	4.77E-08	0.00000161
cardiac muscle contraction (GO:0060048)	75	29	8.85	+	3.28	0.000000681	0.0000191
mitochondrial ATP synthesis coupled electron transport (GO:0042775)	75	29	8.85	+	3.28	0.000000681	0.000019
ADP metabolic process (GO:0046031)	76	29	8.96	+	3.24	0.000000847	0.0000231
sterol transport (GO:0015918)	77	29	9.08	+	3.19	0.00000105	0.0000282
axo-dendritic transport (GO:0008088)	83	29	9.79	+	2.96	0.00000354	0.0000867
negative regulation of protein ubiquitination (GO:0031397)	86	29	10.14	+	2.86	0.00000884	0.000199
regulation of protein dephosphorylation (GO:0035304)	93	29	10.97	+	2.64	0.0000223	0.000464
purine nucleoside bisphosphate metabolic process (GO:0034032)	107	29	12.62	+	2.3	0.000206	0.00335
ribonucleoside bisphosphate metabolic process (GO:0033875)	107	29	12.62	+	2.3	0.000206	0.00334
nucleoside bisphosphate metabolic process (GO:0033865)	107	29	12.62	+	2.3	0.000206	0.00334
mitotic sister chromatid segregation (GO:0000070)	110	29	12.97	+	2.24	0.000409	0.00607
complement activation, classical pathway (GO:0006958)	114	29	13.45	+	2.16	0.000524	0.00754
regulation of axon extension (GO:0030516)	117	29	13.8	+	2.1	0.000967	0.0129
nuclear export (GO:0051168)	119	29	14.04	+	2.07	0.00106	0.014
response to topologically incorrect protein (GO:0035966)	123	29	14.51	+	2	0.002	0.0237
positive regulation of peptide hormone secretion (GO:0090277)	132	29	15.57	+	1.86	0.00418	0.0431
regulation of blood coagulation (GO:0030193)	64	28	7.55	+	3.71	0.000000144	0.00000449
regulation of hemostasis (GO:1900046)	66	28	7.78	+	3.6	0.000000237	0.0000072
negative regulation of wound healing (GO:0061045)	67	28	7.9	+	3.54	0.000000303	0.00000905
regulation of coagulation (GO:0050818)	68	28	8.02	+	3.49	0.000000385	0.0000113
negative regulation of cellular protein catabolic process (GO:1903363)	79	28	9.32	+	3	0.00000415	0.0001
fatty acid catabolic process (GO:0009062)	84	28	9.91	+	2.83	0.0000143	0.000311
response to axon injury (GO:0048678)	87	28	10.26	+	2.73	0.0000207	0.000434
regulation of striated muscle contraction (GO:0006942)	88	28	10.38	+	2.7	0.0000238	0.000493
positive regulation of protein binding (GO:0032092)	98	28	11.56	+	2.42	0.000116	0.00203
response to osmotic stress (GO:0006970)	102	28	12.03	+	2.33	0.000248	0.00395
regulation of oxidoreductase activity (GO:0051341)	102	28	12.03	+	2.33	0.000248	0.00395
negative regulation of extrinsic apoptotic signaling pathway (GO:2001237)	104	28	12.27	+	2.28	0.000293	0.00456
maintenance of location in cell (GO:0051651)	104	28	12.27	+	2.28	0.000293	0.00455
developmental cell growth (GO:0048588)	112	28	13.21	+	2.12	0.000796	0.0109
positive regulation of protein localization to membrane (GO:1905477)	116	28	13.68	+	2.05	0.00148	0.0184
cell growth (GO:0016049)	116	28	13.68	+	2.05	0.00148	0.0184
positive regulation of smooth muscle cell proliferation (GO:0048661)	117	28	13.8	+	2.03	0.00156	0.0193
regulation of calcium ion transport into cytosol (GO:0010522)	117	28	13.8	+	2.03	0.00156	0.0192
cellular response to monosaccharide stimulus (GO:0071326)	118	28	13.92	+	2.01	0.00166	0.0202
cellular response to epidermal growth factor stimulus (GO:0071364)	54	27	6.37	+	4.24	2.85E-08	0.00000099
regulation of actin filament depolymerization (GO:0030834)	56	27	6.61	+	4.09	5.11E-08	0.00000171
purine ribonucleoside triphosphate metabolic process (GO:0009205)	62	27	7.31	+	3.69	0.000000257	0.00000773
regulation of translational initiation (GO:0006446)	69	27	8.14	+	3.32	0.00000136	0.0000361
positive regulation of actin filament bundle assembly (GO:0032233)	69	27	8.14	+	3.32	0.00000136	0.0000361
response to ischemia (GO:0002931)	71	27	8.37	+	3.22	0.00000211	0.0000534
negative regulation of protein-containing complex disassembly (GO:0043242)	83	27	9.79	+	2.76	0.0000263	0.000534
regulation of dendritic spine development (GO:0060998)	84	27	9.91	+	2.73	0.0000299	0.0006

actin filament-based movement (GO:0030048)	87	27	10.26	+	2.63	0.0000458	0.000875
acute inflammatory response (GO:0002526)	89	27	10.5	+	2.57	0.0000937	0.00167
integrin-mediated signaling pathway (GO:0007229)	95	27	11.21	+	2.41	0.000166	0.00277
protein localization to cell junction (GO:1902414)	95	27	11.21	+	2.41	0.000166	0.00277
tissue migration (GO:0090130)	96	27	11.32	+	2.38	0.000186	0.00306
regulation of steroid metabolic process (GO:0019218)	110	27	12.97	+	2.08	0.00121	0.0156
cellular response to glucose stimulus (GO:0071333)	113	27	13.33	+	2.03	0.00205	0.0241
cellular response to hexose stimulus (GO:0071331)	115	27	13.56	+	1.99	0.0023	0.0266
mRNA catabolic process (GO:0006402)	119	27	14.04	+	1.92	0.00403	0.042
regulation of transforming growth factor beta receptor signaling pathway (GO:0017015)	123	27	14.51	+	1.86	0.00493	0.0495
platelet aggregation (GO:0070527)	44	26	5.19	+	5.01	3.82E-09	0.000000152
cortical cytoskeleton organization (GO:0030865)	61	26	7.2	+	3.61	0.000000589	0.0000166
synaptic vesicle recycling (GO:0036465)	63	26	7.43	+	3.5	0.000000957	0.0000259
regulation of focal adhesion assembly (GO:0051893)	65	26	7.67	+	3.39	0.00000153	0.0000401
regulation of cell-substrate junction assembly (GO:0090109)	65	26	7.67	+	3.39	0.00000153	0.0000401
glycolytic process (GO:0006096)	66	26	7.78	+	3.34	0.00000192	0.0000493
ATP generation from ADP (GO:0006757)	67	26	7.9	+	3.29	0.0000024	0.0000605
aerobic electron transport chain (GO:0019646)	67	26	7.9	+	3.29	0.0000024	0.0000604
negative regulation of protein depolymerization (GO:1901880)	73	26	8.61	+	3.02	0.00000841	0.000189
organelle localization by membrane tethering (GO:0140056)	78	26	9.2	+	2.83	0.0000307	0.00061
nucleoside monophosphate metabolic process (GO:0009123)	82	26	9.67	+	2.69	0.0000495	0.000942
response to nerve growth factor (GO:1990089)	84	26	9.91	+	2.62	0.0000656	0.00121
acyl-CoA metabolic process (GO:0006637)	87	26	10.26	+	2.53	0.000146	0.0025
thioester metabolic process (GO:0035383)	87	26	10.26	+	2.53	0.000146	0.0025
mitotic spindle organization (GO:0007052)	88	26	10.38	+	2.5	0.000158	0.00267
endoplasmic reticulum organization (GO:0007029)	88	26	10.38	+	2.5	0.000158	0.00266
regulation of release of sequestered calcium ion into cytosol (GO:0051279)	88	26	10.38	+	2.5	0.000158	0.00266
regulation of calcium ion transmembrane transporter activity (GO:1901019)	89	26	10.5	+	2.48	0.000172	0.00287
midbrain development (GO:0030901)	92	26	10.85	+	2.4	0.000236	0.00377
dicarboxylic acid metabolic process (GO:0043648)	93	26	10.97	+	2.37	0.000265	0.00418
regulation of sodium ion transport (GO:0002028)	96	26	11.32	+	2.3	0.000506	0.0073
ERAD pathway (GO:0036503)	96	26	11.32	+	2.3	0.000506	0.0073
regulation of fatty acid metabolic process (GO:0019217)	100	26	11.8	+	2.2	0.000708	0.0098
regulation of muscle cell apoptotic process (GO:0010660)	102	26	12.03	+	2.16	0.00121	0.0157
regulation of response to oxidative stress (GO:1902882)	102	26	12.03	+	2.16	0.00121	0.0157
positive regulation of axonogenesis (GO:0050772)	103	26	12.15	+	2.14	0.00127	0.0163
carbohydrate biosynthetic process (GO:0016051)	103	26	12.15	+	2.14	0.00127	0.0162
mitochondrial membrane organization (GO:0007006)	105	26	12.38	+	2.1	0.00145	0.0181
negative regulation of intrinsic apoptotic signaling pathway (GO:2001243)	106	26	12.5	+	2.08	0.00156	0.0193
negative regulation of lipid metabolic process (GO:0045833)	106	26	12.5	+	2.08	0.00156	0.0192
negative regulation of angiogenesis (GO:0016525)	107	26	12.62	+	2.06	0.00168	0.0204
negative regulation of blood vessel morphogenesis (GO:2000181)	109	26	12.86	+	2.02	0.00272	0.0307
negative regulation of vasculature development (GO:1901343)	110	26	12.97	+	2	0.00284	0.0318
negative regulation of ion transmembrane transport (GO:0034766)	110	26	12.97	+	2	0.00284	0.0317
regulation of postsynapse organization (GO:0099175)	113	26	13.33	+	1.95	0.00338	0.0365
negative regulation of actin filament polymerization (GO:0030837)	61	25	7.2	+	3.47	0.0000017	0.0000442
negative regulation of proteolysis involved in cellular protein catabolic process (GO:1903051)	67	25	7.9	+	3.16	0.00000648	0.000151
regulation of ATP-dependent activity (GO:0043462)	67	25	7.9	+	3.16	0.00000648	0.00015
protein localization to vacuole (GO:0072665)	67	25	7.9	+	3.16	0.00000648	0.00015
regulation of cardiac muscle hypertrophy (GO:0010611)	72	25	8.49	+	2.94	0.0000177	0.000379
liver regeneration (GO:0097421)	75	25	8.85	+	2.83	0.000045	0.000867
regulation of muscle hypertrophy (GO:0014743)	75	25	8.85	+	2.83	0.000045	0.000866
positive regulation of nucleocytoplasmic transport (GO:0046824)	76	25	8.96	+	2.79	0.0000496	0.000944
regulation of lipase activity (GO:0060191)	80	25	9.44	+	2.65	0.0000819	0.00148

protein localization to mitochondrion (GO:0070585)	81	25	9.55	+	2.62	0.0000943	0.00168
movement in host environment (GO:0052126)	82	25	9.67	+	2.58	0.000109	0.00192
positive regulation of mRNA catabolic process (GO:0061014)	84	25	9.91	+	2.52	0.000212	0.00342
tissue regeneration (GO:0042246)	85	25	10.03	+	2.49	0.000228	0.00365
epithelial cell migration (GO:0010631)	87	25	10.26	+	2.44	0.000273	0.00428
epithelium migration (GO:0090132)	89	25	10.5	+	2.38	0.000338	0.00516
regulation of cellular response to oxidative stress (GO:1900407)	92	25	10.85	+	2.3	0.000678	0.00947
mRNA transport (GO:0051028)	93	25	10.97	+	2.28	0.000721	0.00997
regulation of blood vessel endothelial cell migration (GO:0043535)	95	25	11.21	+	2.23	0.000838	0.0114
mitochondrial respiratory chain complex assembly (GO:0033108)	97	25	11.44	+	2.19	0.001	0.0132
regulation of ATP metabolic process (GO:1903578)	97	25	11.44	+	2.19	0.001	0.0132
positive regulation of ubiquitin-dependent protein catabolic process (GO:2000060)	102	25	12.03	+	2.08	0.00203	0.024
cellular response to hydrogen peroxide (GO:0070301)	103	25	12.15	+	2.06	0.00217	0.0254
neutral lipid metabolic process (GO:0006638)	104	25	12.27	+	2.04	0.00234	0.0269
sarcomere organization (GO:0045214)	41	24	4.84	+	4.96	1.73E-08	0.000000623
positive regulation of substrate adhesion-dependent cell spreading (GO:1900026)	45	24	5.31	+	4.52	6.59E-08	0.00000217
ribonucleoside triphosphate biosynthetic process (GO:0009201)	52	24	6.13	+	3.91	0.000000517	0.0000148
fatty acid beta-oxidation (GO:0006635)	57	24	6.72	+	3.57	0.00000187	0.0000483
positive regulation of dendritic spine development (GO:0060999)	65	24	7.67	+	3.13	0.0000114	0.000252
receptor internalization (GO:0031623)	69	24	8.14	+	2.95	0.0000253	0.000515
neural nucleus development (GO:0048857)	70	24	8.26	+	2.91	0.0000306	0.000609
regulation of cardiac muscle contraction (GO:0055117)	72	24	8.49	+	2.83	0.0000662	0.00122
actin cytoskeleton reorganization (GO:0031532)	74	24	8.73	+	2.75	0.0000808	0.00146
peptidyl-threonine phosphorylation (GO:0018107)	75	24	8.85	+	2.71	0.0000909	0.00163
regulation of cellular response to insulin stimulus (GO:1900076)	79	24	9.32	+	2.58	0.000156	0.00265
positive regulation of DNA biosynthetic process (GO:2000573)	80	24	9.44	+	2.54	0.00018	0.00298
cellular response to nerve growth factor stimulus (GO:1990090)	80	24	9.44	+	2.54	0.00018	0.00298
peptidyl-threonine modification (GO:0018210)	83	24	9.79	+	2.45	0.000358	0.00542
regulation of protein import (GO:1904589)	83	24	9.79	+	2.45	0.000358	0.00542
protein targeting to membrane (GO:0006612)	86	24	10.14	+	2.37	0.000482	0.00705
protein tetramerization (GO:0051262)	90	24	10.62	+	2.26	0.00103	0.0136
cellular response to UV (GO:0034644)	92	24	10.85	+	2.21	0.00119	0.0154
regulation of glucose transmembrane transport (GO:0010827)	93	24	10.97	+	2.19	0.00129	0.0164
ribosome assembly (GO:0042255)	94	24	11.09	+	2.16	0.00141	0.0177
endothelium development (GO:0003158)	99	24	11.68	+	2.06	0.00283	0.0317
negative regulation of ubiquitin-dependent protein catabolic process (GO:2000059)	52	23	6.13	+	3.75	0.00000158	0.0000412
regulation of lamellipodium organization (GO:1902743)	53	23	6.25	+	3.68	0.00000203	0.0000521
energy reserve metabolic process (GO:0006112)	58	23	6.84	+	3.36	0.00000675	0.000155
axonal transport (GO:0098930)	60	23	7.08	+	3.25	0.0000105	0.000235
regulation of microtubule polymerization (GO:0031113)	61	23	7.2	+	3.2	0.0000131	0.000287
cholesterol transport (GO:0030301)	61	23	7.2	+	3.2	0.0000131	0.000286
NADH dehydrogenase complex assembly (GO:0010257)	64	23	7.55	+	3.05	0.0000243	0.000501
mitochondrial respiratory chain complex I assembly (GO:0032981)	64	23	7.55	+	3.05	0.0000243	0.0005
maintenance of protein location in cell (GO:0032507)	66	23	7.78	+	2.95	0.0000361	0.000706
mitotic cytokinesis (GO:0000281)	67	23	7.9	+	2.91	0.0000437	0.000844
establishment of protein localization to mitochondrion (GO:0072655)	74	23	8.73	+	2.64	0.00017	0.00284
regulation of protein import into nucleus (GO:0042306)	77	23	9.08	+	2.53	0.000258	0.00409
negative regulation of RNA catabolic process (GO:1902369)	78	23	9.2	+	2.5	0.000447	0.00658
response to cadmium ion (GO:0046686)	83	23	9.79	+	2.35	0.000689	0.00962
positive regulation of organelle assembly (GO:1902117)	85	23	10.03	+	2.29	0.00132	0.0168
positive regulation of proteasomal ubiquitin-dependent protein catabolic process (GO:0032436)	88	23	10.38	+	2.22	0.00156	0.0193
maternal process involved in female pregnancy (GO:0060135)	89	23	10.5	+	2.19	0.00168	0.0204
glycosyl compound metabolic process (GO:1901657)	89	23	10.5	+	2.19	0.00168	0.0204
body fluid secretion (GO:0007589)	91	23	10.73	+	2.14	0.00199	0.0236

negative regulation of cysteine-type endopeptidase activity (GO:2000117)	94	23	11.09	+	2.07	0.00353	0.0376
positive regulation of endothelial cell proliferation (GO:0001938)	96	23	11.32	+	2.03	0.00395	0.0414
mitochondrial transmembrane transport (GO:1990542)	98	23	11.56	+	1.99	0.00453	0.046
positive regulation of lipid transport (GO:0032370)	98	23	11.56	+	1.99	0.00453	0.046
pattern specification process (GO:0007389)	469	23	55.32	-	0.42	0.00000357	0.0000873
negative regulation of blood coagulation (GO:0030195)	43	22	5.07	+	4.34	0.000000398	0.0000116
substantia nigra development (GO:0021762)	44	22	5.19	+	4.24	0.000000537	0.0000153
negative regulation of hemostasis (GO:1900047)	44	22	5.19	+	4.24	0.000000537	0.0000152
negative regulation of coagulation (GO:0050819)	45	22	5.31	+	4.14	0.000000721	0.00002
purine nucleoside triphosphate biosynthetic process (GO:0009145)	47	22	5.54	+	3.97	0.00000127	0.0000339
lamellipodium organization (GO:0097581)	48	22	5.66	+	3.89	0.00000167	0.0000435
establishment of protein localization to vacuole (GO:0072666)	52	22	6.13	+	3.59	0.00000467	0.000111
presynaptic endocytosis (GO:0140238)	56	22	6.61	+	3.33	0.000012	0.000264
synaptic vesicle endocytosis (GO:0048488)	56	22	6.61	+	3.33	0.000012	0.000264
positive regulation of wound healing (GO:0090303)	58	22	6.84	+	3.22	0.0000186	0.000396
positive regulation of stress fiber assembly (GO:0051496)	58	22	6.84	+	3.22	0.0000186	0.000395
positive regulation of viral process (GO:0048524)	60	22	7.08	+	3.11	0.0000283	0.000569
actin filament bundle assembly (GO:0051017)	60	22	7.08	+	3.11	0.0000283	0.000568
actin polymerization or depolymerization (GO:0008154)	61	22	7.2	+	3.06	0.0000347	0.000681
ribonucleoside monophosphate metabolic process (GO:0009161)	62	22	7.31	+	3.01	0.0000424	0.000823
actin filament bundle organization (GO:0061572)	63	22	7.43	+	2.96	0.0000515	0.000976
endocytic recycling (GO:0032456)	64	22	7.55	+	2.91	0.0000624	0.00116
negative regulation of mRNA catabolic process (GO:1902373)	66	22	7.78	+	2.83	0.000144	0.00248
positive regulation of cell-matrix adhesion (GO:0001954)	67	22	7.9	+	2.78	0.000156	0.00265
positive regulation of smooth muscle cell migration (GO:0014911)	69	22	8.14	+	2.7	0.000192	0.00315
positive regulation of intrinsic apoptotic signaling pathway (GO:2001244)	70	22	8.26	+	2.66	0.000217	0.00349
protein localization to endoplasmic reticulum (GO:0070972)	72	22	8.49	+	2.59	0.000281	0.00439
organelle transport along microtubule (GO:0072384)	74	22	8.73	+	2.52	0.00037	0.00555
regulation of insulin receptor signaling pathway (GO:0046626)	78	22	9.2	+	2.39	0.000813	0.0111
ubiquitin-dependent ERAD pathway (GO:0030433)	80	22	9.44	+	2.33	0.000986	0.0131
regulation of oxidative stress-induced cell death (GO:1903201)	81	22	9.55	+	2.3	0.00109	0.0143
regulation of tissue remodeling (GO:0034103)	86	22	10.14	+	2.17	0.00238	0.0272
regulation of phosphatase activity (GO:0010921)	87	22	10.26	+	2.14	0.00258	0.0294
regulation of organic acid transport (GO:0032890)	91	22	10.73	+	2.05	0.00494	0.0496
cytoplasmic translational initiation (GO:0002183)	30	21	3.54	+	5.93	0.000000014	0.000000513
purine ribonucleoside triphosphate biosynthetic process (GO:0009206)	46	21	5.43	+	3.87	0.000003	0.0000745
retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum (GO:0006890)	49	21	5.78	+	3.63	0.00000652	0.000151
regulation of plasma lipoprotein particle levels (GO:0097006)	52	21	6.13	+	3.42	0.0000134	0.000293
regulation of filopodium assembly (GO:0051489)	55	21	6.49	+	3.24	0.0000264	0.000534
positive regulation of actin filament polymerization (GO:0030838)	55	21	6.49	+	3.24	0.0000264	0.000534
vesicle docking (GO:0048278)	59	21	6.96	+	3.02	0.0000605	0.00113
vesicle cytoskeletal trafficking (GO:0099518)	67	21	7.9	+	2.66	0.000315	0.00484
intermediate filament-based process (GO:0045103)	68	21	8.02	+	2.62	0.000356	0.0054
regulation of glucose import (GO:0046324)	74	21	8.73	+	2.41	0.00108	0.0142
triglyceride metabolic process (GO:0006641)	75	21	8.85	+	2.37	0.00117	0.0152
regulation of intracellular steroid hormone receptor signaling pathway (GO:0033143)	77	21	9.08	+	2.31	0.00141	0.0177
positive regulation of reactive oxygen species metabolic process (GO:2000379)	80	21	9.44	+	2.23	0.00282	0.0316
regulation of response to endoplasmic reticulum stress (GO:1905897)	82	21	9.67	+	2.17	0.00315	0.0347
regulation of telomere maintenance (GO:0032204)	83	21	9.79	+	2.15	0.00337	0.0365
regulation of mitochondrial membrane potential (GO:0051881)	84	21	9.91	+	2.12	0.00363	0.0386
keratinocyte differentiation (GO:0030216)	84	21	9.91	+	2.12	0.00363	0.0385
hydrogen peroxide metabolic process (GO:0042743)	42	20	4.95	+	4.04	0.00000312	0.0000772
glycogen metabolic process (GO:0005977)	48	20	5.66	+	3.53	0.0000149	0.000324
cellular glucan metabolic process (GO:0006073)	48	20	5.66	+	3.53	0.0000149	0.000323

glucan metabolic process (GO:0044042)	49	20	5.78	+	3.46	0.0000189	0.000402
substrate adhesion-dependent cell spreading (GO:0034446)	55	20	6.49	+	3.08	0.0000707	0.00129
cellular protein complex disassembly (GO:0043624)	58	20	6.84	+	2.92	0.000128	0.00221
regulation of striated muscle cell apoptotic process (GO:0010662)	61	20	7.2	+	2.78	0.00034	0.00518
ventricular cardiac muscle tissue development (GO:0003229)	61	20	7.2	+	2.78	0.00034	0.00518
nucleoside metabolic process (GO:0009116)	63	20	7.43	+	2.69	0.00041	0.00607
intermediate filament cytoskeleton organization (GO:0045104)	64	20	7.55	+	2.65	0.000458	0.00671
regulation of sodium ion transmembrane transport (GO:1902305)	65	20	7.67	+	2.61	0.000516	0.00744
negative regulation of intracellular transport (GO:0032387)	66	20	7.78	+	2.57	0.000585	0.00834
mRNA destabilization (GO:0061157)	68	20	8.02	+	2.49	0.000762	0.0105
cellular polysaccharide metabolic process (GO:0044264)	69	20	8.14	+	2.46	0.00138	0.0173
regulation of lipid catabolic process (GO:0050994)	70	20	8.26	+	2.42	0.00146	0.0182
polysaccharide metabolic process (GO:0005976)	71	20	8.37	+	2.39	0.00156	0.0193
regulation of nitric oxide biosynthetic process (GO:0045428)	72	20	8.49	+	2.36	0.00169	0.0204
regulation of protein processing (GO:0070613)	72	20	8.49	+	2.36	0.00169	0.0204
RNA destabilization (GO:0050779)	72	20	8.49	+	2.36	0.00169	0.0204
regulation of protein maturation (GO:1903317)	74	20	8.73	+	2.29	0.00202	0.0239
exocytic process (GO:0140029)	75	20	8.85	+	2.26	0.00223	0.026
regulation of ERBB signaling pathway (GO:1901184)	77	20	9.08	+	2.2	0.00402	0.042
response to cold (GO:0009409)	77	20	9.08	+	2.2	0.00402	0.042
regulation of nitric oxide metabolic process (GO:0080164)	77	20	9.08	+	2.2	0.00402	0.042
cellular response to cAMP (GO:0071320)	78	20	9.2	+	2.17	0.00422	0.0435
regulation of signal transduction by p53 class mediator (GO:1901796)	80	20	9.44	+	2.12	0.00477	0.048
ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway (GO:0043162)	28	19	3.3	+	5.75	9.75E-08	0.00000313
positive regulation of lamellipodium organization (GO:1902745)	38	19	4.48	+	4.24	0.00000315	0.000078
cortical actin cytoskeleton organization (GO:0030866)	38	19	4.48	+	4.24	0.00000315	0.0000779
cardiac muscle hypertrophy (GO:0003300)	39	19	4.6	+	4.13	0.00000423	0.000102
negative regulation of actin filament depolymerization (GO:0030835)	41	19	4.84	+	3.93	0.00000742	0.000169
regulation of lamellipodium assembly (GO:0010591)	41	19	4.84	+	3.93	0.00000742	0.000168
striated muscle hypertrophy (GO:0014897)	41	19	4.84	+	3.93	0.00000742	0.000168
acute-phase response (GO:0006953)	42	19	4.95	+	3.84	0.00000972	0.000217
synaptic vesicle transport (GO:0048489)	42	19	4.95	+	3.84	0.00000972	0.000217
muscle hypertrophy (GO:0014896)	43	19	5.07	+	3.75	0.0000126	0.000278
synaptic vesicle localization (GO:0097479)	48	19	5.66	+	3.36	0.0000425	0.000825
negative regulation of proteasomal protein catabolic process (GO:1901799)	49	19	5.78	+	3.29	0.0000532	0.001
mRNA stabilization (GO:0048255)	55	19	6.49	+	2.93	0.000183	0.00302
positive regulation of axon extension (GO:0045773)	56	19	6.61	+	2.88	0.000221	0.00356
musculoskeletal movement (GO:0050881)	57	19	6.72	+	2.83	0.000266	0.00419
multicellular organismal movement (GO:0050879)	57	19	6.72	+	2.83	0.000266	0.00419
positive regulation of blood vessel endothelial cell migration (GO:0043536)	58	19	6.84	+	2.78	0.000503	0.00727
membrane biogenesis (GO:0044091)	61	19	7.2	+	2.64	0.000667	0.00934
cytoplasmic microtubule organization (GO:0031122)	62	19	7.31	+	2.6	0.000749	0.0103
regulation of alternative mRNA splicing, via spliceosome (GO:0000381)	63	19	7.43	+	2.56	0.000847	0.0115
negative regulation of muscle cell apoptotic process (GO:0010656)	63	19	7.43	+	2.56	0.000847	0.0115
RNA stabilization (GO:0043489)	64	19	7.55	+	2.52	0.000962	0.0128
apoptotic mitochondrial changes (GO:0008637)	68	19	8.02	+	2.37	0.00226	0.0262
modulation by host of symbiont process (GO:0051851)	70	19	8.26	+	2.3	0.00264	0.0299
positive regulation of protein localization to cell periphery (GO:1904377)	71	19	8.37	+	2.27	0.00289	0.0321
regulation of epidermal growth factor receptor signaling pathway (GO:0042058)	72	19	8.49	+	2.24	0.00317	0.0347
response to progesterone (GO:0032570)	73	19	8.61	+	2.21	0.00351	0.0374
tricarboxylic acid cycle (GO:0006099)	30	18	3.54	+	5.09	0.0000008	0.0000219
positive regulation of cell-substrate junction organization (GO:0150117)	35	18	4.13	+	4.36	0.00000421	0.000102
protein targeting to vacuole (GO:0006623)	39	18	4.6	+	3.91	0.0000134	0.000292
protein-lipid complex subunit organization (GO:0071825)	41	18	4.84	+	3.72	0.0000227	0.000473

purine ribonucleoside monophosphate metabolic process (GO:0009167)	45	18	5.31	+	3.39	0.0000602	0.00112
toxin transport (GO:1901998)	48	18	5.66	+	3.18	0.000117	0.00204
purine nucleoside monophosphate metabolic process (GO:0009126)	48	18	5.66	+	3.18	0.000117	0.00204
nucleoside monophosphate biosynthetic process (GO:0009124)	49	18	5.78	+	3.11	0.000144	0.00248
vacuolar localization (GO:1990849)	50	18	5.9	+	3.05	0.000177	0.00295
regulation of monooxygenase activity (GO:0032768)	50	18	5.9	+	3.05	0.000177	0.00294
lysosome localization (GO:0032418)	50	18	5.9	+	3.05	0.000177	0.00294
regulation of posttranscriptional gene silencing (GO:0060147)	51	18	6.02	+	2.99	0.000216	0.00349
regulation of gene silencing by RNA (GO:0060966)	52	18	6.13	+	2.93	0.000263	0.00414
establishment of protein localization to plasma membrane (GO:0061951)	53	18	6.25	+	2.88	0.000318	0.00488
endosome organization (GO:0007032)	54	18	6.37	+	2.83	0.000382	0.00573
Rho protein signal transduction (GO:0007266)	55	18	6.49	+	2.77	0.000746	0.0103
spindle localization (GO:0051653)	56	18	6.61	+	2.73	0.000804	0.011
regulation of cardiac muscle cell apoptotic process (GO:0010665)	58	18	6.84	+	2.63	0.000974	0.013
positive regulation of protein import (GO:1904591)	59	18	6.96	+	2.59	0.00109	0.0143
endosome to lysosome transport (GO:0008333)	60	18	7.08	+	2.54	0.00123	0.0158
regulation of carbohydrate catabolic process (GO:0043470)	63	18	7.43	+	2.42	0.0018	0.0216
cardiac muscle tissue morphogenesis (GO:0055008)	64	18	7.55	+	2.38	0.00307	0.0339
zymogen activation (GO:0031638)	65	18	7.67	+	2.35	0.00326	0.0354
negative regulation of MAP kinase activity (GO:0043407)	65	18	7.67	+	2.35	0.00326	0.0354
cell-cell recognition (GO:0009988)	66	18	7.78	+	2.31	0.0035	0.0374
stress-activated protein kinase signaling cascade (GO:0031098)	68	18	8.02	+	2.24	0.00413	0.0429
hydrogen peroxide catabolic process (GO:0042744)	27	17	3.18	+	5.34	0.000000986	0.0000266
regulation of cytoplasmic transport (GO:1903649)	30	17	3.54	+	4.8	0.00000289	0.0000721
positive regulation of lamellipodium assembly (GO:0010592)	30	17	3.54	+	4.8	0.00000289	0.000072
regulation of the force of heart contraction (GO:0002026)	31	17	3.66	+	4.65	0.00000404	0.0000982
negative regulation of proteasomal ubiquitin-dependent protein catabolic process (GO:0032435)	36	17	4.25	+	4	0.0000184	0.000392
plasma lipoprotein particle organization (GO:0071827)	37	17	4.36	+	3.9	0.0000242	0.000499
ATP biosynthetic process (GO:0006754)	37	17	4.36	+	3.9	0.0000242	0.000498
positive regulation of cardiac muscle hypertrophy (GO:0010613)	40	17	4.72	+	3.6	0.0000526	0.000993
positive regulation of muscle hypertrophy (GO:0014742)	41	17	4.84	+	3.52	0.0000672	0.00123
positive regulation of ATP-dependent activity (GO:0032781)	43	17	5.07	+	3.35	0.000107	0.0019
regulation of actin filament-based movement (GO:1903115)	45	17	5.31	+	3.2	0.000167	0.00279
anterograde axonal transport (GO:0008089)	46	17	5.43	+	3.13	0.000206	0.00335
regulation of gene silencing by miRNA (GO:0060964)	48	17	5.66	+	3	0.00031	0.00478
ventricular cardiac muscle tissue morphogenesis (GO:0055010)	50	17	5.9	+	2.88	0.000456	0.0067
negative regulation of dephosphorylation (GO:0035305)	50	17	5.9	+	2.88	0.000456	0.0067
Golgi to plasma membrane transport (GO:0006893)	51	17	6.02	+	2.83	0.00055	0.00788
regulation of extrinsic apoptotic signaling pathway via death domain receptors (GO:1902041)	51	17	6.02	+	2.83	0.00055	0.00787
protein insertion into membrane (GO:0051205)	51	17	6.02	+	2.83	0.00055	0.00787
positive regulation of protein import into nucleus (GO:0042307)	53	17	6.25	+	2.72	0.00119	0.0154
membrane assembly (GO:0071709)	54	17	6.37	+	2.67	0.00129	0.0165
posttranscriptional gene silencing (GO:0016441)	55	17	6.49	+	2.62	0.00143	0.0178
regulation of sodium ion transmembrane transporter activity (GO:2000649)	56	17	6.61	+	2.57	0.00159	0.0195
peptidyl-proline modification (GO:0018208)	56	17	6.61	+	2.57	0.00159	0.0195
regulation of ubiquitin-protein transferase activity (GO:0051438)	56	17	6.61	+	2.57	0.00159	0.0195
cellular aldehyde metabolic process (GO:0006081)	58	17	6.84	+	2.48	0.00201	0.0238
positive regulation of extrinsic apoptotic signaling pathway (GO:2001238)	59	17	6.96	+	2.44	0.00228	0.0265
regulation of phosphoprotein phosphatase activity (GO:0043666)	59	17	6.96	+	2.44	0.00228	0.0264
response to increased oxygen levels (GO:0036296)	59	17	6.96	+	2.44	0.00228	0.0264
iron ion transport (GO:0006826)	60	17	7.08	+	2.4	0.00258	0.0294
positive regulation of lipase activity (GO:0060193)	60	17	7.08	+	2.4	0.00258	0.0294
regulation of telomere maintenance via telomere lengthening (GO:1904356)	60	17	7.08	+	2.4	0.00258	0.0294
insulin receptor signaling pathway (GO:0008286)	61	17	7.2	+	2.36	0.00446	0.0454

protein activation cascade (GO:0072376)	23	16	2.71	+	5.9	0.000000788	0.0000217
COPII-coated vesicle budding (GO:0090114)	23	16	2.71	+	5.9	0.000000788	0.0000217
positive regulation of posttranscriptional gene silencing (GO:0060148)	32	16	3.77	+	4.24	0.0000187	0.000398
actin filament capping (GO:0051693)	34	16	4.01	+	3.99	0.0000332	0.000656
acetyl-CoA metabolic process (GO:0006084)	35	16	4.13	+	3.88	0.0000437	0.000844
vesicle targeting (GO:0006903)	37	16	4.36	+	3.67	0.0000737	0.00135
nucleobase metabolic process (GO:0009112)	38	16	4.48	+	3.57	0.0000946	0.00169
ribonucleoside monophosphate biosynthetic process (GO:0009156)	39	16	4.6	+	3.48	0.00012	0.0021
lamellipodium assembly (GO:0030032)	39	16	4.6	+	3.48	0.00012	0.0021
translational elongation (GO:0006414)	43	16	5.07	+	3.15	0.000295	0.00458
intermediate filament organization (GO:0045109)	43	16	5.07	+	3.15	0.000295	0.00457
vesicle transport along microtubule (GO:0047496)	43	16	5.07	+	3.15	0.000295	0.00457
regulation of protein localization to cell surface (GO:2000008)	44	16	5.19	+	3.08	0.000364	0.00548
regulation of polysaccharide metabolic process (GO:0032881)	47	16	5.54	+	2.89	0.000657	0.00923
ERBB signaling pathway (GO:0038127)	47	16	5.54	+	2.89	0.000657	0.00923
negative regulation of microtubule polymerization or depolymerization (GO:0031111)	47	16	5.54	+	2.89	0.000657	0.00922
positive regulation of telomere maintenance (GO:0032206)	54	16	6.37	+	2.51	0.00259	0.0294
negative regulation of oxidative stress-induced cell death (GO:1903202)	55	16	6.49	+	2.47	0.00291	0.0323
metaphase plate congression (GO:0051310)	57	16	6.72	+	2.38	0.00372	0.0391
response to morphine (GO:0043278)	57	16	6.72	+	2.38	0.00372	0.0391
positive regulation of glucose transmembrane transport (GO:0010828)	57	16	6.72	+	2.38	0.00372	0.0391
regulation of early endosome to late endosome transport (GO:2000641)	19	15	2.24	+	6.69	0.000000563	0.0000159
viral release from host cell (GO:0019076)	24	15	2.83	+	5.3	0.00000457	0.000109
exit from host cell (GO:0035891)	24	15	2.83	+	5.3	0.00000457	0.000109
exit from host (GO:0035890)	24	15	2.83	+	5.3	0.00000457	0.000109
plasma lipoprotein particle remodeling (GO:0034369)	25	15	2.95	+	5.09	0.0000066	0.000152
protein-lipid complex remodeling (GO:0034368)	25	15	2.95	+	5.09	0.0000066	0.000152
protein-containing complex remodeling (GO:0034367)	27	15	3.18	+	4.71	0.0000132	0.000289
regulation of cytoplasmic translation (GO:2000765)	28	15	3.3	+	4.54	0.0000183	0.000391
clathrin-dependent endocytosis (GO:0072583)	29	15	3.42	+	4.39	0.000025	0.000513
positive regulation of gene silencing by miRNA (GO:2000637)	31	15	3.66	+	4.1	0.0000454	0.000871
modulation by host of viral process (GO:0044788)	34	15	4.01	+	3.74	0.000103	0.00183
negative regulation of striated muscle cell apoptotic process (GO:0010664)	38	15	4.48	+	3.35	0.000272	0.00427
regulation of polysaccharide biosynthetic process (GO:0032885)	39	15	4.6	+	3.26	0.000341	0.00518
cellular response to osmotic stress (GO:0071470)	39	15	4.6	+	3.26	0.000341	0.00517
'de novo' protein folding (GO:0006458)	44	15	5.19	+	2.89	0.000946	0.0127
apoptotic cell clearance (GO:0043277)	44	15	5.19	+	2.89	0.000946	0.0127
protein localization to lysosome (GO:0061462)	44	15	5.19	+	2.89	0.000946	0.0126
mitotic metaphase plate congression (GO:0007080)	45	15	5.31	+	2.83	0.00114	0.0149
tRNA aminoacylation for protein translation (GO:0006418)	45	15	5.31	+	2.83	0.00114	0.0149
neuron projection regeneration (GO:0031102)	45	15	5.31	+	2.83	0.00114	0.0149
negative regulation of cellular response to insulin stimulus (GO:1900077)	46	15	5.43	+	2.76	0.00137	0.0172
adherens junction organization (GO:0034332)	46	15	5.43	+	2.76	0.00137	0.0172
maternal placenta development (GO:0001893)	47	15	5.54	+	2.71	0.00262	0.0297
response to angiotensin (GO:1990776)	47	15	5.54	+	2.71	0.00262	0.0296
regulation of vascular permeability (GO:0043114)	48	15	5.66	+	2.65	0.00282	0.0316
tRNA aminoacylation (GO:0043039)	48	15	5.66	+	2.65	0.00282	0.0315
amino acid activation (GO:0043038)	49	15	5.78	+	2.6	0.00307	0.0339
negative regulation of endocytosis (GO:0045806)	49	15	5.78	+	2.6	0.00307	0.0338
regulation of telomere maintenance via telomerase (GO:0032210)	50	15	5.9	+	2.54	0.00339	0.0367
establishment of spindle localization (GO:0051293)	50	15	5.9	+	2.54	0.00339	0.0366
trabecula morphogenesis (GO:0061383)	53	15	6.25	+	2.4	0.00475	0.0479
regionalization (GO:0003002)	360	15	42.46	-	0.35	0.00000564	0.000132
ATP synthesis coupled proton transport (GO:0015986)	23	14	2.71	+	5.16	0.0000118	0.000262

energy coupled proton transport, down electrochemical gradient (GO:0015985)	23	14	2.71	+	5.16	0.0000118	0.000262
virion assembly (GO:0019068)	27	14	3.18	+	4.4	0.0000455	0.000871
intra-Golgi vesicle-mediated transport (GO:0006891)	30	14	3.54	+	3.96	0.000109	0.00193
positive regulation of focal adhesion assembly (GO:0051894)	30	14	3.54	+	3.96	0.000109	0.00193
endosome transport via multivesicular body sorting pathway (GO:0032509)	30	14	3.54	+	3.96	0.000109	0.00192
multivesicular body sorting pathway (GO:0071985)	34	14	4.01	+	3.49	0.000306	0.00473
response to interleukin-4 (GO:0070670)	35	14	4.13	+	3.39	0.000388	0.0058
axon regeneration (GO:0031103)	35	14	4.13	+	3.39	0.000388	0.00579
negative regulation of protein dephosphorylation (GO:0035308)	36	14	4.25	+	3.3	0.000487	0.00711
positive regulation of telomere maintenance via telomere lengthening (GO:1904358)	36	14	4.25	+	3.3	0.000487	0.0071
negative regulation of lipid transport (GO:0032369)	37	14	4.36	+	3.21	0.000607	0.0086
regulation of cardiac muscle cell contraction (GO:0086004)	37	14	4.36	+	3.21	0.000607	0.0086
regulation of nitric-oxide synthase activity (GO:0050999)	38	14	4.48	+	3.12	0.00075	0.0103
ERK1 and ERK2 cascade (GO:0070371)	38	14	4.48	+	3.12	0.00075	0.0103
purine nucleoside bisphosphate biosynthetic process (GO:0034033)	41	14	4.84	+	2.89	0.00137	0.0173
ribonucleoside bisphosphate biosynthetic process (GO:0034030)	41	14	4.84	+	2.89	0.00137	0.0173
cell-substrate junction organization (GO:0150115)	41	14	4.84	+	2.89	0.00137	0.0172
negative regulation of insulin receptor signaling pathway (GO:0046627)	41	14	4.84	+	2.89	0.00137	0.0172
nucleoside bisphosphate biosynthetic process (GO:0033866)	41	14	4.84	+	2.89	0.00137	0.0172
'de novo' posttranslational protein folding (GO:0051084)	42	14	4.95	+	2.83	0.00165	0.02
positive regulation of sodium ion transport (GO:0010765)	43	14	5.07	+	2.76	0.00197	0.0235
protein depolymerization (GO:0051261)	44	14	5.19	+	2.7	0.00389	0.0408
regulation of amyloid precursor protein catabolic process (GO:1902991)	45	14	5.31	+	2.64	0.00417	0.043
regulation of fatty acid biosynthetic process (GO:0042304)	46	14	5.43	+	2.58	0.00453	0.0461
response to thyroid hormone (GO:0097066)	46	14	5.43	+	2.58	0.00453	0.046
establishment of protein localization to endoplasmic reticulum (GO:0072599)	46	14	5.43	+	2.58	0.00453	0.046
binding of sperm to zona pellucida (GO:0007339)	47	14	5.54	+	2.53	0.00497	0.0496
negative regulation of endothelial cell proliferation (GO:0001937)	47	14	5.54	+	2.53	0.00497	0.0496
mitochondrial ATP synthesis coupled proton transport (GO:0042776)	16	13	1.89	+	6.89	0.00000259	0.0000649
blood coagulation, fibrin clot formation (GO:0072378)	18	13	2.12	+	6.12	0.00000641	0.000149
stress granule assembly (GO:0034063)	22	13	2.59	+	5.01	0.0000306	0.000609
GMP metabolic process (GO:0046037)	23	13	2.71	+	4.79	0.0000433	0.000838
NADH metabolic process (GO:0006734)	26	13	3.07	+	4.24	0.000112	0.00197
response to muscle stretch (GO:0035994)	27	13	3.18	+	4.08	0.00015	0.00257
cholesterol efflux (GO:0033344)	28	13	3.3	+	3.94	0.000199	0.00325
TOR signaling (GO:0031929)	28	13	3.3	+	3.94	0.000199	0.00325
ruffle organization (GO:0031529)	28	13	3.3	+	3.94	0.000199	0.00325
response to nitric oxide (GO:0071731)	30	13	3.54	+	3.67	0.000338	0.00516
nucleus localization (GO:0051647)	32	13	3.77	+	3.44	0.000552	0.00789
positive regulation of telomere maintenance via telomerase (GO:0032212)	32	13	3.77	+	3.44	0.000552	0.00789
cell redox homeostasis (GO:0045454)	33	13	3.89	+	3.34	0.000696	0.00969
regulation of superoxide metabolic process (GO:0090322)	34	13	4.01	+	3.24	0.00087	0.0118
negative regulation of cardiac muscle cell apoptotic process (GO:0010667)	35	13	4.13	+	3.15	0.00108	0.0142
protein localization to cell surface (GO:0034394)	35	13	4.13	+	3.15	0.00108	0.0142
establishment of endothelial barrier (GO:0061028)	35	13	4.13	+	3.15	0.00108	0.0142
cytokinetic process (GO:0032506)	36	13	4.25	+	3.06	0.00133	0.0169
peptide cross-linking (GO:0018149)	36	13	4.25	+	3.06	0.00133	0.0169
purine nucleoside metabolic process (GO:0042278)	36	13	4.25	+	3.06	0.00133	0.0168
regulation of amyloid-beta formation (GO:1902003)	37	13	4.36	+	2.98	0.00163	0.0198
regulation of mitotic spindle organization (GO:0060236)	38	13	4.48	+	2.9	0.00197	0.0235
regulation of glycogen metabolic process (GO:0070873)	38	13	4.48	+	2.9	0.00197	0.0235
protein peptidyl-prolyl isomerization (GO:0000413)	38	13	4.48	+	2.9	0.00197	0.0235
regulation of protein export from nucleus (GO:0046825)	38	13	4.48	+	2.9	0.00197	0.0235
ribonucleoside metabolic process (GO:0009119)	39	13	4.6	+	2.83	0.00238	0.0272

cell-substrate junction assembly (GO:0007044)	40	13	4.72	+	2.76	0.00286	0.0318
endodermal cell differentiation (GO:0035987)	40	13	4.72	+	2.76	0.00286	0.0318
autophagosome maturation (GO:0097352)	40	13	4.72	+	2.76	0.00286	0.0318
epidermal growth factor receptor signaling pathway (GO:0007173)	41	13	4.84	+	2.69	0.00341	0.0368
cellular response to vascular endothelial growth factor stimulus (GO:0035924)	41	13	4.84	+	2.69	0.00341	0.0368
maintenance of protein localization in organelle (GO:0072595)	41	13	4.84	+	2.69	0.00341	0.0367
detection of stimulus (GO:0051606)	1419	13	167.37	-	0.08	1.85E-52	1.85E-49
fibrinolysis (GO:0042730)	14	12	1.65	+	7.27	0.00000433	0.000104
formation of cytoplasmic translation initiation complex (GO:0001732)	15	12	1.77	+	6.78	0.00000705	0.000161
clathrin coat assembly (GO:0048268)	18	12	2.12	+	5.65	0.0000259	0.000527
vesicle cargo loading (GO:0035459)	18	12	2.12	+	5.65	0.0000259	0.000526
cellular response to nitric oxide (GO:0071732)	24	12	2.83	+	4.24	0.000205	0.00333
protein targeting to lysosome (GO:0006622)	25	12	2.95	+	4.07	0.000275	0.0043
regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay (GO:1900151)	25	12	2.95	+	4.07	0.000275	0.0043
purine ribonucleoside monophosphate biosynthetic process (GO:0009168)	26	12	3.07	+	3.91	0.000363	0.00548
mitochondrial electron transport, NADH to ubiquinone (GO:0006120)	27	12	3.18	+	3.77	0.000475	0.00695
regulation of oxidative stress-induced intrinsic apoptotic signaling pathway (GO:1902175)	28	12	3.3	+	3.63	0.000614	0.00869
cellular response to reactive nitrogen species (GO:1902170)	28	12	3.3	+	3.63	0.000614	0.00868
purine nucleoside monophosphate biosynthetic process (GO:0009127)	28	12	3.3	+	3.63	0.000614	0.00868
negative regulation of oxidoreductase activity (GO:0051354)	29	12	3.42	+	3.51	0.000785	0.0107
regulation of glycogen biosynthetic process (GO:0005979)	30	12	3.54	+	3.39	0.000995	0.0132
cellular response to interleukin-4 (GO:0071353)	30	12	3.54	+	3.39	0.000995	0.0132
negative regulation of receptor-mediated endocytosis (GO:0048261)	30	12	3.54	+	3.39	0.000995	0.0132
regulation of glucan biosynthetic process (GO:0010962)	30	12	3.54	+	3.39	0.000995	0.0132
purine ribonucleoside metabolic process (GO:0046128)	31	12	3.66	+	3.28	0.00125	0.016
AMP metabolic process (GO:0046033)	31	12	3.66	+	3.28	0.00125	0.016
protein export from nucleus (GO:0006611)	32	12	3.77	+	3.18	0.00156	0.0193
Golgi to plasma membrane protein transport (GO:0043001)	32	12	3.77	+	3.18	0.00156	0.0193
regulation of intracellular estrogen receptor signaling pathway (GO:0033146)	35	12	4.13	+	2.91	0.00286	0.0318
negative regulation of actin filament bundle assembly (GO:0032232)	36	12	4.25	+	2.83	0.00345	0.0372
chaperone cofactor-dependent protein refolding (GO:0051085)	36	12	4.25	+	2.83	0.00345	0.0372
positive regulation of microtubule polymerization (GO:0031116)	36	12	4.25	+	2.83	0.00345	0.0371
regulation of long-term neuronal synaptic plasticity (GO:0048169)	37	12	4.36	+	2.75	0.00414	0.043
regulation of intrinsic apoptotic signaling pathway in response to DNA damage (GO:1902229)	38	12	4.48	+	2.68	0.00494	0.0495
negative regulation of protein localization to membrane (GO:1905476)	38	12	4.48	+	2.68	0.00494	0.0495
GMP biosynthetic process (GO:0006177)	14	11	1.65	+	6.66	0.0000192	0.000407
positive regulation of cytoplasmic translation (GO:2000767)	16	11	1.89	+	5.83	0.000046	0.00088
cellular response to interleukin-7 (GO:0098761)	17	11	2.01	+	5.49	0.0000686	0.00126
response to interleukin-7 (GO:0098760)	17	11	2.01	+	5.49	0.0000686	0.00126
protein localization to cell-cell junction (GO:0150105)	20	11	2.36	+	4.66	0.000201	0.00327
postsynaptic actin cytoskeleton organization (GO:0098974)	21	11	2.48	+	4.44	0.000277	0.00433
IMP metabolic process (GO:0046040)	23	11	2.71	+	4.05	0.000503	0.0073
plasma membrane repair (GO:0001778)	23	11	2.71	+	4.05	0.000503	0.00729
positive regulation of sodium ion transmembrane transport (GO:1902307)	23	11	2.71	+	4.05	0.000503	0.00728
postsynaptic cytoskeleton organization (GO:0099188)	23	11	2.71	+	4.05	0.000503	0.00728
regulation of complement activation (GO:0030449)	24	11	2.83	+	3.89	0.000664	0.00931
late endosome to vacuole transport (GO:0045324)	25	11	2.95	+	3.73	0.000866	0.0118
establishment of protein localization to mitochondrial membrane (GO:0090151)	25	11	2.95	+	3.73	0.000866	0.0117
nuclear migration (GO:0007097)	27	11	3.18	+	3.45	0.00142	0.0179
peptide catabolic process (GO:0043171)	27	11	3.18	+	3.45	0.00142	0.0178
regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum (GO:0010880)	27	11	3.18	+	3.45	0.00142	0.0178
negative regulation of epidermal growth factor receptor signaling pathway (GO:0042059)	28	11	3.3	+	3.33	0.0018	0.0216
protein localization to Golgi apparatus (GO:0034067)	29	11	3.42	+	3.22	0.00224	0.0261
acyl-CoA biosynthetic process (GO:0071616)	30	11	3.54	+	3.11	0.00278	0.0313

negative regulation of ERBB signaling pathway (GO:1901185)	30	11	3.54	+	3.11	0.00278	0.0313
cellular metabolic compound salvage (GO:0043094)	30	11	3.54	+	3.11	0.00278	0.0313
thioester biosynthetic process (GO:0035384)	30	11	3.54	+	3.11	0.00278	0.0312
negative regulation of extrinsic apoptotic signaling pathway via death domain receptors (GO:1902042)	31	11	3.66	+	3.01	0.00341	0.0368
pyrimidine-containing compound biosynthetic process (GO:0072528)	31	11	3.66	+	3.01	0.00341	0.0368
positive regulation of protein processing (GO:0010954)	32	11	3.77	+	2.91	0.00416	0.0429
regulation of fibrinolysis (GO:0051917)	11	10	1.3	+	7.71	0.0000198	0.000417
COPII-coated vesicle cargo loading (GO:0090110)	14	10	1.65	+	6.06	0.0000816	0.00147
chaperone-mediated autophagy (GO:0061684)	14	10	1.65	+	6.06	0.0000816	0.00147
viral translation (GO:0019081)	15	10	1.77	+	5.65	0.000123	0.00214
positive regulation of telomerase RNA localization to Cajal body (GO:1904874)	15	10	1.77	+	5.65	0.000123	0.00213
positive regulation of exosomal secretion (GO:1903543)	15	10	1.77	+	5.65	0.000123	0.00213
physiological cardiac muscle hypertrophy (GO:0003301)	16	10	1.89	+	5.3	0.000181	0.00299
physiological muscle hypertrophy (GO:0003298)	16	10	1.89	+	5.3	0.000181	0.00299
cell growth involved in cardiac muscle cell development (GO:0061049)	16	10	1.89	+	5.3	0.000181	0.00299
positive regulation by host of viral process (GO:0044794)	17	10	2.01	+	4.99	0.000261	0.00412
regulation of exosomal secretion (GO:1903541)	17	10	2.01	+	4.99	0.000261	0.00412
Rab protein signal transduction (GO:0032482)	18	10	2.12	+	4.71	0.000367	0.00553
regulation of telomerase RNA localization to Cajal body (GO:1904872)	18	10	2.12	+	4.71	0.000367	0.00553
viral budding (GO:0046755)	18	10	2.12	+	4.71	0.000367	0.00552
regulation of ERAD pathway (GO:1904292)	20	10	2.36	+	4.24	0.000691	0.00963
Rac protein signal transduction (GO:0016601)	21	10	2.48	+	4.04	0.000924	0.0124
positive regulation of hemostasis (GO:1900048)	21	10	2.48	+	4.04	0.000924	0.0124
positive regulation of fibroblast migration (GO:0010763)	21	10	2.48	+	4.04	0.000924	0.0124
positive regulation of blood coagulation (GO:0030194)	21	10	2.48	+	4.04	0.000924	0.0124
viral gene expression (GO:0019080)	22	10	2.59	+	3.85	0.00122	0.0157
regulation of lipoprotein particle clearance (GO:0010984)	22	10	2.59	+	3.85	0.00122	0.0157
plasma lipoprotein particle clearance (GO:0034381)	23	10	2.71	+	3.69	0.00158	0.0195
retrograde axonal transport (GO:0008090)	23	10	2.71	+	3.69	0.00158	0.0195
cellular response to prostaglandin stimulus (GO:0071379)	24	10	2.83	+	3.53	0.00203	0.0241
negative regulation of ubiquitin-protein transferase activity (GO:0051444)	24	10	2.83	+	3.53	0.00203	0.0241
positive regulation of coagulation (GO:0050820)	24	10	2.83	+	3.53	0.00203	0.024
positive regulation of lipid storage (GO:0010884)	24	10	2.83	+	3.53	0.00203	0.024
regulation of Rac protein signal transduction (GO:0035020)	24	10	2.83	+	3.53	0.00203	0.024
amyloid-beta clearance (GO:0097242)	24	10	2.83	+	3.53	0.00203	0.024
regulation of platelet-derived growth factor receptor signaling pathway (GO:0010640)	25	10	2.95	+	3.39	0.00258	0.0294
metallo-sulfur cluster assembly (GO:0031163)	26	10	3.07	+	3.26	0.00324	0.0353
iron-sulfur cluster assembly (GO:0016226)	26	10	3.07	+	3.26	0.00324	0.0352
positive regulation of extracellular matrix organization (GO:1903055)	27	10	3.18	+	3.14	0.00403	0.042
negative regulation of phagocytosis (GO:0050765)	27	10	3.18	+	3.14	0.00403	0.042
alternative mRNA splicing, via spliceosome (GO:0000380)	27	10	3.18	+	3.14	0.00403	0.0419
pyrimidine nucleotide biosynthetic process (GO:0006221)	28	10	3.3	+	3.03	0.00496	0.0497
endoplasmic reticulum calcium ion homeostasis (GO:0032469)	28	10	3.3	+	3.03	0.00496	0.0497
mitochondrial calcium ion homeostasis (GO:0051560)	28	10	3.3	+	3.03	0.00496	0.0497
regulation of spindle assembly (GO:0090169)	28	10	3.3	+	3.03	0.00496	0.0496
positive regulation of dendritic spine morphogenesis (GO:0061003)	28	10	3.3	+	3.03	0.00496	0.0496
protein deneddylation (GO:0000338)	10	9	1.18	+	7.63	0.0000549	0.00103
vesicle coating (GO:0006901)	11	9	1.3	+	6.94	0.0000905	0.00163
IRES-dependent viral translational initiation (GO:0075522)	11	9	1.3	+	6.94	0.0000905	0.00162
peripheral nervous system axon regeneration (GO:0014012)	12	9	1.42	+	6.36	0.000144	0.00247
negative regulation of cell size (GO:0045792)	14	9	1.65	+	5.45	0.000328	0.00503
vesicle targeting, to, from or within Golgi (GO:0048199)	14	9	1.65	+	5.45	0.000328	0.00503
negative regulation of microtubule polymerization (GO:0031115)	16	9	1.89	+	4.77	0.000675	0.00943
viral genome replication (GO:0019079)	17	9	2.01	+	4.49	0.000936	0.0126

pyrimidine nucleobase metabolic process (GO:0006206)	17	9	2.01	+	4.49	0.000936	0.0126
regulation of cardiac muscle contraction by calcium ion signaling (GO:0010882)	17	9	2.01	+	4.49	0.000936	0.0125
gas transport (GO:0015669)	18	9	2.12	+	4.24	0.00127	0.0163
NAD metabolic process (GO:0019674)	18	9	2.12	+	4.24	0.00127	0.0163
Golgi to vacuole transport (GO:0006896)	19	9	2.24	+	4.02	0.0017	0.0206
glycogen biosynthetic process (GO:0005978)	19	9	2.24	+	4.02	0.0017	0.0206
glucan biosynthetic process (GO:0009250)	19	9	2.24	+	4.02	0.0017	0.0206
ribosome localization (GO:0033750)	20	9	2.36	+	3.82	0.00224	0.0262
mitotic cytokinetic process (GO:1902410)	20	9	2.36	+	3.82	0.00224	0.0261
ribosomal subunit export from nucleus (GO:0000054)	20	9	2.36	+	3.82	0.00224	0.0261
posttranslational protein targeting to endoplasmic reticulum membrane (GO:0006620)	21	9	2.48	+	3.63	0.00291	0.0323
regulation of mitotic spindle assembly (GO:1901673)	21	9	2.48	+	3.63	0.00291	0.0322
regulation of ryanodine-sensitive calcium-release channel activity (GO:0060314)	22	9	2.59	+	3.47	0.00372	0.0393
regulation of establishment of cell polarity (GO:2000114)	22	9	2.59	+	3.47	0.00372	0.0392
response to hepatocyte growth factor (GO:0035728)	22	9	2.59	+	3.47	0.00372	0.0392
muscle cell cellular homeostasis (GO:0046716)	22	9	2.59	+	3.47	0.00372	0.0392
negative regulation of amyloid precursor protein catabolic process (GO:1902992)	22	9	2.59	+	3.47	0.00372	0.0392
protein-lipid complex assembly (GO:0065005)	23	9	2.71	+	3.32	0.0047	0.0476
cellular response to low-density lipoprotein particle stimulus (GO:0071404)	23	9	2.71	+	3.32	0.0047	0.0476
response to misfolded protein (GO:0051788)	23	9	2.71	+	3.32	0.0047	0.0475
protein insertion into ER membrane (GO:0045048)	23	9	2.71	+	3.32	0.0047	0.0475
early endosome to late endosome transport (GO:0045022)	23	9	2.71	+	3.32	0.0047	0.0475
actin nucleation (GO:0045010)	23	9	2.71	+	3.32	0.0047	0.0474
positive regulation of viral life cycle (GO:1903902)	23	9	2.71	+	3.32	0.0047	0.0474
response to mercury ion (GO:0046689)	23	9	2.71	+	3.32	0.0047	0.0474
anterior/posterior pattern specification (GO:0009952)	232	9	27.36	-	0.33	0.000189	0.00309
CRD-mediated mRNA stabilization (GO:0070934)	9	8	1.06	+	7.54	0.000153	0.00261
positive regulation of establishment of protein localization to telomere (GO:1904851)	10	8	1.18	+	6.78	0.000251	0.00399
negative regulation of amyloid fibril formation (GO:1905907)	11	8	1.3	+	6.17	0.000393	0.00586
regulation of establishment of protein localization to telomere (GO:0070203)	11	8	1.3	+	6.17	0.000393	0.00586
positive regulation of protein localization to Cajal body (GO:1904871)	11	8	1.3	+	6.17	0.000393	0.00585
regulation of protein localization to Cajal body (GO:1904869)	11	8	1.3	+	6.17	0.000393	0.00585
synaptic vesicle budding (GO:0070142)	11	8	1.3	+	6.17	0.000393	0.00584
protein localization to endosome (GO:0036010)	11	8	1.3	+	6.17	0.000393	0.00584
regulation of establishment of protein localization to chromosome (GO:0070202)	12	8	1.42	+	5.65	0.000595	0.00846
negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay (GO:1900152)	12	8	1.42	+	5.65	0.000595	0.00845
oxygen transport (GO:0015671)	12	8	1.42	+	5.65	0.000595	0.00845
phospholipid efflux (GO:0033700)	13	8	1.53	+	5.22	0.000873	0.0118
positive regulation of protein localization to chromosome, telomeric region (GO:1904816)	13	8	1.53	+	5.22	0.000873	0.0118
proteasome assembly (GO:0043248)	13	8	1.53	+	5.22	0.000873	0.0118
high-density lipoprotein particle remodeling (GO:0034375)	13	8	1.53	+	5.22	0.000873	0.0118
negative regulation of monooxygenase activity (GO:0032769)	14	8	1.65	+	4.84	0.00125	0.016
regulation of amyloid fibril formation (GO:1905906)	14	8	1.65	+	4.84	0.00125	0.016
negative regulation of platelet-derived growth factor receptor signaling pathway (GO:0010642)	14	8	1.65	+	4.84	0.00125	0.016
regulation of protein localization to chromosome, telomeric region (GO:1904814)	15	8	1.77	+	4.52	0.00173	0.0209
regulation of plasminogen activation (GO:0010755)	15	8	1.77	+	4.52	0.00173	0.0209
nucleobase biosynthetic process (GO:0046112)	16	8	1.89	+	4.24	0.00236	0.0271
cardiac myofibril assembly (GO:0055003)	16	8	1.89	+	4.24	0.00236	0.0271
actin filament depolymerization (GO:0030042)	16	8	1.89	+	4.24	0.00236	0.0271
tail-anchored membrane protein insertion into ER membrane (GO:0071816)	17	8	2.01	+	3.99	0.00316	0.0347
positive regulation of receptor recycling (GO:0001921)	17	8	2.01	+	3.99	0.00316	0.0347
cellular response to superoxide (GO:0071451)	17	8	2.01	+	3.99	0.00316	0.0347
cellular response to oxygen radical (GO:0071450)	17	8	2.01	+	3.99	0.00316	0.0347
late endosome to vacuole transport via multivesicular body sorting pathway (GO:0032511)	17	8	2.01	+	3.99	0.00316	0.0346

AMP biosynthetic process (GO:0006167)	17	8	2.01	+	3.99	0.00316	0.0346
acetyl-CoA biosynthetic process (GO:0006085)	17	8	2.01	+	3.99	0.00316	0.0346
deoxyribonucleotide biosynthetic process (GO:0009263)	17	8	2.01	+	3.99	0.00316	0.0346
regulation of podosome assembly (GO:0071801)	18	8	2.12	+	3.77	0.00415	0.043
amino-acid betaine metabolic process (GO:0006577)	18	8	2.12	+	3.77	0.00415	0.043
cellular response to prostaglandin E stimulus (GO:0071380)	18	8	2.12	+	3.77	0.00415	0.043
2-oxoglutarate metabolic process (GO:0006103)	18	8	2.12	+	3.77	0.00415	0.0429
protein insertion into mitochondrial membrane (GO:0051204)	18	8	2.12	+	3.77	0.00415	0.0429
actin filament severing (GO:0051014)	18	8	2.12	+	3.77	0.00415	0.0429
protein refolding (GO:0042026)	18	8	2.12	+	3.77	0.00415	0.0429
regulation of Golgi organization (GO:1903358)	18	8	2.12	+	3.77	0.00415	0.0428
positive regulation of early endosome to late endosome transport (GO:2000643)	8	7	0.94	+	7.42	0.000431	0.00637
actin-myosin filament sliding (GO:0033275)	8	7	0.94	+	7.42	0.000431	0.00637
triglyceride-rich lipoprotein particle remodeling (GO:0034370)	8	7	0.94	+	7.42	0.000431	0.00636
establishment or maintenance of cytoskeleton polarity (GO:0030952)	9	7	1.06	+	6.59	0.000697	0.0097
pinocytosis (GO:0006907)	10	7	1.18	+	5.93	0.00108	0.0142
transferrin transport (GO:0033572)	10	7	1.18	+	5.93	0.00108	0.0142
fatty acid beta-oxidation using acyl-CoA dehydrogenase (GO:0033539)	10	7	1.18	+	5.93	0.00108	0.0142
regulation of deoxyribonuclease activity (GO:0032070)	10	7	1.18	+	5.93	0.00108	0.0142
purine ribonucleoside biosynthetic process (GO:0046129)	11	7	1.3	+	5.4	0.0016	0.0196
oxaloacetate metabolic process (GO:0006107)	11	7	1.3	+	5.4	0.0016	0.0196
nucleoside biosynthetic process (GO:0009163)	11	7	1.3	+	5.4	0.0016	0.0196
ribonucleoside biosynthetic process (GO:0042455)	11	7	1.3	+	5.4	0.0016	0.0196
purine nucleoside biosynthetic process (GO:0042451)	11	7	1.3	+	5.4	0.0016	0.0196
regulation of cholesterol esterification (GO:0010872)	11	7	1.3	+	5.4	0.0016	0.0196
nucleobase-containing small molecule biosynthetic process (GO:0034404)	11	7	1.3	+	5.4	0.0016	0.0196
regulation of opsonization (GO:1903027)	12	7	1.42	+	4.95	0.00231	0.0267
NLS-bearing protein import into nucleus (GO:0006607)	12	7	1.42	+	4.95	0.00231	0.0267
synaptic vesicle endosomal processing (GO:0099532)	12	7	1.42	+	4.95	0.00231	0.0267
reverse cholesterol transport (GO:0043691)	12	7	1.42	+	4.95	0.00231	0.0267
plasminogen activation (GO:0031639)	12	7	1.42	+	4.95	0.00231	0.0266
Golgi inheritance (GO:0048313)	12	7	1.42	+	4.95	0.00231	0.0266
organelle inheritance (GO:0048308)	12	7	1.42	+	4.95	0.00231	0.0266
regulation of guanyl-nucleotide exchange factor activity (GO:1905097)	12	7	1.42	+	4.95	0.00231	0.0266
viral budding via host ESCRT complex (GO:0039702)	12	7	1.42	+	4.95	0.00231	0.0266
non-lytic viral release (GO:0046753)	12	7	1.42	+	4.95	0.00231	0.0265
negative regulation of ubiquitin protein ligase activity (GO:1904667)	13	7	1.53	+	4.57	0.00323	0.0353
viral RNA genome replication (GO:0039694)	13	7	1.53	+	4.57	0.00323	0.0352
positive regulation of cytoplasmic transport (GO:1903651)	13	7	1.53	+	4.57	0.00323	0.0352
P-body assembly (GO:0033962)	13	7	1.53	+	4.57	0.00323	0.0352
removal of superoxide radicals (GO:0019430)	14	7	1.65	+	4.24	0.00441	0.0452
glycosyl compound biosynthetic process (GO:1901659)	14	7	1.65	+	4.24	0.00441	0.0452
IMP biosynthetic process (GO:0006188)	14	7	1.65	+	4.24	0.00441	0.0452
regulation of modification of postsynaptic structure (GO:0099159)	14	7	1.65	+	4.24	0.00441	0.0451
carnitine metabolic process (GO:0009437)	14	7	1.65	+	4.24	0.00441	0.0451
positive regulation of actin filament depolymerization (GO:0030836)	14	7	1.65	+	4.24	0.00441	0.0451
purine-containing compound salvage (GO:0043101)	14	7	1.65	+	4.24	0.00441	0.0451
positive regulation of ERAD pathway (GO:1904294)	14	7	1.65	+	4.24	0.00441	0.045
cilium movement (GO:0003341)	172	7	20.29	-	0.35	0.00204	0.024
sensory perception of chemical stimulus (GO:0007606)	1316	7	155.23	-	0.05	1.24E-54	1.64E-51
protein localization to bicellular tight junction (GO:1902396)	6	6	0.71	+	8.48	0.000721	0.00997
negative regulation of fibrinolysis (GO:0051918)	7	6	0.83	+	7.27	0.00122	0.0157
amyloid-beta clearance by transcytosis (GO:0150093)	7	6	0.83	+	7.27	0.00122	0.0157
muscle filament sliding (GO:0030049)	7	6	0.83	+	7.27	0.00122	0.0157

very-low-density lipoprotein particle remodeling (GO:0034372)	7	6	0.83	+	7.27	0.00122	0.0157
complement activation, alternative pathway (GO:0006957)	8	6	0.94	+	6.36	0.00194	0.0233
regulation of ER-associated ubiquitin-dependent protein catabolic process (GO:1903069)	8	6	0.94	+	6.36	0.00194	0.0233
negative regulation of guanyl-nucleotide exchange factor activity (GO:1905098)	8	6	0.94	+	6.36	0.00194	0.0233
positive regulation of cholesterol esterification (GO:0010873)	8	6	0.94	+	6.36	0.00194	0.0233
'de novo' XMP biosynthetic process (GO:0097294)	8	6	0.94	+	6.36	0.00194	0.0233
XMP biosynthetic process (GO:0097293)	8	6	0.94	+	6.36	0.00194	0.0232
XMP metabolic process (GO:0097292)	8	6	0.94	+	6.36	0.00194	0.0232
high-density lipoprotein particle assembly (GO:0034380)	8	6	0.94	+	6.36	0.00194	0.0232
regulation of long-chain fatty acid import into cell (GO:0140212)	9	6	1.06	+	5.65	0.00295	0.0327
negative regulation of endoplasmic reticulum calcium ion concentration (GO:0032471)	9	6	1.06	+	5.65	0.00295	0.0327
voluntary musculoskeletal movement (GO:0050882)	9	6	1.06	+	5.65	0.00295	0.0327
positive regulation of nuclease activity (GO:0032075)	9	6	1.06	+	5.65	0.00295	0.0326
positive regulation of opsonization (GO:1903028)	10	6	1.18	+	5.09	0.00431	0.0443
regulation of mRNA binding (GO:1902415)	10	6	1.18	+	5.09	0.00431	0.0443
tubulin complex assembly (GO:0007021)	10	6	1.18	+	5.09	0.00431	0.0443
positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator (GO:1902255)	10	6	1.18	+	5.09	0.00431	0.0443
negative regulation of nitric-oxide synthase activity (GO:0051001)	10	6	1.18	+	5.09	0.00431	0.0442
aggrephagy (GO:0035973)	5	5	0.59	+	8.48	0.00208	0.0244
COPI-coated vesicle budding (GO:0035964)	5	5	0.59	+	8.48	0.00208	0.0244
establishment or maintenance of actin cytoskeleton polarity (GO:0030950)	5	5	0.59	+	8.48	0.00208	0.0244
response to triglyceride (GO:0034014)	6	5	0.71	+	7.07	0.00348	0.0374
positive regulation of ER-associated ubiquitin-dependent protein catabolic process (GO:1903071)	6	5	0.71	+	7.07	0.00348	0.0374
purine ribonucleoside salvage (GO:0006166)	6	5	0.71	+	7.07	0.00348	0.0373
positive regulation of focal adhesion disassembly (GO:0120183)	6	5	0.71	+	7.07	0.00348	0.0373
regulation of focal adhesion disassembly (GO:0120182)	6	5	0.71	+	7.07	0.00348	0.0373
nucleoside salvage (GO:0043174)	6	5	0.71	+	7.07	0.00348	0.0373
synaptic vesicle budding from presynaptic endocytic zone membrane (GO:0016185)	6	5	0.71	+	7.07	0.00348	0.0372
bradykinin catabolic process (GO:0010815)	6	5	0.71	+	7.07	0.00348	0.0372
cilium-dependent cell motility (GO:0060285)	135	5	15.92	-	0.31	0.0036	0.0383
cilium or flagellum-dependent cell motility (GO:0001539)	135	5	15.92	-	0.31	0.0036	0.0383
detection of chemical stimulus (GO:0009593)	1270	5	149.8	-	0.03	4.37E-55	6.33E-52
detection of stimulus involved in sensory perception (GO:0050906)	1320	5	155.7	-	0.03	1.6E-57	3.19E-54
meiosis I cell cycle process (GO:0061982)	118	4	13.92	-	0.29	0.00473	0.0477
sensory perception of smell (GO:0007608)	1226	3	144.61	-	0.02	6.53E-56	1.04E-52
detection of chemical stimulus involved in sensory perception (GO:0050907)	1236	1	145.79	-	< 0.01	6.48E-60	1.72E-56
response to pheromone (GO:0019236)	97	0	11.44	-	< 0.01	0.0000373	0.000727
detection of chemical stimulus involved in sensory perception of smell (GO:0050911)	1179	0	139.07	-	< 0.01	5.55E-59	1.26E-55

Table S7. Comparison of Log2 abundances of proteins detected in at least 3 out of 4 samples of cardiac EVs from Thiamet G-treated (TG) and non-treated (C) ADHF rats.

#	Description	Gene name	Accession	-log *P*	Difference	C281	C282	C322	C361	TG291	TG292	TG302	TG311
1	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Bckdk PE=1 SV=2	Bckdk	Q00972	1.15113761	0.53399134	21.2075901	21.2801418	21.0388718	20.7315521	21.0143051	20.0314312	20.6941223	20.3823318
2	[Protein ADP-ribosylarginine] hydrolase-like protein 1 OS=Rattus norvegicus OX=10116 GN=Adprhl1 PE=2 SV=1	Adprhl1	Q5XIB3	1.29360113	0.70878839	26.7938309	26.5820847	26.5008831	25.9166508	25.6709328	25.691618	25.2589817	26.3367634
3	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pdk1 PE=1 SV=1	Pdk1	Q63065	1.34467187	0.58665323	24.0417347	24.3541718	23.6106491	24.5189724	23.4955521	23.7583351	23.2289009	23.6961269
4	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pdk2 PE=1 SV=3	Pdk2	F1LMM8	1.69328654	0.47076082	23.5670986	23.7251301	23.3014431	23.8763676	23.1159134	23.3305321	23.217905	22.9226456
5	10 kDa heat shock protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hspe1 PE=1 SV=3	Hspe1	P26772	0.03219935	0.00623798	22.1990776	22.0901222	22.040863	21.9962521	22.0188046	22.0035801	22.0558109	22.2231674
6	14-3-3 protein beta/alpha OS=Rattus norvegicus OX=10116 GN=Ywhab PE=1 SV=3	Ywhab	P35213	1.39758766	0.56281996	20.723772	21.2086334	20.5984898	20.6477699	20.1923332	20.2469158	19.8448429	20.6432934
7	14-3-3 protein epsilon OS=Rattus norvegicus OX=10116 GN=Ywhae PE=1 SV=1	Ywhae	P62260	0.13835351	0.05735397	22.9489307	22.9254227	22.8095684	23.4247894	22.7750111	23.1360016	23.0448704	22.9234123
8	14-3-3 protein eta OS=Rattus norvegicus OX=10116 GN=Ywhah PE=1 SV=2	Ywhah	P68511	0.10617665	-0.0565166	21.432785	20.935051	20.7460766	21.1971989	21.013279	21.3277569	20.8362904	21.3598518
9	14-3-3 protein gamma OS=Rattus norvegicus OX=10116 GN=Ywhag PE=1 SV=2	Ywhag	P61983	0.92304462	0.64230251	23.3519554	23.3127747	22.7654228	24.3789349	22.9145432	22.7350254	22.5448971	23.0454121
10	14-3-3 protein theta OS=Rattus norvegicus OX=10116 GN=Ywhaq PE=1 SV=1	Ywhaq	P68255	0.52878941	-0.2105374	21.8542252	21.9970818	22.2190552	22.3289585	22.3060226	22.1936646	22.722599	22.0191841
11	14-3-3 protein zeta/delta OS=Rattus norvegicus OX=10116 GN=Ywhaz PE=1 SV=1	Ywhaz	A0A0G2JV6	0.24129689	0.13471222	21.1841011	21.4955978	20.6682186	21.5401173	21.0649128	20.8228474	21.1310787	21.3303471
12	2' -5' oligoadenylate synthetase 1K OS=Rattus norvegicus OX=10116 GN=Oas1k PE=4 SV=2	Oas1k	M0RA89	0.11947043	0.07317209	21.8499184	21.8674831	22.3950615	21.8134632	22.1913128	22.218092	21.7609024	21.4629307
13	2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Rattus norvegicus OX=10116 GN=Cnp PE=1 SV=2	Cnp	P13233	0.19614926	0.13474941	18.0051632	17.4492836	17.4117527	18.1630573	17.6617908	17.1955566	17.5155258	18.1173859
14	2,4-dienoyl CoA reductase 1, mitochondrial, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Decr1 PE=1 SV=1	Decr1	G3V734	1.43521673	0.63282728	21.5788193	21.3704948	21.2524376	20.9281445	20.2688942	21.005188	20.3646393	20.9598656
15	26S proteasome non-ATPase regulatory subunit 1 OS=Rattus norvegicus OX=10116 GN=Psmd1 PE=1 SV=1	Psmd1	G3V8B6	0.85222867	0.36637354	23.0322437	23.1107063	22.3459549	23.027029	22.7699451	22.5387993	22.1855106	22.5561848
16	26S proteasome non-ATPase regulatory subunit 10 OS=Rattus norvegicus OX=10116 GN=Psmd10 PE=2 SV=1	Psmd10	Q9Z2X3	0.74980683	1.08427763	19.3874664	17.7709923	18.6278858	18.0861912	19.2077808	16.6574383	16.6107349	17.0594711
17	26S proteasome non-ATPase regulatory subunit 11 OS=Rattus norvegicus OX=10116 GN=Psmd11 PE=1 SV=1	Psmd11	A0A0G2JW1	0.43019399	0.1646347	21.888752	21.509285	21.1974888	21.6669693	21.5740757	21.4532814	21.1520786	21.4245205
18	26S proteasome non-ATPase regulatory subunit 13 OS=Rattus norvegicus OX=10116 GN=Psmd13 PE=1 SV=1	Psmd13	B0BN93	0.27809686	0.19249392	20.8614693	21.1486206	20.3349056	20.9559784	20.510788	20.8777237	20.0509949	21.0914917
19	26S proteasome non-ATPase regulatory subunit 2 OS=Rattus norvegicus OX=10116 GN=Psmd2 PE=1 SV=1	Psmd2	Q4FZT9	0.42863358	0.30528879	22.6694946	21.9540062	21.323307	22.1917095	21.8979607	21.543581	21.4196739	22.0561466
20	26S proteasome non-ATPase regulatory subunit 9 OS=Rattus norvegicus OX=10116 GN=Psmd9 PE=1 SV=1	Psmd9	G3V9P0	0.0126198	-0.0137167	18.3370342	18.2559223	16.9008579	18.0412579	18.0812855	18.1386433	17.467247	17.9027634
21	26S proteasome regulatory subunit 4 OS=Rattus norvegicus OX=10116 GN=Psmc1 PE=1 SV=1	Psmc1	P62193	0.7292318	0.46035385	21.8673496	20.9798775	20.6963844	21.8241272	20.9837952	20.7271137	20.7467728	21.0686417
22	26S proteasome regulatory subunit 6A OS=Rattus norvegicus OX=10116 GN=Psmc3 PE=1 SV=1	Psmc3	Q6P6U2	0.48123701	0.37057114	21.5134735	21.2899246	20.3057652	21.0807171	20.9505558	20.5146427	20.1046429	21.1377544
23	26S proteasome regulatory subunit 6B OS=Rattus norvegicus OX=10116 GN=Psmc4 PE=1 SV=1	Psmc4	Q63570	0.8422683	0.27906036	22.7587528	22.6879559	22.3110199	22.6642456	22.5093899	22.1805286	22.0296402	22.586174
24	26S proteasome regulatory subunit 7 OS=Rattus norvegicus OX=10116 GN=Psmc2 PE=1 SV=1	Psmc2	G3V7L6	0.42709648	0.69220686	21.634325	19.799469	18.7998524	21.2590656	19.9271622	19.0846615	19.3180389	20.394022
25	26S proteasome regulatory subunit 8 OS=Rattus norvegicus OX=10116 GN=Psmc5 PE=1 SV=1	Psmc5	P62198	1.06142655	0.4235239	23.5435009	23.2120094	22.9954739	22.7371922	22.8324642	22.6903057	22.3722115	22.8990993
26	28S ribosomal protein S15, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrps15 PE=2 SV=1	Mrps15	Q5XI37	0.29088434	-0.2200699	17.3053188	18.0601444	17.309063	18.309164	18.1460552	18.1178417	17.4229755	18.1770973
27	28S ribosomal protein S25, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrps25 PE=2 SV=1	Mrps25	Q4QR80	1.00621248	1.06536865	19.507618	18.9611225	17.4765377	19.1696968	17.0595951	17.466753	17.8013935	18.5257587
28	28S ribosomal protein S31, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrps31 PE=2 SV=1	Mrps31	B0BN56	1.28219699	1.59183645	18.6911449	18.8679104	18.6163712	18.6627617	17.1928082	17.6262665	15.2859631	18.3658047
29	28S ribosomal protein S7, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrps7 PE=2 SV=2	Mrps7	Q5I0K8	0.41184117	-0.138164	20.3051434	20.6405926	20.368784	20.3917484	20.6462116	20.3798504	20.3402386	20.8926239
30	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Coq5 PE=2 SV=1	Coq5	Q4G064	1.27428489	0.47668457	24.3508911	23.8419342	24.488657	23.9719028	23.7036152	23.9999962	23.3822727	23.6607628
31	2-oxoglutarate dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ogdh PE=1 SV=1	Ogdh	Q5XI78	1.26475603	0.34007597	26.7431564	26.3294296	26.4910908	26.1814919	26.134449	26.2638645	25.8942871	26.0922642
32	2-oxoisovalerate dehydrogenase subunit alpha OS=Rattus norvegicus OX=10116 GN=Bckdha PE=1 SV=1	Bckdha	F7EV94	0.38560502	0.23262358	23.4881935	23.8304234	23.3330727	23.5494099	23.34655	23.9650784	23.1465206	22.8124561
33	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Bckdhb PE=1 SV=1	Bckdhb	A0A0A0MX	0.4880358	0.3644824	22.7643661	23.0499763	22.0536175	22.546526	22.2568417	22.9873714	21.8990936	21.8132496
34	3'(2'),5'-bisphosphate nucleotidase 1 OS=Rattus norvegicus OX=10116 GN=Bpnt1 PE=1 SV=1	Bpnt1	A0A0G2K0V	1.39677942	0.4008255	20.84515	20.3356571	20.6093884	20.6268291	20.2230148	20.2446098	19.9007206	20.4453773
35	30 kDa adipocyte complement-related protein OS=Rattus norvegicus OX=10116 GN=Adipoq PE=1 SV=1	Adipoq	Q8K3R4	1.59234266	-1.2055964	18.3995419	18.1884899	16.778141	18.381813	19.2673073	19.0212078	18.8634682	19.4183884
36	39S ribosomal protein L11, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrpl11 PE=2 SV=1	Mrpl11	Q5XIE3	0.89453877	1.00384331	18.0740242	16.9691124	16.64711	19.1069965	16.661562	16.4629059	16.7399826	16.9174194
37	39S ribosomal protein L14, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrpl14 PE=1 SV=2	Mrpl14	Q7M0E7	0.16227868	0.39771867	17.9951725	15.8416672	16.3871403	16.6295414	16.9292755	17.0144329	13.8633814	17.4555569
38	39S ribosomal protein L16, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrpl16 PE=2 SV=1	Mrpl16	Q5M818	0.2306537	-0.1305947	22.6536446	22.0469952	22.1124058	21.6703358	22.3093147	22.5025444	22.0006428	22.1932583
39	39S ribosomal protein L22, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrpl22 PE=1 SV=1	Mrpl22	A0A0H2UH	0.74834256	-0.3159671	16.9129601	16.4001808	16.391201	16.0447598	16.8407402	16.9135208	16.4444447	16.8142643
40	39S ribosomal protein L23, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrpl23 PE=2 SV=1	Mrpl23	Q63750	0.32381281	-0.2699542	16.8778419	17.4203777	16.8405972	17.2915401	17.3321514	16.4823685	17.8241787	17.8714752
41	39S ribosomal protein L24, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrpl24 PE=2 SV=1	Mrpl24	Q66H47	0.41639145	0.74402928	16.9444294	16.0772419	16.2416363	16.3445301	16.4643784	16.1309719	13.3762484	16.6601219
42	39S ribosomal protein L38, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrpl38 PE=2 SV=2	Mrpl38	Q5PQN9	0.87142716	0.49425483	17.004879	16.9082069	16.4590759	16.1076012	16.0262127	16.537838	15.6289206	16.3097725
43	39S ribosomal protein L46, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrpl46 PE=2 SV=1	Mrpl46	Q5RK00	0.07196769	-0.0608349	18.853014	19.4360466	18.0096569	18.8631039	18.7143459	18.7394848	18.9945602	18.9567699
44	39S ribosomal protein L9, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mrpl9 PE=2 SV=1	Mrpl9	Q641X9	0.38721058	0.22531939	19.3080254	19.0060406	18.8791656	19.0436878	18.2364731	19.3993931	18.8851643	18.8146114
45	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Rattus norvegicus OX=10116 GN=Hsd17b10 PE=1 SV=1	Hsd17b10	B0BMW2	0.35531447	0.19312191	26.4004841	26.1957588	26.1591015	25.6330643	25.9531593	26.0033379	25.4333134	26.2261105
46	3-hydroxybutyrate dehydrogenase, type 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Bdh1 PE=1 SV=1	Bdh1	A0A0G2JSH	0.85576232	-0.5904999	23.4438877	23.4802723	23.9870281	24.462225	24.8094101	24.2429237	24.8671627	23.8159161
47	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hibadh PE=1 SV=3	Hibadh	P29266	0.16964637	-0.0148196	21.9387379	21.9910984	22.0010204	22.0699501	21.9564133	22.0288887	22.0236835	22.0510998
48	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hibch PE=1 SV=2	Hibch	Q5XIE6	0.76507987	-0.1806703	21.6465816	22.0077801	21.7187958	21.7708397	21.8270664	22.1214695	22.1103668	21.8077755
49	3-ketoacyl-CoA thiolase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acaa2 PE=1 SV=3	Acaa2	G3V9U2	0.75468094	0.30126333	31.4395504	30.5901203	30.8877068	30.8692341	30.7170162	30.5598755	30.4642506	30.840416
50	3-mercaptopyruvate sulfurtransferase OS=Rattus norvegicus OX=10116 GN=Mpst PE=1 SV=3	Mpst	P97532	2.02427627	-0.3828878	20.9777508	20.688282	20.527523	20.8544464	21.0951385	21.2241745	21.1363087	21.1239319
51	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Oxsm PE=1 SV=1	Oxsm	G3V6R7	0.65823056	0.56242895	21.8955936	22.3139458	22.3695717	20.9084797	21.1850548	21.172163	20.9011898	21.9794674
52	40S ribosomal protein S10 OS=Rattus norvegicus OX=10116 GN=Rps10 PE=2 SV=1	Rps10	P63326	1.11501854	0.53568935	21.4181499	21.0220013	20.486454	21.0208321	20.3354931	20.1137123	20.4690552	20.8864193
53	40S ribosomal protein S11 OS=Rattus norvegicus OX=10116 GN=Rps11 PE=1 SV=3	Rps11	P62282	0.30280857	0.40612411	20.6272182	20.2066383	19.888176	21.7023907	20.6441822	20.4137764	19.0138664	20.7281017
54	40S ribosomal protein S12 OS=Rattus norvegicus OX=10116 GN=Rps12 PE=1 SV=1	Rps12	Q6PDW1	0.58297824	0.54549503	18.8275661	19.1468315	18.8874626	20.585762	19.1166325	19.0213776	18.5028687	18.6247635
55	40S ribosomal protein S14 OS=Rattus norvegicus OX=10116 GN=Rps14 PE=2 SV=3	Rps14	P13471	0.14626445	0.08604527	20.4221878	19.7410545	19.9341259	20.5408478	20.1001396	20.3005276	19.7503605	20.1430073
56	40S ribosomal protein S15 OS=Rattus norvegicus OX=10116 GN=Rps15 PE=1 SV=2	Rps15	P62845	0.1128282	0.10537863	15.4323778	15.5917435	14.3353319	15.7810707	14.850337	15.1632204	15.2932062	15.4122458
57	40S ribosomal protein S15a OS=Rattus norvegicus OX=10116 GN=Rps15a PE=1 SV=2	Rps15a	P62246	0.82380461	0.31493044	20.835577	20.7754192	20.4841232	20.9194183	20.2213593	20.3231754	20.2781353	20.9321461
58	40S ribosomal protein S16 OS=Rattus norvegicus OX=10116 GN=Rps16 PE=1 SV=2	Rps16	P62250	0.10243474	-0.0426917	20.2440014	19.6640644	19.9921112	19.8461304	20.0021248	19.76408	19.9405861	20.2102833
59	40S ribosomal protein S17-like OS=Rattus norvegicus OX=10116 GN=LOC100362366 PE=3 SV=1	LOC100362	D3ZFA8	0.51636097	0.25043488	21.5412254	20.8061714	20.8435936	21.5433846	20.9103241	20.9270248	21.1487579	20.7465286
60	40S ribosomal protein S2 OS=Rattus norvegicus OX=10116 GN=Rps2 PE=1 SV=1	Rps2	P27952	0.05832345	0.07528543	18.428091	18.7448864	18.5127869	18.9749508	17.3084888	18.8343353	18.9135857	19.3031635
61	40S ribosomal protein S26 OS=Rattus norvegicus OX=10116 GN=Rps26 PE=3 SV=3	Rps26	P62856	0.71185855	0.34574032	18.3669682	18.1078815	17.4974785	17.8881912	17.8095016	17.260355	17.4969139	17.9107876
62	40S ribosomal protein S27-like OS=Rattus norvegicus OX=10116 GN=Rps27l PE=1 SV=3	Rps27l	P24051	0.24323072	0.11722803	21.1366615	20.4266758	20.3582458	20.7378616	20.4175968	20.5452938	20.4472427	20.7803993
63	40S ribosomal protein S28 OS=Rattus norvegicus OX=10116 GN=Rps28 PE=1 SV=1	Rps28	P62859	1.21310283	0.69781971	18.5479469	18.6838627	18.0849342	18.3569832	17.9984379	17.7900867	16.9299335	18.16399
64	40S ribosomal protein S29 OS=Rattus norvegicus OX=10116 GN=Rps29 PE=1 SV=2	Rps29	P62275	0.30463164	0.20339298	19.9438534	19.6878414	20.4109993	19.312252	19.8212814	19.3438625	19.9893131	19.3869171
65	40S ribosomal protein S3 OS=Rattus norvegicus OX=10116 GN=Rps3 PE=1 SV=1	Rps3	P62909	0.64740944	0.36412716	21.1793156	20.6706104	20.0923386	20.9701176	20.392067	20.4614315	19.9986839	20.6036911
66	40S ribosomal protein S30 OS=Rattus norvegicus OX=10116 GN=LOC100360647 PE=1 SV=1	LOC100360	Q5BJN7	0.23000836	0.41909504	18.7950916	19.0552082	18.7351685	19.0987968	16.9870834	17.5226021	19.7080746	19.7901249
67	40S ribosomal protein S3a OS=Rattus norvegicus OX=10116 GN=LOC100365839 PE=3 SV=1	LOC100365	M0R6L4	0.39981686	0.38238001	16.7244434	18.7312641	18.0697613	17.8160686	17.3650436	17.3725128	17.506834	17.567627
68	40S ribosomal protein S4 OS=Rattus norvegicus OX=10116 GN=Rps4x PE=3 SV=1	Rps4x	A0A0H2UH	1.05461937	-0.6794276	19.6190071	20.0088158	18.9282913	20.325285	20.1086903	20.2189884	20.5273037	20.7441273
69	40S ribosomal protein S5 OS=Rattus norvegicus OX=10116 GN=Rps5 PE=1 SV=1	Rps5	B0BN81	0.40767645	-0.493063	20.2563877	19.3491917	19.4737949	20.1766739	19.2094345	21.0604172	19.7986584	21.15979
70	40S ribosomal protein S6 OS=Rattus norvegicus OX=10116 GN=Rps6 PE=1 SV=1	Rps6	P62755	0.35150277	-0.1754365	19.218483	18.9609566	19.2031574	19.187273	19.2834892	19.5963669	18.748455	19.6433048

71	40S ribosomal protein S7 OS=Rattus norvegicus OX=10116 GN=Rps7 PE=1 SV=1	Rps7	P62083	0.51035675	0.32845736	19.0386314	18.919136	18.4181881	18.9837856	18.1750698	18.6967735	18.0195446	19.1545238
72	40S ribosomal protein S8 OS=Rattus norvegicus OX=10116 GN=Rps8 PE=1 SV=2	Rps8	P62243	0.21878201	0.1703701	19.4602776	19.980072	20.1243973	20.5972157	20.0751133	20.0345802	20.1157646	19.255024
73	40S ribosomal protein S9 OS=Rattus norvegicus OX=10116 GN=Rps9 PE=1 SV=4	Rps9	P29314	0.27184779	-0.1251016	20.7583618	20.4740353	20.3130131	20.3072567	20.4885483	20.3986092	20.4078236	21.0580921
74	40S ribosomal protein SA OS=Rattus norvegicus OX=10116 GN=Rpsa PE=1 SV=3	Rpsa	P38983	0.22723231	0.19370556	20.6771374	19.4722042	19.9366474	19.6411572	19.6488514	19.4896908	19.441597	20.3721848
75	4-trimethylaminobutyraldehyde dehydrogenase OS=Rattus norvegicus OX=10116 GN=Aldh9a1 PE=1 SV=1	Aldh9a1	A0A0G2JSI1	0.0962812	-0.0440016	21.4860611	21.4132042	21.6064796	21.0254211	21.4187241	21.4333286	21.157568	21.6975517
76	5'-AMP-activated protein kinase subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Prkab1 PE=1 SV=4	Prkab1	P80386	0.06523325	0.08735657	17.2557583	19.1598434	18.1917934	18.1299782	18.1086922	18.3927174	17.3223572	18.5641804
77	5'-AMP-activated protein kinase subunit beta-2 OS=Rattus norvegicus OX=10116 GN=Prkab2 PE=1 SV=1	Prkab2	A0A0G2JVK	0.9363066	0.71406698	17.2315884	18.1361809	18.0388355	18.0600014	16.7498627	16.4790592	17.4977722	17.8836441
78	5'-AMP-activated protein kinase subunit gamma-1 OS=Rattus norvegicus OX=10116 GN=Prkag1 PE=1 SV=3	Prkag1	P80385	0.1310188	-0.086422	20.7872448	20.3668442	19.8667603	19.8810139	20.407753	20.1853771	20.0716686	20.5827522
79	5-demethoxyubiquinone hydroxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Coq7 PE=3 SV=4	Coq7	G3V879	0.87859286	1.86771631	22.7986584	22.4342461	22.1334667	19.9615898	19.7649956	22.458744	18.92033	18.713026
80	5'-nucleotidase OS=Rattus norvegicus OX=10116 GN=Nt5c3a PE=1 SV=1	Nt5c3a	B2GUX5	0.81784391	-0.6592917	17.3934593	17.4656277	18.1938248	17.5651436	17.2634239	18.484478	18.8463917	18.6609287
81	5'-nucleotidase OS=Rattus norvegicus OX=10116 GN=Nt5e PE=1 SV=1	Nt5e	P21588	1.03151895	-0.475997	20.7263069	21.1830273	20.4871597	21.2728825	21.2954407	21.41992	21.7835293	21.0744743
82	5'-nucleotidase, cytosolic IA OS=Rattus norvegicus OX=10116 GN=Nt5c1a PE=1 SV=1	Nt5c1a	D3ZVD3	0.575192	0.70121098	19.0530415	19.6524563	19.4294662	18.3171368	17.3096485	18.8454018	17.949894	19.5423126
83	5-oxoprolinase OS=Rattus norvegicus OX=10116 GN=Oplah PE=1 SV=2	Oplah	P97608	0.81838674	1.18993807	18.209507	15.175107	15.6845083	15.9804173	15.6015558	14.4407606	14.7779903	15.4694805
84	6.8 kDa mitochondrial proteolipid OS=Rattus norvegicus OX=10116 GN=Mp68 PE=1 SV=1	Mp68	D3Z9R8	0.44971334	-0.1795225	23.6581764	23.7309647	24.0938587	24.3178082	24.0473232	24.2193222	24.3277149	23.9245377
85	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hspd1 PE=1 SV=1	Hspd1	P63039	1.21808747	0.36010599	28.1836948	28.1273365	27.9848576	27.6102715	27.6963749	27.5583172	27.4024048	27.8086395
86	60S acidic ribosomal protein P0 OS=Rattus norvegicus OX=10116 GN=Rplp0 PE=1 SV=2	Rplp0	P19945	1.10809144	0.62335539	20.7638607	21.3071079	21.0073872	21.6754322	20.6794548	20.2956066	21.1287556	20.1565495
87	60S acidic ribosomal protein P1 OS=Rattus norvegicus OX=10116 GN=Rplp1 PE=3 SV=1	Rplp1	P19944	0.88843034	0.69831324	20.7777882	20.6991177	19.6913414	21.1196117	19.4767399	19.5626259	20.5847397	19.8705006
88	60S acidic ribosomal protein P2 OS=Rattus norvegicus OX=10116 GN=Rplp2 PE=1 SV=2	Rplp2	P02401	0.25864945	0.19893789	20.8581581	21.0035362	20.4936371	21.636404	20.796669	20.6052532	21.37356	20.4205017
89	60S ribosomal protein L10 OS=Rattus norvegicus OX=10116 GN=Rpl10 PE=1 SV=3	Rpl10	Q6PDV7	0.35418577	0.15133238	20.4885674	20.6191444	20.1123047	20.8974838	20.2623444	20.4640865	20.2110538	20.5746861
90	60S ribosomal protein L10a OS=Rattus norvegicus OX=10116 GN=Rpl10a PE=1 SV=2	Rpl10a	P62907	1.30365468	0.38358593	21.3391514	21.3095264	20.8265781	21.3597412	20.6463528	20.9204216	21.0301495	20.7037296
91	60S ribosomal protein L11 OS=Rattus norvegicus OX=10116 GN=Rpl11 PE=1 SV=2	Rpl11	P62914	1.05084758	0.42922258	21.3381977	20.8131237	20.6704254	20.6130924	20.1783123	20.2561932	20.5260792	20.7573643
92	60S ribosomal protein L12 OS=Rattus norvegicus OX=10116 GN=Rpl12 PE=2 SV=1	Rpl12	P23358	0.33159239	0.47644234	20.0804558	20.8479633	20.1206226	22.6019726	20.0397987	20.4950905	20.8315392	20.3788166
93	60S ribosomal protein L13 OS=Rattus norvegicus OX=10116 GN=LOC100360491 PE=3 SV=1	LOC1003604	D3ZRM9	0.01460133	0.008461	21.3388138	21.3889313	20.7252293	21.1241188	20.8778839	21.3906994	21.3030872	20.9715786
94	60S ribosomal protein L14 OS=Rattus norvegicus OX=10116 GN=Rpl14 PE=1 SV=1	Rpl14	B5DEM5	0.41208102	0.41655254	18.3258667	18.4848289	18.5870991	17.4621658	17.4133034	17.480732	18.894598	17.405117
95	60S ribosomal protein L15 OS=Rattus norvegicus OX=10116 GN=Rpl15 PE=1 SV=2	Rpl15	P61314	0.34812248	0.1896615	20.7243595	21.108984	20.5187511	21.0185204	20.886322	20.1051674	20.9375	20.6829796
96	60S ribosomal protein L17 OS=Rattus norvegicus OX=10116 GN=Rpl17 PE=1 SV=2	Rpl17	F1LZX7	0.62070085	-0.3206725	20.3967571	20.3365593	20.8807926	21.2157841	20.9529972	21.0100498	21.383791	20.7657452
97	60S ribosomal protein L18 OS=Rattus norvegicus OX=10116 GN=Rpl18 PE=1 SV=1	Rpl18	A0A0H2UH	0.17048554	-0.0686674	19.4350643	19.6091309	19.8402786	20.1143723	19.7858295	19.832737	19.951685	19.7032642
98	60S ribosomal protein L18a OS=Rattus norvegicus OX=10116 GN=Rpl18a PE=2 SV=1	Rpl18a	P62718	0.17381178	-0.0864968	19.2600117	18.790638	18.915575	19.6208591	19.2840538	19.2586327	19.305233	19.0851517
99	60S ribosomal protein L19 OS=Rattus norvegicus OX=10116 GN=Rpl19 PE=1 SV=1	Rpl19	P84100	0.95557404	0.24308538	19.8873978	19.8323193	20.0598469	20.252533	19.7295094	19.8648529	19.9348049	19.5305882
100	60S ribosomal protein L22 OS=Rattus norvegicus OX=10116 GN=LOC100360057 PE=1 SV=1	LOC1003600	Q6PDV8	0.08300718	0.29380989	18.5033112	18.7833595	14.648736	17.7337036	14.5722399	18.2751579	17.9328918	17.7135811
101	60S ribosomal protein L23 OS=Rattus norvegicus OX=10116 GN=Rpl23 PE=2 SV=1	Rpl23	P62832	0.08740265	-0.0269947	22.1587734	22.0472469	22.0878658	22.0030346	22.2298775	22.3254433	21.859375	21.9902039
102	60S ribosomal protein L24 OS=Rattus norvegicus OX=10116 GN=Rpl24 PE=2 SV=1	Rpl24	P83732	0.51351463	-0.3011179	19.3447666	18.7854366	18.6745281	19.7973175	19.285944	19.4441509	19.4578209	19.6186047
103	60S ribosomal protein L26-like OS=Rattus norvegicus OX=10116 GN=LOC100910721 PE=3 SV=2	LOC1009107	M0R6L3	0.69177644	-0.5727746	16.8656311	17.2022686	15.8104677	17.6088943	17.1899681	17.4355373	17.739584	17.413271
104	60S ribosomal protein L27 OS=Rattus norvegicus OX=10116 PE=1 SV=1	10116	D3ZTK5	0.05747842	-0.0186291	18.2106705	18.2319756	17.937212	18.4282055	18.1726685	18.3823318	18.1630058	18.1645737
105	60S ribosomal protein L34 OS=Rattus norvegicus OX=10116 GN=Rpl34 PE=1 SV=1	Rpl34	B2RZD4	0.32796057	0.06176043	19.6989994	19.4138489	19.5880871	19.5650654	19.4502697	19.5509987	19.6323795	19.3853111
106	60S ribosomal protein L35 OS=Rattus norvegicus OX=10116 GN=Rpl35 PE=1 SV=3	Rpl35	P17078	0.40603636	0.6225872	16.6917343	17.9196739	16.9413567	19.4167728	16.4552135	17.1000423	17.7993908	17.1245422
107	60S ribosomal protein L36a OS=Rattus norvegicus OX=10116 GN=Rpl36a PE=1 SV=2	Rpl36a	P83883	0.01922136	0.01302624	17.2896595	17.4028759	16.830143	17.7508926	17.2364979	17.3575706	17.6257305	17.001667
108	60S ribosomal protein L37a OS=Rattus norvegicus OX=10116 GN=Rpl37a PE=3 SV=1	Rpl37a	A0A0H2UH	0.08979994	0.19436932	16.701601	17.1181812	15.320138	16.6725216	14.211566	17.0309696	16.8869114	16.9055176
109	60S ribosomal protein L4 OS=Rattus norvegicus OX=10116 GN=Rpl4 PE=1 SV=1	Rpl4	Q6P3V9	0.78881422	0.2106595	21.2129459	21.6105003	21.2302418	21.3577366	21.0744591	20.9561863	21.1314526	21.4066887
110	60S ribosomal protein L5 OS=Rattus norvegicus OX=10116 GN=Rpl5 PE=1 SV=3	Rpl5	P09895	0.23335296	0.19782066	18.9591961	19.4991875	17.9750824	18.8851357	18.5082588	18.5346909	19.0235519	18.4608173
111	60S ribosomal protein L6 OS=Rattus norvegicus OX=10116 PE=3 SV=1	10116	F1LQS3	0.1373901	0.07851839	20.36376	20.4654675	20.0904484	21.0895233	20.3523846	20.4370079	20.5487938	20.3569393
112	60S ribosomal protein L7 OS=Rattus norvegicus OX=10116 GN=Rpl7 PE=1 SV=1	Rpl7	B0K031	0.02649389	-0.0096889	20.4047146	20.9366341	20.4570713	20.6908398	20.5576744	20.6444321	20.6292152	20.6966934
113	60S ribosomal protein L9 OS=Rattus norvegicus OX=10116 GN=Rpl9 PE=1 SV=1	Rpl9	P17077	0.37145284	-0.3712344	19.5827179	17.9331493	19.5524254	19.4019279	19.0340519	19.595747	19.8773727	19.4479866
114	6-phosphogluconolactonase OS=Rattus norvegicus OX=10116 GN=Pgls PE=1 SV=1	Pgls	G3V8D5	0.07807124	0.06776381	18.191164	18.1561527	17.8695087	16.9112682	17.7282429	17.8017483	17.4574547	17.8695927
115	A kinase (PRKA) anchor protein 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Akap1 PE=1 SV=2	Akap1	D4A9M6	1.23742547	-0.3287201	19.7153263	19.1728096	19.2483692	19.5320168	19.6958694	19.8085155	19.5978737	19.8811436
116	Ab1-205 OS=Rattus norvegicus OX=10116 GN=Surf4 PE=1 SV=1	Surf4	Q7TP91	0.06588578	-0.0584159	18.9828892	18.8379612	19.2959976	19.6335011	19.5261765	19.4248581	19.5662327	18.4667454
117	Abhydrolase domain-containing 11 OS=Rattus norvegicus OX=10116 GN=Abhd11 PE=1 SV=1	Abhd11	D3ZXK4	0.02108478	-0.0344772	18.539669	17.944313	16.5728264	17.805233	17.6623096	16.7388306	18.1637173	18.4350929
118	ABR, RhoGEF and GTPase-activating protein OS=Rattus norvegicus OX=10116 GN=Abr PE=1 SV=1	Abr	A0A0G2JTR	0.52236889	0.47587776	20.173708	18.7628746	18.6085358	18.8181782	18.6784248	18.5596848	18.1000614	19.1216145
119	Abraxas 2, BRISC complex subunit OS=Rattus norvegicus OX=10116 GN=Abraxas2 PE=1 SV=3	Abraxas2	D4A415	0.57195381	0.85964632	18.3270226	16.680933	16.7922897	16.3449154	16.5999947	16.9015064	14.5404015	16.6646729
120	Ac1002 OS=Rattus norvegicus OX=10116 GN=Adh4 PE=1 SV=1	Adh4	Q7TQ90	0.7070875	-0.3983607	18.3023357	17.512888	17.3719158	17.7710457	18.2349091	17.7307091	17.99827	18.5877399
121	Ac1873 OS=Rattus norvegicus OX=10116 GN=Fga PE=1 SV=1	Fga	Q7TQ70	0.26175764	-0.163928	23.5216026	23.3271637	22.823473	22.6995258	22.9414616	23.5643272	23.002634	23.5190544
122	Acad9 protein OS=Rattus norvegicus OX=10116 GN=Acad9 PE=1 SV=1	Acad9	B1WC61	2.12631891	-0.3225384	23.0726128	22.846035	23.0818348	22.9897652	23.4471245	23.4000225	23.2205448	23.2127094
123	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acat1 PE=1 SV=1	Acat1	P17764	0.00639678	-0.003159	24.1983795	24.3508263	24.6380692	24.7616386	24.5131779	24.5812454	24.6711121	24.1960144
124	Acetyl-CoA carboxylase beta OS=Rattus norvegicus OX=10116 GN=Acacb PE=1 SV=1	Acacb	A0A0G2K1F	1.45473306	0.35462427	23.3090839	23.1872902	23.1206799	23.1193218	23.0156708	22.9467602	22.4690094	22.8864384
125	Acetyl-Coenzyme A dehydrogenase, short chain, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Acads PE=1 SV=1	Acads	Q6IMX3	1.11714622	0.50617599	24.3590679	24.8736076	24.4806747	24.1198502	23.8752575	24.1359062	23.4925728	24.30476
126	Acetyl-coenzyme A synthetase OS=Rattus norvegicus OX=10116 GN=Acss1 PE=3 SV=1	Acss1	D3ZZN3	2.27697247	0.41235542	22.2669334	22.4646778	22.5490742	22.6946106	22.1918316	22.0485001	22.0341644	22.0513783
127	Acetylserotonin O-methyltransferase-like OS=Rattus norvegicus OX=10116 GN=Asmtl PE=1 SV=2	Asmtl	D4AA35	0.65136017	0.32224941	17.2817173	17.3412666	16.9967365	17.0795918	16.5801678	17.2284107	17.2336197	16.3681164
128	Acid ceramidase OS=Rattus norvegicus OX=10116 GN=Asah1 PE=1 SV=1	Asah1	A0A0G2K8T	0.42204043	-0.2385721	21.1620388	21.1866016	20.5929871	20.4831581	20.5944538	21.1877079	21.263773	21.3331394
129	Aconitate hydratase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Aco2 PE=1 SV=2	Aco2	Q9ER34	0.04915674	-0.0066161	27.0309219	26.9179916	27.0827961	27.0349522	26.9515018	27.0467453	26.996685	27.0981941
130	Actin, alpha cardiac muscle 1 OS=Rattus norvegicus OX=10116 GN=Actc1 PE=2 SV=1	Actc1	P68035	0.56557035	-0.134685	27.5227795	27.5621357	27.2386093	27.7262363	27.6012077	27.5618401	27.6514435	27.7740097
131	Actin, alpha skeletal muscle OS=Rattus norvegicus OX=10116 GN=Acta1 PE=1 SV=1	Acta1	P68136	0.72428577	-0.6086721	18.9458218	19.1595955	18.8460655	18.1726303	18.5994968	19.2311611	19.4294224	20.2987213
132	Actin, aortic smooth muscle OS=Rattus norvegicus OX=10116 GN=Acta2 PE=2 SV=1	Acta2	P62738	0.6644613	-1.6933975	19.2951946	16.4685879	13.938221	18.4093323	18.2119045	18.1767998	19.1326828	19.3635387
133	Actin, cytoplasmic 1 OS=Rattus norvegicus OX=10116 GN=Actb PE=1 SV=1	Actb	P60711	0.05880277	-0.0517907	24.0216408	24.6574402	23.8145905	25.1182213	24.2364883	24.4522629	24.4565048	24.6737995
134	Actinin alpha 2 OS=Rattus norvegicus OX=10116 GN=Actn2 PE=1 SV=1	Actn2	D3ZCV0	0.00945035	-0.0182409	18.6831703	19.2979698	20.4746323	20.3028793	20.0728588	20.6813946	19.7141457	18.3632164
135	Actin-related protein 2 OS=Rattus norvegicus OX=10116 GN=Actr2 PE=2 SV=1	Actr2	Q5M7U6	0.19693639	-0.4677663	17.5287018	18.9324627	15.3709621	19.0342369	17.2035122	18.1710167	18.2759113	19.0869884
136	Actin-related protein 2/3 complex subunit 3 OS=Rattus norvegicus OX=10116 GN=Arpc3 PE=1 SV=1	Arpc3	B2GV73	0.54777274	1.23190808	15.7013416	17.1752434	16.64888	19.4207306	13.9692221	16.5369301	16.5510464	16.9613647
137	Actin-related protein 2/3 complex subunit 4 OS=Rattus norvegicus OX=10116 GN=Arpc4 PE=1 SV=1	Arpc4	B2RZ72	0.41232808	0.6916647	16.8866825	16.8043232	15.2439175	18.3212395	17.0886097	15.8441849	15.2265224	16.3301868
138	Actin-related protein 2/3 complex subunit 5 OS=Rattus norvegicus OX=10116 GN=Arpc5 PE=1 SV=1	Arpc5	A0A0G2K58	0.36301983	-0.4459996	16.8388996	17.6457653	16.2432766	15.3093853	17.2817402	16.404707	17.2147503	16.9201279
139	Actin-related protein 3 OS=Rattus norvegicus OX=10116 GN=Actr3 PE=1 SV=1	Actr3	A0A0G2K1C	0.71950319	-0.4362597	18.7665176	17.6712627	17.9726505	18.7353611	18.881115	18.4609547	18.920105	18.6286564
140	Activator of Hsp90 ATPase activity 1 OS=Rattus norvegicus OX=10116 GN=Ahsa1 PE=1 SV=1	Ahsa1	B0BN63	0.02632252	-0.0387459	17.0809746	18.1633205	18.3872471	18.6131058	18.2666531	18.5394707	17.0036564	18.5898514
141	Acyl carrier protein OS=Rattus norvegicus OX=10116 GN=Ndufab1 PE=1 SV=1	Ndufab1	D3ZF13	0.5108927	-0.2645655	24.0225544	24.6723614	24.8087215	24.9302483	24.9299088	24.7963333	25.1812782	24.5846272
142	Acyl-CoA dehydrogenase family, member 10 OS=Rattus norvegicus OX=10116 GN=Acad10 PE=1 SV=2	Acad10	F1LSP2	0.47540126	0.45292759	25.28969	23.3958683	24.299408	24.3900127	24.4320431	23.8136349	23.5285854	23.7890053

143	Acyl-CoA dehydrogenase family, member 8 OS=Rattus norvegicus OX=10116 GN=Acad8 PE=1 SV=2	Acad8	M0RDK9	1.10363683	-0.354794	22.3681812	22.8095398	22.7501335	23.0377579	23.1191673	22.9845886	23.3511944	22.9298382
144	Acyl-CoA synthetase family member 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acsf2 PE=2 SV=1	Acsf2	Q499N5	1.69765769	0.87862492	26.4229736	27.5075665	26.3804741	27.0423584	25.93297	26.123806	26.0148773	25.7672195
145	Acyl-CoA synthetase family member 3 OS=Rattus norvegicus OX=10116 GN=Acsf3 PE=1 SV=1	Acsf3	D3ZUX7	0.07259636	-0.3237286	23.5422115	19.3120327	18.9233437	23.567522	18.8532085	22.968502	22.1547184	22.6635952
146	Acyl-CoA synthetase short-chain family member 2 OS=Rattus norvegicus OX=10116 GN=Acss2 PE=1 SV=1	Acss2	G3V9U0	0.53899605	0.30756187	17.9475918	18.7559776	18.6704273	17.7374783	18.0407791	17.8335114	17.8812275	18.1257095
147	Acyl-CoA thioesterase 11 OS=Rattus norvegicus OX=10116 GN=Acot11 PE=4 SV=3	Acot11	F1LX28	0.52377205	-0.2672029	21.8625755	21.3165245	21.2122116	21.5772552	21.8572769	21.876564	21.2251205	22.0784168
148	Acyl-CoA thioesterase 13 OS=Rattus norvegicus OX=10116 GN=Acot13 PE=1 SV=1	Acot13	D3ZA93	0.90357811	0.30008793	23.3845119	23.2560425	23.3162422	23.0003834	23.0144234	22.8437328	22.6025085	23.2961636
149	Acyl-CoA thioesterase 9 OS=Rattus norvegicus OX=10116 GN=Acot9 PE=1 SV=1	Acot9	Q5U2X8	1.25275055	0.40766478	23.192358	23.1845112	22.8992825	22.5781517	22.6470146	22.5055294	22.3222885	22.7488117
150	Acyl-CoA-binding protein OS=Rattus norvegicus OX=10116 GN=Dbi PE=1 SV=3	Dbi	P11030	0.69795836	0.25604391	20.0266972	19.8641872	20.0244465	20.4751759	19.8408051	19.8957844	19.5244942	20.1052475
151	Acyl-Coenzyme A dehydrogenase, very long chain OS=Rattus norvegicus OX=10116 GN=Acadvl PE=1 SV=1	Acadvl	Q5M9H2	0.09928589	-0.0290341	26.9969139	27.1063786	26.9637661	27.0154934	27.1596737	27.282341	26.8479748	26.908699
152	Acyl-coenzyme A thioesterase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acot2 PE=1 SV=1	Acot2	O55171	0.94306821	0.46538019	22.9721355	22.5355206	23.4337616	22.7538185	22.7313099	22.7426815	22.2430496	22.1166744
153	Acylglycerol kinase OS=Rattus norvegicus OX=10116 GN=Agk PE=1 SV=2	Agk	D3Z9L0	2.11502528	-0.5212598	18.369772	18.4820919	18.7920132	18.5031128	18.9360771	18.8785362	19.3111038	19.1063118
154	Acylphosphatase OS=Rattus norvegicus OX=10116 GN=Acyp2 PE=1 SV=2	Acyp2	D4A1G1	1.41399801	-0.8154845	20.1997318	21.2998657	21.3065529	21.2819958	21.9564133	21.8825092	22.0824108	21.428751
155	Acyl-protein thioesterase 1 OS=Rattus norvegicus OX=10116 GN=Lypla1 PE=1 SV=1	Lypla1	P70470	0.22661446	0.16675615	20.3805389	20.1116657	19.5913754	20.3696842	19.6476707	19.6562424	19.8579044	20.6244221
156	Acyl-protein thioesterase 2 OS=Rattus norvegicus OX=10116 GN=Lypla2 PE=1 SV=1	Lypla2	Q9QYL8	0.00461172	-0.009407	19.1356945	16.3178902	17.2089443	16.7762337	17.7041225	16.7037029	17.1075535	17.9610119
157	Adenine phosphoribosyltransferase OS=Rattus norvegicus OX=10116 GN=Aprt PE=1 SV=1	Aprt	P36972	0.21033409	-0.0440578	20.8434067	20.6054001	20.6688576	20.9125919	20.8844109	20.8190689	20.6852207	20.8177872
158	Adenylate kinase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ak2 PE=1 SV=1	Ak2	A0A0G2JSG	0.09762801	0.03530502	24.0792503	23.6300774	23.8776131	24.0040245	24.0391064	23.7769432	23.9771938	23.6565018
159	Adenylate kinase 4, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ak4 PE=2 SV=1	Ak4	Q9WUS0	1.65100983	0.34502172	24.86689	25.2755241	24.7890854	25.1157932	24.6598225	24.6590366	24.6445198	24.7038269
160	Adenylate kinase isoenzyme 1 OS=Rattus norvegicus OX=10116 GN=Ak1 PE=1 SV=3	Ak1	P39069	2.2222219	1.25472927	23.3695583	23.798872	23.0841599	23.1913643	21.8373775	21.8356857	22.8796883	21.8722858
161	Adenylosuccinate lyase OS=Rattus norvegicus OX=10116 GN=Adsl PE=1 SV=1	Adsl	D3ZW08	0.46643067	-0.8746295	15.3599224	18.9014244	18.2553787	18.8860302	18.7962303	18.7633953	18.8359394	18.5057087
162	Adenylosuccinate synthetase isozyme 1 OS=Rattus norvegicus OX=10116 GN=Adssl1 PE=1 SV=1	Adssl1	M0R629	0.01023329	0.01108646	18.722683	18.052	17.1888733	18.5215721	17.9902287	18.4566059	17.8612175	18.1327305
163	Adenylyl cyclase-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Cap1 PE=1 SV=3	Cap1	Q08163	0.36406417	0.58560705	17.9046288	18.9811497	18.7923908	20.5007572	19.0847664	17.5344868	17.8888111	19.328434
164	Adenylyl cyclase-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Cap2 PE=1 SV=1	Cap2	P52481	0.43060895	0.52689314	24.1297512	23.6925087	23.9165077	22.2868996	23.0451374	23.1543007	22.0160179	23.7026386
165	Adenylyltransferase and sulfurtransferase MOCS3 OS=Rattus norvegicus OX=10116 GN=Mocs3 PE=1 SV=1	Mocs3	D4A8L5	0.02754928	0.05097914	20.6419334	19.2386532	20.6628475	18.1685677	19.9931793	19.4128513	19.1885376	19.913517
166	ADP/ATP translocase 1 OS=Rattus norvegicus OX=10116 GN=Slc25a4 PE=1 SV=3	Slc25a4	Q05962	0.76070788	-0.2131753	28.643364	28.8974018	29.0992756	29.2193394	29.1989155	29.2012672	29.2901344	29.0217648
167	ADP/ATP translocase 2 OS=Rattus norvegicus OX=10116 GN=Slc25a5 PE=1 SV=3	Slc25a5	Q09073	0.82029741	-0.3830423	23.2637177	24.0606766	23.9546528	24.2835312	24.2537842	24.1859493	24.4963799	24.1586342
168	ADP-ribosylation factor 3 OS=Rattus norvegicus OX=10116 GN=Arf3 PE=3 SV=1	Arf3	A0A0G2K9F	0.06947564	-0.0433898	23.2444191	23.3532677	22.4977074	23.3531361	23.1863079	23.1268959	22.9496498	23.3592358
169	ADP-ribosylation factor 4 OS=Rattus norvegicus OX=10116 GN=Arf4 PE=2 SV=2	Arf4	P61751	0.22102466	0.17206097	19.9809799	20.6048164	19.5487347	20.0860538	19.9037247	19.6988392	19.4382172	20.49156
170	ADP-ribosylation factor 5 OS=Rattus norvegicus OX=10116 GN=Arf5 PE=1 SV=2	Arf5	P84083	0.0963081	0.04944754	19.3842831	19.2378864	18.7540913	19.548214	19.1898289	18.9613514	19.3022118	19.2732925
171	ADP-ribosylation factor GTPase activating protein 1 heart isoform OS=Rattus norvegicus OX=10116 GN=Arfgap1 PE=1 SV=1	Arfgap1	Q3S4A4	0.0934027	0.06423831	15.5996981	15.5273943	14.9488182	15.0146961	15.5793772	14.9075518	15.4747143	14.8720102
172	ADP-ribosylation factor-like protein 3 OS=Rattus norvegicus OX=10116 GN=Arl3 PE=1 SV=2	Arl3	F8WG91	1.56333888	0.77737761	16.7732296	17.0911484	15.9378338	16.5086498	15.7910194	16.0924397	15.5570183	15.7608738
173	ADP-ribosylation factor-like protein 8B OS=Rattus norvegicus OX=10116 GN=Arl8b PE=2 SV=1	Arl8b	Q66HA6	1.46213834	-0.3300991	20.5390434	20.5078964	20.5574818	20.9753323	20.9035721	21.007637	21.100811	20.8881302
174	Adrenodoxin, mitochondrial OS=Rattus norvegicus OX=10116 GN=Fdx1 PE=1 SV=1	Fdx1	G3V7L0	0.47732911	0.56936479	17.2075863	17.2102203	16.7347775	16.78479	17.2240734	14.8726263	16.8432484	16.7199669
175	AFG1-like ATPase OS=Rattus norvegicus OX=10116 GN=Afg1l PE=2 SV=1	Afg1l	Q32PX9	1.63924282	0.44268799	24.9625359	24.568737	24.5745087	24.4277802	24.3698349	24.0541058	24.0187912	24.3200779
176	AFG3-like matrix AAA peptidase subunit 2 OS=Rattus norvegicus OX=10116 GN=Afg3l2 PE=1 SV=1	Afg3l2	F1LN92	0.52326155	-0.3817711	22.6791592	23.2255211	23.7081127	23.8446293	23.8171024	23.7335491	24.2236614	23.2101936
177	Aflatoxin B1 aldehyde reductase member 2 OS=Rattus norvegicus OX=10116 GN=Akr7a2 PE=1 SV=1	Akr7a2	A0A0A0MX	0.28412872	0.23805141	18.2316933	18.2602673	17.3826809	18.3260441	17.941433	17.4051876	17.3868675	18.5149918
178	AHNAK nucleoprotein OS=Rattus norvegicus OX=10116 GN=Ahnak PE=1 SV=1	Ahnak	A0A0G2JUA	0.56863925	-0.1711545	25.5677948	25.472393	24.9442158	25.3026047	25.4699287	25.4274635	25.4966946	25.5775394
179	A-kinase anchor protein 12 OS=Rattus norvegicus OX=10116 GN=Akap12 PE=1 SV=1	Akap12	Q5QD51	0.14539682	-0.1577535	16.3743267	16.8409119	15.9548216	16.4489307	16.5488911	15.8493357	17.5877037	16.2640743
180	A-kinase anchor protein 13 OS=Rattus norvegicus OX=10116 GN=Akap13 PE=1 SV=2	Akap13	F1M3G7	0.22213803	0.09313631	18.0930901	18.6622906	18.5321426	18.3780785	18.2785625	18.0753117	18.3068104	18.6323719
181	A-kinase anchor protein SPHKAP OS=Rattus norvegicus OX=10116 GN=Sphkap PE=1 SV=1	Sphkap	A0A0G2K3J	1.19802534	1.24146557	19.558176	19.4644623	19.4844494	19.7405071	17.4601173	19.4695377	19.0213871	17.3306904
182	Alanyl-tRNA editing protein Aarsd1 OS=Rattus norvegicus OX=10116 GN=Aarsd1 PE=1 SV=1	Aarsd1	Q5XI97	0.51548887	1.90446138	19.4985809	24.1417999	20.2917767	16.8326206	19.2195854	18.3041401	16.0886478	19.5345592
183	Aldehyde dehydrogenase family 16 member A1 OS=Rattus norvegicus OX=10116 GN=Aldh16a1 PE=2 SV=1	Aldh16a1	Q3T1L0	0.67697147	0.87375212	18.3061657	19.0238266	17.8809147	16.7299747	17.1826077	17.8415413	15.9926548	17.4290695
184	Aldehyde dehydrogenase family 5, subfamily A1 OS=Rattus norvegicus OX=10116 GN=Aldh5a1 PE=1 SV=1	Aldh5a1	G3V945	0.02795972	-0.0089688	20.8009949	20.8801498	20.714283	20.4361095	20.8559589	20.7170906	20.6907864	20.6035767
185	Aldehyde dehydrogenase family 6, subfamily A1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Aldh6a1 PE=1 SV=1	Aldh6a1	G3V7J0	0.62530932	0.25533724	26.5808086	26.5749073	26.6910172	26.0193043	26.2244396	26.4215298	25.8661728	26.3325462
186	Aldehyde dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Aldh2 PE=1 SV=1	Aldh2	P11884	0.1803981	0.05097103	24.3481426	24.1997929	24.3780594	24.4177094	24.2206554	24.1882935	24.1506863	24.5801849
187	Aldo-keto reductase family 1 member C15 OS=Rattus norvegicus OX=10116 GN=Akr1c15 PE=1 SV=1	Akr1c15	D3ZF77	0.34423089	0.19214058	20.5309849	20.8606052	19.7653179	20.6171379	20.1679249	20.2556133	20.3429184	20.239027
188	Aldose reductase OS=Rattus norvegicus OX=10116 GN=Akr1b1 PE=1 SV=3	Akr1b1	P07943	0.41695586	-0.106935	22.8559742	22.7348175	22.5726967	23.0084572	22.7446899	23.0178604	22.8353672	23.0017681
189	Alkaline phosphatase, tissue-nonspecific isozyme OS=Rattus norvegicus OX=10116 GN=Alpl PE=1 SV=2	Alpl	P08289	0.20133118	-0.3051553	19.5125294	19.4379406	17.3391857	18.5407734	19.6778679	19.1439667	18.1363831	19.0928326
190	Alpha globin OS=Rattus norvegicus OX=10116 GN=Hba-a3 PE=1 SV=2	Hba-a3	Q63910	0.13882358	-0.2744546	19.5084267	19.9313526	18.4835663	18.7816696	19.9788857	17.5812759	19.5166016	20.7260704
191	Alpha glucosidase 2 alpha neutral subunit (Predicted) OS=Rattus norvegicus OX=10116 GN=Ganab PE=1 SV=1	Ganab	D3ZAN3	0.59682648	-0.7594309	16.9606056	17.720665	15.4632587	15.7129135	16.4354267	17.4293652	17.7443027	17.2860718
192	Alpha-1,4 glucan phosphorylase OS=Rattus norvegicus OX=10116 GN=Pygm PE=1 SV=1	Pygm	G3V8V3	0.15731042	0.11892891	24.2902966	23.8906212	23.5953026	23.4542866	23.5643234	24.2940941	23.2214222	23.6749516
193	Alpha-1-antiproteinase OS=Rattus norvegicus OX=10116 GN=Serpina1 PE=1 SV=1	Serpina1	A0A0G2JZ7	0.53428118	-0.2070627	22.2071362	22.0972061	22.1165733	22.5352936	22.0728855	22.4146214	22.5071106	22.7898426
194	Alpha-1-inhibitor 3 OS=Rattus norvegicus OX=10116 GN=A1i3 PE=1 SV=1	A1i3	P14046	0.68959752	-0.2441339	24.6967525	24.9071541	24.3964138	24.2098808	24.6326065	24.9737968	24.7349892	24.8453445
195	Alpha-1-macroglobulin OS=Rattus norvegicus OX=10116 GN=A1m PE=1 SV=1	A1m	Q63041	0.15948713	-0.1145606	23.021286	23.2805614	22.454998	22.2143383	22.5241508	23.1268158	22.874855	22.9036045
196	Alpha-2-HS-glycoprotein OS=Rattus norvegicus OX=10116 GN=Ahsg PE=1 SV=2	Ahsg	P24090	0.48818969	0.30352068	25.6134834	25.9270458	25.0097523	24.7491779	24.9190292	24.8662567	25.0558243	25.2442665
197	Alpha-aminoadipic semialdehyde dehydrogenase OS=Rattus norvegicus OX=10116 GN=Aldh7a1 PE=1 SV=2	Aldh7a1	Q64057	0.37739797	-0.3752818	19.1320152	19.2409439	18.3295422	20.4109592	19.8140831	19.5698128	19.6783733	19.5523186
198	Alpha-centractin OS=Rattus norvegicus OX=10116 GN=Actr1a PE=1 SV=1	Actr1a	P85515	0.15848339	0.03723907	21.0056839	21.0990505	20.7909832	21.1424675	20.9790974	20.9073219	20.9056606	21.0971489
199	Alpha-crystallin B chain OS=Rattus norvegicus OX=10116 GN=Cryab PE=1 SV=1	Cryab	P23928	0.19359432	0.09092951	30.364542	30.2435875	30.0209522	29.6258316	29.9219246	29.9203644	29.820591	30.2283154
200	Alpha-kinase 2 OS=Rattus norvegicus OX=10116 GN=Alpk2 PE=4 SV=3	Alpk2	F1LTG2	0.48233497	0.22451687	22.6262436	21.9536114	22.1887283	22.045208	22.4074345	21.732172	21.8191681	21.9569492
201	Alpha-parvin OS=Rattus norvegicus OX=10116 GN=Parva PE=1 SV=1	Parva	G3V818	0.21004422	-0.0766573	21.2275181	21.3060875	21.1272411	21.5153675	21.0846996	21.6137962	21.2699585	21.514389
202	Alpha-soluble NSF attachment protein OS=Rattus norvegicus OX=10116 GN=Napa PE=1 SV=2	Napa	P54921	0.05324998	0.09658051	18.3347511	20.1807709	18.1617794	19.8443222	17.9363194	19.6138268	19.3993378	19.1858177
203	Amine oxidase OS=Rattus norvegicus OX=10116 GN=Maoa PE=1 SV=1	Maoa	G3V9Z3	0.5197363	-0.6256824	25.5048027	26.9769382	26.1208172	24.4947567	26.214222	25.9923019	26.829607	26.5639133
204	Amine oxidase OS=Rattus norvegicus OX=10116 PE=3 SV=1	10116	A0A0G2JW2	0.90971558	-0.1960773	21.3339958	21.5077057	21.162138	21.0698452	21.3795128	21.5740814	21.3758526	21.5285473
205	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Rattus norvegicus OX=10116 GN=Aimp2 PE=2 SV=1	Aimp2	Q32PX2	0.59401557	0.37298536	20.3510914	20.525507	19.8245831	19.9390144	20.1217976	19.9992008	19.058342	19.968914
206	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 OS=Rattus norvegicus OX=10116 GN=Aimp1 PE=1 SV=1	Aimp1	Q4G079	1.24724244	0.61023951	20.7171974	20.7588692	20.0334396	19.9526253	19.5868073	20.0263519	19.4405842	19.9674301
207	Aminopeptidase N OS=Rattus norvegicus OX=10116 GN=Anpep PE=1 SV=2	Anpep	P15684	0.23463635	-0.556921	15.3157406	19.4063053	18.5616264	18.7025509	18.2568169	19.4375477	18.3042393	18.2153034
208	Aminopeptidase OS=Rattus norvegicus OX=10116 GN=Npepps PE=1 SV=1	Npepps	F1M9V7	0.00117271	-0.001379	21.9610291	21.0963631	21.3580227	21.1017742	22.1174202	21.7061005	20.5945873	21.1045971
209	Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (Glycogen debranching enzyme, glycogen storage disease type III) (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Agl PE=1 SV=1	Agl	D4AEH9	0.07543316	0.11410856	18.312748	16.887928	17.7528839	16.5715141	17.1943817	17.698555	16.2572556	17.9184475
210	Anion exchange protein OS=Rattus norvegicus OX=10116 GN=Slc4a1 PE=1 SV=1	Slc4a1	F8WFT7	0.22117934	-0.288837	23.9427986	25.0700951	23.9943485	24.0481663	24.1940269	25.8225746	24.455946	23.7382088
211	Anionic trypsin-1 OS=Rattus norvegicus OX=10116 GN=Prss1 PE=1 SV=1	Prss1	P00762	0.08649268	0.2772882	17.9577084	17.4031925	17.5077686	16.5048313	18.7193375	18.6907005	13.9501581	16.9041519
212	Ankyrin 1 OS=Rattus norvegicus OX=10116 GN=Ank1 PE=1 SV=1	Ank1	D3Z9Z0	0.3101292	-0.3220348	22.1281452	23.3132858	22.5999641	22.3413296	22.5686169	23.9039688	22.9178181	22.2804604
213	Ankyrin repeat and SOCS box protein 2 OS=Rattus norvegicus OX=10116 GN=Asb2 PE=2 SV=1	Asb2	Q5U2S6	0.79207539	1.08340263	17.3852558	18.4109592	19.7665501	19.8021317	17.1065807	18.3541565	17.2117748	18.3587742
214	Ankyrin repeat and SOCS box-containing 13 OS=Rattus norvegicus OX=10116 GN=Asb13 PE=1 SV=1	Asb13	D3ZEJ6	1.06395407	0.90691471	19.9919567	18.9265633	19.2641869	18.9949207	18.56534	17.6655827	17.975214	19.343832

215	Ankyrin repeat and SOCS box-containing 15 OS=Rattus norvegicus OX=10116 GN=Asb15 PE=4 SV=2	Asb15	F1M9V9	0.84893919	0.58959723	18.2082653	17.3583088	17.4218102	17.1457481	17.4848499	16.8498821	16.269371	17.1716404
216	Ankyrin repeat domain 47 (Predicted) OS=Rattus norvegicus OX=10116 GN=Kank3 PE=1 SV=1	Kank3	B2RYN8	0.60519012	0.31917858	19.849884	19.3956318	19.1840878	18.9847813	19.2005882	18.771513	18.7412167	19.4243526
217	Ankyrin repeat domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Ankrd1 PE=1 SV=1	Ankrd1	Q8R560	1.85608957	0.37071037	23.4218483	23.4784336	23.2776814	23.0755348	22.8918037	22.8201771	22.9568729	23.1018028
218	Annexin A1 OS=Rattus norvegicus OX=10116 GN=Anxa1 PE=1 SV=2	Anxa1	P07150	0.51177761	0.25831604	22.5416451	22.9923534	22.8258591	23.4784126	22.5005245	22.8382683	22.9789944	22.4872189
219	Annexin A2 OS=Rattus norvegicus OX=10116 GN=Anxa2 PE=1 SV=2	Anxa2	Q07936	1.0409819	-0.4132357	24.627079	25.3772984	24.5449467	24.9177055	25.1130924	25.3715057	25.4647274	25.1706467
220	Annexin A3 OS=Rattus norvegicus OX=10116 GN=Anxa3 PE=1 SV=4	Anxa3	P14669	0.53505528	-0.2342782	22.0919132	22.3476791	22.1825237	22.4867821	22.4856186	22.7707443	22.7858162	22.0038319
221	Annexin A5 OS=Rattus norvegicus OX=10116 GN=Anxa5 PE=1 SV=3	Anxa5	P14668	0.41447192	-0.1330781	24.0173988	24.2372322	24.0110626	24.1197758	24.2813034	23.9170475	24.5521698	24.1672611
222	Annexin OS=Rattus norvegicus OX=10116 GN=Anxa11 PE=1 SV=1	Anxa11	Q5XI77	0.18508346	0.1653471	19.7639217	20.4248867	19.8328075	19.9306736	19.2219219	20.2918186	19.3367863	20.4403744
223	Annexin OS=Rattus norvegicus OX=10116 GN=Anxa4 PE=1 SV=1	Anxa4	Q5U362	1.30120702	-0.4388003	20.7819519	21.3193588	20.934351	20.8932095	21.2839737	21.480566	21.7732105	21.1463223
224	Annexin OS=Rattus norvegicus OX=10116 GN=Anxa6 PE=1 SV=1	Anxa6	Q6IMZ3	0.28487513	-0.1447692	23.948885	24.7724667	24.1771507	24.474596	24.2422199	24.779562	24.5153217	24.4150715
225	Annexin OS=Rattus norvegicus OX=10116 GN=Anxa7 PE=1 SV=1	Anxa7	Q6IRJ7	0.528493	-0.3360415	19.1070423	19.3804626	18.4517899	19.7321606	19.3860207	19.6550007	19.2446232	19.7299767
226	Antisecretory factor OS=Rattus norvegicus OX=10116 GN=Psmd4 PE=1 SV=1	Psmd4	O88321	0.80533188	0.36266994	20.8096256	20.4715099	20.266964	20.0786514	20.3649273	19.769022	19.7673473	20.2747746
227	AP-2 complex subunit alpha OS=Rattus norvegicus OX=10116 GN=Ap2a2 PE=1 SV=1	Ap2a2	Q66HM2	0.58615267	-1.0835242	17.3777637	13.919755	16.5124416	16.5546837	17.055027	15.9894667	17.9794655	17.6747818
228	AP-2 complex subunit beta OS=Rattus norvegicus OX=10116 GN=Ap2b1 PE=1 SV=1	Ap2b1	P62944	0.93533998	-1.4396479	14.5707788	18.1319695	17.5255337	16.9606915	18.3897057	18.1255379	18.3703022	18.0620193
229	AP-3 complex subunit mu-1 OS=Rattus norvegicus OX=10116 GN=Ap3m1 PE=1 SV=1	Ap3m1	P53676	0.00652395	-0.0233994	16.7471828	16.6687012	18.2459869	21.7701778	18.5992966	18.5890045	18.292408	18.0449371
230	Apolipoprotein A-I OS=Rattus norvegicus OX=10116 GN=Apoa1 PE=1 SV=2	Apoa1	P04639	0.02109932	-0.0165405	24.4786663	24.8578205	24.3570595	23.7047119	24.3644524	24.1794205	24.2250443	24.6955032
231	Apolipoprotein A-II OS=Rattus norvegicus OX=10116 GN=Apoa2 PE=2 SV=1	Apoa2	P04638	1.10148485	-0.7163544	21.3729801	20.8822231	20.3554592	19.9007988	21.579401	21.0757675	21.4832916	21.2384186
232	Apolipoprotein A-IV OS=Rattus norvegicus OX=10116 GN=Apoa4 PE=1 SV=2	Apoa4	P02651	0.28515951	0.05967474	22.755703	22.8446999	22.7689495	22.6168346	22.7214737	22.6873016	22.4931793	22.8455334
233	Apolipoprotein B-100 OS=Rattus norvegicus OX=10116 GN=Apob PE=1 SV=1	Apob	Q7TMA5	0.46965633	-0.2295747	18.2420006	18.1868649	18.5471344	17.7574615	18.7335281	18.5000648	18.4038906	18.0142765
234	Apolipoprotein C-I OS=Rattus norvegicus OX=10116 GN=Apoc1 PE=3 SV=1	Apoc1	P19939	0.88596307	-0.395092	22.0510731	21.7185287	21.6924725	21.1195965	22.0011711	22.3780289	21.9081726	21.8746662
235	Apolipoprotein C-II (Predicted) OS=Rattus norvegicus OX=10116 GN=Apoc2 PE=1 SV=1	Apoc2	G3V8D4	1.94665648	-0.8880801	20.5269566	20.6987953	20.3024006	20.8768559	21.7574902	21.1289444	21.9490566	21.1218376
236	Apolipoprotein C-III OS=Rattus norvegicus OX=10116 GN=Apoc3 PE=1 SV=1	Apoc3	A0A0G2K8C	1.36381903	-0.421658	22.2477207	21.8232059	21.9835682	21.5262375	22.2423706	22.4465523	22.1670589	22.4113827
237	Apolipoprotein C-IV OS=Rattus norvegicus OX=10116 GN=Apoc4 PE=2 SV=2	Apoc4	P55797	0.38702756	-0.5346649	16.5856571	15.0802631	16.9396839	16.0556526	17.2169304	17.2015762	17.0201015	15.3613081
238	Apolipoprotein E OS=Rattus norvegicus OX=10116 GN=Apoe PE=1 SV=1	Apoe	A0A0G2K15	0.30705502	-0.1739583	26.5659218	25.9938927	26.1885147	25.4635544	26.1690197	26.3052139	26.0752029	26.3582802
239	Apolipoprotein H OS=Rattus norvegicus OX=10116 GN=Apoh PE=1 SV=1	Apoh	Q5I0M1	1.51806948	-0.7577429	22.1409893	22.820507	22.1463585	22.8428402	22.7327518	23.5073986	23.4924526	23.2490635
240	Apolipoprotein M OS=Rattus norvegicus OX=10116 GN=Apom PE=1 SV=2	Apom	P14630	1.4641361	-0.7342758	20.6780186	20.8264198	21.1774559	19.9601498	21.4820538	21.2271156	21.2836514	21.5863266
241	Apolipoprotein N OS=Rattus norvegicus OX=10116 GN=Apon PE=1 SV=1	Apon	Q5M890	0.32679921	0.33155441	17.6378918	18.1906738	17.120224	17.4078426	16.2630596	17.4555836	17.2888317	18.0229397
242	Apoptosis-inducing factor 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Aifm1 PE=1 SV=1	Aifm1	Q9JM53	0.88069893	-0.4207702	23.8326874	24.5681591	24.5952396	24.7532043	24.8539619	24.8182278	25.1865177	24.5736637
243	Apoptotic protease-activating factor 1 OS=Rattus norvegicus OX=10116 GN=Apaf1 PE=1 SV=1	Apaf1	Q9EPV5	0.21446726	0.55797052	18.3042736	16.7323914	14.9220886	19.5157356	16.6454811	16.3150787	16.6089916	17.6730556
244	Aquaporin-1 OS=Rattus norvegicus OX=10116 GN=Aqp1 PE=1 SV=4	Aqp1	P29975	1.37505951	-0.5499725	21.305378	21.5167675	20.9947071	21.6258411	21.8157482	22.355751	21.8906822	21.5804024
245	ARF GTPase-activating protein GIT1 OS=Rattus norvegicus OX=10116 GN=Git1 PE=1 SV=1	Git1	Q9Z272	0.3354657	0.24420404	21.1693573	20.4817963	21.1429424	20.4490681	21.2765026	20.3026371	20.4064922	20.2807159
246	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2 OS=Rattus norvegicus OX=10116 GN=Asap2 PE=1 SV=1	Asap2	A0A0G2K80	0.16466781	0.15248299	22.572752	22.4579468	22.0069084	23.2453938	21.9840145	22.9870033	22.0155811	22.68647
247	Arginine--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Rars PE=1 SV=2	Rars	P40329	1.15165576	0.52499199	21.6070309	22.0231247	21.2097492	21.2062263	20.9837952	20.5991325	21.2302666	21.1329689
248	Arginyl-tRNA synthetase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Rars2 PE=1 SV=1	Rars2	F7FFR1	0.31529002	0.14071751	18.8180599	18.7374268	18.4208813	18.9080505	18.3499241	18.2754841	18.8855896	18.8105507
249	Armadillo repeat containing 6 OS=Rattus norvegicus OX=10116 GN=Armc6 PE=1 SV=1	Armc6	B2RYL4	0.22929687	0.46554756	19.5397453	19.7479076	20.9237499	18.1168499	19.4211788	18.4190311	18.0107632	20.6150894
250	Armadillo repeat-containing 8 OS=Rattus norvegicus OX=10116 GN=Armc8 PE=1 SV=2	Armc8	F1M943	0.70348121	1.11814904	18.6882534	18.5233402	18.7093105	16.1057053	15.9800005	17.2595558	16.3778286	17.9366283
251	Armadillo repeat-containing X-linked protein 3 OS=Rattus norvegicus OX=10116 GN=Armcx3 PE=1 SV=1	Armcx3	Q5XID7	0.66730402	0.38620424	17.54879	17.4904499	17.2685738	17.7047043	16.5804672	17.7178001	17.3873978	16.7820358
252	Arp2/3 complex 34 kDa subunit OS=Rattus norvegicus OX=10116 GN=Arpc2 PE=1 SV=1	Arpc2	A0A0G2K9A	1.145617	0.72048712	21.9427986	21.8151207	22.1671009	21.207056	21.0004005	21.4962063	20.3584251	21.3950958
253	Aspartate aminotransferase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Got1 PE=1 SV=3	Got1	P13221	0.06556173	-0.0150685	23.8720951	23.9602451	24.1343346	24.2303162	24.0745583	24.0804558	24.0614014	24.0408497
254	Aspartate aminotransferase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Got2 PE=1 SV=2	Got2	P00507	0.4912716	-0.1223445	26.3620892	26.1219425	26.4643478	26.0060253	26.2587109	26.4378738	26.3283291	26.418869
255	Aspartate-beta-hydroxylase OS=Rattus norvegicus OX=10116 GN=Asph PE=1 SV=1	Asph	A0A0G2KAI	0.89312647	-0.3446989	20.1387482	20.3496189	20.1428566	20.7758598	20.4272289	20.6404057	21.0322628	20.6859818
256	Aspartate--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Dars PE=1 SV=1	Dars	P15178	0.68931035	0.28588009	22.0377865	22.009409	21.3313847	21.8020515	21.1977139	21.5367432	21.5372639	21.7653904
257	Aspartyl aminopeptidase OS=Rattus norvegicus OX=10116 GN=Dnpep PE=1 SV=1	Dnpep	Q4V8H5	0.02057698	0.01245737	21.092865	21.2306271	20.5921631	20.6340351	20.5360088	21.1159687	20.8247585	21.0231247
258	Asporin OS=Rattus norvegicus OX=10116 GN=Aspn PE=1 SV=1	Aspn	Q5XIH1	0.89765087	0.40594816	19.4484768	18.3633003	18.8514919	19.0016117	18.5404301	18.6332779	18.4526806	18.4146996
259	Ataxin-10 OS=Rattus norvegicus OX=10116 GN=Atxn10 PE=1 SV=1	Atxn10	Q9ER24	0.58704786	0.34500456	19.2253304	18.8884773	18.4692497	18.4698925	18.4488487	18.148241	18.0829258	18.9929161
260	ATIP4 OS=Rattus norvegicus OX=10116 GN=Mtus1 PE=1 SV=1	Mtus1	D2XRB8	1.73401902	0.50050926	20.9436493	20.8003216	20.6206398	20.3429165	20.2170868	20.1780777	20.3657894	19.9445362
261	ATP synthase F(0) complex subunit B1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5pb PE=1 SV=1	Atp5pb	P19511	0.48265908	-0.2147212	26.1894646	26.3304787	26.7196407	26.82514	26.8155518	26.7966385	26.9636822	26.3477364
262	ATP synthase protein 8 OS=Rattus norvegicus OX=10116 GN=Mt-atp8 PE=1 SV=2	Mt-atp8	P11608	0.8649294	-0.2955594	24.2595387	24.598526	24.5621719	24.8793545	24.8500538	24.9074612	25.1450939	24.5792198
263	ATP synthase subunit alpha OS=Rattus norvegicus OX=10116 GN=Atp5f1a PE=1 SV=1	Atp5f1a	F1LP05	1.11783886	-0.1442013	29.998558	29.8141041	30.0688648	29.9505367	30.1266727	30.1840134	30.1078167	29.990366
264	ATP synthase subunit beta OS=Rattus norvegicus OX=10116 GN=Atp5f1b PE=1 SV=1	Atp5f1b	G3V6D3	0.63344033	-0.1679845	29.5501118	29.8506947	30.0340137	29.9802036	29.9538727	30.1752701	30.0778465	29.8799725
265	ATP synthase subunit d, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5pd PE=1 SV=3	Atp5pd	P31399	0.63978915	-0.3139896	26.8712177	27.3152161	27.5685234	27.8534451	27.7946224	27.7269325	27.9255772	27.4172287
266	ATP synthase subunit delta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5f1d PE=1 SV=1	Atp5f1d	G3V7Y3	0.47004354	-0.1835618	25.4833145	25.9787521	25.9149075	26.2323666	26.2132511	26.0249138	26.2285652	25.8768578
267	ATP synthase subunit e, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5me PE=1 SV=3	Atp5me	P29419	0.78054016	-0.3076801	25.4305763	25.6030102	25.9932709	26.0400753	26.0877666	26.1979961	26.29389	25.7180004
268	ATP synthase subunit epsilon, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5f1e PE=1 SV=2	Atp5f1e	P29418	0.10838134	-0.051918	22.9565887	23.2218266	23.6013107	23.5655727	23.4823608	23.2746334	23.5901756	23.205801
269	ATP synthase subunit f, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5mf PE=1 SV=1	Atp5mf	D3ZAF6	0.75867034	-0.3493505	24.0864048	24.5768051	24.5437794	24.9409981	24.9005775	24.8941288	25.2278748	24.5228081
270	ATP synthase subunit g, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5mg PE=1 SV=2	Atp5mg	Q6PDU7	0.50965269	-0.1175995	25.8272362	25.6604271	26.0450058	25.953783	25.7975063	26.0704422	26.0150948	26.0738068
271	ATP synthase subunit gamma OS=Rattus norvegicus OX=10116 GN=Atp5f1c PE=1 SV=1	Atp5f1c	Q6PCU0	0.50129407	-0.1502328	26.668951	26.7950802	27.0437107	27.1274834	27.0646591	27.1484814	27.2072353	26.8157806
272	ATP synthase subunit O, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5po PE=1 SV=1	Atp5po	Q06647	0.88400303	-0.3218894	27.0387211	27.4863281	27.7400055	27.5668373	27.8633785	27.7852688	27.9872684	27.4835339
273	ATP synthase subunit s, mitochondrial OS=Rattus norvegicus OX=10116 GN=Dmac2l PE=2 SV=1	Dmac2l	Q5XIM4	0.80787615	-0.9302204	16.6813507	17.520237	14.9737234	16.7628765	17.3960171	17.3512001	16.9757824	17.9360695
274	ATP synthase-coupling factor 6, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5pf PE=1 SV=1	Atp5pf	P21571	0.87079929	-0.3101053	25.7325516	26.1364307	26.3236809	26.3721142	26.47789	26.5029087	26.6634102	26.1609898
275	ATP/GTP binding protein 1 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Agtpbp1 PE=4 SV=1	Agtpbp1	G3V8G1	0.21104797	-0.0848455	18.5280209	18.3573589	18.7700787	18.1543064	18.5545387	18.7927437	18.4108849	18.3909798
276	ATPase family AAA domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Atad1 PE=1 SV=1	Atad1	A0A0H2UH	0.63990728	-0.2539535	20.3481045	20.7987423	20.77742	20.9815292	20.8037128	20.8505917	21.3793316	20.8879738
277	ATPase family AAA domain-containing protein 3 OS=Rattus norvegicus OX=10116 GN=Atad3 PE=1 SV=1	Atad3	Q3KRE0	0.01032312	-0.0054464	19.3810997	19.413147	19.795723	19.9583626	19.652359	19.4148979	19.9219894	19.5808716
278	ATPase H+-transporting V1 subunit A OS=Rattus norvegicus OX=10116 GN=Atp6v1a PE=1 SV=1	Atp6v1a	D4A133	0.41471677	0.32676363	16.8244438	17.3591385	15.7343388	16.6714382	16.3393021	16.3126278	16.1075783	16.5227966
279	ATPase inhibitor, mitochondrial OS=Rattus norvegicus OX=10116 GN=Atp5if1 PE=3 SV=2	Atp5if1	Q03344	2.29271931	-0.4684043	22.6353531	22.1798229	22.4231167	22.2248344	22.8761406	22.8745251	22.7417507	22.8443279
280	ATP-binding cassette sub-family B member 7, mitochondrial OS=Rattus norvegicus OX=10116 GN=Abcb7 PE=1 SV=1	Abcb7	Q704E8	3.05708919	-1.0919561	18.2858467	18.4027557	18.6109886	18.8523674	19.8931751	19.6745682	19.6742725	19.2777672
281	ATP-binding cassette sub-family B member 8, mitochondrial OS=Rattus norvegicus OX=10116 GN=Abcb8 PE=2 SV=1	Abcb8	Q5RKI8	1.2300458	-0.7420869	19.599844	19.8533421	20.0856915	20.4875565	20.7940559	20.3317947	21.4583645	20.4105663
282	ATP-binding cassette subfamily E member 1 OS=Rattus norvegicus OX=10116 GN=Abce1 PE=1 SV=1	Abce1	D3ZD23	0.0883814	-0.152905	19.6975498	18.1616001	19.0593033	17.0973663	18.5746708	18.7079849	18.0014534	19.3433304
283	ATP-binding cassette sub-family F member 1 OS=Rattus norvegicus OX=10116 GN=Abcf1 PE=1 SV=1	Abcf1	Q6MG08	0.36038472	-0.1431098	19.5404663	19.9451694	19.3742161	19.7946262	20.0006847	19.4764099	19.8448372	19.9049854
284	ATP-binding cassette subfamily F member 2 OS=Rattus norvegicus OX=10116 GN=Abcf2 PE=1 SV=1	Abcf2	A0A096M1V	0.24561335	0.25247955	19.0030003	18.5570068	17.5213757	18.4258022	18.0735302	17.3702965	18.6751347	18.3783054
285	ATP-binding cassette sub-family F member 3 OS=Rattus norvegicus OX=10116 GN=Abcf3 PE=2 SV=1	Abcf3	Q66H39	0.95764011	0.26725864	22.7151432	22.5634499	22.4886475	22.2811871	22.2704067	22.0578632	22.1042137	22.5469093
286	ATP-binding cassette, subfamily A (ABC1), member 8a OS=Rattus norvegicus OX=10116 GN=Abca8a PE=1 SV=3	Abca8a	D3ZCF8	0.23807008	-0.107111	21.963995	22.0925331	21.9537163	21.9357166	22.0905571	22.5574989	21.6878986	22.0384502

287	ATP-dependent 6-phosphofructokinase OS=Rattus norvegicus OX=10116 GN=Pfkm PE=1 SV=1	Pfkm	A0A0G2KB0	0.19936558	0.32762098	24.5510788	25.8633747	23.2520313	25.9636002	24.2948685	24.8628635	24.6132317	24.5486374
288	ATP-dependent 6-phosphofructokinase, platelet type OS=Rattus norvegicus OX=10116 GN=Pfkp PE=1 SV=2	Pfkp	P47860	1.92366774	-0.5949311	18.5327301	18.8773994	18.8322601	19.2403088	19.3853226	19.6892223	19.4833221	19.3045559
289	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Rattus norvegicus OX=10116 GN=Clpx PE=2 SV=1	Clpx	Q5U2U0	1.43646224	0.45525646	23.9924698	23.2496223	23.6107311	23.497757	23.3229008	23.0974808	22.9829407	23.1262321
290	ATP-dependent Clp protease proteolytic subunit OS=Rattus norvegicus OX=10116 GN=Clpp PE=1 SV=1	Clpp	M0RAD5	1.47999754	0.61525011	20.5022755	20.4142818	20.4813843	20.4542809	20.374054	19.8779316	19.285078	19.8541584
291	ATP-dependent RNA helicase SUPV3L1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Supv3l1 PE=2 SV=1	Supv3l1	Q5EBA1	0.08955878	-0.0613408	16.5447521	16.9213371	17.4828548	17.1625748	16.9561596	16.7782726	17.1360016	17.4864483
292	Atrial natriuretic peptide receptor 3 OS=Rattus norvegicus OX=10116 GN=Npr3 PE=2 SV=1	Npr3	P41740	0.07222549	0.10848522	15.8058825	14.5499783	16.4955692	16.6908092	15.4752865	16.3666363	15.9327021	15.3336735
293	Atypical kinase COQ8A, mitochondrial OS=Rattus norvegicus OX=10116 GN=Coq8a PE=2 SV=1	Coq8a	Q5BJQ0	0.35677683	0.20149374	24.7372894	23.9437695	24.422123	24.4489326	24.1442738	24.2230644	23.7508678	24.6279335
294	Atypical kinase COQ8B, mitochondrial OS=Rattus norvegicus OX=10116 GN=Coq8b PE=1 SV=1	Coq8b	Q6AY19	0.09662627	0.16849732	16.7105808	16.0743351	16.0306625	14.9698868	16.5992107	16.1353207	14.2330694	16.1438751
295	Band 4.1-like protein 1-like OS=Rattus norvegicus OX=10116 GN=Epb41l1 PE=1 SV=1	Epb41l1	A0A0G2K0F	1.79797116	1.44737434	19.668396	19.5876122	19.7356949	18.9876556	18.6775455	18.0603218	16.9144382	18.5375557
296	Barrier-to-autointegration factor OS=Rattus norvegicus OX=10116 GN=Banf1 PE=1 SV=1	Banf1	Q9R1T1	0.94805961	-1.5002506	17.5105476	18.5421257	14.9143953	17.9223766	18.8452225	18.9445515	18.3663368	18.7343369
297	Basal cell adhesion molecule OS=Rattus norvegicus OX=10116 GN=Bcam PE=2 SV=1	Bcam	Q9ESS6	1.69853319	-0.3478994	21.7069473	21.5643997	21.5278378	21.3341942	22.0270214	21.9512272	21.88937	21.6573582
298	Basic leucine zipper and W2 domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Bzw2 PE=1 SV=1	Bzw2	Q9WTT7	0.54619122	0.45222044	20.6259365	21.6066685	21.9521313	20.8261814	20.6976604	21.3456383	20.2784061	20.880331
299	Basigin OS=Rattus norvegicus OX=10116 GN=Bsg PE=1 SV=2	Bsg	P26453	0.72113368	-0.2156892	24.019249	24.3158054	23.8280125	24.4698677	24.3338852	24.4058208	24.4155388	24.3404465
300	B-cell receptor-associated protein 31 OS=Rattus norvegicus OX=10116 GN=Bcap31 PE=1 SV=1	Bcap31	Q6AY58	0.22435072	-0.0713921	19.3401241	19.7263241	19.5969334	19.8072853	19.5918636	19.5328274	19.8643341	19.76721
301	Bcl2-associated athanogene 2 OS=Rattus norvegicus OX=10116 GN=Bag2 PE=4 SV=2	Bag2	F1LQH9	1.16882517	-0.7915773	17.7102509	17.3126144	16.7449112	16.1177025	17.8641567	17.5650845	17.7034931	17.919054
302	Bcl2-associated athanogene 3 OS=Rattus norvegicus OX=10116 GN=Bag3 PE=1 SV=1	Bag3	Q5U2U8	0.17131697	0.15307188	21.8836384	21.5932255	20.5216236	21.0312462	21.2469635	21.0552425	20.6606197	21.4546204
303	BCL2-interacting protein 3 OS=Rattus norvegicus OX=10116 GN=Bnip3 PE=1 SV=1	Bnip3	Q9ET45	0.60495135	-0.5003643	18.2512226	18.3353806	18.5442886	17.3299751	18.533886	19.2190914	18.8361721	17.8731747
304	BCL2-like 13 OS=Rattus norvegicus OX=10116 GN=Bcl2l13 PE=1 SV=3	Bcl2l13	D3ZT71	0.75362704	-0.2714643	24.1605759	24.6283722	24.7861614	24.8021564	24.6965637	25.114399	24.9090633	24.7430973
305	BCS1 homolog, ubiquinol-cytochrome c reductase complex chaperone OS=Rattus norvegicus OX=10116 GN=Bcs1l PE=1 SV=1	Bcs1l	Q5XIM0	0.3115174	-0.222095	20.1936932	19.8837185	19.8573685	19.0031853	19.8984222	20.3470707	20.0039063	19.5769463
306	Beta-2-microglobulin OS=Rattus norvegicus OX=10116 GN=B2m PE=1 SV=1	B2m	P07151	0.30531348	-0.2144394	20.8049679	20.7423515	20.3182659	21.1184959	20.2775116	20.9536819	21.2131157	21.3975296
307	Beta-enolase OS=Rattus norvegicus OX=10116 GN=Eno3 PE=1 SV=3	Eno3	P15429	0.14965534	-0.1235352	23.2102013	21.9418316	21.9833794	22.285202	22.2784481	22.4959412	22.3595295	22.7808361
308	Beta-globin OS=Rattus norvegicus OX=10116 GN=Hbb-b1 PE=1 SV=1	Hbb-b1	A0A0G2JTW	0.00561979	-0.0051465	23.5851974	23.9936237	23.1422329	22.8200512	23.0406284	23.7084713	23.1676178	23.6449738
309	Bifunctional purine biosynthesis protein PURH OS=Rattus norvegicus OX=10116 GN=Atic PE=1 SV=2	Atic	O35567	0.60623847	0.2564168	19.2767258	19.6070747	18.8540936	19.3130455	19.0164337	18.6445484	19.1849613	19.1793289
310	Biglycan OS=Rattus norvegicus OX=10116 GN=Bgn PE=1 SV=1	Bgn	P47853	0.32259159	-0.170464	20.3947296	20.7558403	20.463459	20.9781189	20.9470844	20.5234852	21.2668991	20.5365353
311	Biliverdin reductase B OS=Rattus norvegicus OX=10116 GN=Blvrb PE=1 SV=1	Blvrb	B5DF65	0.96007551	0.71349859	21.2792606	21.970623	21.0046215	21.1102276	20.3129253	20.859066	19.9582272	21.3805199
312	Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]-like OS=Rattus norvegicus OX=10116 GN=LOC100910067 PE=4 SV=2	LOC100910(	D3ZH27	0.13218093	0.2678864	14.9514828	15.993885	15.29708	17.8513432	15.049592	16.9242268	15.5408583	15.5075684
313	Blood group Rh(D) polypeptide OS=Rattus norvegicus OX=10116 GN=Rhd PE=2 SV=1	Rhd	O88298	0.30492331	-0.3127229	15.832303	16.4994183	15.4184532	15.4953403	15.4313288	17.0989113	15.8558054	16.1103611
314	Blood vessel epicardial substance OS=Rattus norvegicus OX=10116 GN=Bves PE=1 SV=2	Bves	Q3BCU4	0.1770881	0.1235795	19.3625774	19.5240307	19.3644524	20.1841869	19.8217163	19.5340595	18.9483643	19.6367893
315	Bone marrow stromal antigen 2 OS=Rattus norvegicus OX=10116 GN=Bst2 PE=1 SV=1	Bst2	Q811A2	0.39210039	1.0074061	19.6690407	19.0315361	19.2164192	18.5936813	14.8751087	19.5290432	18.5802937	19.4963493
316	Brain acid soluble protein 1 OS=Rattus norvegicus OX=10116 GN=Basp1 PE=1 SV=2	Basp1	Q05175	0.08439103	-0.0797138	18.0151234	18.7363796	17.5090675	17.2900848	17.6313686	18.14291	18.1153278	17.9799042
317	Branched-chain-amino-acid aminotransferase OS=Rattus norvegicus OX=10116 GN=Bcat2 PE=1 SV=1	Bcat2	G3V8U8	1.42162622	0.70354414	26.8087826	27.0725231	27.1002407	26.2223682	26.1090527	25.9623089	25.7593536	26.5590229
318	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Rattus norvegicus OX=10116 GN=Arfgef1 PE=1 SV=1	Arfgef1	D4A631	0.29052733	0.90596652	15.5216789	18.6880569	18.5791626	17.6705933	17.3186359	13.5831728	17.4493999	18.484417
319	Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Rattus norvegicus OX=10116 GN=Arfgef2 PE=1 SV=1	Arfgef2	Q7TSU1	0.36512747	-0.6085699	15.6782885	18.5589066	18.518343	18.4247093	18.0350018	18.2941532	18.6006355	18.6847363
320	BRISC and BRCA1-A complex member 1 OS=Rattus norvegicus OX=10116 GN=Babam1 PE=1 SV=1	Babam1	Q5XIJ6	2.12334703	0.87255001	18.4048882	18.8617649	18.2040596	18.1314259	17.8245983	17.6468449	17.1291752	17.5113201
321	BRISC and BRCA1-A complex member 2 OS=Rattus norvegicus OX=10116 GN=Babam2 PE=1 SV=1	Babam2	Q6P7Q1	0.54045831	0.39194059	19.3106823	18.8300037	19.1095982	17.9879417	18.3631306	18.5069733	17.9944839	18.8058758
322	BWK-1 OS=Rattus norvegicus OX=10116 GN=Gid8 PE=1 SV=1	Gid8	Q6YDN8	2.25336359	0.8396244	17.8898258	18.2463875	18.08708	17.5456181	17.2938557	16.7296982	17.1225529	17.264307
323	C-1-tetrahydrofolate synthase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Mthfd1 PE=1 SV=1	Mthfd1	G3V6S5	1.19678212	0.71577692	24.4085541	24.8722477	24.1603642	24.1566296	23.7596931	23.8112354	22.9457321	24.2180271
324	C4b-binding protein alpha chain OS=Rattus norvegicus OX=10116 GN=C4bpa PE=1 SV=1	C4bpa	Q5M891	0.28039775	-0.5054278	19.3147125	18.7424812	17.9841709	20.3742771	19.1996403	18.4031792	19.8087139	21.0258198
325	Cadherin 13 OS=Rattus norvegicus OX=10116 GN=Cdh13 PE=1 SV=1	Cdh13	Q8R490	0.47892151	-0.3985915	21.3324242	21.3935642	20.0911903	21.3508587	21.3147888	21.7749443	20.9147396	21.7579308
326	Cadherin-2 OS=Rattus norvegicus OX=10116 GN=Cdh2 PE=1 SV=1	Cdh2	G3V803	0.32695438	-0.4784863	17.4027672	16.6331844	15.6311445	18.3695736	16.9512424	17.4034157	18.0341434	17.5618134
327	Calcium channel, voltage-dependent, alpha 2/delta subunit 2 OS=Rattus norvegicus OX=10116 GN=Cacna2d2 PE=1 SV=2	Cacna2d2	F1M9X7	0.61599926	-0.3152122	18.8792591	18.8987598	18.7928963	18.3013191	18.5874634	18.8244667	19.2778282	19.443325
328	Calcium/calmodulin-dependent protein kinase type 1 OS=Rattus norvegicus OX=10116 GN=Camk1 PE=1 SV=2	Camk1	Q63450	0.6720755	1.25254774	19.1607647	19.8565922	19.764164	16.4342918	16.9549007	18.351759	16.7788677	18.1200943
329	Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Rattus norvegicus OX=10116 GN=Camk2d PE=1 SV=1	Camk2d	P15791	0.10736091	0.05524302	24.1660748	23.837944	23.4586163	23.6579609	23.8397274	23.4447708	23.638628	23.9764977
330	Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Rattus norvegicus OX=10116 GN=Camk2g PE=1 SV=1	Camk2g	P11730	0.04296148	0.0328331	22.6367836	22.3875313	21.8111038	21.6183262	22.1138573	22.0924549	21.7738266	22.3422737
331	Calmodulin-3 OS=Rattus norvegicus OX=10116 GN=Calm3 PE=1 SV=1	Calm3	P0DP31	1.25046991	0.32874107	23.4557133	23.3694916	22.8938904	23.4227409	22.9937878	23.002882	22.821907	23.0082951
332	Calnexin OS=Rattus norvegicus OX=10116 GN=Canx PE=1 SV=1	Canx	P35565	1.35237662	-0.3874569	23.0973816	23.3906364	23.1079216	23.5532856	23.5542068	23.619873	23.9837208	23.5412521
333	Calpain small subunit 1 OS=Rattus norvegicus OX=10116 GN=Capns1 PE=1 SV=3	Capns1	Q64537	0.46413076	-0.515934	18.040823	19.8320713	19.1414909	18.0870953	18.9320869	19.2264442	18.9868202	20.019865
334	Calpain-2 catalytic subunit OS=Rattus norvegicus OX=10116 GN=Capn2 PE=1 SV=3	Capn2	Q07009	0.01167593	-0.014009	21.7339745	21.738842	21.0594902	20.5213985	21.2868843	21.3318596	20.5689697	21.9220276
335	Calreticulin OS=Rattus norvegicus OX=10116 GN=Calr PE=1 SV=1	Calr	P18418	0.38071193	-0.1340351	21.9256306	22.3274517	21.8801441	22.3024216	22.2336178	22.0991096	22.5185013	22.1205597
336	Calsequestrin OS=Rattus norvegicus OX=10116 GN=Casq2 PE=1 SV=2	Casq2	F1M944	2.23808655	0.43601131	27.6628475	27.6842575	27.8328056	27.401392	27.1333675	27.3272305	27.1070576	27.2696018
337	Calumenin OS=Rattus norvegicus OX=10116 GN=Calu PE=1 SV=1	Calu	G3V6S3	1.39712155	0.90811729	21.0931053	21.3576679	21.4024391	20.0843945	19.6644516	20.0155697	20.4369392	20.1881771
338	cAMP-dependent protein kinase inhibitor alpha OS=Rattus norvegicus OX=10116 GN=Pkia PE=1 SV=2	Pkia	P63249	0.72094415	0.47625494	17.5754185	16.9520397	17.9853497	17.3986797	17.376688	16.6880913	16.4928703	17.4488182
339	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Rattus norvegicus OX=10116 GN=Prkar1a PE=1 SV=2	Prkar1a	P09456	0.65360566	0.24281788	22.282177	22.2530422	21.8401928	22.2054844	22.13694	21.9758987	21.4779015	22.0188847
340	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Rattus norvegicus OX=10116 GN=Prkar2a PE=1 SV=4	Prkar2a	P12368	0.20282555	0.19891691	19.9716377	19.8643703	20.1176834	19.4366722	19.5958824	20.6677361	19.3152809	19.0157967
341	Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase OS=Rattus norvegicus OX=10116 GN=Cad PE=1 SV=2	Cad	D4A8A0	1.16850661	0.58453655	23.2794209	23.005022	22.3862267	22.3645973	22.271843	21.8576336	22.0974846	22.4701595
342	Carbonic anhydrase 1 OS=Rattus norvegicus OX=10116 GN=Ca1 PE=1 SV=1	Ca1	B0BNN3	0.98499916	-1.1281052	19.7437572	20.6092205	22.3026428	21.79743	22.2422829	22.0862827	22.5441532	22.0927525
343	Carbonic anhydrase 14 OS=Rattus norvegicus OX=10116 GN=Car14 PE=1 SV=1	Car14	A2IBE0	0.40514702	-0.2112436	17.6002769	17.9134331	17.8432446	18.3973846	18.1100597	18.576992	18.0974255	17.8148365
344	Carbonic anhydrase 2 OS=Rattus norvegicus OX=10116 GN=Ca2 PE=1 SV=2	Ca2	P27139	0.0681125	0.04466915	20.9169827	21.9461708	21.4347172	21.0743599	21.1908646	21.3851681	21.3840504	21.2334709
345	Carbonyl reductase [NADPH] 1 OS=Rattus norvegicus OX=10116 GN=Cbr1 PE=1 SV=2	Cbr1	P47727	2.08542595	0.92329884	21.7959251	21.9077454	21.6646767	21.8780499	20.3874645	21.181757	20.6130524	21.3709278
346	Carbonyl reductase family member 4 OS=Rattus norvegicus OX=10116 GN=Cbr4 PE=2 SV=1	Cbr4	Q7TS56	1.02353348	0.60841179	22.6123924	22.904213	22.0723381	21.9718857	21.6862392	21.6594639	21.3942451	22.3872337
347	Carboxylesterase 1D OS=Rattus norvegicus OX=10116 GN=Ces1d PE=1 SV=2	Ces1d	P16303	0.27900943	-0.4320569	17.673069	20.5284595	19.4886093	19.9173508	20.219305	19.5855694	19.4531746	20.0776672
348	Carboxylic ester hydrolase OS=Rattus norvegicus OX=10116 GN=Ces1c PE=1 SV=3	Ces1c	D3ZGK7	0.41655217	-0.3619049	16.1735783	16.4677448	16.0703545	14.8789082	15.7964697	16.5326862	16.3717976	16.3372517
349	Carboxymethylenebutenolidase homolog OS=Rattus norvegicus OX=10116 GN=Cmbl PE=2 SV=1	Cmbl	Q7TP52	0.02800925	0.01490784	17.9092484	17.7690506	18.2960968	17.9394932	18.1530457	18.2554283	17.6468945	17.7988892
350	Cardiac phospholamban OS=Rattus norvegicus OX=10116 GN=Pln PE=1 SV=1	Pln	P61016	1.33598832	-0.25741	24.6483097	24.7435036	24.5759125	24.8026047	25.0064869	24.7882195	25.1778545	24.8274097
351	Cardiac troponin C OS=Rattus norvegicus OX=10116 GN=Tnnc1 PE=2 SV=1	Tnnc1	Q4PP99	0.53962639	-1.164783	17.3333569	21.3104858	20.575489	20.7849789	21.4574356	20.3596306	20.593998	22.2523785
352	Carnitine O-acetyltransferase OS=Rattus norvegicus OX=10116 GN=Crat PE=1 SV=1	Crat	A0A0H2UI2	2.73001688	0.52703667	22.2345581	21.9534931	22.1080933	22.0313034	21.4895267	21.6656551	21.3605099	21.7036095
353	Carnitine O-palmitoyltransferase 1, liver isoform OS=Rattus norvegicus OX=10116 GN=Cpt1a PE=1 SV=2	Cpt1a	P32198	0.59400935	0.4186573	18.4213772	18.2190914	18.7105103	18.7548885	17.500433	18.4763336	17.6788845	18.7755871
354	Carnitine O-palmitoyltransferase 1, muscle isoform OS=Rattus norvegicus OX=10116 GN=Cpt1b PE=1 SV=1	Cpt1b	Q63704	0.87907101	-0.2629309	24.7294769	24.9803886	25.202673	25.2168446	25.3197689	25.2469826	25.5444775	25.0698776
355	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cpt2 PE=1 SV=1	Cpt2	P18886	0.30115719	0.15307331	25.8537464	26.6608734	25.9447613	26.2494278	26.3182163	25.9323502	26.0504932	25.7954559
356	Casein kinase II subunit alpha OS=Rattus norvegicus OX=10116 GN=Csnk2a1 PE=1 SV=2	Csnk2a1	P19139	0.32473608	-0.6830251	17.7648354	18.2112751	17.9423141	15.1204653	17.2517509	19.5190296	17.4095821	17.5906277
357	Cask-interacting protein 2 OS=Rattus norvegicus OX=10116 GN=Caskin2 PE=1 SV=1	Caskin2	D4A9T0	1.53495495	1.12184381	21.1404114	21.5419331	21.1262283	21.347826	20.7050629	20.6911964	19.0815086	20.1912556
358	Caspase recruitment domain family, member 19 OS=Rattus norvegicus OX=10116 GN=Card19 PE=4 SV=1	Card19	D3ZPP9	0.63670379	-0.3276606	18.4982567	19.26301	19.31143	19.4088497	19.6796131	19.2326164	19.6607857	19.2191734

359	Castration induced prostatic apoptosis-related protein 1 OS=Rattus norvegicus OX=10116 GN=Parm1 PE=1 SV=3	Parm1	F1LQ50	0.83584655	-0.8334663	15.252202	17.3450813	17.1342754	17.147171	17.3298912	17.7330837	17.6302223	17.5193977
360	Catalase OS=Rattus norvegicus OX=10116 GN=Cat PE=1 SV=3	Cat	P04762	0.49975007	0.24433374	20.409399	21.0124607	21.041193	21.0243053	20.424984	20.3106804	20.7491741	21.0251846
361	Catechol O-methyltransferase OS=Rattus norvegicus OX=10116 GN=Comt PE=1 SV=2	Comt	P22734	0.06419473	-0.0917845	16.1255131	17.4272728	15.8653612	15.9169998	16.0114117	17.3989563	15.8375559	16.454361
362	Catenin (Cadherin associated protein), alpha 1 OS=Rattus norvegicus OX=10116 GN=Ctnna1 PE=1 SV=1	Ctnna1	Q5U302	0.1004978	-0.103406	19.4014416	19.4543133	19.3078213	20.287569	19.7432289	18.9460621	19.7534161	20.4220619
363	Catenin (Cadherin associated protein), beta 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ctnnb1 PE=1 SV=1	Ctnnb1	A0A0G2JT9	0.06222197	0.07247305	17.326355	16.5602493	16.5300217	17.2643681	17.1275673	15.8461227	17.4740677	16.9433441
364	Cathepsin B OS=Rattus norvegicus OX=10116 GN=Ctsb PE=1 SV=1	Ctsb	Q6IN22	0.29103171	0.13247776	24.6109142	24.3437729	23.7723236	24.4053841	24.2435055	24.0478649	24.039875	24.2712383
365	Cathepsin D OS=Rattus norvegicus OX=10116 GN=Ctsd PE=1 SV=1	Ctsd	P24268	0.28993242	0.16649103	20.6240253	19.9295902	20.0539722	20.3073235	19.6690598	20.1633911	19.893343	20.5231533
366	Cation-dependent mannose-6-phosphate receptor OS=Rattus norvegicus OX=10116 GN=M6pr PE=1 SV=1	M6pr	Q6AY20	0.05263189	-0.0429645	20.1842537	20.2693024	19.1823483	19.3332329	19.9080696	19.7175751	19.6782246	19.8371258
367	Caveolae-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Cavin1 PE=1 SV=1	Cavin1	G3V8L9	1.62441183	0.68729258	25.6355877	25.5744286	25.9990864	25.2354202	24.6489391	25.3419647	24.6624908	25.0419579
368	Caveolae-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Cavin1 PE=1 SV=1	Cavin1	P85125	0.12620264	-0.3137095	15.4499865	18.7553329	19.1288567	18.7734699	17.4239159	19.0870457	18.2475452	18.6039772
369	Caveolae-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Cavin2 PE=1 SV=3	Cavin2	Q66H98	2.08988645	0.72479296	23.705658	23.6561642	23.9706364	23.2878704	22.9177647	23.2798462	22.7326107	22.7909355
370	Caveolae-associated protein 3 OS=Rattus norvegicus OX=10116 GN=Cavin3 PE=1 SV=1	Cavin3	Q9Z1H9	1.24899668	0.58093596	20.9236317	20.9238358	20.8714352	20.3955879	19.6517105	20.6762123	20.2535381	20.2092857
371	Caveolae-associated protein 4 OS=Rattus norvegicus OX=10116 GN=Cavin4 PE=1 SV=1	Cavin4	B1PRL5	2.15328029	1.02362442	23.9851208	23.48032	24.0419464	23.2127571	22.401968	23.0313358	22.3882217	22.804121
372	Caveolin-1 OS=Rattus norvegicus OX=10116 GN=Cav1 PE=1 SV=3	Cav1	P41350	0.53105817	-0.2193351	23.7176304	23.045435	23.2011318	23.7340603	23.8364391	23.4971886	23.6564922	23.5854778
373	Caveolin-2 OS=Rattus norvegicus OX=10116 GN=Cav2 PE=1 SV=2	Cav2	Q2IBC5	0.97165039	-1.2770414	19.3103561	17.8936043	16.2216911	18.0514946	18.5026417	19.5124493	19.4104919	19.159729
374	Caveolin-3 OS=Rattus norvegicus OX=10116 GN=Cav3 PE=1 SV=1	Cav3	P51638	0.41528762	0.25779104	21.6256561	21.2759819	20.8444443	21.8427849	21.0634766	21.6035881	21.0838528	20.8067856
375	CD151 antigen OS=Rattus norvegicus OX=10116 GN=Cd151 PE=1 SV=2	Cd151	Q9QZA6	1.25915621	-0.3997588	20.4762192	20.3543243	20.3778763	20.894537	20.9763966	20.8616848	21.1995449	20.6643658
376	CD163 antigen (Predicted) OS=Rattus norvegicus OX=10116 GN=Cd163 PE=1 SV=1	Cd163	D3Z9U2	0.0590776	-0.0467238	21.4167233	21.6708069	21.1457691	21.5452633	21.0386639	21.1147823	22.1259499	21.6860619
377	CD1d1 antigen OS=Rattus norvegicus OX=10116 GN=Cd1d1 PE=1 SV=1	Cd1d1	G3V837	0.48648141	-0.6387453	17.8060608	16.4604187	17.5932198	16.9574013	16.3749657	18.7661991	18.0867844	18.1441326
378	CD34 antigen (Predicted) OS=Rattus norvegicus OX=10116 GN=Cd34 PE=1 SV=1	Cd34	B1PLB1	1.03580126	-0.2828145	21.7588825	22.1716385	21.6986542	21.8668613	22.0698395	22.0321655	22.4375401	22.0877495
379	CD34 antigen isoform 2 OS=Rattus norvegicus OX=10116 GN=Cd34 PE=2 SV=1	Cd34	B1PLB2	0.71634167	-0.5849304	15.8679543	17.5879459	17.2550907	17.224411	17.2667923	17.6598415	17.8132496	17.5352402
380	CD48 antigen OS=Rattus norvegicus OX=10116 GN=Cd48 PE=1 SV=1	Cd48	P10252	1.49262957	-0.6631289	20.3121452	20.2337093	19.7181835	19.4420986	20.6384048	20.6187572	20.8312263	20.2702637
381	CD59 glycoprotein OS=Rattus norvegicus OX=10116 GN=Cd59 PE=1 SV=2	Cd59	P27274	1.31703285	-0.4476357	21.2944107	21.2830029	20.9635296	21.4763851	21.731781	22.048933	21.6928482	21.3343086
382	CD9 antigen OS=Rattus norvegicus OX=10116 GN=Cd9 PE=1 SV=2	Cd9	P40241	0.48125817	-0.2624931	20.5560131	20.7268772	19.6603909	20.0569725	20.4053555	20.4779873	20.6465359	20.5203476
383	CD99 molecule (Xg blood group) OS=Rattus norvegicus OX=10116 GN=Cd99 PE=1 SV=1	Cd99	B4F7A5	1.11745125	-0.5041242	19.925415	20.1765003	20.2297859	20.3526211	21.1397095	20.134819	20.8854771	20.5408134
384	Cdc42 effector protein 1 OS=Rattus norvegicus OX=10116 GN=Cdc42ep1 PE=1 SV=1	Cdc42ep1	A1A5P0	0.55474395	0.29498339	17.6285152	16.8271313	17.5477085	17.3546486	17.1872482	16.8283443	16.70895	17.4535275
385	CDGSH iron sulfur domain 2 OS=Rattus norvegicus OX=10116 GN=Cisd2 PE=1 SV=1	Cisd2	D4AAE9	0.07798994	-0.0520406	17.5383205	18.2515888	18.2249393	18.6530914	18.3905544	18.1464825	18.2418079	18.0972576
386	CDGSH iron sulfur domain 3 OS=Rattus norvegicus OX=10116 GN=Cisd3 PE=1 SV=1	Cisd3	A0A0G2JW3	0.55274782	0.21469164	23.5231419	22.7897663	22.9985371	23.0847092	23.0889626	22.7320881	22.7162647	23.0000725
387	CDGSH iron-sulfur domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Cisd1 PE=3 SV=1	Cisd1	B0K020	0.84123877	-0.3670964	25.0519581	25.5604801	25.6325188	25.9351177	25.808939	25.8985462	26.24683	25.6941452
388	Cell adhesion molecule 3 OS=Rattus norvegicus OX=10116 GN=Cadm3 PE=1 SV=1	Cadm3	A0A0G2K87	0.22193565	-0.1905298	19.4879875	19.6108913	19.2475414	18.6745491	19.0566959	19.0136642	19.5184498	20.1942787
389	Cell cycle and apoptosis regulator 2 OS=Rattus norvegicus OX=10116 GN=Ccar2 PE=1 SV=1	Ccar2	F1LM55	0.09456093	0.04668379	20.5640106	19.7474499	20.2110291	20.2660923	20.1598892	19.9883442	20.1551609	20.2984524
390	Cell cycle control protein OS=Rattus norvegicus OX=10116 GN=Tmem30a PE=1 SV=1	Tmem30a	A0A0G2JXG	0.37669273	-0.1389856	16.2844505	16.6659584	16.176033	16.3033218	16.8491802	16.39571	16.4287624	16.3120537
391	Cell division control protein 42 homolog OS=Rattus norvegicus OX=10116 GN=Cdc42 PE=1 SV=2	Cdc42	Q8CFN2	0.29882258	-0.0671539	22.1684723	22.2458878	22.1171722	22.2478523	22.3393517	21.9963741	22.3576527	22.3546219
392	Cerebral dopamine neurotrophic factor OS=Rattus norvegicus OX=10116 GN=Cdnf PE=3 SV=1	Cdnf	P0C5I0	0.22160644	-0.4252105	16.4767685	14.4467154	17.8633289	16.70998	15.9606485	16.8426647	17.0956917	17.2986298
393	Ceruloplasmin OS=Rattus norvegicus OX=10116 GN=Cp PE=1 SV=1	Cp	A0A0G2K9I	1.16438395	-0.6303186	20.2034836	21.1714439	19.9650116	20.1033306	20.9253426	20.8500385	21.1935806	20.9955826
394	cGMP-inhibited 3',5'-cyclic phosphodiesterase A OS=Rattus norvegicus OX=10116 GN=Pde3a PE=1 SV=1	Pde3a	Q62865	0.20190808	0.15230894	21.2232838	20.5929699	20.4625187	20.1128864	20.4120731	20.7718067	19.928627	20.6699162
395	Chaperonin containing Tcp1, subunit 6A (Zeta 1) OS=Rattus norvegicus OX=10116 GN=Cct6a PE=1 SV=1	Cct6a	Q3MHS9	0.51685442	0.3013401	22.4575615	22.3010387	22.2963428	21.5484867	21.7873497	22.0669441	21.3848648	22.1589108
396	Chaperonin subunit 8 (Theta) (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Cct8 PE=1 SV=1	Cct8	D4ACB8	1.42381008	0.66696739	21.6861477	22.2585144	21.4453316	21.7096844	21.3521423	21.1793251	20.5712605	21.3290806
397	Charged multivesicular body protein 6 OS=Rattus norvegicus OX=10116 GN=Chmp6 PE=1 SV=1	Chmp6	D3ZDR2	0.57824276	-0.551156	18.4709511	18.8125992	17.8381844	17.004961	18.6378059	18.0100384	18.9878731	18.6956024
398	Chloride intracellular channel protein 1 OS=Rattus norvegicus OX=10116 GN=Clic1 PE=1 SV=1	Clic1	Q6MG61	0.7008743	1.03126001	16.7275486	17.3691177	16.7139759	18.7423286	15.0209007	16.0198212	17.423027	16.9641819
399	Chloride intracellular channel protein 5 OS=Rattus norvegicus OX=10116 GN=Clic5 PE=1 SV=1	Clic5	Q9EPT8	1.03568045	1.83178306	18.6163216	18.8491039	18.4256535	16.89048	16.9173546	16.4452515	14.1530104	17.9388103
400	Chloride intracellular channel protein OS=Rattus norvegicus OX=10116 GN=Clic4 PE=1 SV=1	Clic4	G3V8C4	0.49345583	0.30559826	21.9762821	22.8326931	22.4726448	21.7629929	21.7684612	21.8201199	21.8410091	22.3926296
401	CHMP family, member 7 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Chmp7 PE=1 SV=1	Chmp7	D4A7H9	0.50232851	0.37600899	17.625494	17.6602745	16.8057861	16.6615467	16.9700584	16.8199711	16.2135658	17.24547
402	Choline transporter-like protein 2 OS=Rattus norvegicus OX=10116 GN=Slc44a2 PE=2 SV=1	Slc44a2	B4F795	0.2425686	0.2598896	19.9237595	18.7003536	18.8798828	20.1547375	19.1114826	18.8548317	18.818121	19.8347397
403	Choline-phosphate cytidylyltransferase A OS=Rattus norvegicus OX=10116 GN=Pcyt1a PE=1 SV=2	Pcyt1a	P19836	0.85717603	-1.6208394	16.035017	18.3166504	13.9151354	15.9612808	17.0831394	17.225008	18.0903873	18.3129063
404	Chromosome segregation 1-like OS=Rattus norvegicus OX=10116 GN=Cse1l PE=1 SV=1	Cse1l	D3ZPR0	0.63266309	0.38760567	24.486927	23.4736004	23.3067837	23.9071827	23.1693878	23.3936596	23.3016491	23.7593746
405	Citramalyl-CoA lyase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Clybl PE=2 SV=2	Clybl	Q5I0K3	0.78194723	-0.7812066	18.7720909	20.3608818	20.3680916	20.8690529	20.7128811	21.3235855	21.0204048	20.4380722
406	Citrate synthase OS=Rattus norvegicus OX=10116 GN=Cs PE=1 SV=1	Cs	G3V936	0.63025073	0.17237806	25.9341526	26.0250645	26.055624	25.5727749	25.7311611	25.8651695	25.5385323	25.7632408
407	Clathrin heavy chain OS=Rattus norvegicus OX=10116 GN=Cltc PE=1 SV=1	Cltc	F1M779	0.14607217	-0.0983849	24.1599464	24.7923698	23.8479424	24.2313995	23.8663826	24.5469551	24.4641552	24.5477047
408	Clathrin interactor 1 OS=Rattus norvegicus OX=10116 GN=Clint1 PE=1 SV=1	Clint1	Q6DGF2	0.87040284	-1.255527	16.8746147	14.3369827	16.9941387	17.6036453	17.5455933	17.8877316	17.645237	17.7529278
409	Clathrin light chain A OS=Rattus norvegicus OX=10116 GN=Clta PE=1 SV=1	Clta	P08081	0.58251615	0.31978464	20.9368877	21.4366093	20.5897827	21.0155239	20.8842735	21.0110493	20.1468563	20.657486
410	Clathrin light chain B OS=Rattus norvegicus OX=10116 GN=Cltb PE=1 SV=1	Cltb	P08082	0.70210034	-0.534348	19.9410419	20.7581863	19.9044304	21.3216133	20.7021961	21.0085621	21.3804359	20.9714699
411	Clusterin OS=Rattus norvegicus OX=10116 GN=Clu PE=1 SV=2	Clu	P05371	0.10550203	0.09640074	21.6976795	22.3371639	21.4640179	20.8687744	21.3526878	21.2270546	21.5033264	21.8989639
412	Coagulation factor C homolog (Limulus polyphemus) (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Coch PE=2 SV=1	Coch	B1H259	0.7689008	1.546597	17.0466499	17.0179214	17.3374691	20.0572624	17.2378635	14.3631744	16.5619431	17.1099339
413	Coagulation factor IX OS=Rattus norvegicus OX=10116 GN=F9 PE=2 SV=2	F9	P16296	1.25159702	0.55879831	22.0231304	22.3468227	21.9737549	21.4502678	21.2667408	21.1133842	21.3812504	21.7974072
414	Coagulation factor X OS=Rattus norvegicus OX=10116 GN=F10 PE=1 SV=1	F10	A0A0H2UH	0.07556038	0.16338873	18.2372799	17.4028778	19.5259075	16.9940128	19.3143921	16.7090778	17.6363907	17.8466625
415	Coagulation factor XII OS=Rattus norvegicus OX=10116 GN=F12 PE=1 SV=1	F12	A0A0H2UI1	1.0947517	-0.4730163	17.2138367	16.9746056	16.9004536	17.4085159	17.6680355	17.4210491	18.100441	17.1999512
416	Coagulation factor XIII A chain OS=Rattus norvegicus OX=10116 GN=F13a1 PE=2 SV=3	F13a1	O08619	0.64622208	0.79301524	16.3795452	17.2871342	16.3334675	16.668026	14.3675232	15.7772379	16.6888542	16.6624966
417	Coatomer subunit alpha OS=Rattus norvegicus OX=10116 GN=Copa PE=1 SV=1	Copa	G3V6T1	0.43212207	-0.1589756	20.9173813	20.7035313	20.3457222	20.3633881	20.898098	20.5476818	20.6396656	20.8804798
418	Coatomer subunit beta OS=Rattus norvegicus OX=10116 GN=Copb1 PE=1 SV=1	Copb1	P23514	0.22187175	-0.2755232	19.0169182	19.0145035	18.7373238	18.1354923	19.0988522	18.0198689	18.7044907	20.1831188
419	Coatomer subunit beta' OS=Rattus norvegicus OX=10116 GN=Copb2 PE=1 SV=3	Copb2	O35142	0.35352386	0.47405887	17.4698086	17.7332878	17.0814476	17.8173923	17.6689472	17.2744198	15.4293642	17.8329697
420	Coatomer subunit epsilon OS=Rattus norvegicus OX=10116 GN=Cope PE=1 SV=3	Cope	G3V8Q1	0.03378466	0.0433321	19.4054527	18.9922085	17.8386974	18.0825672	17.856823	18.6155739	18.9971828	18.6760178
421	Coatomer subunit gamma OS=Rattus norvegicus OX=10116 GN=Copg1 PE=1 SV=1	Copg1	A0A0G2K1F	1.00942325	-0.9728742	18.7211857	16.7410278	17.7844067	17.6327286	19.113966	18.209959	18.1872044	19.259716
422	COBW domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Cbwd1 PE=2 SV=2	Cbwd1	Q99MB4	0.63772496	0.39397907	20.1928902	20.3467903	19.7459717	20.2955074	19.6490231	19.6234379	19.2471581	20.4856243
423	Coenzyme A synthase OS=Rattus norvegicus OX=10116 GN=Coasy PE=1 SV=1	Coasy	Q5XIA5	0.89422478	0.62960815	20.1696892	20.2744217	18.9859657	19.9873905	19.4572487	19.3005104	19.4994755	18.6417999
424	Coenzyme Q10 homolog A (Yeast) (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Coq10a PE=4 SV=1	Coq10a	D3ZX74	0.05343037	0.04110098	19.9651756	19.3691521	19.6352577	19.7858257	19.9430599	19.0086498	19.5618954	20.0774021
425	Cofilin 2 OS=Rattus norvegicus OX=10116 GN=Cfl2 PE=1 SV=1	Cfl2	M0RC65	0.48121104	-0.1793656	19.0225849	18.883646	18.3991146	18.8744278	18.8591251	18.9885368	18.7981148	19.2514591
426	Cofilin-1 OS=Rattus norvegicus OX=10116 GN=Cfl1 PE=1 SV=3	Cfl1	P45592	0.26355101	0.10348701	20.9305763	20.8508797	20.639492	21.2793255	20.6388226	20.700243	20.9207363	21.0265236
427	Coiled-coil domain-containing 141 OS=Rattus norvegicus OX=10116 GN=Ccdc141 PE=1 SV=2	Ccdc141	D3ZEY0	0.40777684	0.61512923	16.9127617	16.4616566	18.6489105	16.8769264	16.6346188	15.9090872	16.008112	17.8879204
428	Coiled-coil domain-containing 186 OS=Rattus norvegicus OX=10116 GN=Ccdc186 PE=1 SV=1	Ccdc186	A0A0G2K8I	0.34699634	0.72789979	18.076149	16.8545685	17.4652901	17.503624	17.4843712	17.3987885	14.1747389	17.9301338
429	Coiled-coil domain-containing protein 127 OS=Rattus norvegicus OX=10116 GN=Ccdc127 PE=2 SV=2	Ccdc127	Q6PEB9	0.3713467	-0.4720366	15.272912	15.571209	15.1833792	16.2740002	15.547616	14.9582939	16.5070133	17.1767235
430	Coiled-coil domain-containing protein 47 OS=Rattus norvegicus OX=10116 GN=Ccdc47 PE=2 SV=1	Ccdc47	Q5U2X6	0.17880301	0.27897573	16.4906845	16.724165	15.1604958	16.8792591	16.7995777	16.079174	14.7155638	16.5443859

431	Coiled-coil domain-containing protein 51 OS=Rattus norvegicus OX=10116 GN=Ccdc51 PE=1 SV=1	Ccdc51	A0A0G2JXH	0.66900916	-0.2204599	20.7945766	20.9401035	21.1790543	21.2719479	21.4050217	21.2447205	21.4667206	20.9510593
432	Coiled-coil-helix-coiled-coil-helix domain containing 10 OS=Rattus norvegicus OX=10116 GN=Chchd10 PE=1 SV=1	Chchd10	Q63ZY8	0.18061934	0.40827179	20.8121071	17.5179901	17.5753002	17.2345886	18.5988998	17.4863892	17.6003609	17.821249
433	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial-like OS=Rattus norvegicus OX=10116 GN=LOC100911516 PE=4 SV=1	LOC100911	M0R785	0.4657454	-0.8929067	22.4631214	21.1604195	21.1070385	18.7067623	22.573967	21.5904388	20.822649	22.0219135
434	Cold shock domain-containing protein E1 OS=Rattus norvegicus OX=10116 GN=Csde1 PE=2 SV=1	Csde1	P18395	0.67474334	0.57786989	19.6843338	20.7695827	20.5299454	19.2616005	19.3151436	19.5409966	19.0348263	20.0430164
435	Collagen type VI alpha 1 chain OS=Rattus norvegicus OX=10116 GN=Col6a1 PE=1 SV=1	Col6a1	D3ZUL3	0.02005093	-0.0372324	20.6243382	19.9686165	19.8458767	18.0983086	20.1838646	18.7813969	19.5781689	20.1426392
436	Collagen type VI alpha 2 chain OS=Rattus norvegicus OX=10116 GN=Col6a2 PE=1 SV=2	Col6a2	F1LNH3	0.44827916	0.60986471	18.7557716	19.6181259	18.4607449	17.5647717	17.1624527	18.6128941	17.3101234	18.874485
437	Complement C3 OS=Rattus norvegicus OX=10116 GN=C3 PE=1 SV=1	C3	M0RBF1	0.02568554	-0.0143538	23.1176987	23.2713375	22.8328819	22.9004211	22.7000465	22.9384174	23.0650654	23.4762249
438	Complement C4A OS=Rattus norvegicus OX=10116 GN=C4a PE=4 SV=2	C4a	M0RB00	0.02830866	-0.0467663	18.0437851	18.0798187	18.4358387	17.9507351	18.1147728	18.2772217	16.7923203	19.512928
439	Complement C7 OS=Rattus norvegicus OX=10116 GN=C7 PE=1 SV=1	C7	A0A0G2K7Y	0.80276709	-0.332108	21.7630463	22.0576019	22.3963966	22.6382675	22.3980446	22.615818	22.7203903	22.4494915
440	Complement C8 alpha chain OS=Rattus norvegicus OX=10116 GN=C8a PE=1 SV=1	C8a	D3ZWD6	0.32789125	0.63833714	17.5845318	18.0721836	15.5967379	16.9461327	16.8907738	16.3301888	14.7195559	17.705719
441	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=C1qbp PE=1 SV=2	C1qbp	O35796	0.71008126	-0.5185418	23.6886654	22.3947906	22.7373943	22.9669399	24.0178013	23.3860607	22.9175453	23.5405502
442	Complement component receptor 1-like protein OS=Rattus norvegicus OX=10116 GN=Cr1l PE=1 SV=1	Cr1l	A0A0G2K7V	0.55664568	-0.657073	17.7015724	19.5691643	19.2128029	20.2165737	19.4414082	19.9928951	20.0389462	19.8551559
443	Complement factor H OS=Rattus norvegicus OX=10116 GN=Cfh PE=1 SV=1	Cfh	G3V9R2	0.96388099	-0.8810358	16.1914349	17.8120728	17.4778481	16.3670387	17.3619652	18.1763172	17.5069199	18.3273354
444	Component of oligomeric golgi complex 2 OS=Rattus norvegicus OX=10116 GN=Cog2 PE=1 SV=1	Cog2	D3ZT01	0.45969902	0.36550903	17.9429607	17.8513279	17.3142395	16.5724087	16.6814766	17.2772026	16.8554401	17.4047813
445	Component of oligomeric golgi complex 3 OS=Rattus norvegicus OX=10116 GN=Cog3 PE=1 SV=1	Cog3	Q5XHZ8	1.29133453	0.96408749	17.6676464	18.9963989	18.5072536	17.8709793	16.5566845	17.3567657	17.6178627	17.6546154
446	Component of oligomeric golgi complex 4 OS=Rattus norvegicus OX=10116 GN=Cog4 PE=1 SV=1	Cog4	D3ZZM3	0.5312708	0.59728575	19.0291672	19.1737671	18.8506889	17.386343	17.6183853	18.7085094	17.3578033	18.3661251
447	Component of oligomeric golgi complex 5 OS=Rattus norvegicus OX=10116 GN=Cog5 PE=1 SV=1	Cog5	A0A0G2K9P	0.15866735	-0.3460302	18.4816551	18.535408	18.4872398	15.2167511	18.2653484	17.5426311	18.2159214	18.081274
448	Conserved helix-loop-helix ubiquitous kinase OS=Rattus norvegicus OX=10116 GN=Chuk PE=1 SV=1	Chuk	G3V926	0.19169321	0.28154516	19.3289852	17.3383732	18.5808182	17.2450981	18.0631752	17.3539066	17.4146137	18.5353985
449	COP9 signalosome complex subunit 3 OS=Rattus norvegicus OX=10116 GN=Cops3 PE=1 SV=1	Cops3	Q68FW9	0.03741133	0.03629708	15.6256199	15.9144154	16.5217171	16.2239761	16.5311909	15.2509604	16.2085972	16.1497917
450	COP9 signalosome complex subunit 4 OS=Rattus norvegicus OX=10116 GN=Cops4 PE=1 SV=1	Cops4	Q68FS2	0.01535332	-0.0407164	14.4717693	16.1796722	16.1719208	16.9276085	15.8205338	14.0449018	16.544241	17.5041599
451	COP9 signalosome complex subunit 8 OS=Rattus norvegicus OX=10116 GN=Cops8 PE=2 SV=1	Cops8	Q6P4Z9	0.54225287	-0.5683093	16.4352932	17.4007874	16.2334595	16.2526398	16.983099	17.4740601	16.1282558	18.0100021
452	Copine-7 OS=Rattus norvegicus OX=10116 GN=Cpne7 PE=1 SV=1	Cpne7	H1UBN0	0.38186001	-0.1837196	16.9158497	17.5548172	17.4823666	17.5636368	17.4527645	17.7249794	17.8521442	17.2216606
453	COX assembly mitochondrial protein OS=Rattus norvegicus OX=10116 GN=Cmc1 PE=1 SV=2	Cmc1	D3ZTN2	0.52082648	-0.7374907	15.845993	15.384304	17.4794998	17.5608196	17.4681816	17.928669	16.3447704	17.4789581
454	COX15 homolog, cytochrome c oxidase assembly protein (Yeast), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Cox15 PE=1 SV=1	Cox15	D4A414	0.55456031	-0.8269932	15.8741369	18.3069935	18.2001381	18.8060341	18.4917889	19.0762043	18.90028	18.0270023
455	C-reactive protein OS=Rattus norvegicus OX=10116 GN=Crp PE=1 SV=1	Crp	A0A0G2K8V	0.67105159	-0.2049589	18.9378338	19.1018295	18.7585564	18.6894073	18.7743168	19.0568199	19.1583023	19.3180237
456	Creatine kinase B-type OS=Rattus norvegicus OX=10116 GN=Ckb PE=1 SV=2	Ckb	P07335	0.14473517	0.1315918	23.1542416	24.0724926	23.791666	22.9801731	23.3319149	23.1486492	22.9716549	24.0199871
457	Creatine kinase M-type OS=Rattus norvegicus OX=10116 GN=Ckm PE=1 SV=1	Ckm	A0A0G2JSP9	0.20880467	0.08970165	26.5772781	26.7352352	26.963068	26.5206947	26.6612778	26.7268829	26.2071838	26.8421249
458	Creatine kinase S-type, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ckmt2 PE=1 SV=1	Ckmt2	A0A0G2JVQ	0.2489227	0.05052185	26.117012	26.2241669	26.1516724	26.3767185	26.1959724	26.2891693	26.1777973	26.0045433
459	Creatine kinase S-type, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ckmt2 PE=1 SV=2	Ckmt2	P09605	0.32500945	-0.0944724	28.4917774	28.8016167	28.703207	29.0468807	28.937439	28.9167404	28.8215847	28.7456074
460	CTP synthase OS=Rattus norvegicus OX=10116 GN=Ctps1 PE=1 SV=1	Ctps1	B1WC02	0.70917864	0.55175543	20.1493874	20.1079655	20.1666908	18.9660683	19.4120235	19.3536625	18.6382332	19.779171
461	C-type lectin domain family 10 member A OS=Rattus norvegicus OX=10116 GN=Clec10a PE=1 SV=1	Clec10a	P49301	0.01442961	-0.0137143	18.8541794	19.5675888	18.3618031	19.1834888	18.8283978	19.3390503	19.31353	18.5409393
462	C-type lectin domain family 2, member G OS=Rattus norvegicus OX=10116 GN=Clec2g PE=1 SV=1	Clec2g	A0A0G2JVV	0.48156094	-0.636843	17.166048	17.5967178	16.5734234	15.4240236	17.8542366	17.4633446	16.2368851	17.7531185
463	Cullin 2 OS=Rattus norvegicus OX=10116 GN=Cul2 PE=1 SV=1	Cul2	A0A0G2K76	0.04263811	0.03898191	19.8530979	19.9450054	19.6902103	18.9837151	19.3965702	19.3387032	19.3084335	20.2723942
464	Cullin 4A OS=Rattus norvegicus OX=10116 GN=Cul4a PE=1 SV=1	Cul4a	B2RYJ3	0.12315445	0.13950491	17.2702084	17.9768295	16.8417034	17.2849445	17.0062599	16.8277302	16.7338295	18.2478466
465	Cullin 9 OS=Rattus norvegicus OX=10116 GN=Cul9 PE=1 SV=2	Cul9	D3ZZP8	0.41469969	-0.2452607	19.9271011	20.9715385	20.6636639	20.8751392	20.655304	21.1523666	20.9014721	20.709343
466	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus OX=10116 GN=Cand1 PE=1 SV=1	Cand1	P97536	0.11863081	0.16530132	18.8837547	18.3624649	17.7467213	18.7104721	18.7017746	17.1418839	17.9656849	19.2328644
467	Cullin-associated NEDD8-dissociated protein 2 OS=Rattus norvegicus OX=10116 GN=Cand2 PE=4 SV=1	Cand2	A0A0G2K13	0.12327334	0.11510611	25.7965202	25.1271	25.2062225	24.6027889	25.2104473	25.0882816	24.3898201	25.5836582
468	Cyclin-dependent kinase 11B OS=Rattus norvegicus OX=10116 GN=Cdk11b PE=1 SV=3	Cdk11b	D4A3G2	0.97040048	0.95735216	18.1743011	16.0116768	17.2730446	16.708004	16.5610943	15.5372849	16.0008545	16.2383842
469	Cyclin-dependent kinase 16 OS=Rattus norvegicus OX=10116 GN=Cdk16 PE=1 SV=1	Cdk16	Q68G39	0.8078874	1.66680694	18.5224037	17.6158295	18.5313034	15.0874977	16.7478199	16.3224831	16.083477	13.9360266
470	Cyclin-dependent-like kinase 5 OS=Rattus norvegicus OX=10116 GN=Cdk5 PE=1 SV=1	Cdk5	Q03114	0.9045666	1.03248072	18.8951015	18.2537479	17.8900089	16.6977673	16.4188652	17.930624	16.7270355	16.5301781
471	Cystatin-B OS=Rattus norvegicus OX=10116 GN=Cstb PE=1 SV=1	Cstb	P01041	0.17432302	-0.1367536	18.8042107	18.4916	18.7709236	19.1580658	19.1059208	18.1575832	19.4177055	19.0906048
472	Cystatin-C OS=Rattus norvegicus OX=10116 GN=Cst3 PE=1 SV=2	Cst3	P14841	0.23303927	-0.0772595	18.435154	18.8426666	18.6685028	18.9621696	18.8218765	18.8435383	18.9406872	18.6114292
473	Cysteine and glycine-rich protein 3 OS=Rattus norvegicus OX=10116 GN=Csrp3 PE=1 SV=1	Csrp3	G3V7U0	0.20187195	-0.1018419	23.9376278	23.5752335	23.3028793	23.7634754	23.6061554	23.4108162	23.9109249	24.0586872
474	Cysteine conjugate-beta lyase 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Kyat1 PE=1 SV=1	Kyat1	G3V827	0.20726367	0.41164494	19.1095695	19.5875149	17.1432648	17.4609375	17.0463715	18.8383503	17.0171604	18.7528248
475	Cysteine desulfurase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Nfs1 PE=1 SV=1	Nfs1	Q3MHT2	1.06771511	0.4493084	25.5848427	25.2430038	25.3571892	24.6496429	24.7348404	24.7671623	24.549551	24.9858913
476	Cysteine-rich protein 1 OS=Rattus norvegicus OX=10116 GN=Crip1 PE=1 SV=2	Crip1	P63255	0.88471188	-0.2440276	17.2498684	17.4072247	17.0952187	16.8535137	17.5066757	17.2457199	17.2916012	17.5379391
477	Cysteine-rich protein 2 OS=Rattus norvegicus OX=10116 GN=Crip2 PE=2 SV=1	Crip2	P36201	0.37379741	-0.1561198	23.2024803	23.0980244	22.8346024	22.7595959	22.8007736	23.2141914	23.0099678	23.4942493
478	Cytochrome b OS=Rattus norvegicus OX=10116 GN=Mt-Cyb PE=3 SV=3	Mt-Cyb	P00159	0.61732833	-0.2887864	22.5168304	22.873558	23.0386562	23.4720974	23.4066277	23.0233116	23.4507618	23.1755867
479	Cytochrome b-245 beta chain OS=Rattus norvegicus OX=10116 GN=Cybb PE=1 SV=2	Cybb	Q9ERL1	0.24134043	-0.4277024	18.0856113	18.1815357	15.6560535	17.7380238	16.6962261	17.8858089	18.2509689	18.5390301
480	Cytochrome b5 OS=Rattus norvegicus OX=10116 GN=Cyb5a PE=1 SV=2	Cyb5a	P00173	0.67760382	-0.4233303	20.2433872	20.2379875	19.8668766	21.0350704	20.8868999	21.0659714	20.8597794	20.2639923
481	Cytochrome b5 type B OS=Rattus norvegicus OX=10116 GN=Cyb5b PE=1 SV=2	Cyb5b	P04166	0.94469681	-0.6092854	18.1754856	18.7821846	18.0301952	17.905159	18.6987972	18.168335	19.41749	19.0455437
482	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Uqcrc1 PE=1 SV=1	Uqcrc1	Q68FY0	0.68401182	-0.3559537	27.2085724	27.8298512	28.0751743	28.2189503	28.2149372	28.1279373	28.4874344	27.926054
483	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Uqcrc2 PE=1 SV=2	Uqcrc2	P32551	0.91196547	-0.2919745	27.4943771	27.9134312	28.0517445	28.1538506	28.1791878	28.2006855	28.3800697	28.0213585
484	Cytochrome b-c1 complex subunit 6, mitochondrial OS=Rattus norvegicus OX=10116 GN=Uqcrh PE=3 SV=1	Uqcrh	Q5M9I5	0.99684262	-0.423389	24.6975212	25.2229004	25.3631668	25.2449226	25.607935	25.5258064	25.9350967	25.1532288
485	Cytochrome b-c1 complex subunit 7 OS=Rattus norvegicus OX=10116 GN=Uqcrb PE=1 SV=1	Uqcrb	B2RYS2	0.54799769	-0.2787437	26.6409931	27.1065006	27.3382263	27.5231647	27.5226784	27.3595791	27.7537766	27.0878258
486	Cytochrome b-c1 complex subunit 8 OS=Rattus norvegicus OX=10116 GN=Uqcrq PE=3 SV=1	Uqcrq	Q7TQ16	0.68518922	-0.3499384	24.4347324	24.6298542	25.0688858	25.3462429	25.2155399	25.1564026	25.5799084	24.927618
487	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Rattus norvegicus OX=10116 GN=Uqcrfs1 PE=1 SV=2	Uqcrfs1	P20788	1.15231659	-0.4512029	25.896616	26.2983875	26.6257057	26.6413136	26.7480984	26.7929764	27.1164379	26.6093216
488	Cytochrome c heme lyase OS=Rattus norvegicus OX=10116 GN=Hccs PE=1 SV=1	Hccs	D3ZL85	0.90676361	-0.609499	20.6750813	21.3855572	21.8633347	22.0488472	22.0175228	22.2716007	22.3985138	21.7231789
489	Cytochrome C oxidase assembly factor 3 OS=Rattus norvegicus OX=10116 GN=Coa3 PE=1 SV=1	Coa3	D3Z9I1	1.33480599	-0.4623632	20.8505325	21.0638771	21.2982082	20.6599827	21.2026081	21.4230194	21.7745361	21.3218899
490	Cytochrome c oxidase assembly factor COX20 OS=Rattus norvegicus OX=10116 GN=Cox20 PE=1 SV=1	Cox20	D3ZYU4	0.80929845	-0.5059142	20.5752831	20.9868393	21.2325611	21.7206192	21.6500549	21.4856091	22.1723423	21.2309532
491	Cytochrome C oxidase assembly protein COX17 OS=Rattus norvegicus OX=10116 GN=Cox17 PE=1 SV=1	Cox17	Q76MV3	0.06552771	0.04719687	18.5815334	18.2083683	18.2708187	18.4533749	18.696682	18.0440769	18.7830276	17.8015213
492	Cytochrome c oxidase subunit 1 OS=Rattus norvegicus OX=10116 GN=Mtco1 PE=2 SV=3	Mtco1	P05503	1.02916847	-0.4775305	22.5978317	23.2175026	23.3177814	23.4072056	23.4235401	23.4596024	24.0746288	23.492672
493	Cytochrome c oxidase subunit 2 OS=Rattus norvegicus OX=10116 GN=Mtco2 PE=1 SV=3	Mtco2	P00406	1.53755832	-0.4500513	26.3034039	26.5206966	26.7474174	26.8646469	26.9823437	27.1495266	27.2740517	26.8304482
494	Cytochrome c oxidase subunit 3 OS=Rattus norvegicus OX=10116 GN=Mtco3 PE=1 SV=5	Mtco3	P05505	1.04878444	-0.5060091	21.264225	21.092123	21.1255894	21.6649246	21.8963718	21.785059	22.258091	21.2313766
495	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox4i1 PE=1 SV=1	Cox4i1	P10888	1.04827111	-0.3981276	26.3861389	26.7766399	26.8008251	27.2102833	27.1050739	27.2688236	27.4319496	26.9605503
496	Cytochrome c oxidase subunit 5A, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox5a PE=1 SV=1	Cox5a	P11240	0.90956673	-0.3850474	25.9241924	26.3942509	26.4701195	26.7514191	26.6162567	26.7602234	27.1367836	26.5669079
497	Cytochrome c oxidase subunit 5B, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox5b PE=1 SV=2	Cox5b	P12075	0.89836461	-0.3791299	26.0088215	26.4283199	26.5562439	26.895752	26.7706261	26.8865738	27.1349831	26.6134739
498	Cytochrome c oxidase subunit 6A, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox6a2 PE=3 SV=1	Cox6a2	G3V8M4	0.24033982	-0.2106814	23.8002281	24.574358	24.6796646	25.1723862	24.6133842	24.5180092	25.406023	24.5319462
499	Cytochrome c oxidase subunit 6A1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox6a1 PE=1 SV=2	Cox6a1	P10818	0.6798323	-1.8582444	15.0026035	18.7428131	19.2057533	20.8376999	19.9773254	20.0903225	21.6685143	19.4856853
500	Cytochrome c oxidase subunit 6C-2 OS=Rattus norvegicus OX=10116 GN=Cox6c2 PE=1 SV=3	Cox6c2	P11951	0.73370792	-0.3679614	25.8299942	26.1243191	26.1283112	26.7538414	26.5769405	26.5391216	26.9615612	26.2306881
501	Cytochrome c oxidase subunit 7A2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox7a2 PE=1 SV=1	Cox7a2	P35171	1.24396963	-0.7990994	23.5362606	23.8901978	24.3934269	25.0485039	24.9215126	25.1824169	25.146389	24.8144684
502	Cytochrome c oxidase subunit 7A2-like OS=Rattus norvegicus OX=10116 GN=Cox7a2l PE=1 SV=1	Cox7a2l	D3ZYX8	0.73903558	-0.3578715	22.4310284	23.0208149	23.0955772	23.3145256	23.2639961	23.2141151	23.7385883	23.0767326

503	Cytochrome c oxidase subunit 7B, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox7b PE=1 SV=3	Cox7b	P80431	0.91020611	-0.3158188	23.6753654	23.7209053	23.6998768	24.1193619	24.358017	24.1041183	24.2878704	23.7287788
504	Cytochrome c oxidase subunit 7C, mitochondrial OS=Rattus norvegicus OX=10116 GN=Cox7c PE=1 SV=2	Cox7c	P80432	0.70975441	-0.3743114	24.4141083	24.1579914	24.6906528	25.1168499	25.0320873	24.8928814	25.3472881	24.6045914
505	Cytochrome c oxidase subunit OS=Rattus norvegicus OX=10116 GN=Cox6b1 PE=1 SV=1	Cox6b1	D3ZD09	1.1702043	-0.4383311	26.1724873	26.467474	26.5885201	26.9751511	26.8197079	27.010046	27.2795143	26.8476887
506	Cytochrome c-1 OS=Rattus norvegicus OX=10116 GN=Cyc1 PE=1 SV=3	Cyc1	D3ZFQ8	0.73697221	-0.4289775	25.8299084	26.4238129	26.6705399	26.9670944	26.9437389	27.0242004	27.1708603	26.4684658
507	Cytoglobin OS=Rattus norvegicus OX=10116 GN=Cygb PE=1 SV=1	Cygb	Q921A4	0.05962995	0.0645442	17.9770393	18.0379734	18.7044353	17.7213287	17.2753429	17.9269161	18.8294487	18.1508923
508	Cytoplasmic aconitate hydratase OS=Rattus norvegicus OX=10116 GN=Aco1 PE=1 SV=1	Aco1	G3V6S2	0.16385575	0.34435225	17.4346848	18.9186592	18.9224701	18.7223415	18.9613953	18.9443855	15.9795265	18.7354393
509	Cytoplasmic dynein 1 heavy chain 1 OS=Rattus norvegicus OX=10116 GN=Dync1h1 PE=1 SV=2	Dync1h1	M0R9X8	0.53001728	0.30751467	26.7348671	26.7985325	25.9720383	26.1541882	26.0176754	26.4929066	25.6868172	26.2321682
510	Cytoplasmic dynein 1 intermediate chain 2 OS=Rattus norvegicus OX=10116 GN=Dync1i2 PE=1 SV=3	Dync1i2	G3V9V3	0.6914684	0.27397919	23.8461971	23.5636692	23.1135693	23.1190338	23.0791187	23.2173843	22.9736252	23.2764244
511	Cytoplasmic dynein 1 light intermediate chain 1 OS=Rattus norvegicus OX=10116 GN=Dync1li1 PE=1 SV=1	Dync1li1	Q9QXU8	0.56466155	0.39465046	23.0171223	22.7014198	21.8835144	21.9926605	21.8284245	22.3894615	21.6033821	22.1948471
512	Cytoplasmic dynein 1 light intermediate chain 2 OS=Rattus norvegicus OX=10116 GN=Dync1li2 PE=1 SV=1	Dync1li2	Q62698	0.73620209	0.36580944	21.3144646	21.2578888	20.430666	20.7562256	20.6676559	20.7016754	20.2113895	20.7152863
513	Cytoskeleton-associated protein 4 OS=Rattus norvegicus OX=10116 GN=Ckap4 PE=1 SV=2	Ckap4	D3ZH41	1.22447036	-0.9765458	18.9120483	19.0483475	17.6542645	19.4901371	19.6034584	19.4470444	20.1386662	19.8218117
514	Cytosol aminopeptidase OS=Rattus norvegicus OX=10116 GN=Lap3 PE=1 SV=1	Lap3	Q68FS4	1.3286825	0.52370739	25.4356499	25.2745667	24.8298264	24.6086636	24.4735146	24.5724201	24.30126	24.7066822
515	Cytosolic acyl coenzyme A thioester hydrolase OS=Rattus norvegicus OX=10116 GN=Acot7 PE=1 SV=4	Acot7	Q64559	0.67209766	0.5268116	21.5535278	21.009058	21.4008007	22.0495453	21.7890949	20.5276318	20.4552364	21.1337223
516	Cytosolic Fe-S cluster assembly factor NUBP2 OS=Rattus norvegicus OX=10116 GN=Nubp2 PE=1 SV=1	Nubp2	Q68FS1	0.46976115	0.36144114	21.225193	20.6248894	20.8524265	19.9370441	20.4859104	20.3949795	19.6623783	20.6505203
517	Cytosolic non-specific dipeptidase OS=Rattus norvegicus OX=10116 GN=Cndp2 PE=1 SV=1	Cndp2	Q6Q0N1	0.03265244	-0.0308943	16.2334309	16.9063759	16.7292366	16.2901859	16.5764179	16.8868294	15.7786484	17.0409107
518	D-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=D2hgdh PE=3 SV=1	D2hgdh	P84850	0.39363855	-0.3126435	22.9047356	24.1141186	24.203249	24.044733	23.9420242	24.6273232	23.9352551	24.0128078
519	DCN1-like protein OS=Rattus norvegicus OX=10116 GN=NEWGENE_1582994 PE=1 SV=1	NEWGENE_	A0A0U1RRI	1.32136644	0.58476782	19.7152977	19.7757359	20.4585094	19.5148716	19.0719128	19.468399	19.0899143	19.4951172
520	DDHD domain-containing 2 OS=Rattus norvegicus OX=10116 GN=Ddhd2 PE=1 SV=2	Ddhd2	D3ZJ91	0.21888624	0.15997386	16.1976318	16.4493618	15.5065441	16.1524487	16.3047142	15.3265457	16.1244297	15.9104013
521	D-dopachrome decarboxylase OS=Rattus norvegicus OX=10116 GN=Ddt PE=1 SV=3	Ddt	P80254	0.64603317	0.19136429	20.323164	20.3211231	20.266201	20.6387939	20.1619701	19.9250164	20.2182102	20.4786282
522	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3 OS=Rattus norvegicus OX=10116 GN=Ddx3 PE=1 SV=1	Ddx3	A0A0G2K9N	0.69470773	0.15025043	23.3058109	23.0410843	23.036829	22.930788	23.0002556	22.9240475	22.7398109	23.0493965
523	DEAD-box helicase 19A OS=Rattus norvegicus OX=10116 GN=Ddx19b PE=1 SV=1	Ddx19b	A0A0G2JZQ	0.49961182	0.37025642	18.9284782	19.3697128	19.2426376	19.4471378	19.5261078	18.0611668	19.2057648	18.7139015
524	Death-associated protein 3 OS=Rattus norvegicus OX=10116 GN=Dap3 PE=1 SV=1	Dap3	F7EZZ0	0.82441974	0.41881514	21.6543331	21.7803802	20.884798	21.9363632	20.9457169	21.1298428	21.0879669	21.4170876
525	Decorin OS=Rattus norvegicus OX=10116 GN=Dcn PE=1 SV=1	Dcn	Q01129	0.08190238	-0.053967	22.2721882	21.9877377	22.0400391	21.248455	22.0632362	21.7750912	21.8105259	22.1154346
526	Dehydrogenase/reductase SDR family member 4 OS=Rattus norvegicus OX=10116 GN=Dhrs4 PE=2 SV=2	Dhrs4	Q8VID1	0.48417072	0.31701899	21.6303463	21.3911896	22.1657562	22.5852985	21.9548569	21.5526619	21.3350716	21.6619244
527	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ech1 PE=1 SV=2	Ech1	Q62651	0.25686964	0.1115799	22.5163383	21.8240528	22.531971	22.4369888	22.2230263	22.1774979	22.0996284	22.3628788
528	Dematin actin-binding protein OS=Rattus norvegicus OX=10116 GN=Dmtn PE=1 SV=1	Dmtn	B2GUY4	0.13182395	-0.2480929	15.0546789	17.4035892	15.2079306	16.5401192	15.388629	17.466301	16.2923431	16.0514164
529	DENN domain-containing protein 5A OS=Rattus norvegicus OX=10116 GN=Dennd5a PE=2 SV=1	Dennd5a	G3V7Q0	0.35308591	0.26382017	19.4707279	19.0188046	18.0496864	18.686882	18.8262424	18.2463322	18.5383587	18.5598869
530	Deoxyguanosine kinase OS=Rattus norvegicus OX=10116 GN=Dguok PE=1 SV=1	Dguok	D3ZDE4	0.77554623	-0.2360144	17.2282009	16.8168602	17.2301483	17.2237873	17.3025627	17.2420559	17.6857986	17.2126369
531	Dermatopontin OS=Rattus norvegicus OX=10116 GN=Dpt PE=1 SV=1	Dpt	B2RZ77	0.09054929	0.12692308	18.9227066	18.1556606	17.0060234	17.3934574	18.5899391	17.4571762	17.4914227	17.4316177
532	Desmin OS=Rattus norvegicus OX=10116 GN=Des PE=1 SV=2	Des	P48675	0.11354484	0.12835121	20.1275082	19.9584522	20.6618881	20.0912094	20.3423862	21.0607014	19.5763378	19.3462276
533	Desmoplakin OS=Rattus norvegicus OX=10116 GN=Dsp PE=1 SV=1	Dsp	F1LMV6	0.40084375	0.94415903	17.733511	16.8120155	17.1042061	21.2750549	17.2579403	17.3817749	17.4487991	17.0596371
534	Destrin OS=Rattus norvegicus OX=10116 GN=Dstn PE=1 SV=3	Dstn	Q7M0E3	0.36100372	-0.1490145	19.3128777	19.3412704	19.0056381	19.5764523	19.1528282	19.7944088	19.3702469	19.5148125
535	Deubiquitinating protein VCIP135 OS=Rattus norvegicus OX=10116 GN=Vcpip1 PE=1 SV=2	Vcpip1	Q8CF97	0.37514894	0.31819391	19.733572	19.4080715	19.961319	18.8401928	18.6543503	19.0332623	19.0267372	19.9560299
536	D-glutamate cyclase OS=Rattus norvegicus OX=10116 GN=Dglucy PE=1 SV=1	Dglucy	D4A9W3	0.29302077	-0.2165952	18.1408958	17.5472069	18.6207409	18.6466637	18.6970997	18.7220345	17.9946117	18.4081421
537	Diablo homolog (Drosophila) OS=Rattus norvegicus OX=10116 GN=Diablo PE=1 SV=1	Diablo	Q5RK17	0.46763327	-0.3330598	18.9114571	19.8365231	19.7303753	20.3042488	20.009407	19.8143806	20.431303	19.8597527
538	Diacylglycerol kinase alpha OS=Rattus norvegicus OX=10116 GN=Dgka PE=2 SV=1	Dgka	P51556	2.15377707	1.38899612	17.6869678	17.6988316	17.3129368	18.1982136	16.5758648	16.606905	16.70327	15.4549255
539	Diacylglycerol kinase zeta OS=Rattus norvegicus OX=10116 GN=Dgkz PE=1 SV=1	Dgkz	O08560	0.3576375	-0.4469523	18.1612358	17.6715717	18.0833244	15.969593	17.8663864	17.8468361	17.5752373	18.3850746
540	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex OS=Rattus norvegicus OX=10116 GN=Dbt PE=1 SV=1	Dbt	B2GV15	0.83076892	0.41412067	24.6027737	25.0624046	24.7204857	24.8422985	24.4707451	24.9879322	24.2031937	23.9096088
541	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex OS=Rattus norvegicus OX=10116 GN=Pdhx PE=1 SV=1	Pdhx	A0A0G2JZH	1.70689215	0.54400873	25.3284016	24.9598217	25.2198467	24.5584316	24.4355717	24.5187302	24.4446125	24.4915524
542	Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Dlst PE=1 SV=1	Dlst	G3V6P2	1.40421536	0.37055588	25.8475189	25.3508377	25.6279869	25.5755424	25.1440277	25.4917946	25.033947	25.2498932
543	Dihydrolipoyl dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Dld PE=1 SV=1	Dld	Q6P6R2	1.53104458	0.2015543	27.0292854	27.1551094	27.1393948	26.9962406	27.0541611	26.812767	26.8110828	26.8358021
544	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Rattus norvegicus OX=10116 GN=Dlat PE=1 SV=3	Dlat	P08461	1.1779177	0.297122	26.0905838	26.0945187	25.9281139	26.1727619	25.8034687	26.1095142	25.5905266	25.5939808
545	Dihydropyrimidinase-related protein 2 OS=Rattus norvegicus OX=10116 GN=Dpysl2 PE=1 SV=1	Dpysl2	P47942	0.14200092	0.11472368	20.3186321	20.8400288	20.3672123	19.7244358	19.9865303	20.6593876	19.7474289	20.3980675
546	Dihydropyrimidinase-related protein 3 OS=Rattus norvegicus OX=10116 GN=Dpysl3 PE=1 SV=2	Dpysl3	Q62952	0.09140966	0.18614459	17.1538029	16.8391705	15.4267559	15.1428738	16.6347752	16.4568462	16.4039688	14.3224344
547	Dipeptidyl peptidase 4 OS=Rattus norvegicus OX=10116 GN=Dpp4 PE=1 SV=1	Dpp4	A0A0G2K23	0.45232035	-0.2705312	18.689682	17.5365696	17.6433372	18.2144356	18.3272362	18.2589397	18.3241901	18.2557831
548	Disks large homolog 1 OS=Rattus norvegicus OX=10116 GN=Dlg1 PE=1 SV=1	Dlg1	Q62696	0.50758022	0.44778252	19.567091	18.3307209	17.650383	18.3247929	18.1654568	17.9118176	17.9165516	18.0880318
549	Distal membrane arm assembly complex 1 OS=Rattus norvegicus OX=10116 GN=Dmac1 PE=1 SV=2	Dmac1	D4AEL3	0.7704403	-0.3377423	17.3879719	17.729969	17.8648682	17.8692989	18.1607647	17.6641426	18.5122089	17.8659611
550	Distal membrane-arm assembly complex protein 2 OS=Rattus norvegicus OX=10116 GN=Dmac2 PE=2 SV=1	Dmac2	Q5I0I4	0.10648736	-0.0938716	16.6643238	17.6047344	16.5209885	16.5547543	17.0667858	16.7099972	17.418766	16.5247383
551	DNA damage-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ddb1 PE=1 SV=1	Ddb1	G3V8T4	0.73638709	1.92188358	19.2117691	19.1362534	18.356638	17.5890923	17.7119083	18.6597004	13.1158314	17.1187782
552	DNA polymerase delta-interacting protein 2 OS=Rattus norvegicus OX=10116 GN=Poldip2 PE=1 SV=3	Poldip2	E9PT51	1.55842201	0.57103014	21.5532265	21.4505463	21.661026	21.4391117	20.4459667	20.8814487	21.2169018	21.2754726
553	DNA repair protein RAD50 OS=Rattus norvegicus OX=10116 GN=Rad50 PE=1 SV=1	Rad50	Q9JIL8	0.59717252	1.22915053	18.8196297	17.8831825	18.2013206	17.8104973	18.0825386	14.1259737	17.8750916	17.7144241
554	DNA-directed RNA polymerase subunit beta OS=Rattus norvegicus OX=10116 GN=Polr2b PE=1 SV=1	Polr2b	G3V8Y5	0.94931712	0.52228785	22.1626492	21.0366955	21.4555416	21.6648445	21.4553871	20.698761	21.0058517	21.0705795
555	DnaJ (Hsp40) homolog, subfamily A, member 2 OS=Rattus norvegicus OX=10116 GN=Dnaja2 PE=1 SV=1	Dnaja2	Q5M9H7	1.23007221	0.51201296	21.1545105	21.0959301	20.8558121	20.8213139	20.6689148	20.2171326	20.0542984	20.9391689
556	DnaJ (Hsp40) homolog, subfamily A, member 4 OS=Rattus norvegicus OX=10116 GN=Dnaja4 PE=1 SV=1	Dnaja4	Q4QR73	0.51687539	0.56210947	20.8071365	19.8957882	19.4244041	18.7817707	19.1235714	18.5999508	19.0694599	19.8676796
557	DnaJ (Hsp40) homolog, subfamily B, member 4 OS=Rattus norvegicus OX=10116 GN=Dnajb4 PE=1 SV=1	Dnajb4	Q5XIP0	0.11456772	0.1173501	20.6723804	20.1139164	20.1512222	19.239933	20.3470364	19.9256554	19.2624779	20.1728821
558	DnaJ (Hsp40) homolog, subfamily C, member 11 OS=Rattus norvegicus OX=10116 GN=Dnajc11 PE=1 SV=1	Dnajc11	B1WBY5	0.01990579	0.01672411	21.4020233	20.5253162	20.215807	20.5222397	20.9960823	20.3845425	20.6146431	20.6032219
559	DnaJ heat shock protein family (Hsp40) member A3 OS=Rattus norvegicus OX=10116 GN=Dnaja3 PE=1 SV=1	Dnaja3	A0A0G2K5F	0.10062025	-0.0432773	21.580183	21.2052002	21.3730469	20.921299	21.3019295	21.5093441	21.1472149	21.2943497
560	DnaJ heat shock protein family (Hsp40) member B2 OS=Rattus norvegicus OX=10116 GN=Dnajb2 PE=1 SV=1	Dnajb2	B2RYA8	0.4504985	-0.7345574	14.7613039	17.8440933	17.2036514	17.7739506	17.5099773	17.5312996	17.915472	17.5644798
561	DnaJ heat shock protein family (Hsp40) member B5 OS=Rattus norvegicus OX=10116 GN=Dnajb5 PE=4 SV=1	Dnajb5	A0A0G2K9H	0.01104337	0.00982475	20.4391537	21.4191551	20.5715981	21.3954945	20.6106415	21.3053398	21.0117893	20.8583317
562	DnaJ homolog subfamily A member 1 OS=Rattus norvegicus OX=10116 GN=Dnaja1 PE=1 SV=1	Dnaja1	P63036	0.14714227	-0.1426575	15.8011503	16.7289619	17.2681675	17.239027	17.2944736	16.7697506	16.6639729	16.8797398
563	DnaJ homolog subfamily C member 5 OS=Rattus norvegicus OX=10116 GN=Dnajc5 PE=1 SV=1	Dnajc5	P60905	0.84901053	-0.5480506	17.3537998	17.2653046	17.0813503	15.9755926	17.4163876	17.4947872	17.6007957	17.3562794
564	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Rattus norvegicus OX=10116 GN=Ddost PE=2 SV=1	Ddost	Q641Y0	0.76184331	-0.3078618	18.1249065	18.6489258	18.1229382	17.9370537	18.1664829	18.5806789	18.7743034	18.5438061
565	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Rattus norvegicus OX=10116 GN=Rpn1 PE=1 SV=1	Rpn1	Q6P7A7	0.07376625	-0.1050453	18.8518143	18.5297432	19.1346893	19.6267872	18.3441067	18.7345257	20.4434965	19.0510864
566	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Rattus norvegicus OX=10116 GN=Rpn2 PE=2 SV=2	Rpn2	P25235	1.19455749	-0.9529262	16.5374336	16.6787472	16.3311234	16.0219688	18.3212261	17.6551552	16.6947002	16.7098961
567	Double-stranded RNA-binding protein Staufen homolog 2 OS=Rattus norvegicus OX=10116 GN=Stau2 PE=1 SV=1	Stau2	Q68SB1	0.23165244	-0.1327734	19.2841167	19.2202549	19.1924229	19.5274506	19.5311222	19.2477779	19.9989204	18.9775181
568	Dual specificity mitogen-activated protein kinase kinase 1 OS=Rattus norvegicus OX=10116 GN=Map2k1 PE=1 SV=2	Map2k1	Q01986	1.19958339	0.36645651	21.1635685	21.1170177	20.8258476	21.0283356	20.7507305	20.4417515	20.4414253	21.0350361
569	Dual-specificity phosphatase 3 OS=Rattus norvegicus OX=10116 GN=Dusp3 PE=1 SV=1	Dusp3	A0A0G2K3I	0.36681736	0.66572666	19.0686073	18.7228661	19.016077	16.8341274	18.6279736	17.6371651	16.1430798	18.5705528
570	Dynactin subunit 1 OS=Rattus norvegicus OX=10116 GN=Dctn1 PE=1 SV=1	Dctn1	A0A0G2K42	0.4346455	-0.4023824	22.002182	21.9075699	20.6400909	20.9332027	21.6764374	21.9450169	21.190897	22.2802238
571	Dynamin-1-like protein OS=Rattus norvegicus OX=10116 GN=Dnm1l PE=1 SV=1	Dnm1l	O35303	0.03830886	0.02871037	23.1170311	22.7811642	22.4230614	22.692667	22.746748	22.4925041	22.336544	23.3232861
572	Dynamin-2 OS=Rattus norvegicus OX=10116 GN=Dnm2 PE=1 SV=1	Dnm2	P39052	0.94051657	-0.2171173	22.4221001	22.7419891	22.4410172	22.8507557	22.9038162	22.7917194	22.9136715	22.7151241
573	Dynamin-like 120 kDa protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Opa1 PE=1 SV=1	Opa1	Q2TA68	0.70393429	-0.3206444	22.9256897	23.4107513	23.5389061	23.7046585	23.7570686	23.6010056	24.0940399	23.4104691
574	Dynein assembly factor 4, axonemal OS=Rattus norvegicus OX=10116 GN=Dnaaf4 PE=1 SV=1	Dnaaf4	Q5VJS5	0.06733748	0.06135035	18.1785984	17.6174793	18.0004807	18.4168568	17.5701427	18.7829056	17.9704113	17.6445541

575	Dynein light chain 1, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Dynll1 PE=1 SV=1	Dynll1	P63170	0.205245	0.79440284	19.7100582	19.5464001	17.9288635	15.0295191	19.0343208	17.7777481	14.0995159	18.1256447
576	Dynein light chain 2, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Dynll2 PE=1 SV=1	Dynll2	Q78P75	1.33067448	0.41456223	21.8705521	21.9116974	21.6853638	21.3196735	21.4355278	20.9993153	21.3499603	21.3442345
577	Dynein light chain roadblock-type 1 OS=Rattus norvegicus OX=10116 GN=Dynlrb1 PE=1 SV=3	Dynlrb1	P62628	0.36815943	0.44221926	18.5978718	17.341301	18.785841	19.1264286	19.0493259	17.6991386	17.5611057	17.772995
578	Dynein light chain Tctex-type 3 OS=Rattus norvegicus OX=10116 GN=Dynlt3 PE=1 SV=1	Dynlt3	Q5XI90	0.31156126	0.33935308	19.4098816	19.2088623	17.9328022	18.2615051	18.0745182	19.1382217	17.8143921	18.4285069
579	Dysferlin OS=Rattus norvegicus OX=10116 GN=Dysf PE=1 SV=1	Dysf	A0A0G2K7E	1.28311186	-0.4826646	22.2239609	22.2097626	22.2604046	22.9104748	22.7801571	23.1671696	22.9041634	22.6837711
580	Dystonin OS=Rattus norvegicus OX=10116 GN=Dst PE=1 SV=3	Dst	D3ZC56	0.35446088	-0.214282	20.3760681	19.9764481	20.1425724	19.8868542	19.6980553	20.8249645	20.4826984	20.2333527
581	Dystrobrevin OS=Rattus norvegicus OX=10116 GN=Dtna PE=1 SV=3	Dtna	D4A772	0.06638696	0.04006577	19.5295696	18.9839554	18.6972561	19.3153954	19.0648003	18.8751907	19.0198364	19.406086
582	Dystroglycan 1 OS=Rattus norvegicus OX=10116 GN=Dag1 PE=1 SV=1	Dag1	F1M8K0	0.06903085	-0.0799704	19.5731163	19.2964287	19.3993454	19.1077976	19.3478317	20.2700119	18.3607311	19.7179947
583	Dystrophin OS=Rattus norvegicus OX=10116 GN=Dmd PE=1 SV=2	Dmd	P11530	0.92143482	0.45318985	23.4136887	23.642828	23.7661114	22.9384232	22.8965321	23.272789	22.5420437	23.236927
584	Dystrophin OS=Rattus norvegicus OX=10116 GN=Dmd PE=1 SV=2	Dmd	Q7TPH3	1.34156562	0.53650188	17.6554165	17.635561	17.7079144	17.7694511	16.7115593	17.7219143	17.1636257	17.0252361
585	E3 ubiquitin-protein ligase NHLRC1 OS=Rattus norvegicus OX=10116 GN=Nhlrc1 PE=2 SV=1	Nhlrc1	Q6IMG5	0.36635884	-0.5734239	18.2518768	18.2609749	17.2348194	15.6598606	17.8743343	18.6742973	17.8903294	17.2622662
586	E3 ubiquitin-protein ligase OS=Rattus norvegicus OX=10116 GN=Nedd4 PE=1 SV=1	Nedd4	A0A0G2K8P	0.8976994	0.78948593	21.6303253	21.8559914	22.1372814	20.3608437	20.8448238	20.5956478	20.1932526	21.1927738
587	E3 ubiquitin-protein ligase RNF123 OS=Rattus norvegicus OX=10116 GN=Rnf123 PE=1 SV=1	Rnf123	F1LMI7	0.1852705	0.12104082	18.8775368	18.1159363	17.857254	18.5423985	18.5671692	18.1852951	18.006794	18.149704
588	E3 ubiquitin-protein ligase TRIP12 OS=Rattus norvegicus OX=10116 GN=Trip12 PE=1 SV=1	Trip12	F1LP64	0.52067771	1.92752743	16.2429047	16.8248005	15.0881443	14.2684183	16.1108437	15.0933456	8.95898628	14.5509825
589	E3 ubiquitin-protein ligase UBR4 OS=Rattus norvegicus OX=10116 GN=Ubr4 PE=1 SV=1	Ubr4	F1LQI5	2.16927972	0.82859945	21.4926033	21.5590401	21.1649628	21.3801365	20.4204235	21.1027164	20.2461357	20.5130692
590	E3 ubiquitin-protein transferase MAEA OS=Rattus norvegicus OX=10116 GN=Maea PE=2 SV=2	Maea	Q5RKJ1	0.40757792	0.41679811	18.9874935	17.0265656	18.5332394	18.2426815	18.1254768	17.9715977	17.6430912	17.3826218
591	E3 UFM1-protein ligase 1 OS=Rattus norvegicus OX=10116 GN=Ufl1 PE=1 SV=1	Ufl1	B2GV24	0.84661536	-0.3533363	18.8766727	19.5402832	19.508112	19.6828556	19.8815098	19.6163216	19.9910355	19.532402
592	Echinoderm microtubule-associated protein-like 1 OS=Rattus norvegicus OX=10116 GN=Eml1 PE=1 SV=2	Eml1	M0RDD8	0.07688591	0.07482624	19.7938957	19.6577454	19.1225262	19.2742538	19.1406822	20.0728397	18.6466846	19.6889095
593	Ecm29 proteasome adaptor and scaffold OS=Rattus norvegicus OX=10116 GN=Ecpas PE=1 SV=3	Ecpas	F1M446	1.12677955	0.44689178	22.0571423	21.7058811	21.8948326	22.6298637	21.582262	21.7002525	21.4831104	21.7345276
594	Ectonucleoside triphosphate diphosphohydrolase 1 OS=Rattus norvegicus OX=10116 GN=Entpd1 PE=3 SV=3	Entpd1	F1M0G3	0.82012246	-0.6288514	20.0410557	18.3291492	18.9922523	18.6782284	19.7165527	19.8279552	19.6505394	19.3610439
595	Ectonucleoside triphosphate diphosphohydrolase 2 OS=Rattus norvegicus OX=10116 GN=Entpd2 PE=1 SV=1	Entpd2	F1M7N2	0.89010085	-0.5787792	19.7850933	20.7506065	20.9432201	19.9117985	21.0423641	20.4795551	21.144125	21.0397911
596	Egl nine homolog 3 OS=Rattus norvegicus OX=10116 GN=Egln3 PE=4 SV=1	Egln3	G3V6N9	0.49849057	-0.4045472	14.2340307	13.2140989	12.9935131	13.367692	13.6942177	14.6072645	13.605792	13.5202494
597	EH domain-binding protein 1-like 1 OS=Rattus norvegicus OX=10116 GN=Ehbp1l1 PE=1 SV=1	Ehbp1l1	A0A0G2K6R	1.83463359	0.6236825	21.6716423	21.2327766	21.2464161	20.9346695	20.4245625	20.820425	20.5163212	20.8294659
598	EH domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Ehd1 PE=1 SV=1	Ehd1	Q641Z6	0.0569589	0.01896715	23.724453	23.7487526	23.4764957	23.7081795	23.4500237	23.7477722	23.5121346	23.8720818
599	EH domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Ehd2 PE=1 SV=1	Ehd2	Q4V8H8	0.54148896	0.25039959	24.3815365	25.0567284	24.1207542	24.520071	24.2480602	24.1326427	24.1840763	24.5127125
600	EH-domain-containing 4 OS=Rattus norvegicus OX=10116 GN=Ehd4 PE=1 SV=1	Ehd4	Q8R3Z7	0.12349922	0.05538845	23.1962528	22.9761105	22.5388851	22.6781139	22.7008018	22.8682842	22.6242218	22.9745007
601	ELAV-like protein 1 OS=Rattus norvegicus OX=10116 GN=Elavl1 PE=1 SV=1	Elavl1	B5DF91	1.11846065	-1.1789417	18.5021763	16.8098583	16.339325	16.6535339	17.692028	18.0028076	18.4371548	18.88867
602	Electron transfer flavoprotein beta subunit lysine methyltransferase OS=Rattus norvegicus OX=10116 GN=Etfbkmt PE=2 SV=1	Etfbkmt	Q6P7Q0	0.37263951	0.41797304	18.7847099	17.7290306	18.4795971	17.0340576	18.3055687	17.1525993	17.0919724	17.8053627
603	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Rattus norvegicus OX=10116 GN=Etfa PE=1 SV=4	Etfa	P13803	0.22224314	0.19712353	28.8691502	28.5563087	28.9609756	27.8804207	28.6184578	28.5050926	27.6091404	28.7456703
604	Electron transfer flavoprotein subunit beta OS=Rattus norvegicus OX=10116 GN=Etfb PE=1 SV=3	Etfb	Q68FU3	0.4019099	0.32022047	27.1466141	27.1865635	27.3228416	26.2205086	26.7705345	26.7392311	25.9659328	27.1199474
605	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Etfdh PE=1 SV=1	Etfdh	Q66HF3	0.47240212	-0.2466722	25.6522636	26.1159191	26.3436985	26.6176014	26.5147133	26.5587978	26.5687656	26.0738945
606	Elongation factor 1-alpha 2 OS=Rattus norvegicus OX=10116 GN=Eef1a2 PE=1 SV=1	Eef1a2	P62632	0.42997524	0.22980022	25.8600368	25.7447681	25.1055164	26.1668148	25.3833408	25.4528294	25.3884602	25.733305
607	Elongation factor 1-alpha OS=Rattus norvegicus OX=10116 GN=LOC100360413 PE=3 SV=1	LOC100360	M0R757	0.18790725	0.12756252	24.7219219	24.564846	23.7226372	24.445343	24.1116371	23.9592228	24.2232018	24.6504364
608	Elongation factor 1-delta OS=Rattus norvegicus OX=10116 GN=Eef1d PE=1 SV=2	Eef1d	Q68FR9	0.35195448	0.35075283	20.4732838	19.4562759	19.1514435	20.1645908	19.5958233	19.7552853	18.5805283	19.9109459
609	Elongation factor 1-gamma OS=Rattus norvegicus OX=10116 GN=Eef1g PE=2 SV=3	Eef1g	Q68FR6	0.58027813	0.44767237	21.2246933	21.4618874	20.7964497	20.6987648	20.4185486	20.480629	20.0049343	21.4869938
610	Elongation factor 2 OS=Rattus norvegicus OX=10116 GN=Eef2 PE=1 SV=4	Eef2	P05197	0.19393369	0.05408621	22.9378223	22.7692757	22.8195992	23.0318871	22.8873043	22.7601089	22.6305103	23.0643158
611	Elongation factor G, mitochondrial OS=Rattus norvegicus OX=10116 GN=Gfm1 PE=1 SV=2	Gfm1	Q07803	0.3674285	0.45129728	20.4659081	19.0667458	20.7250519	19.7515011	19.0893288	19.5365067	18.952774	20.6254082
612	Elongation factor Ts, mitochondrial OS=Rattus norvegicus OX=10116 GN=Tsfm PE=2 SV=1	Tsfm	Q9QYU2	0.93056415	0.86255836	23.5936031	24.5509949	24.6352901	22.6814976	23.1887608	23.1213512	22.7109356	22.9901047
613	Elongation factor Tu, mitochondrial OS=Rattus norvegicus OX=10116 GN=Tufm PE=1 SV=1	Tufm	P85834	0.74669846	0.18867731	29.1969051	28.6879025	29.0724983	28.8877087	28.8278217	28.6659603	28.6958237	28.9006996
614	Elongation factor-like GTPase 1 OS=Rattus norvegicus OX=10116 GN=Efl1 PE=1 SV=2	Efl1	D3ZXJ5	0.49363013	-0.2875838	18.1672897	18.8206825	19.1066456	18.4761047	19.2413902	18.7183933	19.1974697	18.5638046
615	Elongator complex protein 1 OS=Rattus norvegicus OX=10116 GN=Elp1 PE=1 SV=2	Elp1	F1LP76	0.14248258	-0.0972705	21.4375916	20.9589043	20.9137535	20.2870789	20.6945972	21.0469074	21.0446625	21.200243
616	Elongator complex protein 2 OS=Rattus norvegicus OX=10116 GN=Elp2 PE=2 SV=1	Elp2	Q496Z0	0.02452668	-0.0931399	19.8017349	18.6380329	14.938653	16.9057121	18.2892914	15.4259472	18.4398556	18.5015984
617	Elongator complex protein 3 OS=Rattus norvegicus OX=10116 GN=Elp3 PE=1 SV=2	Elp3	D4ACM1	0.58040415	-0.6656117	18.1613178	17.5487919	16.2545872	16.2266655	17.713562	18.2102222	17.0664997	17.8635254
618	Elongin-B OS=Rattus norvegicus OX=10116 GN=Elob PE=1 SV=1	Elob	P62870	0.65738848	0.22186565	21.5682659	21.3961182	21.2145729	21.1408958	21.1858921	20.939333	20.86516	21.4420052
619	Elongin-C OS=Rattus norvegicus OX=10116 GN=Eloc PE=1 SV=1	Eloc	P83941	0.61165467	0.23933983	21.2672806	21.1473522	20.9663582	20.6097851	20.9582653	20.5554867	20.5531597	20.9665051
620	Embigin OS=Rattus norvegicus OX=10116 GN=Emb PE=1 SV=1	Emb	O88775	0.4277804	-0.647469	16.6758385	18.1052895	16.9212418	17.1498432	17.4421959	19.4648094	17.9062462	16.6288376
621	Endonuclease G OS=Rattus norvegicus OX=10116 GN=Endog PE=1 SV=1	Endog	Q3V5X8	0.23250508	-0.4587321	25.0000668	23.8037338	25.4199638	22.3832989	24.8967571	24.6564426	23.4719467	25.4168453
622	Endophilin-B1 OS=Rattus norvegicus OX=10116 GN=Sh3glb1 PE=2 SV=1	Sh3glb1	Q6AYE2	1.41535369	0.49785089	21.768713	21.3662071	21.5179977	21.2291489	21.1028023	20.9303284	20.5800934	21.2774391
623	Endoplasmic reticulum chaperone BiP OS=Rattus norvegicus OX=10116 GN=Hspa5 PE=1 SV=1	Hspa5	P06761	1.17032814	-0.2181063	24.6558571	24.8329334	24.4890289	24.7540951	24.8989277	24.7836437	25.0797749	24.8419933
624	Endoplasmin OS=Rattus norvegicus OX=10116 GN=Hsp90b1 PE=1 SV=1	Hsp90b1	A0A0A0MY	0.35872308	-0.1095181	22.3602219	22.5948486	22.2030563	22.5996361	22.4684601	22.4386921	22.8170242	22.4716587
625	Enoyl CoA hydratase domain-containing 2 OS=Rattus norvegicus OX=10116 GN=Echdc2 PE=1 SV=1	Echdc2	D3ZIL6	0.95707321	0.4501605	21.5692844	21.8924446	21.7533894	21.0883961	21.3175907	21.0312614	20.7068043	21.447216
626	Enoyl-[acyl-carrier-protein] reductase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mecr PE=1 SV=1	Mecr	A0A140TAE	3.26534423	0.94242239	20.0895081	20.1534538	20.3169594	20.5980759	19.2788906	19.1978912	19.3264542	19.5850716
627	Enoyl-CoA delta isomerase 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Eci1 PE=1 SV=1	Eci1	P23965	0.84812853	0.39962196	25.3192902	24.6781788	25.0960541	25.0224247	24.2448349	24.8324776	24.3643894	25.075758
628	Enoyl-CoA delta isomerase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Eci2 PE=1 SV=1	Eci2	Q5XIC0	0.23698118	0.08694458	23.9109554	23.3519897	23.6309319	23.6355991	23.6501808	23.3753223	23.3961697	23.760025
629	Enoyl-CoA hydratase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Echs1 PE=1 SV=1	Echs1	P14604	0.49221274	-0.160182	23.210741	23.1490059	23.6659985	23.6697426	23.4723549	23.5666332	23.6885071	23.6087208
630	Epithelial membrane protein 3 OS=Rattus norvegicus OX=10116 GN=Emp3 PE=2 SV=1	Emp3	Q9QYW5	0.66432263	-1.2950256	14.6153555	18.7878761	18.0128765	18.0176277	18.3537941	18.7709484	18.8021927	18.686903
631	Epsilon 1 globin OS=Rattus norvegicus OX=10116 GN=Hbe1 PE=1 SV=1	Hbe1	O88752	0.12611196	-0.4635155	18.4121571	18.8458843	18.0456734	13.4011374	17.8927364	17.8631001	16.1319504	18.6711273
632	ER membrane protein complex subunit 1 OS=Rattus norvegicus OX=10116 GN=Emc1 PE=1 SV=1	Emc1	D4A994	0.82917922	-0.444932	16.4680977	16.4987335	15.6227303	16.3452797	16.6360893	16.8769188	16.9874191	16.2141418
633	Erlin-2 OS=Rattus norvegicus OX=10116 GN=Erlin2 PE=1 SV=1	Erlin2	B5DEH2	0.63652413	-0.2137585	19.3140163	18.8105869	19.340868	19.2514858	19.4830036	19.2327118	19.2196579	19.6366177
634	Erythrocyte membrane protein band 4.1 OS=Rattus norvegicus OX=10116 GN=Epb41 PE=1 SV=1	Epb41	A0A0G2K16	0.00794862	0.01268768	20.2743473	21.4463768	19.723526	20.6267376	19.9235477	21.6322956	20.4756432	19.9887505
635	Erythrocyte membrane protein band 4.1-like 2 OS=Rattus norvegicus OX=10116 GN=Epb41l2 PE=1 SV=2	Epb41l2	D3ZM69	0.42876086	0.22352457	19.8832207	20.3106518	19.7735176	19.4978867	19.5552177	19.2923012	19.6648903	20.0587692
636	Erythrocyte membrane protein band 4.2 OS=Rattus norvegicus OX=10116 GN=Epb42 PE=1 SV=1	Epb42	B5DF57	0.08650656	-0.1742706	19.0427361	20.8673401	19.4821491	18.88978	19.7928829	21.3379803	19.1306705	18.7175541
637	ES1 protein homolog, mitochondrial OS=Rattus norvegicus OX=10116 PE=1 SV=2	10116	P56571	0.26232085	0.12961769	28.5487309	28.0213146	28.6658592	28.1799545	28.3919334	27.8509083	28.2061462	28.4484005
638	Estradiol 17-beta-dehydrogenase 8 OS=Rattus norvegicus OX=10116 GN=Hsd17b8 PE=1 SV=1	Hsd17b8	Q6MGB5	0.85236812	0.42082596	23.8230515	24.1545258	23.3968468	23.211237	23.310915	23.1779213	22.9017735	23.5117474
639	Ethanolamine-phosphate cytidylyltransferase OS=Rattus norvegicus OX=10116 GN=Pcyt2 PE=1 SV=1	Pcyt2	O88637	0.47259683	0.36824131	18.9078197	18.1000443	18.730257	18.6219521	18.767107	17.7544575	17.6290874	18.7364559
640	ETHE1, persulfide dioxygenase OS=Rattus norvegicus OX=10116 GN=Ethe1 PE=1 SV=1	Ethe1	B0BNJ4	0.20150139	0.0790143	20.1961727	19.784977	19.8054714	20.0738354	20.0695534	19.5425301	19.9913425	19.9409733
641	Eukaryotic translation initiation factor 2 subunit beta OS=Rattus norvegicus OX=10116 GN=Eif2s2 PE=1 SV=1	Eif2s2	Q6P685	0.57061006	-0.9283309	17.6173782	17.6088142	17.6900482	14.7031345	18.32551	17.9662209	17.3746548	17.6663132
642	Eukaryotic translation initiation factor 3 subunit B OS=Rattus norvegicus OX=10116 GN=Eif3b PE=1 SV=1	Eif3b	Q4G061	1.22315046	0.97770071	19.3309727	18.7804718	19.1381378	17.7668343	18.3697891	17.2861462	17.9323406	17.5173378
643	Eukaryotic translation initiation factor 3 subunit E OS=Rattus norvegicus OX=10116 GN=LOC100909481 PE=3 SV=1	LOC100909	A0A0G2K27	0.61473141	0.76056623	20.1721745	20.0450706	19.5089188	19.1010914	19.4298553	19.5085545	19.4963818	17.3501987
644	Eukaryotic translation initiation factor 3 subunit F OS=Rattus norvegicus OX=10116 GN=Eif3f PE=1 SV=3	Eif3f	D4AC36	0.14614904	0.28813601	18.70368	17.7891846	16.6894455	16.2795105	16.7208843	17.575388	15.8304443	18.18256
645	Eukaryotic translation initiation factor 3 subunit I OS=Rattus norvegicus OX=10116 GN=Eif3i PE=2 SV=1	Eif3i	B0BNA7	0.53726145	0.4114151	19.2916756	19.0592861	18.3506355	19.2361507	19.0156937	18.6246738	17.7671242	18.8845959
646	Eukaryotic translation initiation factor 4 gamma, 1 OS=Rattus norvegicus OX=10116 GN=Eif4g1 PE=1 SV=1	Eif4g1	D3ZU13	0.18307384	0.14954376	20.2817001	20.1717625	19.5417099	19.6973686	19.5561123	19.6891117	19.3178101	20.531332

647	Eukaryotic translation initiation factor 4, gamma 2 OS=Rattus norvegicus OX=10116 GN=Eif4g2 PE=1 SV=2	Eif4g2	F1LN59	0.17306137	-0.3525555	17.3374786	17.6864185	18.1187382	16.7134438	15.703969	18.3522663	18.1296024	19.0804634
648	Eukaryotic translation initiation factor 4A1 OS=Rattus norvegicus OX=10116 GN=Eif4a1 PE=1 SV=1	Eif4a1	Q6P3V8	1.46734788	0.50299311	22.6877804	22.7354603	22.4241409	22.3183975	22.0255222	22.0725346	21.6519604	22.4037895
649	Eukaryotic translation initiation factor 4E OS=Rattus norvegicus OX=10116 GN=Eif4e PE=1 SV=1	Eif4e	A0A1W2Q6	0.86514825	0.90523338	19.6281338	19.5406208	19.5281639	21.631609	18.9569931	19.0690117	19.3995247	19.2820644
650	Eukaryotic translation initiation factor 5A-1 OS=Rattus norvegicus OX=10116 GN=Eif5a PE=1 SV=3	Eif5a	Q3T1J1	2.0984451	0.46484804	20.8503113	21.1816311	21.3404999	21.0495453	20.5778656	20.5816097	20.5870094	20.8161106
651	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ecsit PE=1 SV=1	Ecsit	Q5XIC2	0.1707403	0.09087324	20.9752178	20.5063114	20.5566845	21.2566242	20.7254219	20.6485558	21.0202217	20.5371456
652	Exocyst complex component 1 OS=Rattus norvegicus OX=10116 GN=Exoc1 PE=1 SV=1	Exoc1	A0A0G2K2V	0.14248753	-0.2597494	15.4767246	17.3318367	17.1940918	14.8208752	16.7162571	15.7781944	16.2251854	17.142889
653	Exocyst complex component 2 OS=Rattus norvegicus OX=10116 GN=Exoc2 PE=1 SV=1	Exoc2	F1LMB9	0.87163803	1.07127166	18.6389427	18.0386295	18.6581383	18.8607235	17.5199108	15.8257589	17.9685898	18.5970879
654	Exocyst complex component 3 OS=Rattus norvegicus OX=10116 GN=Exoc3 PE=1 SV=1	Exoc3	Q62825	0.1840902	0.13049793	16.071104	17.2024651	17.217762	16.7474174	16.8215103	16.6314583	16.5194435	16.7443447
655	Exocyst complex component 4 OS=Rattus norvegicus OX=10116 GN=Exoc4 PE=1 SV=1	Exoc4	Q62824	1.71243415	0.80313158	20.3144093	19.6484604	20.0856628	19.3812962	19.2053318	18.828783	18.8053074	19.3778801
656	Exocyst complex component 5 OS=Rattus norvegicus OX=10116 GN=Exoc5 PE=1 SV=1	Exoc5	P97878	0.44456932	0.24252748	18.8779469	18.5503082	18.055851	17.9849224	18.288002	17.7718792	18.1489906	18.2900467
657	Exocyst complex component 7 OS=Rattus norvegicus OX=10116 GN=Exoc7 PE=1 SV=1	Exoc7	O54922	0.81797209	1.00343966	18.3686943	17.754631	18.034111	17.0444431	16.8402081	16.8945198	15.4003057	18.0530872
658	Exocyst complex component 8 OS=Rattus norvegicus OX=10116 GN=Exoc8 PE=1 SV=1	Exoc8	O54924	0.94512903	1.010252	18.6924915	18.0168457	19.0096416	17.9332161	17.7881584	17.5467815	16.0335903	18.2426567
659	Exocyst complex component OS=Rattus norvegicus OX=10116 GN=Exoc6 PE=1 SV=2	Exoc6	F1M0F4	0.21749905	0.12735939	22.4232254	21.7027702	21.7076664	21.5495968	21.9668217	21.4532547	21.5468254	21.9069195
660	Exportin 5 OS=Rattus norvegicus OX=10116 GN=Xpo5 PE=1 SV=1	Xpo5	D3ZQE8	0.01745575	0.02577829	16.4542274	16.7849121	16.199585	15.2268572	15.8596163	16.0690041	15.4474888	17.1863594
661	Exportin 7 OS=Rattus norvegicus OX=10116 GN=Xpo7 PE=1 SV=1	Xpo7	A0A0G2JWA	0.237197	0.27157855	17.2514668	17.4494534	16.999279	15.7556305	16.7198944	16.9755116	16.8582516	15.8158579
662	F-actin-capping protein subunit alpha-2 OS=Rattus norvegicus OX=10116 GN=Capza2 PE=1 SV=1	Capza2	Q3T1K5	0.0095909	-0.0336151	16.7963791	16.7552128	13.6779232	18.3109531	16.8714886	17.6188946	16.6631794	14.5213661
663	F-actin-capping protein subunit beta OS=Rattus norvegicus OX=10116 GN=Capzb PE=1 SV=1	Capzb	A0A0G2JYB	0.15593136	0.20572424	18.8963146	19.2127266	20.4025345	20.7247944	20.2070789	19.2187042	19.7719116	19.2157784
664	FAD synthase OS=Rattus norvegicus OX=10116 GN=Flad1 PE=1 SV=2	Flad1	D4A4P4	0.13153028	-0.293694	16.3418655	15.8501778	18.1421909	17.8032284	18.5347099	16.498724	18.2711773	16.0076275
665	FAD-dependent oxidoreductase domain containing 1 OS=Rattus norvegicus OX=10116 GN=Foxred1 PE=1 SV=1	Foxred1	D3ZEH2	0.18845288	0.12798882	22.5472889	23.1346436	21.9808178	22.1883011	22.1258965	22.4189034	22.2807064	22.5135899
666	Fam49b protein OS=Rattus norvegicus OX=10116 GN=Fam49b PE=1 SV=1	Fam49b	B2GUZ9	0.06605109	0.14563131	16.8669319	14.2641087	15.7765121	14.8525219	16.0489311	15.4457245	15.9622631	13.7206306
667	Family with sequence similarity 120A OS=Rattus norvegicus OX=10116 GN=Fam120a PE=1 SV=2	Fam120a	D4AB03	0.25789686	0.74893999	19.1318378	18.9931717	18.6021557	17.6872196	19.2188835	18.4668655	14.4659252	19.2669506
668	Family with sequence similarity 186, member B OS=Rattus norvegicus OX=10116 GN=Fam186b PE=4 SV=1	Fam186b	D4ADP4	0.66525196	1.46334338	19.0475197	19.0932713	18.2513733	21.6547146	15.7935362	18.824791	19.0085983	18.5665798
669	Family with sequence similarity 210, member B OS=Rattus norvegicus OX=10116 GN=Fam210b PE=1 SV=1	Fam210b	B2RYM8	3.06479037	-0.6182127	17.9263668	18.0967484	18.0965519	17.701252	18.623621	18.5322227	18.6478329	18.4900932
670	Family with sequence similarity 49, member A OS=Rattus norvegicus OX=10116 GN=Fam49a PE=1 SV=1	Fam49a	B0BN65	0.16960296	-0.2178919	15.3201132	17.2734871	16.5665379	16.8780632	16.4766846	16.8644695	16.1744213	17.3941936
671	FAST kinase domain-containing protein 4 OS=Rattus norvegicus OX=10116 GN=Tbrg4 PE=2 SV=1	Tbrg4	Q5M9G9	0.90194022	0.49535275	21.113245	21.3093128	21.4334602	20.8770962	20.1971493	20.7842808	20.4247017	21.3455715
672	FAST kinase domains 1 OS=Rattus norvegicus OX=10116 GN=Fastkd1 PE=4 SV=1	Fastkd1	D3ZFR0	0.39602573	0.61477757	14.103899	16.0957546	14.1150351	14.4891205	13.2501774	13.9049349	13.6908941	15.4986925
673	Fatty acid-binding protein 5 OS=Rattus norvegicus OX=10116 GN=Fabp5 PE=1 SV=3	Fabp5	P55053	0.28955142	-0.504236	17.9388504	17.8217068	17.6862297	15.0734816	17.3271885	18.1195431	17.151556	17.9389248
674	Fatty acid-binding protein, adipocyte OS=Rattus norvegicus OX=10116 GN=Fabp4 PE=1 SV=1	Fabp4	A0A0G2K58	0.03060181	0.00983238	22.4610748	22.3843231	22.470808	22.6034145	22.3373699	22.5811939	22.2671223	22.6946049
675	Fatty acid-binding protein, heart OS=Rattus norvegicus OX=10116 GN=Fabp3 PE=1 SV=2	Fabp3	P07483	0.22900832	0.06076288	25.7125473	25.5177116	25.7144051	26.0250034	25.7007694	25.6543789	25.729435	25.6420326
676	Fatty aldehyde dehydrogenase OS=Rattus norvegicus OX=10116 GN=Aldh3a2 PE=1 SV=1	Aldh3a2	A0A0G2JY4	0.22176077	0.148839	17.979435	17.5273972	16.8479233	17.0942039	17.3487568	17.1878757	16.9358749	17.3810959
677	F-box only protein 6 OS=Rattus norvegicus OX=10116 GN=Fbxo6 PE=1 SV=1	Fbxo6	Q923V4	0.33372837	0.13077688	16.9570675	17.2194042	16.6654644	17.0368805	16.9078331	16.7214661	17.1424599	16.58395
678	F-box protein 40 OS=Rattus norvegicus OX=10116 GN=Fbxo40 PE=4 SV=2	Fbxo40	F1LXQ1	0.00934033	0.00413656	21.5011463	20.9974365	21.3941002	21.2276516	21.1043758	21.477972	21.419548	21.1018925
679	Fermitin family member 2 OS=Rattus norvegicus OX=10116 GN=Fermt2 PE=1 SV=1	Fermt2	A0A0G2JW0	0.30904967	0.20336342	21.7730808	21.1687832	21.3001499	21.2903786	21.6003437	20.5952873	20.9643688	21.558939
680	Ferritin heavy chain OS=Rattus norvegicus OX=10116 GN=Fth1 PE=1 SV=3	Fth1	P19132	0.36669002	0.14745188	22.0927505	22.3945961	21.6050854	21.9163494	21.8738136	21.8920708	21.6967525	21.956337
681	Ferrochelatase OS=Rattus norvegicus OX=10116 GN=Fech PE=1 SV=1	Fech	D3ZBM3	1.04679157	0.18014097	23.917448	23.7840385	23.8435974	23.8781471	23.5292549	23.5294628	23.8298702	23.8140793
682	Fetub protein OS=Rattus norvegicus OX=10116 GN=Fetub PE=1 SV=1	Fetub	Q6IRS6	0.14305027	0.08997631	19.9286137	20.4998512	19.9921494	20.1827145	20.0466061	20.0589485	19.5755177	20.5623512
683	Fibrillin 1 OS=Rattus norvegicus OX=10116 GN=Fbn1 PE=1 SV=1	Fbn1	G3V9M6	0.15692506	0.13522339	25.3863735	24.8000984	24.7767162	24.5798473	24.4767895	24.3600311	24.5825005	25.5828209
684	Fibrinogen beta chain OS=Rattus norvegicus OX=10116 GN=Fgb PE=1 SV=4	Fgb	P14480	0.45852859	-0.1635256	23.7356968	23.6425858	23.2163124	23.4743481	23.3857803	23.8524017	23.6206379	23.8642254
685	Fibrinogen gamma chain OS=Rattus norvegicus OX=10116 GN=Fgg PE=1 SV=3	Fgg	P02680	1.28965547	-0.3527136	23.3177509	23.2442036	22.8414173	23.1675358	23.3015022	23.7528973	23.3768902	23.5504723
686	Fibronectin OS=Rattus norvegicus OX=10116 GN=Fn1 PE=1 SV=2	Fn1	A0A096P6L8	0.83471204	0.30393982	21.9853935	21.6116371	21.8060551	21.4407749	21.4800758	21.3158627	21.0864601	21.7457027
687	Fibronectin type III and SPRY domain-containing 1-like OS=Rattus norvegicus OX=10116 GN=Fsd1l PE=4 SV=1	Fsd1l	A0A0G2JZ60	0.57255405	0.67766714	18.65275	18.4824371	18.8695946	17.8145275	18.2524796	16.3112221	18.5915203	17.9534187
688	Fibulin-5 OS=Rattus norvegicus OX=10116 GN=Fbln5 PE=2 SV=1	Fbln5	Q9WVH8	0.79807299	0.83014727	20.4454784	19.4475651	20.2092934	19.154007	19.7132282	18.3168316	18.2116127	19.6940823
689	Filamin A OS=Rattus norvegicus OX=10116 GN=Flna PE=1 SV=1	Flna	C0JPT7	0.27354165	-0.4173207	21.5039558	20.7239475	19.4780083	20.177906	19.7522793	20.8528385	20.930542	22.0174408
690	Filamin-C OS=Rattus norvegicus OX=10116 GN=Flnc PE=1 SV=1	Flnc	D3ZHA0	0.01966572	0.02017498	20.769022	20.5352917	19.3828087	20.1012897	20.3039551	20.4055481	19.6728439	20.3253651
691	Flotillin-1 OS=Rattus norvegicus OX=10116 GN=Flot1 PE=2 SV=2	Flot1	Q9Z1E1	0.00301548	0.00308084	19.4286423	18.9713326	18.6927547	19.9791756	19.2495193	18.7715034	19.3317947	19.7067642
692	Flotillin-2 OS=Rattus norvegicus OX=10116 GN=Flot2 PE=1 SV=1	Flot2	Q9Z2S9	0.36691367	-0.2702308	19.3992615	19.5333767	19.100853	19.4986935	19.2557583	20.3527336	19.9570389	19.0475769
693	Folliculin OS=Rattus norvegicus OX=10116 GN=Flcn PE=1 SV=1	Flcn	Q76JQ2	0.98586192	1.14325786	18.2823315	16.4738369	16.6291714	16.4156647	14.7801008	15.6103115	16.3093109	16.5282497
694	Formin-like 3 OS=Rattus norvegicus OX=10116 GN=Fmnl3 PE=1 SV=1	Fmnl3	A0A0G2JXC	0.72466181	0.31670618	21.6119137	20.9364319	20.6848812	21.1060352	21.0040264	20.773016	20.6151905	20.6802044
695	Four and a half LIM domains 1 OS=Rattus norvegicus OX=10116 GN=Fhl1 PE=1 SV=1	Fhl1	Q6P792	0.68393819	-0.3851514	19.4398766	20.1528244	19.2451439	19.833107	19.8042889	19.7893066	20.0496559	20.568306
696	Four and a half LIM domains protein 2 OS=Rattus norvegicus OX=10116 GN=Fhl2 PE=1 SV=1	Fhl2	O35115	1.01198322	1.09924984	20.9674587	21.5154362	20.0711937	20.0844231	18.782362	20.800848	19.3899174	19.2683849
697	Fragile X mental retardation syndrome-related protein 1 OS=Rattus norvegicus OX=10116 GN=Fxr1 PE=1 SV=1	Fxr1	Q5XI81	0.69525688	0.14128685	21.6633339	21.478529	21.3298988	21.6353264	21.5352364	21.236227	21.3985977	21.3718796
698	Fructose-bisphosphate aldolase A OS=Rattus norvegicus OX=10116 GN=Aldoa PE=1 SV=2	Aldoa	P05065	0.5710288	-0.1288919	25.584631	25.5540943	25.5655975	25.9736042	25.7772884	25.7410603	25.8795013	25.7956448
699	FRY microtubule-binding protein OS=Rattus norvegicus OX=10116 GN=Fry PE=1 SV=3	Fry	E9PTY6	0.74849659	1.16423464	18.5374527	16.3214722	17.8481121	18.7563171	17.4297676	16.4018211	15.3329372	17.6418896
700	FTS and Hook-interacting protein OS=Rattus norvegicus OX=10116 GN=Fam160a2 PE=1 SV=1	Fam160a2	Q66H54	0.86627214	1.28363204	16.3668499	16.9547424	17.0418243	16.2333851	16.4087276	14.8083525	13.5961914	16.6490021
701	Fumarate hydratase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Fh PE=1 SV=1	Fh	P14408	0.01289767	0.00256443	24.5091057	24.3260021	24.3772411	24.2096653	24.3430977	24.4086399	24.2880745	24.3719444
702	Fumarylacetoacetate hydrolase domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Fahd2 PE=1 SV=1	Fahd2	B2RYW9	1.83723068	-0.4831314	19.853138	19.2696323	19.4615154	19.5996761	20.0200214	20.0899677	20.1718483	19.83465
703	FUN14 domain-containing 2 OS=Rattus norvegicus OX=10116 GN=Fundc2 PE=1 SV=1	Fundc2	D3ZAQ0	0.55022892	-0.5888662	18.7332058	18.5961647	19.8628159	19.1150417	20.0415649	18.5271339	20.420126	19.6738682
704	FXYD domain-containing ion transport regulator OS=Rattus norvegicus OX=10116 GN=Fxyd1 PE=1 SV=1	Fxyd1	A0A0H2UH	0.32849402	-0.1650147	21.6662731	21.3355446	21.0447502	21.7891273	21.8164158	21.7993984	21.6320629	21.2478771
705	FYVE, RhoGEF and PH domain-containing 5 OS=Rattus norvegicus OX=10116 GN=Fgd5 PE=1 SV=2	Fgd5	F1LTE6	0.14068838	0.26607585	16.7499771	16.0248051	15.5460148	18.5983887	16.3190536	15.8069201	16.8204384	16.9084702
706	G patch domain-containing 8 OS=Rattus norvegicus OX=10116 GN=Gpatch8 PE=1 SV=3	Gpatch8	F1M4M5	0.08488577	0.14560604	19.5286846	19.8682423	20.2370529	22.1568966	20.6685448	20.1764126	20.5721531	19.7913418
707	G protein beta subunit-like, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Mlst8 PE=1 SV=1	Mlst8	G3V7F1	0.17096546	0.16120768	19.3914585	19.0323124	18.4392757	18.1132965	18.5341244	18.6375465	18.0302181	19.1296234
708	G protein nucleolar 3-like OS=Rattus norvegicus OX=10116 GN=Gnl3l PE=4 SV=3	Gnl3l	D3ZMZ9	0.31631849	0.60804176	19.2843418	16.995451	17.7461872	17.6273117	17.9459724	16.0681477	16.3833656	18.8236389
709	G protein-coupled receptor 21 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Rabgap1 PE=1 SV=1	Rabgap1	D3ZX42	1.99383452	2.23362041	18.6219406	18.5864258	17.6330853	17.8862553	16.1312389	15.1971579	15.0326328	17.4321957
710	G protein-coupled receptor kinase interacting ArfGAP 2 OS=Rattus norvegicus OX=10116 GN=Git2 PE=1 SV=1	Git2	Q66H91	0.68214328	0.80615687	17.8818398	17.397295	17.3536224	16.0466404	17.2386856	15.2485781	16.3729534	16.594553
711	Galactose-4-epimerase, UDP, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Gale PE=1 SV=1	Gale	Q4QRB0	0.37554055	0.25027418	19.7791653	19.2661877	19.459938	18.7908421	19.6366444	18.7085648	19.0882607	18.8615665
712	Galectin-1 OS=Rattus norvegicus OX=10116 GN=Lgals1 PE=1 SV=2	Lgals1	P11762	1.10531746	-0.3467255	21.9976349	22.3322811	22.2831135	22.6761074	22.7975445	22.6180859	22.8134327	22.4469757
713	Galectin-3-binding protein OS=Rattus norvegicus OX=10116 GN=Lgals3bp PE=1 SV=2	Lgals3bp	O70513	1.54970072	-0.9036396	16.0457668	16.89044	16.5854721	15.7394686	16.828207	17.4323711	17.5927677	17.0223598
714	Gamma-tubulin complex component OS=Rattus norvegicus OX=10116 GN=Tubgcp3 PE=1 SV=1	Tubgcp3	A0A0G2JUU	0.39992827	-0.1724639	20.480526	20.0067043	19.7353535	19.8344269	20.3671265	20.0478573	20.3260326	20.0058498
715	Gap junction alpha-1 protein OS=Rattus norvegicus OX=10116 GN=Gja1 PE=1 SV=2	Gja1	P08050	0.31436874	0.43487692	19.5299225	18.9456234	18.3153057	19.8830624	19.4136009	19.0011215	19.1807327	17.3389511
716	GCN1 eIF2 alpha kinase activator-like 1 OS=Rattus norvegicus OX=10116 GN=Gcn1 PE=1 SV=3	Gcn1	F1LRI5	1.1678674	0.54305506	23.2172165	22.6282902	22.5114307	22.2345791	22.1105099	22.0521927	21.8133163	22.4432774
717	Gelsolin OS=Rattus norvegicus OX=10116 GN=Gsn PE=1 SV=1	Gsn	Q68FP1	0.29886595	-0.7183745	17.9336777	18.8824978	15.8927736	20.5744991	18.7238026	18.5663528	19.6577187	19.2090721
718	Gem (nuclear organelle)-associated protein 5 OS=Rattus norvegicus OX=10116 GN=Gemin5 PE=1 SV=2	Gemin5	D3ZGD0	0.48945137	0.46146178	17.8424835	15.9912586	16.5686703	16.3227119	16.5911598	16.1087322	15.9101591	16.2692261

719	General vesicular transport factor p115 OS=Rattus norvegicus OX=10116 GN=Uso1 PE=1 SV=1	Uso1	P41542	0.23135872	0.21526194	19.8145638	19.5431404	19.0571213	18.5997543	18.4035702	19.0557098	19.007431	19.686821
720	GLI pathogenesis-related 2 OS=Rattus norvegicus OX=10116 GN=Glipr2 PE=1 SV=3	Glipr2	F1M5V2	0.21286563	0.21284771	19.288187	20.2088127	19.6663647	19.347456	18.4355392	19.6336555	19.5983868	19.991848
721	Glioblastoma amplified sequence OS=Rattus norvegicus OX=10116 GN=Nipsnap2 PE=1 SV=1	Nipsnap2	Q5RK08	0.18120141	-0.0343342	24.4222851	24.415596	24.3678818	24.5311184	24.3198414	24.4321079	24.487709	24.6345596
722	Globin a1 OS=Rattus norvegicus OX=10116 GN=LOC103694855 PE=1 SV=1	LOC1036948	Q62669	0.25667007	-0.1158805	23.5946445	24.1661777	23.4278851	23.5672588	23.5486393	23.9188442	23.8480759	23.9039288
723	Globin c2 OS=Rattus norvegicus OX=10116 GN=Hba-a2 PE=1 SV=1	Hba-a2	A0A0G2JSV	0.52149769	-0.1801004	27.5050087	27.8896084	27.4960594	27.56077	27.4368191	28.0504608	27.8165169	27.8680515
724	Glucan (1,4-alpha-), branching enzyme 1 OS=Rattus norvegicus OX=10116 GN=Gbe1 PE=1 SV=1	Gbe1	A0A0G2JTB	0.60917703	1.27002311	17.8252125	18.1659164	18.5850754	16.541048	17.14991	14.3443136	16.0233364	18.5195999
725	Glucocorticoid receptor OS=Rattus norvegicus OX=10116 GN=Nr3c1 PE=1 SV=2	Nr3c1	P06536	0.47694693	0.58940363	21.3392906	19.857748	20.6312237	20.2694626	19.7587566	20.7864952	18.7028408	20.4920177
726	Glucose-6-phosphate 1-dehydrogenase OS=Rattus norvegicus OX=10116 GN=G6pdx PE=1 SV=3	G6pdx	P05370	0.3423935	0.3842566	16.6183147	15.736434	14.8627787	16.3360958	15.502965	15.3842506	14.8779202	16.251461
727	Glucose-6-phosphate isomerase OS=Rattus norvegicus OX=10116 GN=Gpi PE=1 SV=1	Gpi	Q6P6V0	0.81395116	-0.207612	22.2779427	22.2470436	22.4106026	22.7131977	22.4712353	22.7731953	22.5389137	22.6958904
728	Glutamate dehydrogenase 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Glud1 PE=1 SV=2	Glud1	P10860	0.16257824	-0.1110168	23.6436996	23.5801105	23.6102562	22.8844223	23.3870869	23.7925682	23.0789566	23.903944
729	Glutaminase kidney isoform, mitochondrial OS=Rattus norvegicus OX=10116 GN=Gls PE=1 SV=2	Gls	P13264	0.59757452	1.42231655	18.7660427	19.5773201	19.6456203	17.6601353	18.191246	18.2790489	14.4685287	19.0210285
730	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2 OS=Rattus norvegicus OX=10116 GN=Gfpt2 PE=1 SV=3	Gfpt2	Q4KMC4	0.01946057	-0.0395379	21.1141357	20.5316849	20.0308857	18.6926308	19.5321217	19.4455662	20.119524	21.4302769
731	Glutamine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Qars PE=1 SV=1	Qars	Q66H61	1.00583464	0.63674641	19.7487335	19.8036919	18.8688164	19.5302658	18.2959232	18.5820637	19.2274132	19.2991219
732	Glutamyl aminopeptidase OS=Rattus norvegicus OX=10116 GN=Enpep PE=1 SV=2	Enpep	P50123	0.51861093	-0.9413748	16.4671459	18.2155056	17.3955479	17.2011776	19.4870014	18.7660275	18.7329521	16.0588951
733	Glutamyl-prolyl-tRNA synthetase OS=Rattus norvegicus OX=10116 GN=Eprs PE=1 SV=1	Eprs	A0A0G2JZI2	1.01591087	0.47546101	23.0321674	23.2875862	22.6876965	22.6211281	22.639782	22.5018978	21.8912868	22.6937675
734	Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial OS=Rattus norvegicus OX=10116 GN=Qrsl1 PE=2 SV=1	Qrsl1	Q5FWT5	0.50026611	-0.5680108	15.8235779	17.9076958	17.8711452	17.5983353	17.6175575	18.2955914	17.8544846	17.705164
735	Glutaredoxin 5 OS=Rattus norvegicus OX=10116 GN=Glrx5 PE=1 SV=1	Glrx5	D4ADD7	0.90661651	0.86096811	19.0524216	19.4032249	20.0562439	18.9688702	18.6485538	19.1197357	17.3050785	18.9635201
736	Glutaredoxin-3 OS=Rattus norvegicus OX=10116 GN=Glrx3 PE=1 SV=2	Glrx3	Q9JLZ1	0.77022503	1.04013467	18.3364735	18.0925484	18.6734219	17.5300121	18.1768093	15.9192095	16.1707573	18.2051411
737	Glutaryl-CoA dehydrogenase OS=Rattus norvegicus OX=10116 GN=Gcdh PE=1 SV=1	Gcdh	D3ZT90	0.38528082	0.23487282	22.9897461	22.4993019	22.3907623	21.9235096	22.2877464	22.0702477	21.9008942	22.6049404
738	Glutathione peroxidase 1 OS=Rattus norvegicus OX=10116 GN=Gpx1 PE=1 SV=4	Gpx1	P04041	0.25232188	-0.1075106	22.6382904	22.1907845	22.007391	21.9290695	22.250597	22.4878597	22.1480885	22.3090324
739	Glutathione peroxidase 3 OS=Rattus norvegicus OX=10116 GN=Gpx3 PE=2 SV=2	Gpx3	P23764	0.33158667	0.37911654	17.576952	18.3096199	17.7788849	16.7760563	16.270153	17.3888416	17.207468	18.0585842
740	Glutathione S-transferase alpha-3 OS=Rattus norvegicus OX=10116 GN=Gsta3 PE=1 SV=3	Gsta3	P04904	0.02619197	0.01363802	19.1245766	19.7804489	19.0995502	19.2684765	19.3298225	19.3119926	19.4861565	19.0905285
741	Glutathione S-transferase kappa 1 OS=Rattus norvegicus OX=10116 GN=Gstk1 PE=1 SV=3	Gstk1	P24473	1.44300123	0.53343821	23.8605709	23.7939606	23.3200703	23.3064041	23.2185898	23.0855808	22.6537743	23.1893082
742	Glutathione S-transferase Mu 2 OS=Rattus norvegicus OX=10116 GN=Gstm2 PE=1 SV=2	Gstm2	P08010	0.04631528	0.0244565	22.3279209	22.7552013	22.9142151	22.7339344	22.8789978	22.4252605	22.9072514	22.421936
743	Glutathione S-transferase Mu 5 OS=Rattus norvegicus OX=10116 GN=Gstm5 PE=1 SV=3	Gstm5	Q9Z1B2	0.33054916	0.11125183	16.5334167	16.4496593	16.3853188	16.2725029	16.6105957	16.0671043	16.0914955	16.4266949
744	Glutathione S-transferase omega-1 OS=Rattus norvegicus OX=10116 GN=Gsto1 PE=1 SV=2	Gsto1	Q9Z339	0.41135407	-0.216433	19.0761662	18.4863853	19.153059	19.5292969	19.4799042	19.143631	19.3645992	19.1225052
745	Glutathione S-transferase P OS=Rattus norvegicus OX=10116 GN=Gstp1 PE=1 SV=2	Gstp1	P04906	0.06785625	0.08534336	18.5451927	20.003315	20.1630192	20.3484364	19.9095993	19.4684105	19.301321	20.039259
746	Glutathione S-transferase, theta 3 OS=Rattus norvegicus OX=10116 GN=Gstt3 PE=1 SV=1	Gstt3	D3Z8I7	0.3749721	-0.8159022	18.5135784	18.2152748	19.7330761	15.3472633	18.8448238	18.7236938	18.3064327	19.1978512
747	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus OX=10116 GN=Gapdh PE=1 SV=3	Gapdh	P04797	0.19202722	0.10928965	28.5618458	28.1175938	28.0118523	27.8835506	27.9658985	28.2795162	27.5855083	28.3067608
748	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus OX=10116 PE=1 SV=1	10116	M0R660	0.23915103	-0.1075754	23.3724098	23.2023659	23.1951065	22.6896324	23.1077938	23.3917236	22.9782753	23.4120235
749	Glycerate kinase OS=Rattus norvegicus OX=10116 GN=Glyctk PE=1 SV=1	Glyctk	Q0VGK3	1.55798564	0.86069345	19.2252541	18.8682976	19.3101959	18.8989334	18.870739	17.6153297	17.9408703	18.4329681
750	Glycerol kinase OS=Rattus norvegicus OX=10116 GN=Gk PE=1 SV=1	Gk	A0A0G2K78	1.04618912	-0.5214176	17.2479362	16.4822693	17.5205326	17.414835	17.6835709	17.6969109	17.9477711	17.4229908
751	Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Rattus norvegicus OX=10116 GN=Gpd1l PE=1 SV=1	Gpd1l	D3ZAP9	0.445084	0.32209206	20.1276379	20.2096176	19.2784882	20.095171	19.6348743	19.3484287	19.1721592	20.2670841
752	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Rattus norvegicus OX=10116 GN=Gpd1 PE=1 SV=4	Gpd1	O35077	0.7785877	-0.4334455	20.1357784	20.6834984	20.9706554	21.378809	21.4749012	21.1577873	21.0721874	21.1976471
753	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Gpd2 PE=1 SV=1	Gpd2	P35571	0.73685261	-0.8566942	16.0333214	15.6798458	17.0989342	17.8139839	16.9871883	18.1535473	17.8578072	17.0543194
754	Glycine C-acetyltransferase OS=Rattus norvegicus OX=10116 GN=Gcat PE=1 SV=1	Gcat	A0A0G2K2C	0.01332659	0.01025438	22.7254429	21.873045	21.8421497	22.3426571	22.429575	21.8883762	21.9586754	22.4656506
755	Glycine cleavage system H protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Gcsh PE=2 SV=1	Gcsh	Q5I0P2	0.68178189	0.32286024	18.5398026	18.044838	18.3190422	18.580677	17.8915482	17.6084232	18.5066586	18.1862888
756	Glycine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Gars PE=1 SV=1	Gars	G3V7G8	0.07435259	0.14994979	15.321125	17.0978565	17.5418034	15.4459915	14.8608427	16.783493	16.5898685	16.572773
757	Glycogen [starch] synthase, muscle OS=Rattus norvegicus OX=10116 GN=Gys1 PE=1 SV=1	Gys1	A2RRU1	0.30250167	0.2437458	20.2979259	20.3036709	19.5446148	19.6965694	19.2785587	20.4854984	19.3761768	19.7275639
758	Glycogen phosphorylase, brain form (Fragment) OS=Rattus norvegicus OX=10116 GN=Pygb PE=1 SV=3	Pygb	P53534	0.91299795	0.69475937	22.4805088	22.5795765	21.6972885	22.3622055	21.4653721	22.4790764	20.8810158	21.5150776
759	Glycogenin-1 OS=Rattus norvegicus OX=10116 GN=Gyg1 PE=1 SV=1	Gyg1	A0A0G2JXP	0.11662841	0.10016775	21.3802834	21.0601711	20.2650814	20.3000889	20.5818615	21.0014839	20.2589436	20.7626648
760	Glycophorin-C OS=Rattus norvegicus OX=10116 GN=Gypc PE=1 SV=1	Gypc	Q6XFR6	0.28129079	-0.223495	17.8267345	18.2324638	17.3180008	17.9580231	18.0724277	18.6647701	18.1344337	17.3575706
761	Glypican-1 OS=Rattus norvegicus OX=10116 GN=Gpc1 PE=2 SV=1	Gpc1	Q6P7Q2	2.21000956	-0.5520186	21.5267067	21.6178036	21.1373138	21.5819683	22.0038776	22.1766109	21.8219185	22.0694599
762	GMP reductase OS=Rattus norvegicus OX=10116 GN=Gmpr PE=3 SV=1	Gmpr	F1LRV6	0.50509726	0.29152584	20.2822514	19.170084	19.8822899	19.5554714	19.1217537	19.613945	19.3712368	19.6170578
763	GMP synthase [glutamine-hydrolyzing] OS=Rattus norvegicus OX=10116 GN=Gmps PE=1 SV=1	Gmps	Q4V7C6	0.74224073	0.44043064	18.8651962	19.0208454	17.8004932	18.804039	18.0235481	18.1742554	18.1051331	18.4259148
764	Golgi apparatus protein 1 OS=Rattus norvegicus OX=10116 GN=Glg1 PE=1 SV=1	Glg1	G3V8G5	0.96542659	-0.7150116	18.3853836	20.0101948	19.6205349	19.8237114	20.0949516	20.0283775	20.4556561	20.1208858
765	Golgi brefeldin A-resistant guanine nucleotide exchange factor 1 OS=Rattus norvegicus OX=10116 GN=Gbf1 PE=1 SV=2	Gbf1	F1M8X9	0.37241773	0.53640652	15.1367655	15.409481	14.8112125	17.2653732	15.9840078	14.6577206	14.8125257	15.0229521
766	Golgi reassembly-stacking protein 2 OS=Rattus norvegicus OX=10116 GN=Gorasp2 PE=1 SV=1	Gorasp2	Q68G33	0.47951426	0.44590235	18.1311741	18.5481625	18.2199154	18.3371181	18.2897778	16.6372738	18.1275921	18.3981171
767	Golgi to ER traffic protein 4 OS=Rattus norvegicus OX=10116 GN=Get4 PE=1 SV=2	Get4	F1LXF5	1.68904435	-1.6725173	17.3079453	16.1334858	16.3118534	16.2714062	16.7924252	18.6444321	18.6156845	18.6622181
768	Golgin subfamily A member 2 OS=Rattus norvegicus OX=10116 GN=Golga2 PE=1 SV=1	Golga2	A0A0G2K97	0.83802257	0.67171574	19.5086937	17.8460331	18.6171913	18.3255711	18.2442093	18.0512791	17.3361149	17.979023
769	Golgin subfamily A member 4 OS=Rattus norvegicus OX=10116 GN=Golga4 PE=1 SV=1	Golga4	A0A0G2JUE	1.09055576	0.64468241	19.4184074	19.2792511	18.3386974	18.7556515	18.168108	18.7850895	17.9202518	18.3398285
770	GPRIN family member 3 OS=Rattus norvegicus OX=10116 GN=Gprin3 PE=1 SV=2	Gprin3	D3ZF21	0.87853806	-0.4083633	21.2600212	21.0309696	21.1516628	21.9115124	21.7821331	21.6898327	21.4485989	22.0670547
771	G-protein signalling modulator 1 (AGS3-like, C. elegans), isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Gpsm1 PE=1 SV=1	Gpsm1	G3V9X2	0.30468382	-0.262464	18.0828094	18.0957432	18.4978561	18.9768448	17.9002056	19.307312	18.8654861	18.630106
772	Granulin, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Grn PE=4 SV=1	Grn	G3V8V1	0.02767071	0.04292727	18.1934204	19.4391975	19.2333717	19.1216412	19.3161049	17.5978394	19.53755	19.3644276
773	G-rich RNA sequence-binding factor 1 OS=Rattus norvegicus OX=10116 GN=Grsf1 PE=1 SV=2	Grsf1	F1LRK4	0.03787662	0.02892208	22.6139755	22.1027908	21.9574451	21.47542	22.1764526	21.6465263	22.0715904	22.1393738
774	Growth arrest-specific protein 6 OS=Rattus norvegicus OX=10116 GN=Gas6 PE=1 SV=1	Gas6	Q63772	0.46431367	0.23720837	19.6098137	19.1863861	19.5828915	19.6227169	19.5396652	19.2374306	19.5836372	18.6922417
775	Growth factor receptor-bound protein 14 OS=Rattus norvegicus OX=10116 GN=Grb14 PE=1 SV=1	Grb14	O88900	0.19514502	0.119133	21.9904709	21.7172031	21.8680744	21.0536842	21.5647659	21.5335503	21.2356548	21.8189297
776	Growth hormone-inducible transmembrane protein OS=Rattus norvegicus OX=10116 GN=Ghitm PE=2 SV=1	Ghitm	Q5XIA8	0.63989953	-0.2605352	20.662302	21.022892	21.0646896	21.1972275	21.4001656	21.0774994	21.6059227	20.9056644
777	GrpE protein homolog OS=Rattus norvegicus OX=10116 GN=Grpel1 PE=1 SV=1	Grpel1	A0A0G2JZA	0.96816805	0.41395044	19.9883213	20.2668362	19.6869202	19.8254642	19.1371479	19.5743504	19.9959049	19.4043369
778	GTP:AMP phosphotransferase AK3, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ak3 PE=1 SV=1	Ak3	Q6P2A5	0.02008187	0.0138526	23.4387207	23.4632645	23.2678089	23.4087029	23.3485622	23.1118832	23.0222607	24.0403805
779	GTPase HRas OS=Rattus norvegicus OX=10116 GN=Hras PE=1 SV=2	Hras	P20171	0.04075636	0.13149166	18.4890957	18.755846	18.1884899	14.5409908	18.0784035	17.0508595	16.0208855	18.2983074
780	GTP-binding nuclear protein Ran OS=Rattus norvegicus OX=10116 GN=Ran PE=1 SV=3	Ran	P62828	0.25808984	-0.1407967	20.1624165	20.0427017	19.8804512	20.1704369	20.3292351	20.3681965	19.5809135	20.5408478
781	GTP-binding protein 6 (putative) OS=Rattus norvegicus OX=10116 GN=Gtpbp6 PE=1 SV=1	Gtpbp6	D3ZLF0	0.34741077	0.54214859	16.8555565	19.0625114	18.4327602	19.3516788	18.4123764	16.8364124	18.4158802	17.8692436
782	GTP-binding protein OS=Rattus norvegicus OX=10116 GN=Rrad PE=3 SV=1	Rrad	G3V7K9	2.70824837	0.58982468	21.861454	22.0431061	21.7750854	22.0505676	21.0829487	21.4603176	21.3627434	21.4649048
783	GTP-binding protein Rheb OS=Rattus norvegicus OX=10116 GN=Rheb PE=1 SV=1	Rheb	Q62639	1.1980715	0.61266637	16.0687485	16.7615395	16.482481	16.7451439	15.7391758	16.0834026	15.3933268	16.3913422
784	GTP-binding protein SAR1b OS=Rattus norvegicus OX=10116 GN=Sar1b PE=2 SV=1	Sar1b	Q5HZY2	0.364459	-0.2767906	17.8208294	18.1122189	16.8788681	18.198349	18.2249012	17.9046021	17.7253151	18.2626095
785	Guanine deaminase OS=Rattus norvegicus OX=10116 GN=Gda PE=1 SV=1	Gda	Q9JKB7	0.42213194	-0.2704077	20.116333	21.0429077	20.0803165	20.3301468	20.2154942	20.80369	21.0426216	20.589529
786	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Rattus norvegicus OX=10116 GN=Gnai2 PE=1 SV=3	Gnai2	P04897	1.33430897	-0.2451148	23.3001671	23.5294342	23.1887131	23.4252434	23.4488049	23.7215939	23.6982918	23.5553265
787	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Rattus norvegicus OX=10116 GN=Gng5 PE=3 SV=1	Gng5	P63219	0.41264066	1.17832112	20.6279869	19.9457932	19.5622616	19.7063427	20.0446434	19.8964901	20.1238136	15.0641527
788	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Gnb1 PE=1 SV=4	Gnb1	P54311	1.77388813	-0.4302387	21.0625916	21.4323711	20.9668121	21.1313782	21.3686237	21.6363029	21.769228	21.5399532
789	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Rattus norvegicus OX=10116 GN=Gnb2 PE=1 SV=4	Gnb2	P54313	1.21364496	-0.3113489	22.2010479	22.5932083	22.6697254	22.7798977	22.8478508	22.7714176	23.0092278	22.8607788
790	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 OS=Rattus norvegicus OX=10116 GN=Gnb3 PE=1 SV=1	Gnb3	P52287	1.18379379	-0.4899082	20.5071754	20.0738239	20.024683	19.6388893	20.2181053	20.5239353	20.8149567	20.6472073

791	Guanine nucleotide-binding protein G(o) subunit alpha OS=Rattus norvegicus OX=10116 GN=Gnao1 PE=1 SV=2	Gnao1	P59215	1.14861039	-0.689476	18.415453	19.5360565	18.5469036	18.7279987	18.9403172	19.7228298	19.7491379	19.572031
792	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Rattus norvegicus OX=10116 GN=Gnas PE=1 SV=1	Gnas	P63095	0.67642156	-0.2616148	20.6022491	20.7001648	20.0034065	20.6553307	20.5439625	20.8937435	20.911068	20.6588364
793	Guanine nucleotide-binding protein subunit alpha-13 OS=Rattus norvegicus OX=10116 GN=Gna13 PE=1 SV=1	Gna13	Q6Q7Y5	0.23178769	-0.1303673	17.4693718	17.470953	16.9832344	17.859621	17.6281338	17.2225266	17.8972664	17.5567226
794	Guanine nucleotide-binding protein subunit gamma OS=Rattus norvegicus OX=10116 GN=Gng10 PE=1 SV=1	Gng10	Q3KRE3	1.13653156	-1.5809581	15.4777422	18.7450027	17.8753109	16.9868603	19.0023079	18.2282581	19.1555004	19.0226822
795	Guanine nucleotide-binding protein subunit gamma OS=Rattus norvegicus OX=10116 GN=Gng12 PE=1 SV=1	Gng12	G3V6P8	1.01982458	-0.1715336	20.5465546	20.7359982	20.5255718	20.4708939	20.7772923	20.9090843	20.6271648	20.6516113
796	Guanylate kinase 1 OS=Rattus norvegicus OX=10116 GN=Guk1 PE=1 SV=2	Guk1	E9PTV0	0.48615225	0.42641973	17.1429043	16.8408184	15.8512774	16.8065434	16.6976967	15.6897974	15.7966137	16.7517567
797	Gup1, glycerol uptake/transporter homolog (Yeast) (Predicted) OS=Rattus norvegicus OX=10116 GN=Hhatl PE=3 SV=1	Hhatl	D4A9P9	1.00068869	-0.3287272	21.6105766	21.8226929	21.5997314	22.1465473	21.9807529	22.166235	22.4179401	21.9295292
798	Haloacid dehalogenase-like hydrolase domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Hdhd2 PE=1 SV=1	Hdhd2	Q6QI86	0.35665416	0.44338727	17.1532421	16.7961922	16.9398861	17.242712	16.8321686	16.8380089	17.5861893	15.1021166
799	Haptoglobin OS=Rattus norvegicus OX=10116 GN=Hp PE=1 SV=3	Hp	P06866	0.69429805	-0.6510739	19.9759979	19.0672321	19.8207531	20.6117115	19.8232994	21.125227	20.1090336	21.0224304
800	HBS1-like protein OS=Rattus norvegicus OX=10116 GN=Hbs1l PE=1 SV=1	Hbs1l	A0A0G2K2P	0.74474473	0.71706676	22.4975033	21.92906	23.2030678	22.9855099	22.7857246	21.3033867	21.2933044	22.3644581
801	Heat shock 27kD protein family, member 7 (Cardiovascular) OS=Rattus norvegicus OX=10116 GN=Hspb7 PE=2 SV=1	Hspb7	B5DFG4	0.01003908	0.03509712	17.9048977	18.4638634	17.7424812	15.1144495	18.6875496	14.7418871	17.1701088	18.4857578
802	Heat shock 27kDa protein 1 OS=Rattus norvegicus OX=10116 GN=Hspb1 PE=1 SV=1	Hspb1	G3V913	0.25596964	0.26177025	26.8623314	26.8575363	26.2738056	25.4371529	26.1229858	25.7819786	25.6906662	26.7881145
803	Heat shock 27kDa protein 3 OS=Rattus norvegicus OX=10116 GN=Hspb3 PE=3 SV=1	Hspb3	G3V7G6	1.33085164	1.5006876	20.3672886	21.1344204	20.6194839	21.781683	19.0662537	20.9538288	18.5978699	19.2821732
804	Heat shock 70 kDa protein 1A OS=Rattus norvegicus OX=10116 GN=Hspa1a PE=2 SV=1	Hspa1a	P0DMW0	0.07637084	0.13075972	20.9799004	20.6409683	20.3163624	21.6073761	20.9990063	19.805666	20.008709	22.2081871
805	Heat shock 70 kDa protein 4 OS=Rattus norvegicus OX=10116 GN=Hspa4 PE=1 SV=1	Hspa4	F1LRV4	0.72330771	0.3275795	21.4573021	22.0100479	21.1648922	21.1279926	20.9731808	21.0705242	21.0431328	21.3630791
806	Heat shock 70 kDa protein 4L OS=Rattus norvegicus OX=10116 GN=Hspa4l PE=1 SV=1	Hspa4l	F7F2F3	0.44245148	0.83805728	17.3910217	18.9553795	18.4762001	16.5822964	17.2287006	18.1286278	15.1197901	17.5755501
807	Heat shock cognate 71 kDa protein OS=Rattus norvegicus OX=10116 GN=Hspa8 PE=1 SV=1	Hspa8	P63018	0.0186828	0.00945473	27.3534126	26.7812748	26.6816139	26.7189159	26.9535732	26.7397423	26.781517	27.0225658
808	Heat shock protein 105 kDa OS=Rattus norvegicus OX=10116 GN=Hsph1 PE=1 SV=1	Hsph1	Q66HA8	0.00979132	0.00639868	19.6537094	20.3123455	19.4862232	19.9252205	19.9134998	19.903347	20.0582218	19.4768353
809	Heat shock protein 75 kDa, mitochondrial OS=Rattus norvegicus OX=10116 GN=Trap1 PE=1 SV=1	Trap1	Q5XHZ0	1.68832628	0.46028042	23.1170406	22.983654	23.3334064	23.4162884	22.6935577	23.0756187	22.6203995	22.6196918
810	Heat shock protein beta-2 OS=Rattus norvegicus OX=10116 GN=Hspb2 PE=3 SV=1	Hspb2	O35878	1.66541208	0.90768766	22.5931377	23.148138	22.8395576	22.8442516	21.705368	22.6390896	21.3713913	22.0784855
811	Heat shock protein beta-6 OS=Rattus norvegicus OX=10116 GN=Hspb6 PE=1 SV=1	Hspb6	P97541	1.17636156	0.39885521	26.9484367	27.0522118	26.7116356	26.5105286	26.3181953	26.2151184	26.3016224	26.7924557
812	Heat shock protein beta-8 OS=Rattus norvegicus OX=10116 GN=Hspb8 PE=1 SV=1	Hspb8	Q9EPX0	0.42091819	0.43815708	19.9855137	19.9596786	18.5854473	19.5631981	18.6283283	19.5683384	18.4273796	19.7171631
813	Heat shock protein family A (Hsp70) member 12B OS=Rattus norvegicus OX=10116 GN=Hspa12b PE=1 SV=3	Hspa12b	D3ZVM5	0.18531032	0.09462166	23.5141449	23.5266094	23.3393593	23.100811	23.1403942	22.9980755	23.181797	23.7821712
814	Heat shock protein HSP 90-alpha OS=Rattus norvegicus OX=10116 GN=Hsp90aa1 PE=1 SV=3	Hsp90aa1	P82995	0.19446041	0.11439896	22.2012215	22.0581417	21.6569424	22.0664635	21.723732	21.7503986	21.5812187	22.4698238
815	Heat shock protein HSP 90-beta OS=Rattus norvegicus OX=10116 GN=Hsp90ab1 PE=1 SV=4	Hsp90ab1	P34058	0.43387058	0.22449684	26.0058231	25.8693504	25.7274303	25.6022263	25.477047	25.5306206	25.137289	26.1618862
816	Heme oxygenase 2 OS=Rattus norvegicus OX=10116 GN=Hmox2 PE=1 SV=1	Hmox2	P23711	0.20228955	-0.61902	16.5169888	16.8560886	13.5043869	16.5131893	17.0363655	13.7431297	17.8199425	17.2672958
817	Hemoglobin subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Hbb PE=1 SV=3	Hbb	P02091	0.3901067	-0.1185703	28.1045513	28.4073772	27.9785347	27.9332695	28.0086212	28.374052	28.2104053	28.3049355
818	Hemoglobin subunit beta-2 OS=Rattus norvegicus OX=10116 PE=1 SV=2	10116	P11517	0.52179251	-0.2453494	23.2342262	23.6363735	23.1965427	23.1574821	23.0688286	23.9672756	23.6444397	23.5254784
819	Hemopexin OS=Rattus norvegicus OX=10116 GN=Hpx PE=1 SV=3	Hpx	P20059	1.72299314	-0.3699117	21.9680691	22.0132904	21.8284149	21.9192104	22.0167446	22.322279	22.321064	22.5485439
820	Hermansky-Pudlak syndrome 5 protein homolog OS=Rattus norvegicus OX=10116 GN=Saa4 PE=1 SV=1	Saa4	Q7TMC3	0.2657762	0.10395193	24.189724	24.3944378	23.7796841	24.0944157	23.9161987	23.9157391	23.9071102	24.3034058
821	Heterogeneous nuclear ribonucleoprotein C, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Hnrnpc PE=1 SV=1	Hnrnpc	A0A0G2JXW	2.09860079	-1.3291297	18.2149372	17.2737923	16.9028568	17.9736195	18.7047844	18.6954327	18.9303741	19.3511333
822	Heterogeneous nuclear ribonucleoprotein H OS=Rattus norvegicus OX=10116 GN=Hnrnph1 PE=1 SV=1	Hnrnph1	A0A0G2JTG	0.46204564	0.60003853	19.6794052	20.0334034	19.4897118	18.7534885	19.2638245	18.6497669	17.5891304	20.053133
823	Heterogeneous nuclear ribonucleoprotein H2 OS=Rattus norvegicus OX=10116 GN=Hnrnph2 PE=1 SV=1	Hnrnph2	Q6AY09	0.09615082	0.23506546	17.8339329	16.2571335	17.2797356	17.9056244	17.5530434	14.6971302	18.2625408	17.8234501
824	Heterogeneous nuclear ribonucleoprotein K OS=Rattus norvegicus OX=10116 GN=Hnrnpk PE=1 SV=1	Hnrnpk	Q5D059	0.08214168	0.05101347	21.0859795	21.0731163	20.5256062	21.235939	21.0229759	20.5471554	20.832552	21.3139038
825	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus OX=10116 GN=Hnrnpm PE=1 SV=1	Hnrnpm	F1M3D3	0.64472652	0.40626526	22.4082603	21.8304653	21.5806351	21.3562317	21.3945808	21.8112316	20.8533573	21.4913616
826	Heterogeneous nuclear ribonucleoprotein R OS=Rattus norvegicus OX=10116 GN=Hnrnpr PE=1 SV=1	Hnrnpr	Q566E4	0.19977347	0.40061164	15.6269999	16.6039257	16.4979973	17.0670223	13.8870697	16.4084282	16.8227291	17.0752716
827	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus OX=10116 GN=Hnrnpu PE=1 SV=1	Hnrnpu	A0A0G2JZ5	1.27163422	1.04936934	19.7186699	20.1951237	19.4346104	21.0087814	19.5903511	18.3637543	18.8695183	19.3360844
828	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus OX=10116 GN=Hnrnpa2b1 PE=1 SV=1	Hnrnpa2b1	F1LNF1	1.25420303	0.83169031	19.2671719	19.6054726	19.4744301	20.6422653	18.5746765	18.7630768	18.9465237	19.3783016
829	Hexokinase-1 OS=Rattus norvegicus OX=10116 GN=Hk1 PE=1 SV=4	Hk1	P05708	2.29643631	-1.156208	19.3131828	20.5922928	20.1005917	19.9872227	21.0904045	21.2992039	21.1568737	21.07164
830	HIG1 domain family member 1A, mitochondrial OS=Rattus norvegicus OX=10116 GN=Higd1a PE=1 SV=2	Higd1a	Q8VH49	1.11570595	-0.555264	19.0002975	19.6986389	19.8326168	19.7636089	20.0701962	20.0718994	20.6055336	19.768589
831	HIG1 domain family, member 2A OS=Rattus norvegicus OX=10116 GN=Higd2a PE=2 SV=1	Higd2a	B2GV65	1.92476961	-0.6505976	18.9830265	19.177084	19.5385151	19.5417995	19.8049793	19.8862877	20.3139133	19.837635
832	High affinity immunoglobulin epsilon receptor subunit gamma OS=Rattus norvegicus OX=10116 GN=Fcer1g PE=1 SV=1	Fcer1g	P20411	0.32507983	0.65983534	17.0470982	17.4988346	16.6581001	17.0130157	16.7070656	13.9198895	17.4296875	17.5210648
833	High density lipoprotein binding protein (Vigilin) OS=Rattus norvegicus OX=10116 GN=Hdlbp PE=1 SV=1	Hdlbp	Q3KRF2	0.37205537	0.24283314	19.0256786	19.5599155	19.2322063	19.2537289	18.9198513	18.3443146	19.2844143	19.5516167
834	High mobility group protein B1 OS=Rattus norvegicus OX=10116 GN=Hmgb1 PE=1 SV=2	Hmgb1	P63159	0.6481338	-0.7671251	17.6896019	16.7471027	16.3593044	17.0327396	17.2684326	18.6315289	16.5548134	18.4424744
835	Histidine rich calcium binding protein, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Hrc PE=1 SV=1	Hrc	G3V8S6	0.47342602	-0.365242	21.0283566	21.3239231	21.8542652	22.1484222	22.2261391	21.2724037	22.3522186	21.9651737
836	Histidine triad nucleotide binding protein 2 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Hint2 PE=1 SV=1	Hint2	D4AB01	0.40869174	0.36327887	19.9696598	19.9305611	20.5830002	19.1160583	19.6356487	19.316843	19.0073147	20.1863575
837	Histidine triad nucleotide-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Hint1 PE=1 SV=5	Hint1	P62959	0.12039857	-0.0393915	20.0681095	20.0355549	20.384182	20.2072334	20.0566177	20.058588	20.425148	20.3122921
838	Histidine triad nucleotide-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Hint3 PE=1 SV=1	Hint3	F1M9G8	0.81721222	-0.3525639	17.263649	17.5986481	17.4329948	18.0960789	17.9036541	17.7492657	18.2920818	17.8566246
839	Histidine-rich glycoprotein OS=Rattus norvegicus OX=10116 GN=Hrg PE=1 SV=1	Hrg	A0A0G2K3C	0.81609215	-0.9114065	17.5015068	18.2065182	16.3357296	18.6800632	19.0210094	18.4194279	18.8867817	18.0422249
840	Histone cell cycle regulation defective interacting protein 5 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Nfu1 PE=1 SV=1	Nfu1	D3ZA85	0.52927582	0.37785769	18.0930748	17.1882305	18.2327061	17.7245121	17.5001869	17.2208767	16.9582195	18.0478096
841	Histone cluster 1 H1 family member d OS=Rattus norvegicus OX=10116 GN=Hist1h1d PE=1 SV=2	Hist1h1d	M0R7B4	0.36338498	-0.4020753	19.6526356	19.5057793	19.2956066	21.0998936	20.4628658	20.8737698	19.7212105	20.1043701
842	Histone H2A type 4 OS=Rattus norvegicus OX=10116 PE=2 SV=2	10116	Q00728	0.12832484	-0.3109546	20.4763718	19.8785286	19.6418152	23.3881512	21.5530281	21.7046165	20.5322552	20.8387852
843	Histone H2B OS=Rattus norvegicus OX=10116 GN=Hist1h2bd PE=3 SV=2	Hist1h2bd	D3ZWM5	0.07969817	0.18837214	20.8024616	20.6697426	20.5302105	23.9826221	21.6776772	21.5760727	21.0836754	20.8941231
844	Histone H3 OS=Rattus norvegicus OX=10116 GN=Hist2h3c2 PE=1 SV=1	Hist2h3c2	D3ZJ08	0.00474387	0.01819992	19.8290977	18.3098927	18.7715988	23.8654575	20.5693283	20.4072342	19.5960236	20.130661
845	Histone H4 OS=Rattus norvegicus OX=10116 GN=Hist1h4b PE=1 SV=2	Hist1h4b	P62804	0.01052054	0.03383303	21.0425262	20.0387535	20.3993244	24.6768436	21.9377556	21.6820965	21.1918602	21.2104034
846	Histone-binding protein RBBP7 OS=Rattus norvegicus OX=10116 GN=Rbbp7 PE=2 SV=1	Rbbp7	Q71UF4	0.58373494	0.58930683	19.7238503	19.6978931	18.4816952	18.4808865	18.1488323	17.858881	18.7469101	19.2724743
847	Hormone-sensitive lipase OS=Rattus norvegicus OX=10116 GN=Lipe PE=1 SV=3	Lipe	P15304	0.40305591	-0.5484235	17.4904461	16.4188881	14.7823668	16.9256191	17.2309475	16.6199722	16.8461838	17.1139107
848	Hsc70-interacting protein OS=Rattus norvegicus OX=10116 GN=St13 PE=1 SV=1	St13	P50503	0.23270996	-0.3312376	17.7504654	17.4636478	17.3789043	15.3084364	17.2571545	17.3267326	17.0243759	17.6181412
849	Hsd17b4 protein OS=Rattus norvegicus OX=10116 GN=Hsd17b4 PE=1 SV=1	Hsd17b4	Q6IN39	2.16914756	-1.203342	16.7462959	17.0406303	16.5632114	17.6081772	18.0133381	18.1002598	18.7524376	17.9056473
850	Hsp90 co-chaperone Cdc37 OS=Rattus norvegicus OX=10116 GN=Cdc37 PE=1 SV=1	Cdc37	A0A140TAC	0.44101542	-0.3986263	19.1325264	18.02001	18.6024685	17.5989513	18.6205597	18.2214584	18.7946758	19.3117676
851	HtrA serine peptidase 2 OS=Rattus norvegicus OX=10116 GN=Htra2 PE=1 SV=1	Htra2	B0BNB9	1.76263877	-0.419189	19.9946613	19.8013306	19.7562752	19.9134789	20.3917732	20.1221619	20.5631676	20.0653992
852	Huntingtin interacting protein 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Hip1 PE=1 SV=1	Hip1	G3V8Y8	0.30681358	-0.6067128	17.8978329	18.3192825	16.961113	15.583395	16.3444672	17.6400681	18.1180668	19.0858727
853	Huntingtin OS=Rattus norvegicus OX=10116 GN=Htt PE=1 SV=1	Htt	P51111	0.76558769	0.64662814	15.8298187	15.892746	15.1466551	16.8207016	14.9626379	15.7935467	14.8015423	15.545682
854	Hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Adhfe1 PE=1 SV=1	Adhfe1	Q4QQW3	0.27420593	0.18566513	18.6088295	17.8030491	17.9681206	18.0424328	17.7750797	18.4475002	17.4120808	18.0451107
855	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hadh PE=2 SV=1	Hadh	Q9WVK7	0.03043665	-0.0062141	25.2023945	25.1750984	25.3998222	25.2354584	25.3154469	25.1215191	25.3396492	25.2610149
856	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hmgcl PE=2 SV=1	Hmgcl	P97519	0.13518852	0.10462761	19.6550655	19.649025	19.5479279	20.2133579	20.3271465	19.7585297	19.2179432	19.3432465
857	Hydroxysteroid dehydrogenase-like protein 2 OS=Rattus norvegicus OX=10116 GN=Hsdl2 PE=2 SV=1	Hsdl2	Q4V8F9	1.02181814	0.33619738	25.2712517	25.0860882	24.963686	25.0470104	24.8280869	24.5638351	24.4647522	25.1665726
858	Hypothetical protein LOC681410 OS=Rattus norvegicus OX=10116 GN=LOC681410 PE=1 SV=3	LOC681410	F1M3H8	0.23849449	0.3454895	20.6024952	19.970953	19.9325333	18.9192123	19.2683468	18.512886	19.4779434	20.7840595
859	Hypothetical protein MGC:15854 OS=Rattus norvegicus OX=10116 GN=RGD1302996 PE=1 SV=1	RGD130299	G3V628	0.26611515	-0.5668683	18.6695671	18.8630314	18.9656506	15.5212154	19.0305576	18.70014	17.7511024	18.8051376
860	Hypoxanthine-guanine phosphoribosyltransferase OS=Rattus norvegicus OX=10116 GN=Hprt1 PE=1 SV=1	Hprt1	P27605	0.00554312	-0.0027242	21.2216873	21.4401875	21.3033104	21.1840363	21.3300266	21.3555546	20.8669186	21.6076183
861	Hypoxia up-regulated protein 1 OS=Rattus norvegicus OX=10116 GN=Hyou1 PE=1 SV=1	Hyou1	Q63617	0.39202609	0.36751223	18.9037647	19.7934837	19.217865	18.9180851	18.8995724	18.9838181	17.8849869	19.5947723
862	IBA57, iron-sulfur cluster assembly OS=Rattus norvegicus OX=10116 GN=Iba57 PE=1 SV=1	Iba57	D4ADG2	0.02774178	0.05358219	18.7579536	16.3199863	19.1670055	18.1638241	17.8579559	18.507246	17.5740376	18.2552013

863	Ig gamma-2A chain C region OS=Rattus norvegicus OX=10116 GN=Igg-2a PE=1 SV=1	Igg-2a	P20760	0.05351642	0.07207203	20.0625324	20.9467392	19.7338257	20.3304291	21.0626526	20.2442646	20.3433113	19.1350098
864	Ig gamma-2B chain C region OS=Rattus norvegicus OX=10116 GN=Igh-1a PE=1 SV=1	Igh-1a	P20761	0.0315828	-0.0661526	16.1822166	17.5637226	16.9073715	17.4236546	17.3192787	16.0100651	16.1840401	18.8281918
865	Ig kappa chain C region, A allele OS=Rattus norvegicus OX=10116 PE=1 SV=1	10116	P01836	2.57476433	-0.831615	19.9184666	20.2113991	20.3441849	19.7322006	21.1049156	20.767292	20.6818581	20.9786453
866	Immunoglobulin-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Igbp1 PE=2 SV=2	Igbp1	O08836	0.34601308	0.80242682	19.0195427	19.0156822	19.6407547	19.7469788	19.7019653	15.6424637	19.6281013	19.2407207
867	Importin 5 OS=Rattus norvegicus OX=10116 GN=Ipo5 PE=1 SV=1	Ipo5	D4A781	1.93302646	-1.1448517	18.0957355	19.2369156	19.1828976	18.760479	19.9533215	20.4791031	19.741663	19.6813469
868	Importin 9 OS=Rattus norvegicus OX=10116 GN=Ipo9 PE=1 SV=2	Ipo9	D4A857	0.49707324	-0.2985005	14.862318	14.9325542	15.1996822	14.1762257	15.2260303	15.0082808	14.6735611	15.4569101
869	Importin subunit alpha OS=Rattus norvegicus OX=10116 GN=LOC100359600 PE=3 SV=1	LOC100359(	M0R7I0	0.81715608	0.89189625	20.7510014	21.4892883	21.293541	19.8338871	20.5095158	19.3633938	19.173357	20.7538662
870	Importin subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Kpnb1 PE=1 SV=1	Kpnb1	F2Z3Q8	0.22893155	0.20808363	18.8428879	19.0558071	18.4303474	18.7709293	18.7179623	17.6293297	18.6487522	19.2715931
871	Inhibitor of kappaB kinase beta, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Ikbkb PE=1 SV=1	Ikbkb	G3V8H5	0.08650225	-0.0563846	21.3834362	21.1965141	21.2763958	20.479538	20.894577	21.167284	21.0489082	21.4506531
872	Inosine-5'-monophosphate dehydrogenase 2 OS=Rattus norvegicus OX=10116 GN=Impdh2 PE=1 SV=1	Impdh2	E9PU28	0.06596153	-0.2534761	21.3943233	22.8713856	16.9810715	22.4414787	20.8483105	21.7657661	21.2660656	20.8220215
873	Inositol polyphosphate-5-phosphatase A OS=Rattus norvegicus OX=10116 GN=Inpp5a PE=1 SV=1	Inpp5a	D3ZZX1	0.11855724	-0.1272798	17.2257328	16.5568008	16.6906052	16.7711792	16.5098743	18.0275288	16.8066254	16.4094086
874	Insulin-like growth factor 2 receptor OS=Rattus norvegicus OX=10116 GN=Igf2r PE=1 SV=1	Igf2r	G3V824	1.68396833	-1.2011981	18.105484	18.6416626	18.4565353	17.0219631	18.9944916	19.3842793	19.0869522	19.5647144
875	Integrin alpha 5 (Mapped) OS=Rattus norvegicus OX=10116 GN=Itga5 PE=1 SV=1	Itga5	A0A0G2K1E	0.36785005	-0.3268285	18.5781116	19.3127232	18.4120045	17.6826191	18.8944626	18.4987011	19.3341637	18.5654449
876	Integrin alpha-7 OS=Rattus norvegicus OX=10116 GN=Itga7 PE=1 SV=2	Itga7	Q63258	0.50966119	-0.2158728	21.83918	21.9358273	21.246006	22.0535469	22.0450344	22.1632195	21.8336525	21.8961449
877	Integrin beta OS=Rattus norvegicus OX=10116 GN=Itgb1 PE=1 SV=1	Itgb1	A0A0G2JSK	0.92550114	-0.2635708	22.7698765	22.9814625	22.5359421	22.9787407	22.9962368	23.371748	23.0192146	22.9331055
878	Integrin beta OS=Rattus norvegicus OX=10116 GN=Itgb3 PE=1 SV=2	Itgb3	M0RCF3	1.83286657	-1.3547256	15.8242579	16.5771351	16.3095284	16.0665913	18.3060074	18.0453281	16.9308586	16.9142208
879	Integrin subunit alpha V OS=Rattus norvegicus OX=10116 GN=Itgav PE=1 SV=3	Itgav	F1LZX9	0.24720057	-0.2709866	17.8138752	17.6866951	17.227211	16.0421867	17.836422	17.7196789	17.2768822	17.0209312
880	Integrin-linked protein kinase OS=Rattus norvegicus OX=10116 GN=Ilk PE=2 SV=1	Ilk	Q99J82	1.35099572	0.87350368	23.7052822	24.6088562	24.1066113	24.5914898	23.1928158	23.0140648	23.1337814	24.1775627
881	Inter alpha-trypsin inhibitor, heavy chain 4 OS=Rattus norvegicus OX=10116 GN=Itih4 PE=1 SV=1	Itih4	Q5EBC0	0.93548362	-0.5405469	19.3058357	19.2539825	18.4059315	19.0143604	19.2522449	19.3156281	19.4172287	20.157196
882	Inter-alpha-trypsin inhibitor heavy chain 2 OS=Rattus norvegicus OX=10116 GN=Itih2 PE=1 SV=3	Itih2	D3ZFH5	0.1700221	0.21621132	18.3441162	17.4429169	17.2521477	16.093626	17.4467411	16.7130966	16.8613663	17.2467575
883	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Rattus norvegicus OX=10116 GN=Itih3 PE=1 SV=3	Itih3	D3ZBS2	0.24770672	-0.5130742	18.401207	17.8690128	18.1426163	15.3215876	18.6577396	18.227747	16.6222363	18.2789974
884	Interferon gamma-induced GTPase OS=Rattus norvegicus OX=10116 GN=Igtp PE=1 SV=2	Igtp	F7F469	0.8004313	0.67287302	18.3378086	18.6608162	16.957943	17.9388142	17.0387764	17.8670063	17.0471935	17.2509136
885	Interferon-induced GTP-binding protein Mx1 OS=Rattus norvegicus OX=10116 GN=Mx1 PE=1 SV=1	Mx1	P18588	0.11742175	0.2418561	15.5696964	16.644352	16.1772175	17.9887524	15.1569223	15.7040529	16.8709946	17.680624
886	Interferon-induced GTP-binding protein Mx2 OS=Rattus norvegicus OX=10116 GN=Mx2 PE=2 SV=1	Mx2	P18589	0.28314435	1.22625422	20.8718472	16.2635593	13.8033772	20.3393898	17.2285347	16.7955036	14.7874136	17.5617046
887	Interferon-induced transmembrane protein 3 OS=Rattus norvegicus OX=10116 GN=ifitm3 PE=2 SV=1	ifitm3	P26376	0.70276095	-0.52317	18.3768902	19.1340904	18.3384247	17.6134071	19.0784111	18.3472004	19.169426	18.9604549
888	IQ motif containing GTPase activating protein 1 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Iqgap1 PE=1 SV=1	Iqgap1	G3V7Q7	0.11195469	0.10676622	21.2169876	21.3112812	20.7787933	20.6121387	20.8597889	20.6699123	20.2422714	21.7201633
889	IQ motif-containing GTPase-activating protein 2 OS=Rattus norvegicus OX=10116 GN=Iqgap2 PE=1 SV=3	Iqgap2	F1LW74	0.9995807	0.4121995	19.7709637	20.0743523	20.2050152	19.6141968	19.8084164	19.1467609	19.30896	19.7515926
890	Isochorismatase domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Isoc2 PE=2 SV=1	Isoc2	Q5U3Z3	1.51754505	2.38415742	19.2529755	18.9762878	18.5905991	18.8602962	16.5343628	18.8126602	15.9375286	14.8589773
891	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Idh3B PE=2 SV=1	Idh3B	Q68FX0	0.6599139	0.1833353	27.8138866	27.5974045	27.5729923	27.3933067	27.458704	27.4110966	27.1408138	27.6336346
892	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Idh3g PE=1 SV=2	Idh3g	P41565	0.14460511	-0.158298	20.0232372	19.8116264	18.2392159	19.6340122	19.6259613	19.2896729	19.7109318	19.7147179
893	Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Idh3a PE=1 SV=2	Idh3a	F1LNF7	0.5858969	0.23450136	27.5820637	27.5909805	27.3163509	26.9217663	27.1921062	27.2022858	26.8111076	27.2676563
894	Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Idh3g PE=1 SV=1	Idh3g	Q5XIJ3	0.8802799	0.22849369	27.2159328	27.0768394	27.0636349	26.7759628	26.8043404	26.7505245	26.6091194	27.0544109
895	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Rattus norvegicus OX=10116 GN=Idh1 PE=1 SV=1	Idh1	P41562	0.24485327	0.16461325	18.9914799	19.2835636	19.2468052	19.2664242	18.7913418	19.3242493	19.5965557	18.4176731
896	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus OX=10116 GN=Idh2 PE=1 SV=2	Idh2	P56574	1.02881447	0.32700253	29.460947	30.0983849	29.4477825	29.5861492	29.3832378	29.1768475	29.2794418	29.4457264
897	Isoleucine-tRNA synthetase (Predicted) OS=Rattus norvegicus OX=10116 GN=Iars PE=1 SV=2	Iars	F1LS86	0.52856092	0.23776627	20.0550957	20.4277058	19.7115459	20.1971493	19.8161163	20.274828	19.7283382	19.6211491
898	Isoleucyl-tRNA synthetase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Iars2 PE=1 SV=1	Iars2	A0A0G2K26	0.16843496	0.18855381	21.0339165	20.2602806	21.6514397	20.1108437	20.5405197	21.2623692	20.1383553	20.361021
899	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ivd PE=1 SV=2	Ivd	P12007	1.28439333	0.48682404	26.7575111	26.5933151	26.0547504	26.223444	26.070097	25.6464691	25.8014679	26.1636906
900	IST1 homolog OS=Rattus norvegicus OX=10116 GN=Ist1 PE=2 SV=1	Ist1	Q568Z6	0.12672631	-0.2166159	16.3855286	17.4451084	16.1635151	16.3413868	17.8459454	17.259243	15.1884165	16.9083977
901	Junction plakoglobin OS=Rattus norvegicus OX=10116 GN=Jup PE=1 SV=1	Jup	Q6P0K8	0.24298885	0.28211832	19.497448	19.2810535	19.7247982	21.137619	19.6223621	20.0952892	19.053957	19.7408371
902	Junctophilin-2 OS=Rattus norvegicus OX=10116 GN=Jph2 PE=1 SV=1	Jph2	Q2PS20	0.2088739	-0.1219459	21.6828232	21.6550999	20.9651165	21.9482002	21.5794449	21.4867496	21.7323627	21.9404659
903	Kelch-like family member 31 OS=Rattus norvegicus OX=10116 GN=Klhl31 PE=4 SV=1	Klhl31	D3ZLT6	1.16820823	0.7130785	21.5028667	21.5888824	21.1770668	20.5371265	20.682663	20.1130638	20.1567497	21.001152
904	Kelch-like protein 22 OS=Rattus norvegicus OX=10116 GN=Klhl22 PE=1 SV=1	Klhl22	A0A0G2KA(	0.32321872	0.35148096	19.4440479	19.461689	18.3844604	17.8288918	18.4773159	17.9815388	18.2352009	19.0191097
905	Kelch-like protein 24 OS=Rattus norvegicus OX=10116 GN=Klhl24 PE=1 SV=1	Klhl24	Q56A24	0.20067339	0.1310606	18.5962925	18.2333431	17.6606026	17.8080292	18.1136684	17.9975815	17.5121861	18.150589
906	Kelch-like protein 41 OS=Rattus norvegicus OX=10116 GN=Klhl41 PE=1 SV=1	Klhl41	Q9ER30	0.14302585	0.19288445	20.5276031	18.8112717	18.8014374	18.7113247	19.0185623	19.2242775	18.2963791	19.5408802
907	Keratin 16 OS=Rattus norvegicus OX=10116 GN=Krt16 PE=1 SV=1	Krt16	Q6IFU9	0.62455351	1.40933657	19.5007248	19.7686386	18.9651394	23.4530525	18.5938244	19.6893692	18.3412724	19.4257431
908	Keratin 71 OS=Rattus norvegicus OX=10116 GN=Krt71 PE=2 SV=2	Krt71	D3ZXB7	0.01666577	0.027807	15.932497	16.0647945	15.6003351	17.7805119	15.7963724	16.5614491	15.9069185	17.0021706
909	Keratin 76 OS=Rattus norvegicus OX=10116 GN=Krt76 PE=2 SV=1	Krt76	Q6IFZ5	0.65669385	1.25923824	18.4089394	18.1105194	18.7039394	17.8704929	17.7166309	17.9173698	14.3163185	18.1066189
910	Keratin, type I cytoskeletal 10 OS=Rattus norvegicus OX=10116 GN=Krt10 PE=1 SV=1	Krt10	A0A0G2K2V	0.05326945	0.06690693	23.7512474	24.0594196	23.5310249	25.3438168	23.7318687	24.4351273	23.8820324	24.3688526
911	Keratin, type I cytoskeletal 14 OS=Rattus norvegicus OX=10116 GN=Krt14 PE=2 SV=1	Krt14	Q6IFV1	0.15049347	0.28944826	23.4460106	23.8596306	22.9379654	26.1473198	23.4631748	24.1649837	23.4864178	24.118557
912	Keratin, type I cytoskeletal 17 OS=Rattus norvegicus OX=10116 GN=Krt17 PE=1 SV=1	Krt17	Q6IFU8	0.48477589	1.47216415	19.5353203	19.1967258	18.6410999	24.4631824	19.2589722	19.7107124	18.3985004	18.5794868
913	Keratin, type I cytoskeletal 42 OS=Rattus norvegicus OX=10116 GN=Krt42 PE=3 SV=1	Krt42	Q6IFU7	0.10267423	0.41699839	18.2928352	18.0029736	16.5269508	22.711813	16.7826138	19.5056934	17.9805679	19.5977039
914	Keratin, type II cytoskeletal 1 OS=Rattus norvegicus OX=10116 GN=Krt1 PE=1 SV=1	Krt1	A0A0G2JST	0.01141993	0.01336861	23.2788925	23.5206642	22.7037354	24.1710148	22.9276409	23.9251404	23.0245304	23.7435207
915	Keratin, type II cytoskeletal 2 epidermal OS=Rattus norvegicus OX=10116 GN=Krt2 PE=3 SV=1	Krt2	Q6IG02	0.07098468	-0.0681334	22.1925545	22.1290321	21.9335918	23.0050125	21.9706345	23.0886879	22.1106319	22.3627701
916	Keratin, type II cytoskeletal 5 OS=Rattus norvegicus OX=10116 GN=Krt5 PE=1 SV=1	Krt5	A0A0G2K50	0.0134068	0.0141511	25.4975891	25.5103951	25.1231632	26.6233215	25.3645821	26.0363064	25.5204086	25.7765675
917	Keratin, type II cytoskeletal 5 OS=Rattus norvegicus OX=10116 GN=Krt5 PE=1 SV=1	Krt5	Q6P6Q2	0.26389813	0.62539244	21.6169186	21.2882195	20.2900505	24.7468109	21.1742611	21.7845917	21.1312447	21.3503323
918	Keratin, type II cytoskeletal 6A OS=Rattus norvegicus OX=10116 GN=Krt6a PE=1 SV=1	Krt6a	Q4FZU2	0.00723111	0.00882006	22.6233921	22.6709862	21.9831505	23.7096634	22.3470783	23.1659775	22.456913	22.9819431
919	Keratin, type II cytoskeletal 73 OS=Rattus norvegicus OX=10116 GN=Krt73 PE=1 SV=1	Krt73	Q6IG03	0.09102638	-0.0918031	23.3845901	23.2188301	22.7625904	24.1112061	23.0460548	24.0344448	23.0965137	23.6674156
920	Keratin, type II cytoskeletal 75 OS=Rattus norvegicus OX=10116 GN=Krt75 PE=1 SV=1	Krt75	A0A0H2UH	0.34191222	1.31970501	17.3221703	19.6415558	17.6250477	24.3786907	18.3558731	19.0005169	17.6803761	18.6518784
921	Keratin, type II cytoskeletal 8 OS=Rattus norvegicus OX=10116 GN=Krt8 PE=1 SV=3	Krt8	Q10758	0.35018721	0.58854151	19.6627426	20.7970963	19.8365536	22.360527	20.0249176	21.1169968	19.8099747	19.3508644
922	Ketimine reductase mu-crystallin OS=Rattus norvegicus OX=10116 GN=Crym PE=1 SV=1	Crym	Q9QYU4	0.07381079	0.0636096	18.769846	17.7080727	18.9288559	18.7666512	18.6084862	18.6274471	18.0949631	18.5880909
923	KH domain-containing, RNA-binding, signal transduction-associated protein 2 OS=Rattus norvegicus OX=10116 GN=Khdrbs2 PE=1 SV=1	Khdrbs2	Q920F3	0.00076677	-0.0004759	17.6419926	17.533947	17.1371632	17.4292431	17.5674191	17.0881157	17.2214241	17.8672905
924	Kinectin 1 OS=Rattus norvegicus OX=10116 GN=Ktn1 PE=1 SV=2	Ktn1	D4A4Z9	0.09512479	-0.0975633	16.5699234	17.0033665	16.635603	17.1383953	16.630003	16.0968838	17.5712261	17.4394283
925	Kinesin light chain 4 OS=Rattus norvegicus OX=10116 GN=Klc4 PE=1 SV=1	Klc4	Q5PQM2	1.84611245	-0.4164171	20.3724613	20.423975	20.8453083	20.6316586	20.8856907	21.1079044	21.0544548	20.8910217
926	Kinesin-1 heavy chain OS=Rattus norvegicus OX=10116 GN=Kif5b PE=1 SV=1	Kif5b	Q2PQA9	0.7785153	0.25600386	21.3087769	21.5360489	21.0500145	20.9417648	20.8703194	20.734417	21.0613976	21.1464558
927	Kinesin-like protein KIF1B OS=Rattus norvegicus OX=10116 GN=Kif1b PE=1 SV=2	Kif1b	O88658	1.20832808	1.70748377	17.9256535	17.923502	16.5721111	17.8646469	15.8204603	13.9966536	16.7202549	16.9186096
928	Kininogen-1 OS=Rattus norvegicus OX=10116 GN=Kng1 PE=2 SV=1	Kng1	P08934	0.36442099	0.44769526	19.7501106	20.6188755	19.8602886	18.4900818	19.3468723	19.3415051	18.4101753	19.8300228
929	KN motif and ankyrin repeat domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Kank2 PE=1 SV=2	Kank2	D3ZD05	0.16054353	-0.4617538	18.2611504	18.148632	17.8061161	13.7326126	17.6411572	16.8948479	17.4759998	17.7835217
930	Kynurenine--oxoglutarate transaminase 3 OS=Rattus norvegicus OX=10116 GN=Kyat3 PE=2 SV=1	Kyat3	Q58FK9	0.05582847	-0.0763483	17.942894	18.6525784	19.2452316	17.4536247	18.8049908	18.308382	17.6480751	18.838274
931	L-2-hydroxyglutarate dehydrogenase OS=Rattus norvegicus OX=10116 GN=L2hgdh PE=1 SV=1	L2hgdh	D3ZVS2	0.86162807	0.34526062	22.444273	22.4253426	21.9552689	22.3071079	21.942009	21.6050644	21.8116512	22.3922253
932	Lactadherin OS=Rattus norvegicus OX=10116 GN=Mfge8 PE=2 SV=1	Mfge8	P70490	0.54540149	-0.2598038	20.628273	21.0235023	20.291647	21.1963291	21.1103935	20.9918919	21.2461166	20.8305645
933	Lactamase, beta OS=Rattus norvegicus OX=10116 GN=Lactb PE=1 SV=1	Lactb	D3ZFJ6	0.83423564	-1.2046926	17.1965427	17.5255547	17.5957355	14.7924452	18.0057869	17.2735558	18.0239239	18.625782
934	Lactate dehydrogenase D OS=Rattus norvegicus OX=10116 GN=Ldhd PE=1 SV=1	Ldhd	A0A0G2K1V	0.24700142	0.15658379	23.9889126	23.068388	23.8062153	23.1448727	23.2447033	23.6565628	23.1287403	23.352047

935	Lactoylglutathione lyase OS=Rattus norvegicus OX=10116 GN=Glo1 PE=1 SV=3	Glo1	Q6P7Q4	0.23384909	0.16386175	18.7582874	18.8709507	18.795023	18.8710861	17.8314934	18.845705	18.8716679	19.0910339
936	Laforin OS=Rattus norvegicus OX=10116 GN=Epm2a PE=2 SV=2	Epm2a	Q91XQ2	0.17324172	0.19285059	17.530508	17.7376556	18.2838345	17.7293987	18.1238766	17.8314953	18.1120892	16.4425335
937	Laminin subunit alpha 5 OS=Rattus norvegicus OX=10116 GN=Lama5 PE=1 SV=2	Lama5	F1MAN8	0.79186779	0.425282	20.257143	19.5573711	19.6424828	19.8963108	19.9626064	19.0916233	19.0498905	19.5480595
938	Laminin subunit beta-2 OS=Rattus norvegicus OX=10116 GN=Lamb2 PE=1 SV=1	Lamb2	M0R6K0	0.01406938	-0.0069633	19.5453358	20.1403961	19.5240936	19.7787552	19.6842346	19.9803257	19.5737553	19.7781181
939	Laminin subunit gamma 1 OS=Rattus norvegicus OX=10116 GN=Lamc1 PE=1 SV=1	Lamc1	F1MAA7	0.25408662	-0.1824336	20.3295822	20.3693485	20.444355	21.1000137	20.6357975	20.7456837	21.3535271	20.2380257
940	Large proline-rich protein BAG6 OS=Rattus norvegicus OX=10116 GN=Bag6 PE=1 SV=2	Bag6	Q6MG49	0.61658132	0.40189123	21.5937786	20.7343063	20.8434086	20.817522	20.5629234	20.1853542	20.3685493	21.2646236
941	LDL receptor-related protein 1 OS=Rattus norvegicus OX=10116 GN=Lrp1 PE=1 SV=1	Lrp1	G3V928	1.23511191	-0.3423615	18.8280334	19.2623596	19.2048626	19.1740932	19.4399948	19.3152142	19.7736282	19.3099575
942	Lectin, mannose-binding 2 OS=Rattus norvegicus OX=10116 GN=Lman2 PE=1 SV=1	Lman2	B0BNG3	0.5613531	-0.3874722	18.8459988	18.803606	19.5079613	19.7464714	19.1364899	19.3658962	20.0805569	19.8709831
943	Legumain OS=Rattus norvegicus OX=10116 GN=Lgmn PE=1 SV=1	Lgmn	Q5PPG2	0.06588003	-0.1269393	18.8907661	18.5473785	16.539093	17.6894112	18.4628372	17.6286201	19.0414257	17.041523
944	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Lrpprc PE=1 SV=2	Lrpprc	F1LM33	1.88977888	0.75096655	23.2305832	23.7428875	23.7017765	23.2114544	22.731308	22.7691059	22.3057423	23.0766792
945	Leucine-rich repeat-containing 10 OS=Rattus norvegicus OX=10116 GN=LOC100911101 PE=1 SV=1	LOC100911	D4AAU8	0.27917181	0.33110619	21.6125126	20.6725388	21.1743698	19.793541	20.3510838	20.3727322	19.8900185	21.314703
946	Leucine-rich repeat-containing 14B OS=Rattus norvegicus OX=10116 GN=Lrrc14b PE=4 SV=1	Lrrc14b	D3ZJ80	0.79815122	-0.4627261	17.2274227	18.0594273	18.1092796	18.0712585	17.8150978	18.6371841	18.2490826	18.6169281
947	Leucine-rich repeat-containing protein 59 OS=Rattus norvegicus OX=10116 GN=Lrrc59 PE=1 SV=1	Lrrc59	Q5RJR8	0.33058092	-0.2442484	15.5975456	16.3640652	16.4779491	16.8327618	16.3430195	16.521452	17.0750656	16.3097782
948	Leucyl-cystinyl aminopeptidase OS=Rattus norvegicus OX=10116 GN=Lnpep PE=1 SV=1	Lnpep	P97629	0.24907882	-0.1333876	20.3965778	20.7556477	20.0863514	20.2775993	20.2647495	20.8334064	20.7643318	20.1872387
949	Leucyl-tRNA synthetase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Lars2 PE=1 SV=1	Lars2	A0A0G2K9E	0.12346256	-0.3295867	18.5042133	19.1169357	15.6793547	19.1466064	18.8608913	19.275198	16.77668	18.8526878
950	Leukocyte surface antigen CD47 OS=Rattus norvegicus OX=10116 GN=Cd47 PE=1 SV=1	Cd47	P97829	0.66184174	-0.3289123	18.700182	19.5931549	19.164938	19.1514473	19.2234039	19.9258404	19.4370365	19.3390903
951	LIM and cysteine-rich domains 1 OS=Rattus norvegicus OX=10116 GN=Lmcd1 PE=1 SV=1	Lmcd1	Q6AYF2	0.27508002	-0.3994961	19.7683182	19.3946743	17.0909634	18.6057243	19.4005642	18.9929676	19.0404968	19.0236359
952	LIM and senescent cell antigen-like-containing domain protein OS=Rattus norvegicus OX=10116 GN=Lims1 PE=1 SV=1	Lims1	C0KUC6	0.65220359	0.40229559	22.4265232	23.1122799	21.7516689	22.6536007	21.9765644	21.983305	22.039259	22.335762
953	LIM and senescent cell antigen-like-containing domain protein OS=Rattus norvegicus OX=10116 GN=Lims2 PE=1 SV=1	Lims2	A0A0G2KAI	0.08619026	-0.2003622	17.6875076	17.7863426	14.5991554	17.719038	16.9566154	17.3161564	17.9008865	16.4198341
954	LIM domain-binding 3 OS=Rattus norvegicus OX=10116 GN=Ldb3 PE=1 SV=1	Ldb3	A0A096MJ0	0.27442484	-0.1917577	23.8723984	23.2501888	22.8405857	22.9860573	23.5643959	23.5455875	22.9067059	23.6995716
955	LIM domain-binding 3 OS=Rattus norvegicus OX=10116 GN=Ldb3 PE=1 SV=1	Ldb3	A0A096MKI	0.39643073	0.27433681	19.8747425	19.3164463	18.6342545	19.3635464	19.1145573	18.668026	19.4383526	18.8707066
956	Lipin 1 OS=Rattus norvegicus OX=10116 GN=Lpin1 PE=1 SV=1	Lpin1	A0A0G2JW0	0.02102655	-0.0390472	17.2863407	16.4791508	16.8444309	14.8365488	16.7131748	16.0438461	15.6683474	17.1772919
957	Lipoprotein lipase OS=Rattus norvegicus OX=10116 GN=Lpl PE=1 SV=1	Lpl	Q06000	0.06344288	-0.0561533	21.6892891	21.1304226	20.6242085	21.1134529	20.8448372	20.8723335	21.2473698	21.8174458
958	Lipoyl synthase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Lias PE=2 SV=1	Lias	Q5XIH4	0.03232631	-0.0501223	18.1813412	18.563158	18.180687	16.4142494	18.0362377	17.2176056	18.0172806	18.2688007
959	L-lactate dehydrogenase A chain OS=Rattus norvegicus OX=10116 GN=Ldha PE=1 SV=1	Ldha	P04642	0.2867421	-0.0660295	24.29105	24.1881657	24.1573944	24.4276581	24.2711906	24.484478	24.154892	24.4178257
960	L-lactate dehydrogenase B chain OS=Rattus norvegicus OX=10116 GN=Ldhb PE=1 SV=2	Ldhb	P42123	0.03420313	-0.0083075	26.5965691	26.3141975	26.4859447	26.6990662	26.545723	26.5631084	26.4902802	26.5298958
961	LOC682908 protein OS=Rattus norvegicus OX=10116 GN=Rcc1 PE=1 SV=1	Rcc1	B1H227	0.14481822	-0.3332651	17.0773716	14.4206505	16.9599895	15.7980499	16.9244747	16.6084671	14.615098	17.441082
962	LOC683667 protein OS=Rattus norvegicus OX=10116 GN=Sri PE=1 SV=1	Sri	B0BNJ1	0.17647683	0.36922312	18.5199852	17.364399	16.0557861	16.7433872	14.9745312	17.133297	17.7743568	17.3244801
963	Lon protease homolog, mitochondrial OS=Rattus norvegicus OX=10116 GN=Lonp1 PE=2 SV=1	Lonp1	Q924S5	0.8181877	0.4544363	26.8611412	26.6626816	27.0557194	26.1648083	26.3994732	26.17276	25.7062378	26.6481342
964	Long-chain fatty acid transport protein 1 OS=Rattus norvegicus OX=10116 GN=Slc27a1 PE=1 SV=1	Slc27a1	Q6GMM8	1.05816519	-0.4665837	20.1692657	20.0344639	20.5608521	20.8684902	21.0584621	20.5908794	21.1206322	20.7294331
965	Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acadl PE=1 SV=1	Acadl	P15650	3.80893254	0.19918633	26.0055428	26.0361195	26.0738201	26.0990238	25.839262	25.8861217	25.8582954	25.8340816
966	Long-chain-fatty-acid--CoA ligase 1 OS=Rattus norvegicus OX=10116 GN=Acsl1 PE=1 SV=1	Acsl1	P18163	0.68742692	-0.2792726	26.3812943	26.5876598	26.853714	27.0977421	26.9880962	27.0336304	27.2999802	26.7157936
967	Low molecular weight phosphotyrosine protein phosphatase OS=Rattus norvegicus OX=10116 GN=Acp1 PE=1 SV=2	Acp1	Z4YNF4	0.04170222	0.03937578	17.8351479	17.5144596	17.5115299	17.8456402	17.6808338	17.8824463	18.2286491	16.7573452
968	LRP16 protein OS=Rattus norvegicus OX=10116 GN=Macrod1 PE=1 SV=1	Macrod1	A0A0G2K5F	1.24039923	0.35965681	23.2493858	23.0653782	23.3592606	22.950573	22.9082184	22.6659908	22.5299606	23.0818005
969	Lumican OS=Rattus norvegicus OX=10116 GN=Lum PE=1 SV=1	Lum	P51886	0.01406723	0.01055956	20.2696552	20.0832958	19.7132378	19.4094429	19.9739132	19.7848625	19.4437752	20.2308426
970	L-xylulose reductase OS=Rattus norvegicus OX=10116 GN=Dcxr PE=1 SV=1	Dcxr	Q920P0	0.43780054	0.20955181	16.8581409	17.3062916	16.6851425	16.3415699	16.4424648	16.6232662	16.5076008	16.7796059
971	LYR motif-containing 4 OS=Rattus norvegicus OX=10116 GN=Lyrm4 PE=1 SV=1	Lyrm4	D3ZYM7	0.46285458	0.47124362	16.6405983	16.5106087	16.7878494	16.5355034	16.939106	14.8974218	16.0686626	16.6843948
972	Lys-63-specific deubiquitinase BRCC36 OS=Rattus norvegicus OX=10116 GN=Brcc3 PE=2 SV=1	Brcc3	B2RYM5	0.51083167	0.47398376	20.7298088	20.300951	20.010601	21.9112339	20.0437756	20.4354668	20.2581844	20.3192329
973	Lysine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Kars PE=1 SV=1	Kars	Q5XIM7	2.10351553	0.3450098	20.8040962	21.0259056	20.6666679	20.9195576	20.5859318	20.5451908	20.3880215	20.5170441
974	Lysophospholipid acyltransferase 5 OS=Rattus norvegicus OX=10116 GN=Lpcat3 PE=2 SV=1	Lpcat3	Q5FVN0	0.92772549	-0.333499	20.6258259	20.0786057	20.1845703	20.0493469	20.5137711	20.9076061	20.3062439	20.5447235
975	Lysosome membrane protein 2 OS=Rattus norvegicus OX=10116 GN=Scarb2 PE=1 SV=2	Scarb2	P27615	0.03117484	-0.0321503	18.7583294	19.4373112	19.4579678	19.4446659	19.720644	18.4057579	19.7126141	19.3878593
976	Lysosome-associated membrane glycoprotein 1 OS=Rattus norvegicus OX=10116 GN=Lamp1 PE=1 SV=1	Lamp1	P14562	0.5804314	-0.1940999	21.9022579	22.1862698	21.5181561	22.1120892	22.1567364	22.2235088	21.998085	22.1168423
977	Lysosome-associated membrane glycoprotein 2 OS=Rattus norvegicus OX=10116 GN=Lamp2 PE=1 SV=3	Lamp2	P17046	1.19585061	-0.4516754	17.6566353	18.2761116	17.8578434	17.6104984	17.9620533	18.4823055	18.5197239	18.2437077
978	m-AAA protease-interacting protein 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Maip1 PE=2 SV=1	Maip1	Q6AY04	0.22172499	-0.2844815	18.1753254	19.1610355	19.3090725	20.3471527	19.8472881	19.9915867	19.4584045	18.8332329
979	Macrophage migration inhibitory factor OS=Rattus norvegicus OX=10116 GN=Mif PE=1 SV=4	Mif	P30904	0.01445287	-0.0096498	20.2606659	20.8173485	21.2105885	20.7150383	20.6084328	20.6824169	20.6547928	21.0965977
980	Maestro heat-like repeat family member 1 OS=Rattus norvegicus OX=10116 GN=Mroh1 PE=1 SV=1	Mroh1	A0A0G2JV0	1.13868699	0.49766397	20.0758743	19.5915718	19.9932079	19.5881729	19.412199	19.5680599	18.7567081	19.521204
981	MAGUK p55 subfamily member 7 OS=Rattus norvegicus OX=10116 GN=Mpp7 PE=2 SV=2	Mpp7	Q5U2Y3	0.59119842	0.55226231	17.9428272	18.2382412	18.0241585	18.7372398	18.0447617	18.0559006	18.1545086	16.4782467
982	Major prion protein OS=Rattus norvegicus OX=10116 GN=Prnp PE=1 SV=2	Prnp	P13852	0.8599891	-1.862546	18.493	15.1892929	14.9934158	19.0531216	18.7202873	18.5450745	19.3917446	18.5219078
983	Major vault protein OS=Rattus norvegicus OX=10116 GN=Mvp PE=1 SV=1	Mvp	A0A140TAE	0.47744894	0.33972311	22.7292919	22.510828	21.8511391	23.1092377	21.7693558	22.0811558	22.3515854	22.6395073
984	Makorin, ring finger protein, 2 OS=Rattus norvegicus OX=10116 GN=Mkrn2 PE=1 SV=1	Mkrn2	Q5XI23	0.80048482	0.58282089	19.5941906	20.0603733	19.0773582	19.4529991	18.8641319	18.6443958	19.8345051	18.5106049
985	Malate dehydrogenase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Mdh1 PE=1 SV=3	Mdh1	O88989	0.06538413	0.01923895	26.5300484	26.2166023	26.1371307	26.1438828	26.2165241	26.1552715	26.2013054	26.3776073
986	Malate dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mdh2 PE=1 SV=2	Mdh2	P04636	0.87044454	-0.0857143	27.1125984	27.0168304	27.1928291	27.2064781	27.1942368	27.2375164	27.1665764	27.2732639
987	Maleylacetoacetate isomerase OS=Rattus norvegicus OX=10116 GN=Gstz1 PE=1 SV=2	Gstz1	P57113	0.21664865	-0.2869315	18.1608391	19.2049484	18.672514	18.9448376	20.3215542	19.0724697	18.0385628	18.6982784
988	Malic enzyme OS=Rattus norvegicus OX=10116 GN=Me3 PE=3 SV=2	Me3	F1M5N4	0.08772875	-0.0550418	18.7900162	19.2709026	18.7356148	19.2845211	19.3217697	18.9996128	18.6192513	19.3605881
989	Malonyl-CoA decarboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mlycd PE=1 SV=1	Mlycd	Q920F5	0.67008736	0.42985439	18.5763798	17.7061005	18.5614033	17.8858643	17.8441219	17.243927	17.661993	18.2602882
990	Mannan-binding lectin serine protease 1 OS=Rattus norvegicus OX=10116 GN=Masp1 PE=1 SV=1	Masp1	A0A0H2UH	0.02409206	-0.0390816	16.1795883	17.0498714	17.1878433	17.7244415	17.4844303	15.7741089	17.831646	17.2078857
991	Mannose receptor, C type 1 OS=Rattus norvegicus OX=10116 GN=Mrc1 PE=1 SV=3	Mrc1	D3ZD31	0.29035792	-0.1895657	21.433939	22.1716385	21.2695274	21.4115047	21.4006596	21.4977303	22.0702209	22.0762615
992	Mannose-binding protein A OS=Rattus norvegicus OX=10116 GN=Mbl1 PE=1 SV=1	Mbl1	P19999	0.80122975	-0.5312319	19.4743881	19.5212669	19.6098976	18.5383987	19.9066582	19.1895046	20.1120453	20.0606709
993	MAP kinase-activated protein kinase 3 OS=Rattus norvegicus OX=10116 GN=Mapkapk3 PE=2 SV=1	Mapkapk3	Q66H84	0.16819542	-0.0656571	23.0399132	23.5113811	23.4842949	23.4160767	23.5655785	23.6233711	23.3573151	23.1680298
994	Map2k3 protein OS=Rattus norvegicus OX=10116 GN=Map2k3 PE=1 SV=1	Map2k3	B1H230	0.88859443	0.69206715	22.3123474	23.0319214	21.7494984	23.2550945	21.8091469	21.755743	22.4472771	21.5684261
995	MAP7 domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Map7d1 PE=1 SV=1	Map7d1	D4A644	0.02623843	-0.0292563	20.371664	19.5698414	18.9488297	19.656208	19.8259373	19.5141716	19.0785961	20.2448635
996	Mast cell protease 1 OS=Rattus norvegicus OX=10116 GN=Mcpt1 PE=1 SV=3	Mcpt1	P09650	0.1177268	0.10045719	18.4468479	17.7536545	18.0471458	18.6654568	18.2093124	17.6983204	18.7827263	17.8209171
997	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acadm PE=1 SV=1	Acadm	P08503	2.07685214	0.54066563	26.1977329	26.4233761	26.2194309	25.7900391	25.6866417	25.6332684	25.4855537	25.6624527
998	Membrane palmitoylated protein 6 OS=Rattus norvegicus OX=10116 GN=Mpp6 PE=1 SV=1	Mpp6	A0A0G2K4N	0.00057161	0.00034857	21.2630577	20.8084221	20.8536587	20.3688698	20.8572311	21.0518494	20.6429424	20.740591
999	Membrane-associated progesterone receptor component 2 OS=Rattus norvegicus OX=10116 GN=Pgrmc2 PE=1 SV=1	Pgrmc2	Q5XIU9	0.5830306	-0.479311	18.6082439	19.8730011	19.6279583	20.1160431	20.116848	19.9492741	20.518158	19.5582104
1000	Metalloendopeptidase OMA1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Oma1 PE=3 SV=1	Oma1	D3ZS74	0.27808165	-0.1828327	17.6527023	18.5702953	18.8638744	18.5305672	18.6075211	18.4062271	18.7792816	18.5557404
1001	Metalloreductase STEAP4 OS=Rattus norvegicus OX=10116 GN=Steap4 PE=1 SV=1	Steap4	Q4V8K1	0.75044127	-1.1088197	15.5156584	17.854435	15.7025185	16.1631641	16.3321495	18.3783226	18.1176929	16.8428898
1002	Metastasis-associated 1 family, member 2 OS=Rattus norvegicus OX=10116 GN=Mta2 PE=1 SV=1	Mta2	B2GV01	0.17655555	-0.2181876	15.8477602	17.5370216	17.3477669	17.8121452	17.7150917	17.6241245	16.8801899	17.1980381
1003	Metaxin 1 OS=Rattus norvegicus OX=10116 GN=Mtx1 PE=1 SV=1	Mtx1	A0A0G2JU4	2.54548738	-0.3705225	20.1304188	20.0306339	20.0741463	19.8356247	20.4991856	20.3280258	20.3206348	20.4050674
1004	Metaxin 2 OS=Rattus norvegicus OX=10116 GN=Mtx2 PE=1 SV=1	Mtx2	Q5U1Z9	0.99579165	-0.689218	20.9741211	21.7271671	22.4128761	22.3977089	22.5245285	22.5144234	22.855154	22.3746395
1005	Methanethiol oxidase OS=Rattus norvegicus OX=10116 GN=Selenbp1 PE=1 SV=1	Selenbp1	Q8VIF7	0.31678046	-0.1373167	20.117136	20.6603069	20.6880283	20.2888718	20.7001305	20.2984238	20.476368	20.8286877
1006	Methionine aminopeptidase 2 OS=Rattus norvegicus OX=10116 GN=Metap2 PE=1 SV=2	Metap2	P38062	0.09065332	-0.1162801	17.9636555	17.0271168	17.4361916	17.9586239	17.5735874	16.6126957	18.2965794	18.3678455

1007	Methionyl-tRNA synthetase OS=Rattus norvegicus OX=10116 GN=Mars PE=1 SV=1	Mars	D3Z941	0.62329701	0.50566816	20.0054321	20.2249374	19.4429398	18.8097229	19.1624565	19.5039501	18.4867153	19.3072376
1008	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mccc2 PE=2 SV=1	Mccc2	Q5XIT9	0.74742749	0.28699207	27.4142265	26.9250431	27.3015118	26.7930489	26.9590206	27.0504036	26.52775	26.7486877
1009	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mccc1 PE=1 SV=1	Mccc1	F1LP30	0.98602653	0.32125425	27.5238323	27.2117519	27.4177837	27.0674858	27.1297379	27.2454357	26.6430454	26.9176178
1010	Methylenetetrahydrofolate dehydrogenase (NADP+-dependent) 1-like OS=Rattus norvegicus OX=10116 GN=Mthfd1l PE=1 SV=1	Mthfd1l	B2GUZ3	0.47545279	0.48905516	19.8413582	19.9852543	20.1455898	18.8530788	19.8947144	18.630146	18.5460491	19.798151
1011	Methylglutaconyl-CoA hydratase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Auh PE=1 SV=2	Auh	F1LU71	0.9660441	-0.2198424	20.5116787	20.6672039	20.4647007	20.7156563	20.8095512	20.8650913	21.0214882	20.5424786
1012	Methylmalonyl CoA mutase OS=Rattus norvegicus OX=10116 GN=Mmut PE=1 SV=2	Mmut	D3ZKG1	0.89644398	0.7156105	19.5161533	20.1700592	18.5582008	19.4457016	18.8184986	19.3034401	18.4643688	18.2413654
1013	Methylthioribose-1-phosphate isomerase OS=Rattus norvegicus OX=10116 GN=Mri1 PE=1 SV=1	Mri1	Q5HZE4	0.96323146	0.72824717	21.8326569	21.9278011	22.3708649	21.2917957	21.852623	21.0033245	20.3342686	21.3199139
1014	Methyltransferase like 7A, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Mettl7a PE=1 SV=1	Mettl7a	Q3KRE2	1.22067473	-1.4240508	17.6903095	17.1555023	17.0110207	15.027195	18.0274048	17.9626904	17.8581352	18.7320004
1015	Methyltransferase-like 15 OS=Rattus norvegicus OX=10116 GN=Mettl15 PE=1 SV=1	Mettl15	F7F172	1.47263317	0.51565933	19.5555363	19.0123291	19.4945412	19.145647	18.7081738	19.1754036	18.6984749	18.563364
1016	MICOS complex subunit Mic10 OS=Rattus norvegicus OX=10116 GN=Minos1 PE=3 SV=1	Minos1	B2RYW8	0.30963793	0.16060448	22.0141373	21.751976	21.687851	21.1484737	21.5970917	21.4054832	21.7602272	21.1972179
1017	MICOS complex subunit MIC60 OS=Rattus norvegicus OX=10116 GN=Immt PE=1 SV=1	Immt	A0A0G2JVH	0.69084243	-0.3085055	25.714859	25.9970055	26.3555107	26.5193958	26.4285202	26.4522476	26.7608299	26.1791954
1018	MICOS complex subunit OS=Rattus norvegicus OX=10116 GN=Apoo PE=1 SV=2	Apoo	M0R7V3	0.96460221	-0.4219794	22.1570072	22.6027603	22.8093166	22.9101696	23.1005173	22.9754848	23.4055729	22.6855965
1019	MICOS complex subunit OS=Rattus norvegicus OX=10116 GN=Apool PE=1 SV=1	Apool	Q5U1W6	0.40049948	-0.2590394	21.5463715	21.8403492	22.4067039	22.5435619	22.2472687	22.3221836	22.7832794	22.0204124
1020	MICOS complex subunit OS=Rattus norvegicus OX=10116 GN=Chchd3 PE=1 SV=1	Chchd3	D3ZUX5	0.68300826	-0.3498034	24.0088921	24.190033	24.5413818	24.8025322	24.7298603	24.697567	25.1787338	24.3358917
1021	Microsomal glutathione S-transferase 1 OS=Rattus norvegicus OX=10116 GN=Mgst1 PE=1 SV=3	Mgst1	P08011	0.74055154	-0.5473499	16.0881062	16.2404671	16.6653728	17.4290943	17.3461933	17.0576382	17.5745926	16.634016
1022	Microsomal glutathione S-transferase 3 OS=Rattus norvegicus OX=10116 GN=Mgst3 PE=1 SV=1	Mgst3	D4ADS4	1.20829794	-0.4437318	22.1468563	22.6232777	22.8416615	22.5156746	22.6508751	23.0257149	23.2739563	22.9518509
1023	Microtubule-associated protein 1A OS=Rattus norvegicus OX=10116 GN=Map1a PE=1 SV=1	Map1a	A0A0G2K5C	1.29402281	0.35365486	22.4819489	22.3757668	22.0094967	22.4347935	21.9264488	22.1271343	22.1195126	21.7142906
1024	Microtubule-associated protein 1B OS=Rattus norvegicus OX=10116 GN=Map1b PE=1 SV=3	Map1b	P15205	0.14594352	0.16188335	17.8983669	19.1092644	17.8198872	18.8154335	18.215826	17.9357777	19.020319	17.8234959
1025	Microtubule-associated protein 4 OS=Rattus norvegicus OX=10116 GN=Map4 PE=1 SV=1	Map4	Q5M7W5	0.21178394	-0.1703382	21.2498341	20.5178146	20.0356407	20.3044052	20.204361	20.740799	20.7315845	21.1123028
1026	Microtubule-associated protein RP/EB family member 2 OS=Rattus norvegicus OX=10116 GN=Mapre2 PE=1 SV=1	Mapre2	Q3B8Q0	0.30348562	0.31489372	20.6423225	21.0475521	20.9100609	19.1877537	19.9964046	20.1111832	20.0528126	20.3677139
1027	Microtubule-associated serine/threonine kinase family member 4 OS=Rattus norvegicus OX=10116 GN=Mast4 PE=1 SV=2	Mast4	M0R3L1	0.18524406	0.12443256	20.0428543	19.1857281	19.2366714	18.8218689	19.2393875	19.2276192	19.0414028	19.280983
1028	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Rattus norvegicus OX=10116 GN=Slc25a11 PE=1 SV=1	Slc25a11	G3V6H5	1.25532946	-0.4270329	24.3938541	24.8667259	24.9424915	25.0104713	25.3048649	25.1625729	25.4969139	24.9573231
1029	Mitochondrial amidoxime reducing component 2 OS=Rattus norvegicus OX=10116 GN=Marc2 PE=1 SV=2	37316	D3Z900	0.5361012	-0.3318319	18.629076	18.6705647	18.203619	18.0787983	18.5306282	19.2690144	18.9592438	18.1504993
1030	Mitochondrial antiviral-signaling protein OS=Rattus norvegicus OX=10116 GN=Mavs PE=1 SV=1	Mavs	Q66HG9	0.21564799	-0.2346849	19.1696911	19.2864895	20.0699501	19.9551773	19.9954395	18.9889812	20.7676334	19.6679935
1031	Mitochondrial carnitine/acylcarnitine carrier protein OS=Rattus norvegicus OX=10116 GN=Slc25a20 PE=1 SV=1	Slc25a20	P97521	0.23510948	-0.1499596	23.7677631	24.0773048	24.3196068	24.7555752	24.3859253	24.4184494	24.7278595	23.987854
1032	Mitochondrial carrier 1 OS=Rattus norvegicus OX=10116 GN=Mtch1 PE=1 SV=1	Mtch1	B0BN30	0.14176068	-0.1562028	18.6256142	19.0864944	18.5237885	19.6677742	19.4477348	19.0223866	19.7862034	18.2721577
1033	Mitochondrial carrier 2 OS=Rattus norvegicus OX=10116 GN=Mtch2 PE=1 SV=1	Mtch2	A0A0G2K45	0.73276273	-0.4488363	22.2048321	22.9516678	23.1651497	23.4237118	23.2808056	23.3936176	23.7780323	23.0882511
1034	Mitochondrial coenzyme A transporter SLC25A42 OS=Rattus norvegicus OX=10116 GN=Slc25a42 PE=1 SV=1	Slc25a42	B1H271	0.03561735	0.02799606	19.198246	18.1974945	19.2988873	19.2510109	19.1253147	18.846426	18.9957733	18.8661404
1035	Mitochondrial elongation factor 2 OS=Rattus norvegicus OX=10116 GN=Mief2 PE=1 SV=2	Mief2	D3ZS35	0.02828421	0.05497313	18.2681961	16.6647282	18.3024082	18.2948284	18.4591656	18.2044373	16.2501755	18.3964901
1036	Mitochondrial fission 1 protein OS=Rattus norvegicus OX=10116 GN=Fis1 PE=1 SV=1	Fis1	P84817	1.1457865	-0.4430833	22.1385651	22.1616497	22.2809238	21.5846233	22.465416	22.282629	22.8573399	22.3327103
1037	Mitochondrial fission process 1 OS=Rattus norvegicus OX=10116 GN=Mtfp1 PE=1 SV=1	Mtfp1	Q5XIG9	0.68548743	-0.4085107	19.4951839	20.5056686	20.2393303	20.7601662	20.7897129	20.7155609	20.7434444	20.3856735
1038	Mitochondrial import inner membrane translocase subunit Tim10 B OS=Rattus norvegicus OX=10116 GN=Timm10b PE=1 SV=1	Timm10b	A0A096MK4	0.04475901	-0.0660553	16.6941261	16.6394997	16.8210621	18.2972984	17.0319405	16.3264313	17.8254585	17.5323772
1039	Mitochondrial import inner membrane translocase subunit Tim10 OS=Rattus norvegicus OX=10116 GN=Timm10 PE=3 SV=1	Timm10	P62074	0.76027439	-0.496685	18.9895763	19.4437294	18.7697315	19.779808	19.9144955	19.8760948	20.1051598	19.0738354
1040	Mitochondrial import inner membrane translocase subunit Tim13 OS=Rattus norvegicus OX=10116 GN=Timm13 PE=3 SV=1	Timm13	P62076	0.09494132	-0.0263395	22.1565933	22.3670406	22.1399441	22.5139637	22.3501472	22.257925	22.4412346	22.233593
1041	Mitochondrial import inner membrane translocase subunit Tim17-A OS=Rattus norvegicus OX=10116 GN=Timm17a PE=2 SV=1	Timm17a	O35092	0.77133729	-1.2491908	15.1855068	17.9611244	18.1419334	16.6718311	17.056181	18.4937496	18.9786873	18.4285412
1042	Mitochondrial import inner membrane translocase subunit Tim21 OS=Rattus norvegicus OX=10116 GN=Timm21 PE=2 SV=1	Timm21	Q5U2X7	0.60514947	-0.3940744	20.6709404	20.7687759	21.3888893	21.1782246	21.7947235	21.2266445	21.8197689	20.741991
1043	Mitochondrial import inner membrane translocase subunit Tim23 OS=Rattus norvegicus OX=10116 GN=Timm23 PE=2 SV=1	Timm23	O35093	2.02598534	-1.2134309	17.4772701	17.4832249	18.2090969	17.0204105	18.917532	18.2248421	19.2176132	18.6837387
1044	Mitochondrial import inner membrane translocase subunit TIM44 OS=Rattus norvegicus OX=10116 GN=Timm44 PE=1 SV=1	Timm44	G3V640	0.27189108	-0.1188712	22.6922092	22.6065197	22.7144604	23.1915054	22.7878971	23.0889931	23.1612644	22.642025
1045	Mitochondrial import inner membrane translocase subunit Tim8 A OS=Rattus norvegicus OX=10116 GN=Timm8a PE=1 SV=1	Timm8a	Q9WVA1	0.35280991	-0.1817417	20.271431	20.8442154	20.8187809	21.0744076	20.9899654	20.8047447	21.3020248	20.6390667
1046	Mitochondrial import inner membrane translocase subunit Tim8 B OS=Rattus norvegicus OX=10116 GN=Timm8b PE=3 SV=1	Timm8b	P62078	0.49302498	0.29815006	20.479805	20.0814686	19.5572834	20.2654114	19.8047771	20.0726738	20.0641842	19.249733
1047	Mitochondrial import inner membrane translocase subunit Tim9 OS=Rattus norvegicus OX=10116 GN=Timm9 PE=1 SV=3	Timm9	Q9WV97	0.82011465	-0.4150214	20.2248135	20.3748341	20.0224419	21.0600986	20.7563362	20.720747	21.1762161	20.6889744
1048	Mitochondrial import receptor subunit TOM20 homolog OS=Rattus norvegicus OX=10116 GN=Tomm20 PE=1 SV=2	Tomm20	Q62760	1.39714513	-1.4269295	16.5148621	18.8706017	17.4580612	17.4869747	19.1767426	18.9935131	19.5344296	18.3335323
1049	Mitochondrial import receptor subunit TOM22 homolog OS=Rattus norvegicus OX=10116 GN=Tomm22 PE=1 SV=1	Tomm22	Q75Q41	0.44505195	-0.2217598	20.2422676	20.7620277	20.8533249	20.9639912	20.7605629	20.9452171	21.3567162	20.6461544
1050	Mitochondrial import receptor subunit TOM34 OS=Rattus norvegicus OX=10116 GN=Tomm34 PE=1 SV=1	Tomm34	Q3KRD5	0.175845	0.28907681	18.3722343	18.2502518	17.4339027	16.3039417	17.5875359	16.1767235	17.2290668	18.2106972
1051	Mitochondrial import receptor subunit TOM40 homolog OS=Rattus norvegicus OX=10116 GN=Tomm40 PE=1 SV=1	Tomm40	G3V8F5	0.26609954	-0.7313192	15.13659	19.210638	18.4493084	19.6340561	19.0537395	17.5650978	19.931942	18.80509
1052	Mitochondrial import receptor subunit TOM70 OS=Rattus norvegicus OX=10116 GN=Tomm70 PE=1 SV=1	Tomm70	Q75Q39	0.86866646	-0.5037436	20.1201134	21.0238876	20.8271809	21.2491989	21.122467	20.9649124	21.6608429	21.487133
1053	Mitochondrial intermediate peptidase OS=Rattus norvegicus OX=10116 GN=Mipep PE=1 SV=1	Mipep	A0A0G2K4T	2.20957017	1.28744268	19.7044888	18.7698898	19.0151062	18.7220974	18.0081577	17.7974586	17.1511421	18.1050529
1054	Mitochondrial intermembrane space import and assembly protein 40 OS=Rattus norvegicus OX=10116 GN=Chchd4 PE=2 SV=1	Chchd4	Q5BJN5	1.00694936	-0.544034	18.7057838	19.5091686	19.7784538	19.7034092	19.9323444	20.0260792	20.2717953	19.6427326
1055	Mitochondrial proton/calcium exchanger protein OS=Rattus norvegicus OX=10116 GN=Letm1 PE=1 SV=1	Letm1	Q5XIN6	0.61125311	-0.3353863	22.6093464	22.9328251	23.2700558	23.423811	23.4018726	23.1633949	23.9171791	23.0951366
1056	Mitochondrial pyruvate carrier 1 OS=Rattus norvegicus OX=10116 GN=Mpc1 PE=3 SV=1	Mpc1	P63031	0.91485457	-0.2598495	22.5088062	22.5599499	22.7118263	23.0058556	23.002861	22.819931	23.1950855	22.8079586
1057	Mitochondrial pyruvate carrier 2 OS=Rattus norvegicus OX=10116 GN=Mpc2 PE=2 SV=1	Mpc2	P38718	1.01485775	-0.189384	23.531332	23.6658878	23.7733612	23.6113415	23.8334141	23.8300705	24.0381527	23.6378212
1058	Mitochondrial ribosomal protein L12 OS=Rattus norvegicus OX=10116 GN=Mrpl12 PE=1 SV=1	Mrpl12	D3ZXF9	0.71657459	0.60335636	20.3426838	19.3215923	19.1109562	19.7779388	19.2963753	19.4169769	19.3078461	18.1185474
1059	Mitochondrial ribosomal protein L19 OS=Rattus norvegicus OX=10116 GN=Mrpl19 PE=1 SV=1	Mrpl19	D4A4A9	0.11127559	0.23838878	18.3687859	17.7704334	17.4374275	15.3616829	15.7239428	17.3644276	17.0813713	17.815033
1060	Mitochondrial ribosomal protein L1-like OS=Rattus norvegicus OX=10116 GN=LOC100359687 PE=1 SV=3	LOC1003596	D3ZFE9	0.18580564	-0.1049089	18.8512039	19.262104	18.8257523	18.6993961	18.4658756	19.19981	19.2525196	19.1398869
1061	Mitochondrial ribosomal protein L28 OS=Rattus norvegicus OX=10116 GN=Mrpl28 PE=1 SV=1	Mrpl28	D3ZJY1	0.11008043	-0.133409	18.3368607	17.3124466	18.39048	16.9361248	18.2631721	18.2268848	17.1469784	17.8725128
1062	Mitochondrial ribosomal protein L45 OS=Rattus norvegicus OX=10116 GN=Mrpl45 PE=1 SV=1	Mrpl45	D4A104	0.69474847	0.4390707	20.4938374	19.627634	20.3722897	19.282238	19.4913864	19.7712059	19.3637238	19.3934002
1063	Mitochondrial ribosomal protein L47 OS=Rattus norvegicus OX=10116 GN=Mrpl47 PE=1 SV=1	Mrpl47	Q3B8R7	0.08438797	0.23124838	18.2586918	17.5710716	18.221405	14.8034573	17.8847866	17.5261784	17.155405	15.3632622
1064	Mitochondrial ribosomal protein L53 OS=Rattus norvegicus OX=10116 GN=Mrpl53 PE=1 SV=1	Mrpl53	B2RYW4	0.40878251	-0.5471888	16.6862736	15.4071264	14.2557507	16.5786896	16.4089603	15.8327379	16.511282	16.363615
1065	Mitochondrial ribosomal protein S11 OS=Rattus norvegicus OX=10116 GN=Mrps11 PE=1 SV=1	Mrps11	D4A040	0.36007388	0.22618008	20.0452137	19.8989544	19.7665672	20.418045	19.787981	20.1660233	19.1566315	20.1134243
1066	Mitochondrial ribosomal protein S12 OS=Rattus norvegicus OX=10116 GN=Mrps12 PE=1 SV=1	Mrps12	D3ZQX3	0.41125195	0.53966355	17.2782421	16.449789	16.9437408	16.8219986	17.2357826	14.7496672	16.4217339	16.9279327
1067	Mitochondrial ribosomal protein S14 OS=Rattus norvegicus OX=10116 GN=Mrps14 PE=1 SV=1	Mrps14	B2RYT4	0.0073109	-0.0077453	19.6329441	18.8925133	18.9452171	18.5258236	19.1665878	19.2169495	18.2156029	19.428339
1068	Mitochondrial ribosomal protein S16 OS=Rattus norvegicus OX=10116 GN=Mrps16 PE=1 SV=1	Mrps16	D4A7X1	2.75719613	1.48426414	17.8276844	17.4222622	16.7178898	17.6882896	16.1126747	15.6485834	15.78372	16.1740913
1069	Mitochondrial ribosomal protein S18B OS=Rattus norvegicus OX=10116 GN=Mrps18b PE=1 SV=1	Mrps18b	F6Q5K7	0.52260722	0.37660027	19.4077969	20.1652203	19.4278469	19.8133526	19.3563499	20.0856743	19.088583	18.7772083
1070	Mitochondrial ribosomal protein S2 OS=Rattus norvegicus OX=10116 GN=Mrps2 PE=1 SV=1	Mrps2	D3ZY44	0.0400645	0.06939459	18.9398594	18.8913841	18.0942554	16.6625576	17.3886757	18.1106472	18.0466881	18.7644672
1071	Mitochondrial ribosomal protein S21 OS=Rattus norvegicus OX=10116 GN=Mrps21 PE=2 SV=1	Mrps21	B2RYT0	0.19658902	-0.2466569	20.7785759	20.9479942	20.0698643	18.9791222	20.3514194	20.5640526	19.9166279	20.9300842
1072	Mitochondrial ribosomal protein S22 OS=Rattus norvegicus OX=10116 GN=Mrps22 PE=1 SV=1	Mrps22	Q0D2L2	0.92055292	0.71264601	19.7330589	19.6509781	20.1770363	18.9968586	19.3183613	19.1048088	18.0097046	19.2744732
1073	Mitochondrial ribosomal protein S30 OS=Rattus norvegicus OX=10116 GN=Mrps30 PE=1 SV=1	Mrps30	D4A833	0.14407825	-0.2886231	16.0696144	16.0093651	13.3751202	16.2563839	16.2454262	15.5428762	14.8557205	16.220953
1074	Mitochondrial ribosomal protein S35 OS=Rattus norvegicus OX=10116 GN=Mrps35 PE=1 SV=1	Mrps35	D4A9Z6	1.59055519	0.94129562	19.2288723	19.3154469	19.2143745	18.4940662	18.0864353	18.8217926	17.5979443	17.9814053
1075	Mitochondrial ribosomal protein S36 OS=Rattus norvegicus OX=10116 GN=Mrps36 PE=1 SV=1	Mrps36	M0R776	0.66287811	0.22207022	22.5635719	22.0468178	22.3522797	21.9948978	22.1795902	22.1442051	21.952198	21.793293
1076	Mitochondrial ribosomal protein S5 OS=Rattus norvegicus OX=10116 GN=Mrps5 PE=1 SV=1	Mrps5	D3ZYT2	0.16489282	0.13796902	21.1446896	20.9635391	20.0223408	20.7119637	20.4384136	20.8244362	20.0466156	20.9811916
1077	Mitochondrial ribosomal protein S6 OS=Rattus norvegicus OX=10116 GN=Mrps6 PE=1 SV=2	Mrps6	F1M6D0	1.33398982	0.67019844	20.3787746	20.306181	20.1483917	20.0292568	19.4180183	19.6879654	18.9256783	20.1501484
1078	Mitochondrial ribosomal protein S9 OS=Rattus norvegicus OX=10116 GN=Mrps9 PE=1 SV=1	Mrps9	B0BN68	0.95598158	1.3242588	19.6175804	19.6841164	18.9883556	20.5892048	17.4626617	18.2143402	17.6894703	20.2157497

1079	Mitochondrial translational initiation factor 2 OS=Rattus norvegicus OX=10116 GN=Mtif2 PE=1 SV=2	Mtif2	F7FDM3	1.31205464	0.68028927	21.6212425	21.6034908	22.0196495	20.9524174	20.6405163	21.1754627	20.5309029	21.1287613
1080	Mitochondrial-processing peptidase subunit alpha OS=Rattus norvegicus OX=10116 GN=Pmpca PE=1 SV=1	Pmpca	Q68FX8	0.50301206	0.73121929	18.92943	18.8870907	20.2089939	17.0142708	17.8412971	17.9245377	18.0418625	18.3072109
1081	Mitofusin-1 OS=Rattus norvegicus OX=10116 GN=Mfn1 PE=1 SV=1	Mfn1	Q8R4Z9	0.20965527	-0.163887	19.6269703	19.1405067	20.2319279	20.381216	19.7361107	19.9282017	20.3195457	20.0523109
1082	Mitofusin-2 OS=Rattus norvegicus OX=10116 GN=LOC100911485 PE=1 SV=1	LOC100911	F7FHF7	0.38939054	1.24527359	16.3746662	18.6305351	18.2566833	22.6238136	18.4799633	17.4665089	18.4910297	16.4671021
1083	Mitogen-activated protein kinase 3 OS=Rattus norvegicus OX=10116 GN=Mapk3 PE=1 SV=5	Mapk3	P21708	0.00076498	0.00039148	20.1849785	20.4940128	20.0759048	19.9162579	20.1187077	20.0746841	19.9655724	20.5106239
1084	Mitogen-activated protein kinase 8 OS=Rattus norvegicus OX=10116 GN=Mapk8 PE=1 SV=1	Mapk8	P49185	0.42365327	0.58541155	17.4034367	16.7995014	15.9755993	14.9303827	15.8828993	14.82302	15.8674707	16.1938839
1085	Mitogen-activated protein kinase kinase 4 OS=Rattus norvegicus OX=10116 GN=Map2k4 PE=1 SV=3	Map2k4	F1LP57	0.05583546	0.08108568	16.8380852	17.6664867	16.9744987	16.8754139	17.2188835	16.7991276	15.8654137	18.1467171
1086	Mitogen-activated protein kinase kinase kinase 20 OS=Rattus norvegicus OX=10116 GN=Map3k20 PE=1 SV=1	Map3k20	D4AE17	0.3719789	-0.3359456	17.7328682	17.3109493	17.3331451	17.4433308	17.5011349	17.2150879	17.5372791	18.910574
1087	Mitogen-activated protein kinase kinase kinase 5 OS=Rattus norvegicus OX=10116 GN=Map3k5 PE=1 SV=3	Map3k5	D3ZZH6	3.08105125	0.83352947	21.1292973	20.8406391	20.7566528	20.5846577	20.1495419	20.0544548	19.9657612	19.8073711
1088	Mitogen-activated protein kinase OS=Rattus norvegicus OX=10116 GN=Mapk14 PE=1 SV=1	Mapk14	G3V617	1.14273767	1.9171145	19.4248486	20.2887993	19.6010799	18.6370373	16.58111	15.9685774	18.1646633	19.5689564
1089	Mitogen-activated protein kinase-activated protein kinase 2 OS=Rattus norvegicus OX=10116 GN=Mapkapk2 PE=1 SV=3	Mapkapk2	F1M9C0	0.23211326	0.22868133	16.8575554	17.5359535	17.3859997	16.7007961	17.3020954	17.3219662	15.8793211	17.0621967
1090	MMS19 homolog, cytosolic iron-sulfur assembly component OS=Rattus norvegicus OX=10116 GN=Mms19 PE=1 SV=1	Mms19	M0R6T4	0.98200371	0.68825436	17.1098747	16.9506626	18.0138588	16.9191227	16.5510769	15.9149094	17.1324081	16.642107
1091	Moesin OS=Rattus norvegicus OX=10116 GN=Msn PE=1 SV=1	Msn	A0A096MK3	0.25405758	-0.1800251	20.4634113	21.0998859	20.4258633	21.5042706	20.6818733	21.1796379	21.2262249	21.1257954
1092	MON2 homolog, regulator of endosome-to-Golgi-trafficking OS=Rattus norvegicus OX=10116 GN=Mon2 PE=1 SV=3	Mon2	D3ZCG3	0.51066206	1.28543329	18.2140007	18.4869938	18.456377	18.3777409	13.6481743	18.0924339	18.1364861	18.5162849
1093	Monocarboxylate transporter 1 OS=Rattus norvegicus OX=10116 GN=Slc16a1 PE=1 SV=1	Slc16a1	P53987	0.564252	-0.1785741	22.1358261	22.0997639	21.6420956	22.2873898	22.2969151	22.2691174	22.240036	22.0733032
1094	Monoglyceride lipase OS=Rattus norvegicus OX=10116 GN=Mgll PE=1 SV=1	Mgll	Q8R431	0.41360309	-0.4421725	16.9052811	18.2126102	18.3725319	18.5024719	18.6697102	18.4024715	19.0432816	17.646122
1095	Muringlobulin-1 OS=Rattus norvegicus OX=10116 GN=LOC297568 PE=1 SV=1	LOC297568	A0A0G2K92	0.43661194	1.30019927	19.8190498	20.0133305	18.5957031	18.1916714	14.1025515	19.2218437	19.1011887	18.9933739
1096	Muringlobulin-1 OS=Rattus norvegicus OX=10116 GN=Mug1 PE=1 SV=2	Mug1	D4A6E3	1.08381989	-0.4811959	20.0198536	20.3328018	20.1752968	19.7893448	20.033823	20.8851223	20.4661064	20.857029
1097	Musashi RNA-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Msi2 PE=1 SV=3	Msi2	F1LWE6	0.63400042	1.41394162	18.345026	16.5690384	13.9816961	17.2028122	15.2405653	15.871006	15.7513618	13.5798731
1098	Muscarinic acetylcholine receptor M2 OS=Rattus norvegicus OX=10116 GN=Chrm2 PE=1 SV=2	Chrm2	P10980	0.45982241	0.24418497	18.6533871	18.8712521	18.6395206	18.2689571	17.8781452	18.7887802	18.1929569	18.5964947
1099	Myadm protein OS=Rattus norvegicus OX=10116 GN=Myadm PE=1 SV=1	Myadm	Q05BA4	0.71810134	-0.2869544	20.2577114	20.7029686	20.3347816	21.0210991	20.9209805	20.6825008	21.0668316	20.7940655
1100	Myeloid leukemia factor 2 OS=Rattus norvegicus OX=10116 GN=Mlf2 PE=1 SV=1	Mlf2	D3ZPN3	0.5251301	-0.3129702	22.1868382	22.5213432	22.9592056	23.1324787	22.7595272	23.3637085	23.2522469	22.6762638
1101	Myeloperoxidase OS=Rattus norvegicus OX=10116 GN=Mpo PE=1 SV=1	Mpo	A0A0G2K1A	0.55726272	1.5892086	16.4728985	16.588604	15.88132	21.0741959	16.4270306	16.3111382	16.7080345	14.2139807
1102	Myl6 protein OS=Rattus norvegicus OX=10116 GN=Myl6 PE=2 SV=1	Myl6	B2GV99	0.36933834	-0.2709684	19.3483829	20.1601696	19.0695457	19.6112747	20.0106316	19.4535217	19.4668694	20.3422241
1103	Myoferlin OS=Rattus norvegicus OX=10116 GN=Myof PE=1 SV=1	Myof	A0A0G2K69	1.18656319	1.52926016	19.8908386	19.826952	19.3303909	17.0817165	17.561758	17.5495224	17.8045483	17.0970287
1104	Myoglobin OS=Rattus norvegicus OX=10116 GN=Mb PE=1 SV=3	Mb	Q9QZ76	0.11132079	0.0245986	28.0746021	27.7590466	27.9363728	28.0892448	27.9116688	27.8937416	28.0218983	27.9335632
1105	Myomesin 2 OS=Rattus norvegicus OX=10116 GN=Myom2 PE=1 SV=1	Myom2	G3V7K1	0.28661034	0.19423676	26.5182762	26.0648441	26.6733952	25.9518719	26.3914242	26.0200577	25.5178699	26.5020885
1106	Myosin light chain 3 OS=Rattus norvegicus OX=10116 GN=Myl3 PE=1 SV=2	Myl3	P16409	0.43542455	-0.3554058	22.2555981	23.3689232	23.4500465	23.0917702	23.4776993	24.0397472	22.9436874	23.1268272
1107	Myosin light chain kinase 3 OS=Rattus norvegicus OX=10116 GN=Mylk3 PE=1 SV=1	Mylk3	E9PT87	1.8947296	0.87221813	22.8196926	23.3645973	22.2654953	23.0203667	22.0351315	21.9651852	21.7610798	22.219883
1108	Myosin light chain kinase OS=Rattus norvegicus OX=10116 GN=Mylk PE=1 SV=2	Mylk	D3ZFU9	0.58784132	0.32750082	20.9157543	21.3264351	20.2277451	20.3322792	20.2739334	20.4948215	20.4033012	20.3201542
1109	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform OS=Rattus norvegicus OX=10116 GN=Myl2 PE=1 SV=2	Myl2	P08733	0.08169832	-0.0912671	21.557806	22.5779476	22.6024532	22.1203117	22.5061607	23.0369835	21.5073071	22.1731358
1110	Myosin, heavy polypeptide 9, non-muscle OS=Rattus norvegicus OX=10116 GN=Myh9 PE=1 SV=1	Myh9	G3V6P7	0.3905707	-0.5222092	20.5632305	21.2236004	19.9782276	22.291954	21.2287121	20.8749218	22.3035488	21.7386665
1111	Myosin-4 OS=Rattus norvegicus OX=10116 GN=Myh4 PE=1 SV=1	Myh4	Q29RW1	0.16326601	-0.1739411	16.017828	17.2541409	17.5629959	17.5012169	17.0149307	17.4706135	16.8549995	17.6914024
1112	Myosin-6 OS=Rattus norvegicus OX=10116 GN=Myh6 PE=1 SV=2	Myh6	G3V885	0.23430592	-0.252799	24.5964947	25.9006119	26.0123711	25.4037628	25.7693367	26.5462704	25.265501	25.3433285
1113	Myosin-7 OS=Rattus norvegicus OX=10116 GN=Myh7 PE=1 SV=1	Myh7	G3V8B0	1.53360278	-0.7392969	21.6926785	22.0069294	21.6848392	21.6237144	22.2011623	23.170763	22.0756874	22.5177364
1114	Myosin-binding protein C, cardiac-type OS=Rattus norvegicus OX=10116 GN=Mybpc3 PE=1 SV=2	Mybpc3	P56741	0.2357426	-0.1904874	26.9990788	27.2586441	26.9172058	27.3374271	27.2901936	26.5235672	27.4243851	28.0361595
1115	Myristoylated alanine-rich C-kinase substrate OS=Rattus norvegicus OX=10116 GN=Marcks PE=1 SV=2	Marcks	P30009	1.05515837	-0.3514299	21.6204567	21.8025074	21.5993862	21.4079819	21.7727509	21.6869526	22.3700047	22.0063438
1116	N(alpha)-acetyltransferase 15, NatA auxiliary subunit OS=Rattus norvegicus OX=10116 GN=Naa15 PE=1 SV=2	Naa15	D3ZD89	0.09270392	-0.1601768	16.2288208	14.424778	14.598896	16.9222889	15.4786291	16.1233749	15.6408472	15.5726395
1117	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Rattus norvegicus OX=10116 GN=Ddah2 PE=1 SV=1	Ddah2	Q6MG60	0.27152058	-0.6128225	14.8312263	18.7417831	18.4556866	17.6043053	18.5388699	18.3778801	17.7918034	17.3757381
1118	N-acetylneuraminate lyase OS=Rattus norvegicus OX=10116 GN=Npl PE=2 SV=1	Npl	Q66H59	0.9291623	0.70376539	20.7525024	19.4697609	19.3408871	20.2289867	19.7169266	18.8778877	18.9712467	19.4110146
1119	NAD(P)(+)--arginine ADP-ribosyltransferase OS=Rattus norvegicus OX=10116 GN=Art3 PE=3 SV=1	Art3	A0A0G2K8S	1.93730202	-0.7063661	19.5770149	19.7467995	19.6382179	19.9946098	20.0950985	20.7090797	20.7785015	20.1994267
1120	NAD(P)H-hydrate epimerase OS=Rattus norvegicus OX=10116 GN=Naxe PE=2 SV=1	Naxe	B0BNM1	0.46728251	0.39101601	16.0336857	16.049902	16.5884609	16.8760777	16.1974792	15.0955925	16.5712662	16.1197243
1121	NAD-dependent protein deacetylase OS=Rattus norvegicus OX=10116 GN=Sirt2 PE=1 SV=1	Sirt2	A0A0G2JW1	1.27159957	-0.6414819	19.0438175	20.0079784	19.7945728	19.8877773	20.2440567	19.9304066	20.4748878	20.6507225
1122	NAD-dependent protein deacetylase OS=Rattus norvegicus OX=10116 GN=Sirt3 PE=1 SV=1	Sirt3	C6ZII9	0.00218447	-0.0034547	20.1258392	18.651968	20.6460514	20.5875263	20.4622593	19.3028049	20.1776295	20.08251
1123	NAD-dependent protein deacylase sirtuin-5, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sirt5 PE=2 SV=1	Sirt5	Q68FX9	1.08065387	0.66895914	21.6959915	21.9375668	21.7829704	20.6776676	20.7929363	20.53405	20.8444538	21.2469196
1124	NAD-dependent protein lipoamidase sirtuin-4, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sirt4 PE=3 SV=1	Sirt4	G3V641	0.4271185	0.98388052	17.7911091	17.76474	18.0774307	18.2035923	18.0363617	13.9463768	18.2918568	17.6267548
1125	NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, assembly factor 1 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ndufaf1 PE=1 SV=2	Ndufaf1	F1LWG4	0.00571481	-0.0027232	20.0489559	19.9363518	20.3387623	20.5704269	20.4207096	20.2233639	20.0958462	20.1654701
1126	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 11 (Predicted) OS=Rattus norvegicus OX=10116 GN=Ndufb11 PE=1 SV=1	Ndufb11	D4A7L4	0.61212909	-0.3643236	23.6051941	24.250124	24.5259171	24.6388664	24.705286	24.58181	24.9843445	24.2059555
1127	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 2 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Ndufb2 PE=1 SV=1	Ndufb2	B2RYU0	0.69774977	-0.4169888	19.5441341	20.4215965	20.3571281	20.507452	20.8116951	20.6295624	20.9514389	20.1055698
1128	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 5 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Ndufb5 PE=1 SV=1	Ndufb5	D4A565	0.93106331	-0.3441734	23.5536728	24.2318096	24.1417847	24.2946491	24.3529091	24.3542862	24.6314926	24.259922
1129	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 6 (Predicted) OS=Rattus norvegicus OX=10116 GN=Ndufb6 PE=1 SV=1	Ndufb6	D3ZZ21	0.62850604	-0.3464513	22.6467934	23.4267807	23.6789207	23.4889011	23.7078705	23.6203709	23.9673653	23.3315945
1130	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 7 (Predicted) OS=Rattus norvegicus OX=10116 GN=Ndufb7 PE=1 SV=1	Ndufb7	D3ZLT1	0.75910349	-0.3923726	24.2465572	24.8544235	25.1507301	25.2117577	25.3832417	25.1598129	25.5342522	24.9556522
1131	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 9 OS=Rattus norvegicus OX=10116 GN=Ndufb9 PE=1 SV=1	Ndufb9	B2RYW3	0.49717858	-0.2828026	24.6617069	25.3082733	25.4648781	25.6755543	25.6322823	25.4857597	25.8979912	25.2255898
1132	NADH dehydrogenase (Ubiquinone) Fe-S protein 3 (Predicted), isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Ndufs3 PE=1 SV=1	Ndufs3	D3ZG43	0.7140249	-0.331212	25.264452	25.8112259	25.972065	26.0919476	26.2593307	26.056345	26.3783035	25.7705593
1133	NADH dehydrogenase (Ubiquinone) Fe-S protein 5 OS=Rattus norvegicus OX=10116 GN=Ndufs5 PE=1 SV=1	Ndufs5	B5DEL8	0.41022349	-0.2496681	24.1384106	25.0286942	25.1735744	25.1348114	25.2442112	24.9564629	25.3622799	24.9112091
1134	NADH dehydrogenase (Ubiquinone) Fe-S protein 7 OS=Rattus norvegicus OX=10116 GN=Ndufs7 PE=1 SV=1	Ndufs7	Q5RJN0	0.24905719	-0.1399684	24.6651764	25.1209526	25.2472935	25.3232937	25.4329662	25.0093765	25.6106205	24.8636265
1135	NADH dehydrogenase (Ubiquinone) Fe-S protein 8 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ndufs8 PE=1 SV=1	Ndufs8	B0BNE6	0.63550652	-0.3125377	24.5912971	25.1348915	25.3365383	25.5133705	25.6148968	25.3625336	25.6949711	25.1538467
1136	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 OS=Rattus norvegicus OX=10116 GN=Ndufaf3 PE=2 SV=1	Ndufaf3	O08776	0.92030045	-0.275054	22.4429436	22.8437195	23.1284904	22.7165585	23.1501617	22.9232922	23.1350384	23.0234356
1137	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4 OS=Rattus norvegicus OX=10116 GN=Ndufaf4 PE=1 SV=1	Ndufaf4	Q9NQR8	0.3923015	0.5225873	19.7011852	18.9730015	19.2472878	20.5817051	18.7183971	18.4616985	20.4868603	18.7458744
1138	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufa10 PE=1 SV=1	Ndufa10	Q561S0	0.62040679	-0.4770546	24.7840176	25.6232452	25.9439602	26.2309895	26.2134247	26.1212139	26.5342293	25.621563
1139	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufa10l1 PE=3 SV=1	Ndufa10l1	A0A1W2Q6	1.08593603	-0.8046126	20.0219536	20.2254925	20.4616642	20.5497093	21.007225	20.6528473	22.1887569	20.6284409
1140	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=Rattus norvegicus OX=10116 GN=Ndufa11 PE=2 SV=1	Ndufa11	Q80W89	0.2694325	-0.1180053	21.9201221	22.3825645	22.497757	22.6911354	22.6723499	22.5250912	22.3052025	22.4609566
1141	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Rattus norvegicus OX=10116 GN=Ndufa12 PE=1 SV=2	Ndufa12	F1LXA0	0.86059856	-0.3773065	24.8303967	25.4732819	25.686451	25.5678844	25.8533134	25.6902714	26.0170174	25.5066376
1142	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Rattus norvegicus OX=10116 GN=Ndufa2 PE=1 SV=1	Ndufa2	D3ZS58	0.53865118	-0.228477	24.7762547	25.1865177	25.2412281	25.2540817	25.4911594	25.3114586	25.658123	24.9112492
1143	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Rattus norvegicus OX=10116 GN=Ndufa5 PE=1 SV=3	Ndufa5	Q63362	0.78901746	-0.3854551	24.6458035	25.072134	25.3805313	25.381958	25.5987091	25.5175476	25.8565388	25.0494518
1144	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Rattus norvegicus OX=10116 GN=Ndufa6 PE=1 SV=1	Ndufa6	D4A3V2	0.69824252	-0.3565416	24.4206104	25.0253716	25.2109833	25.2832832	25.4151764	25.244751	25.7151165	24.9913712
1145	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Rattus norvegicus OX=10116 GN=Ndufa8 PE=1 SV=1	Ndufa8	A0A0G2JVL	0.65055999	-0.2895255	25.1948185	25.6586685	25.8026962	26.0015869	26.1169872	25.7524033	26.2231236	25.7233582
1146	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufa9 PE=1 SV=2	Ndufa9	Q5BK63	0.80714935	-0.3295541	25.0931282	25.5285282	25.8696823	25.6027031	25.9695454	25.7904148	26.113369	25.538929
1147	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 OS=Rattus norvegicus OX=10116 GN=Ndufb1 PE=3 SV=1	Ndufb1	P0DN35	0.13448149	-0.1021481	22.5432339	23.2173786	23.4315987	23.7765617	23.3933048	23.1082783	23.6606426	23.2151394
1148	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufb8 PE=1 SV=1	Ndufb8	B2RYS8	0.92571042	-0.4837384	23.3434525	24.1405182	24.3047314	24.4313087	24.5609398	24.6161537	24.7327614	24.2451096
1149	NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Rattus norvegicus OX=10116 GN=Ndufc2 PE=1 SV=1	Ndufc2	Q5PQZ9	0.57244249	-0.3305664	23.6150379	24.4574127	24.5588455	24.6734886	24.8291054	24.6285133	24.8492851	24.3201466
1150	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufv1 PE=1 SV=1	Ndufv1	Q5XIH3	0.77224982	-0.3377638	26.3509464	26.9419575	27.1798038	27.1088448	27.3407116	27.1219025	27.4705563	26.9994373

1151	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufv2 PE=1 SV=2	Ndufv2	P19234	0.74261886	-0.299315	25.3186264	25.6109562	25.8940449	25.9087791	26.122427	25.9780941	26.2362194	25.592926
1152	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufv3 PE=3 SV=1	Ndufv3	Q6PCU8	0.98376377	-1.0236106	20.7257175	21.8708344	21.4422398	22.9864006	22.8829575	22.4456043	23.4378014	22.3532715
1153	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufs2 PE=1 SV=1	Ndufs2	Q641Y2	0.94688421	-0.4177761	25.7001247	26.2428303	26.5231686	26.532732	26.7787476	26.6106739	26.8997211	26.3808174
1154	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufs4 PE=1 SV=1	Ndufs4	Q5XIF3	0.56760273	-0.302042	24.7953548	25.3822517	25.6223698	25.6872559	25.8766499	25.5637569	25.9369717	25.3180218
1155	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Rattus norvegicus OX=10116 GN=LOC100912599 PE=1 SV=1	LOC100912599	D3ZCZ9	0.76375238	-0.4964466	24.0361462	24.8790855	25.2780495	25.247282	25.5228367	25.2699089	25.6249981	25.008606
1156	NADH:ubiquinone oxidoreductase complex assembly factor 2 OS=Rattus norvegicus OX=10116 GN=Ndufaf2 PE=1 SV=1	Ndufaf2	A0A0G2JZF9	1.15162199	-0.3796821	16.4845486	16.9560661	16.8533859	16.9513206	17.0264244	17.2884712	17.5169106	16.9322433
1157	NADH:ubiquinone oxidoreductase subunit A1 OS=Rattus norvegicus OX=10116 GN=Ndufa1 PE=1 SV=2	Ndufa1	G3V9S6	0.84728617	-0.4453654	21.6092205	22.2780666	22.4792404	22.258358	22.6808357	22.5644379	23.0259418	22.1351318
1158	NADH:ubiquinone oxidoreductase subunit A13 OS=Rattus norvegicus OX=10116 GN=Ndufa13 PE=1 SV=1	Ndufa13	D3ZE15	1.04966304	-0.4890013	24.6086712	24.8316307	25.0753021	25.1964016	25.6848354	25.3984432	25.7346001	24.850132
1159	NADH:ubiquinone oxidoreductase subunit A7 OS=Rattus norvegicus OX=10116 GN=Ndufa7 PE=1 SV=1	Ndufa7	A9UMV9	0.38988498	-0.2262206	24.865181	25.3490047	25.350769	25.735096	25.7992573	25.4116516	25.8886147	25.1054096
1160	NADH:ubiquinone oxidoreductase subunit B10 OS=Rattus norvegicus OX=10116 GN=Ndufb10 PE=1 SV=1	Ndufb10	D4A0T0	0.55238778	-0.3207283	25.3323059	25.9353428	26.2378826	26.351965	26.4254265	26.1552925	26.6076736	25.9520168
1161	NADH:ubiquinone oxidoreductase subunit B3 OS=Rattus norvegicus OX=10116 GN=Ndufb3 PE=1 SV=1	Ndufb3	D4A4P3	0.59624195	-0.3810325	23.2201939	24.1919861	24.2329712	24.3239536	24.4596119	24.3576946	24.7105598	23.9653683
1162	NADH:ubiquinone oxidoreductase subunit B4 OS=Rattus norvegicus OX=10116 GN=Ndufb4 PE=1 SV=1	Ndufb4	F1LPG5	0.42361835	-0.2594881	24.3859119	25.0743065	25.3532925	25.3975296	25.3664932	25.2114372	25.666996	25.0040665
1163	NADH-cytochrome b5 reductase 3 OS=Rattus norvegicus OX=10116 GN=Cyb5r3 PE=1 SV=2	Cyb5r3	P20070	1.20567072	-0.608789	20.5514736	20.9837265	21.1826458	20.747942	21.3379135	20.9139423	21.6727715	21.9763165
1164	NADH-cytochrome b5 reductase OS=Rattus norvegicus OX=10116 GN=Cyb5r1 PE=1 SV=1	Cyb5r1	G3V9S0	0.03920722	-0.0206966	22.7646484	22.2617722	22.4862232	22.0924778	22.7464008	22.2547665	22.379034	22.3077068
1165	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ndufs1 PE=1 SV=1	Ndufs1	Q66HF1	0.86992391	-0.3098354	27.4232712	27.9234943	28.1408062	28.0189304	28.2810707	28.1281509	28.3625774	27.9740448
1166	NADH-ubiquinone oxidoreductase chain 1 OS=Rattus norvegicus OX=10116 GN=Mtnd1 PE=1 SV=3	Mtnd1	P03889	0.60342422	-0.3004956	20.4987736	21.1210423	21.2602539	20.8188572	21.0082684	21.152277	21.7075443	21.0328197
1167	NADH-ubiquinone oxidoreductase chain 3 OS=Rattus norvegicus OX=10116 GN=Mtnd3 PE=3 SV=3	Mtnd3	P05506	0.71796626	-0.3771915	21.3411961	22.1491642	22.3801498	22.2905617	22.2292557	22.4887218	22.6518269	22.3000336
1168	NADH-ubiquinone oxidoreductase chain 4 OS=Rattus norvegicus OX=10116 GN=Mtnd4 PE=3 SV=3	Mtnd4	P05508	0.17200906	-0.1282697	21.1234989	21.4051914	21.3507137	21.8280582	21.7657604	21.3934383	22.1107216	20.9506207
1169	NADH-ubiquinone oxidoreductase chain 4L OS=Rattus norvegicus OX=10116 GN=Mtnd4l PE=3 SV=3	Mtnd4l	P05507	0.86225567	-1.33283	14.2916355	17.3918324	17.1094532	17.3871899	18.1661091	17.9850445	17.3201332	18.040144
1170	NADH-ubiquinone oxidoreductase chain 5 OS=Rattus norvegicus OX=10116 GN=Mtnd5 PE=3 SV=3	Mtnd5	P11661	0.53013204	-0.3036704	23.2925453	24.1735554	24.2071323	24.023365	24.417366	24.1131058	24.5354404	23.8453674
1171	NADPH--cytochrome P450 reductase OS=Rattus norvegicus OX=10116 GN=Por PE=1 SV=3	Por	P00388	0.04867263	0.05591297	19.231226	19.8316231	19.4641075	20.9727097	19.7283497	19.6735764	20.1533871	19.7207012
1172	N-alpha-acetyltransferase 11 OS=Rattus norvegicus OX=10116 GN=Naa11 PE=2 SV=1	Naa11	Q4V8K3	0.2140311	0.15614176	18.3764286	18.4550552	17.7600307	18.5959225	18.5692635	18.0275631	18.4079838	17.5580597
1173	Nascent polypeptide-associated complex subunit alpha OS=Rattus norvegicus OX=10116 GN=Naca PE=1 SV=1	Naca	M0R9L0	0.01808786	-0.0187097	19.3786106	19.2377892	20.0774879	20.1058865	19.8848763	19.4548302	20.3803368	19.1545696
1174	Natriuretic peptides A OS=Rattus norvegicus OX=10116 GN=Nppa PE=1 SV=1	Nppa	P01161	0.27687979	-0.4113955	16.33111	18.7057304	17.2612572	16.5695171	16.9202099	17.3414726	18.270174	17.9813404
1175	NDUFA4, mitochondrial complex-associated OS=Rattus norvegicus OX=10116 GN=Ndufa4 PE=1 SV=1	Ndufa4	B2RZD6	1.30014273	-0.4085379	26.1164742	26.4689178	26.5438652	26.7919064	26.8519382	26.9252892	27.1110725	26.6670151
1176	Nebulette OS=Rattus norvegicus OX=10116 GN=Nebl PE=1 SV=1	Nebl	A0A0G2JWS	0.23492614	0.36907005	20.6988277	19.2338772	18.8301411	19.2646523	19.8367176	17.820652	18.9936752	19.9001732
1177	Nebulin-related-anchoring protein OS=Rattus norvegicus OX=10116 GN=Nrap PE=1 SV=1	Nrap	D4A4K6	0.08261449	0.11026859	21.5404911	20.0070362	20.0098763	20.9591904	20.2280731	20.0530472	20.4000683	21.394331
1178	Nectin cell adhesion molecule 2 OS=Rattus norvegicus OX=10116 GN=Nectin2 PE=1 SV=1	Nectin2	A0A0G2KA7	2.55681502	0.94388103	21.2015858	20.749157	21.399477	20.7398453	19.9706306	20.36059	20.0764675	19.9068527
1179	Negative regulator of ubiquitin-like proteins 1 OS=Rattus norvegicus OX=10116 GN=Nub1 PE=1 SV=1	Nub1	F7ES73	0.1824845	-0.0937314	21.845089	21.6917763	22.044487	21.5315228	21.5540047	21.8717499	21.7245483	22.3374977
1180	N-ethylmaleimide sensitive fusion protein, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Nsf PE=1 SV=3	Nsf	F1LQ81	1.30661763	0.55563116	21.4828987	21.7413654	21.124939	21.1122475	20.5557308	20.9020958	20.5364208	21.2446785
1181	Netrin-1 OS=Rattus norvegicus OX=10116 GN=Ntn1 PE=1 SV=1	Ntn1	Q924Z9	2.04559859	-1.6074715	16.8030491	18.2846031	18.3640385	18.5642204	19.6864109	19.2508411	19.8257198	19.6828251
1182	Neural cell adhesion molecule 1 OS=Rattus norvegicus OX=10116 GN=Ncam1 PE=1 SV=1	Ncam1	P13596	0.66022926	-0.6646295	20.5987072	20.8046169	18.7298203	20.2607059	20.5486126	20.6077385	21.0535259	20.8424911
1183	Neuroplastin OS=Rattus norvegicus OX=10116 GN=Nptn PE=1 SV=2	Nptn	P97546	0.3454816	-0.3256278	17.1410694	18.4114532	17.805521	17.3617725	17.300005	18.4570885	18.5103931	17.7548409
1184	Neutral cholesterol ester hydrolase 1 OS=Rattus norvegicus OX=10116 GN=Nceh1 PE=1 SV=1	Nceh1	B2GV54	0.01860378	0.01506901	20.9928169	19.8388729	20.6800041	20.1629677	20.1579914	20.521452	20.3553982	20.5795441
1185	Nexilin OS=Rattus norvegicus OX=10116 GN=Nexn PE=1 SV=1	Nexn	A0A0G2K6I	0.38912566	-0.2145214	16.5930424	16.8513699	17.3890457	17.0347958	17.1918488	16.7209167	17.2503033	17.5632706
1186	NF-kappa-B essential modulator OS=Rattus norvegicus OX=10116 GN=Ikbkg PE=2 SV=1	Ikbkg	Q6TMG5	0.74348517	0.51373816	21.5532875	20.7039757	21.1119995	20.4553318	20.3505268	20.5107746	19.8749657	21.0333748
1187	NFKB inhibitor interacting Ras-like protein 2 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Nkiras2 PE=1 SV=1	Nkiras2	D3ZCK2	0.40968569	0.36143494	18.1612186	17.4840965	16.6418285	17.5299034	17.1048222	17.5667229	16.4548988	17.2448635
1188	Nicotinamide nucleotide transhydrogenase OS=Rattus norvegicus OX=10116 GN=Nnt PE=1 SV=1	Nnt	Q5BJZ3	0.74088018	-0.3203349	27.4997196	27.951664	28.196888	28.3450756	28.3509502	28.3867245	28.5117836	28.0252285
1189	Nicotinamide phosphoribosyltransferase OS=Rattus norvegicus OX=10116 GN=Nampt PE=1 SV=1	Nampt	Q80Z29	1.04983168	0.63775921	22.7322865	22.3459377	22.2471237	21.9266853	21.1631699	22.148922	21.2635632	22.1253414
1190	Nicotinamide-nucleotide adenylyltransferase OS=Rattus norvegicus OX=10116 GN=Nmnat3 PE=1 SV=1	Nmnat3	F7F588	1.02956089	0.63700914	21.708046	22.188282	21.8212986	20.795557	20.8552818	21.3514805	20.9164314	20.8419533
1191	Nicotinate phosphoribosyltransferase OS=Rattus norvegicus OX=10116 GN=Naprt PE=1 SV=1	Naprt	G3V709	0.03544862	0.03749752	17.0470982	16.111721	16.7905312	16.9558163	16.7934246	15.8520641	17.2624264	16.8472614
1192	Nidogen-1 OS=Rattus norvegicus OX=10116 GN=Nid1 PE=1 SV=1	Nid1	F1LM84	0.34295803	0.56275296	17.7981758	17.3624496	15.5632982	17.0289745	15.5327778	17.4414654	15.4757252	17.051918
1193	Nischarin OS=Rattus norvegicus OX=10116 GN=Nisch PE=2 SV=2	Nisch	Q4G017	0.64551294	0.22699356	21.1506882	20.8121223	21.0597191	20.4394989	20.7386818	20.6910324	20.4839478	20.6403923
1194	Nitric oxide synthase-interacting protein OS=Rattus norvegicus OX=10116 GN=Nosip PE=1 SV=1	Nosip	D3ZH12	0.62195652	0.97284865	19.156271	17.1290226	17.2911968	17.8264656	17.1282501	15.5259886	16.5330811	18.3242416
1195	NLR family member X1 OS=Rattus norvegicus OX=10116 GN=Nlrx1 PE=2 SV=1	Nlrx1	Q5FVQ8	0.03540466	0.05859423	21.1464005	23.3644161	21.1323776	22.4795914	21.9773655	21.609911	22.4320774	21.8690548
1196	N-lysine methyltransferase SMYD2 OS=Rattus norvegicus OX=10116 GN=Smyd2 PE=1 SV=1	Smyd2	Q7M6Z3	0.70293525	0.55440378	22.7218609	22.6835957	22.3781452	21.3510265	21.6391048	21.7541981	21.251358	22.2723522
1197	N-myc downstream regulated gene 2, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Ndrg2 PE=1 SV=1	Ndrg2	A0A0G2JSU	1.28880114	-0.5122385	22.8363476	23.3830471	23.2651901	23.7137794	24.0234013	23.7848969	23.9170876	23.5219326
1198	NOL1/NOP2/Sun domain family, member 4 (Predicted) OS=Rattus norvegicus OX=10116 GN=Nsun4 PE=1 SV=1	Nsun4	D4A099	0.19377381	0.17036247	17.1151161	16.8528843	16.328968	17.0645294	16.5699577	17.5211964	16.1648502	16.4240437
1199	Non-specific lipid-transfer protein OS=Rattus norvegicus OX=10116 GN=Scp2 PE=1 SV=1	Scp2	A0A0G2KA0	0.93883926	0.69615793	19.1750622	19.8141708	19.6284904	19.6298599	19.1929932	17.9262943	18.7747192	19.5689449
1200	Non-specific serine/threonine protein kinase OS=Rattus norvegicus OX=10116 GN=Prkaa2 PE=1 SV=1	Prkaa2	G3V715	0.42896136	0.19260645	21.7800598	21.9308472	21.2648811	21.336525	21.2776031	21.2767048	21.2584743	21.729105
1201	NSFL1 cofactor p47 OS=Rattus norvegicus OX=10116 GN=Nsfl1c PE=1 SV=1	Nsfl1c	O35987	0.24117664	-0.8229966	19.3687534	19.5355835	19.139452	14.1435776	19.5463963	19.4512901	17.5283165	18.9533501
1202	Nuclear factor kappa B subunit 2 OS=Rattus norvegicus OX=10116 GN=Nfkb2 PE=1 SV=1	Nfkb2	Q5U2Z4	0.5591368	1.34627223	20.0192986	19.1474552	18.9327087	17.3789387	19.3995953	16.303751	15.4205103	18.9694557
1203	Nuclear factor NF-kappa-B p105 subunit OS=Rattus norvegicus OX=10116 GN=Nfkb1 PE=1 SV=2	Nfkb1	F1LQH2	0.37079154	-0.1863694	17.8264198	18.0046749	17.8590393	18.4058533	18.3396263	18.3503475	18.4541035	17.6973877
1204	Nuclear mitotic apparatus protein 1 OS=Rattus norvegicus OX=10116 GN=Numa1 PE=1 SV=2	Numa1	F7FF45	1.45912123	-0.3567638	22.6291599	23.132822	22.9970169	22.8514671	23.2402878	23.4691448	23.1143723	23.2137165
1205	Nucleobindin-1 OS=Rattus norvegicus OX=10116 GN=Nucb1 PE=1 SV=1	Nucb1	Q63083	0.06302104	-0.0505238	19.5110722	18.959528	18.8078365	19.2381325	19.4305248	18.5224247	19.6115246	19.1541901
1206	Nucleoside diphosphate kinase B OS=Rattus norvegicus OX=10116 GN=Nme2 PE=1 SV=1	Nme2	P19804	0.31839931	-0.0797758	23.6022949	23.5813599	24.0037498	23.8468666	23.8560905	23.9159164	23.8043194	23.7770481
1207	Nucleoside diphosphate kinase OS=Rattus norvegicus OX=10116 GN=Nme6 PE=3 SV=1	Nme6	R9PXW5	0.18224536	0.12228394	18.1073208	17.7620335	17.4539471	17.1172924	17.3802986	17.6304359	17.1137543	17.8269691
1208	Nucleoside-triphosphatase, cancer-related OS=Rattus norvegicus OX=10116 GN=Ntpcr PE=1 SV=1	Ntpcr	D4A478	0.08939438	0.2736578	18.9115219	20.2804604	16.8246174	20.8955231	19.0950871	19.3508701	17.140192	20.2313423
1209	Nucleosome assembly protein 1-like 4 OS=Rattus norvegicus OX=10116 GN=Nap1l4 PE=1 SV=1	Nap1l4	A0A0H2UH	0.516614	0.66125345	18.7272644	19.7307434	19.3844776	18.3863106	18.953577	18.380455	16.9884682	19.261282
1210	Nucleotide-binding protein-like OS=Rattus norvegicus OX=10116 GN=Nubpl PE=1 SV=1	Nubpl	D3ZFQ3	0.48740809	-0.4351959	21.5322208	20.8375854	21.0220261	20.7398014	22.0104237	20.3993874	21.8630638	21.5995426
1211	Nudix hydrolase 8 OS=Rattus norvegicus OX=10116 GN=Nudt8 PE=1 SV=1	Nudt8	D3ZEH6	0.11987457	0.48213005	18.6947498	18.5648479	15.2900276	18.6698647	17.9495544	19.1198025	13.661459	18.560154
1212	Obg-like ATPase 1 OS=Rattus norvegicus OX=10116 GN=Ola1 PE=2 SV=1	Ola1	A0JPJ7	1.47238496	0.87898064	22.585228	23.7701454	22.3483486	23.0425415	22.1853313	22.0390358	21.8687706	22.1372032
1213	Obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF OS=Rattus norvegicus OX=10116 GN=Obscn PE=1 SV=1	Obscn	A0A0G2K8N	0.31200148	0.29909897	21.9538097	20.8755226	20.6628857	20.1787453	20.7787762	20.3298607	20.4005051	20.9654255
1214	Obscurin-like protein 1 OS=Rattus norvegicus OX=10116 GN=Obsl1 PE=2 SV=3	Obsl1	D3ZZ80	0.051532	-0.0245237	19.169117	19.0294952	19.2320309	18.6046944	19.1534805	18.8623276	18.899538	19.2180862
1215	OCIA domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Ociad1 PE=1 SV=1	Ociad1	Q5XIG4	0.25909737	-0.2534375	21.0924702	21.9837093	22.22155	22.7380314	22.050066	22.0618343	22.8821793	22.0554314
1216	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ogt PE=1 SV=1	Ogt	A0A0G2K3V	1.91348215	1.39747286	21.7836933	21.7794304	22.1752243	20.8133545	20.2805843	20.4907513	19.4817486	20.7087269
1217	Omega-amidase NIT2 OS=Rattus norvegicus OX=10116 GN=Nit2 PE=1 SV=1	Nit2	Q497B0	0.07535059	-0.0907321	20.4808502	19.8264465	19.7202244	18.574543	19.6063271	20.2259655	19.4153461	19.7173538
1218	Ornithine aminotransferase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Oat PE=1 SV=1	Oat	P04182	0.33416062	0.38179421	16.9765968	16.5790138	16.7324657	16.7556763	14.9974012	17.0503864	16.4526405	17.0161476
1219	OXA1L, mitochondrial inner membrane protein OS=Rattus norvegicus OX=10116 GN=Oxa1l PE=1 SV=1	Oxa1l	D3ZRH1	0.80009766	-0.8137088	16.6643448	16.1946754	16.6191006	17.4334698	17.507328	17.3735371	18.6954231	16.5901375
1220	Oxidative stress-responsive kinase 1 OS=Rattus norvegicus OX=10116 GN=Oxsr1 PE=1 SV=1	Oxsr1	D3ZUC9	0.8708884	0.39388132	19.558382	19.0636177	19.2552872	19.067482	18.7224922	18.6606541	18.5641804	19.421917
1221	Oxidoreductase NAD-binding domain containing 1 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Oxnad1 PE=1 SV=1	Oxnad1	D4A0Y4	0.26342376	0.14163065	17.3767529	17.318655	17.2634201	17.5543652	17.6444664	17.144289	16.683012	17.4749031
1222	Oxysterol-binding protein OS=Rattus norvegicus OX=10116 GN=Osbp PE=1 SV=2	Osbp	D4A9D8	0.14121347	-0.2172735	16.6748066	17.2393456	15.001689	16.8651428	16.6743889	16.5543423	15.9605007	17.4608459

1223	Pantothenate kinase 4 OS=Rattus norvegicus OX=10116 GN=Pank4 PE=1 SV=1	Pank4	G3V7T3	1.22016167	0.68856144	22.0663357	21.4158535	20.9195251	22.0113087	21.0963402	20.5659676	20.9154873	21.0809822
1224	Paraplegin OS=Rattus norvegicus OX=10116 GN=Spg7 PE=2 SV=2	Spg7	Q7TT47	0.01376856	0.00516939	20.0895081	20.0175991	20.3670673	20.5432091	20.2189903	20.3492508	20.2077484	20.2207165
1225	Parvin, beta OS=Rattus norvegicus OX=10116 GN=Parvb PE=1 SV=1	Parvb	D3ZKG5	0.8792247	0.4438386	19.7794113	19.7927856	19.6023006	19.603075	19.3603497	19.3411789	18.5568352	19.7438545
1226	PDZ and LIM domain protein 5 OS=Rattus norvegicus OX=10116 GN=Pdlim5 PE=1 SV=2	Pdlim5	Q62920	0.3741566	-0.2832751	20.549202	20.3035622	19.8967247	21.1628761	20.2678242	20.9018822	20.6808605	21.1948986
1227	Pentatricopeptide repeat domain 2 OS=Rattus norvegicus OX=10116 GN=Ptcd2 PE=4 SV=1	Ptcd2	D4A9I4	0.73353562	0.30516195	20.9746056	20.9156494	21.1717262	20.5191422	20.5176849	20.7443409	20.2022533	20.8961964
1228	Pentatricopeptide repeat domain 3 OS=Rattus norvegicus OX=10116 GN=Ptcd3 PE=1 SV=1	Ptcd3	A0A0G2JU1	0.65955441	0.9429903	20.7680149	20.1934834	20.5255299	20.0124531	20.0290985	19.8703213	17.4583912	20.369709
1229	Peptide deformylase OS=Rattus norvegicus OX=10116 GN=Pdf PE=1 SV=2	Pdf	F1LVY9	0.63711477	-0.4287238	16.0203915	16.6603374	17.2488194	17.1844425	16.9707413	17.1542816	17.6384716	17.0653915
1230	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase OS=Rattus norvegicus OX=10116 GN=Ngly1 PE=2 SV=2	Ngly1	Q5XI55	1.41585845	1.03302431	18.3577824	17.9794102	18.2655106	18.4553413	17.6528282	16.3053017	16.9624043	18.0054131
1231	Peptidyl-prolyl cis-trans isomerase A OS=Rattus norvegicus OX=10116 GN=Ppia PE=1 SV=2	Ppia	P10111	0.0614427	0.02182055	22.223196	22.1963024	21.9297791	22.4021816	21.9562397	22.2493038	22.1362705	22.3223629
1232	Peptidyl-prolyl cis-trans isomerase B OS=Rattus norvegicus OX=10116 GN=Ppib PE=1 SV=3	Ppib	P24368	0.21049842	0.13501549	18.336031	18.4841003	18.6108322	19.3797131	18.5849876	18.3529587	18.482996	18.8496723
1233	Peptidyl-prolyl cis-trans isomerase F, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ppif PE=1 SV=2	Ppif	P29117	0.36772551	-0.2216949	20.0521584	19.4641533	20.1106491	20.4784565	20.3973103	20.2030735	20.5576019	19.8342113
1234	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Rattus norvegicus OX=10116 GN=Fkbp1a PE=1 SV=3	Fkbp1a	Q62658	0.37204373	0.09890461	19.7801514	19.8519726	19.7130871	19.9286861	19.7747746	19.4650993	19.666729	19.9716759
1235	Peptidylprolyl isomerase OS=Rattus norvegicus OX=10116 GN=Fkbp2 PE=1 SV=1	Fkbp2	D3ZZR9	1.7932173	0.80614924	17.5172691	17.0019054	17.0035133	16.7002449	16.5075607	15.7885313	16.1711578	16.531086
1236	Peptidylprolyl isomerase OS=Rattus norvegicus OX=10116 GN=Fkbp3 PE=1 SV=1	Fkbp3	G3V6L9	1.00376901	-0.6182282	15.7532911	16.8274555	16.3869228	17.1989155	17.1722183	17.0720692	17.0615463	17.3336639
1237	Perilipin 4 OS=Rattus norvegicus OX=10116 GN=Plin4 PE=4 SV=2	Plin4	M0R7S5	0.69635887	0.33135796	26.3765697	25.4871426	25.5492344	25.7425461	25.1788254	25.5951462	25.3920326	25.6640568
1238	Perilipin OS=Rattus norvegicus OX=10116 GN=Plin2 PE=1 SV=1	Plin2	F6QBA3	1.42602753	0.97328901	18.2380199	19.5003033	19.6401482	19.4147949	18.6041985	18.1449566	17.7966232	18.354332
1239	Perilipin OS=Rattus norvegicus OX=10116 GN=Plin3 PE=1 SV=1	Plin3	M0RA08	0.29077795	0.15960884	22.106451	21.16292	21.8960571	21.513834	21.5432987	21.2761097	21.4877911	21.7336273
1240	Perilipin-5 OS=Rattus norvegicus OX=10116 GN=Plin5 PE=1 SV=1	Plin5	M0R7Z9	0.09185503	0.09759712	15.7414856	16.3660698	16.8113365	17.3264217	16.3478279	17.0327396	16.2490807	16.2252769
1241	Peroxidasin OS=Rattus norvegicus OX=10116 GN=Pxdn PE=4 SV=1	Pxdn	A0A0G2JWI	0.82752461	0.70579433	20.6382046	19.8242149	19.9240589	19.1539612	19.5084877	19.2870216	18.3063202	19.6154327
1242	Peroxiredoxin 3 OS=Rattus norvegicus OX=10116 GN=Prdx3 PE=1 SV=1	Prdx3	G3V7I0	0.15763218	0.07906103	22.8517056	22.3475132	22.3175774	22.3896008	22.4958763	22.2092323	22.1220036	22.7630405
1243	Peroxiredoxin 5, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Prdx5 PE=1 SV=1	Prdx5	A0A0G2JSS8	0.08931013	0.03401995	21.9443207	21.6131115	22.062603	22.2564316	21.8890686	21.8787918	22.0079308	21.9645958
1244	Peroxiredoxin-2 OS=Rattus norvegicus OX=10116 GN=Prdx2 PE=1 SV=1	Prdx2	A0A0G2JSH	0.0098564	0.00247955	22.4542179	22.4476376	22.2362309	22.4486008	22.2412567	22.5584793	22.365799	22.4112339
1245	Peroxiredoxin-6 OS=Rattus norvegicus OX=10116 GN=Prdx6 PE=1 SV=3	Prdx6	O35244	1.11343529	-0.1771145	22.8831978	22.840456	22.8896885	23.0246143	22.9296856	23.0388527	23.0998383	23.278038
1246	Peroxisomal trans-2-enoyl-CoA reductase OS=Rattus norvegicus OX=10116 GN=Pecr PE=1 SV=1	Pecr	A0A0G2JVC	0.47204997	0.32093716	21.5670109	22.0809212	22.0804081	21.3538017	21.744566	20.9264603	21.1498013	21.9775658
1247	Phenylalanine--tRNA ligase alpha subunit OS=Rattus norvegicus OX=10116 GN=Farsa PE=1 SV=1	Farsa	Q505J8	0.05625082	0.0562911	20.2349892	20.6056652	20.38978	20.1975689	20.1881409	20.8313942	19.3810596	20.8022442
1248	Phenylalanyl-tRNA synthetase subunit beta OS=Rattus norvegicus OX=10116 GN=Farsb PE=1 SV=1	Farsb	Q68FT7	0.18462108	0.19445872	16.5799007	16.4852734	15.668788	16.0703163	16.3813515	15.3423929	15.4843245	16.8183746
1249	Phosphatase domain-containing, paladin 1 OS=Rattus norvegicus OX=10116 GN=Pald1 PE=1 SV=1	Pald1	D3ZCT5	0.51222287	0.29406404	18.6176434	17.7230244	17.5492039	17.9881935	18.030426	17.4819031	17.5868759	17.6026039
1250	Phosphate carrier protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Slc25a3 PE=1 SV=1	Slc25a3	Q6IRH6	0.51100451	-0.2445617	26.659132	27.2490864	27.4087677	27.5463753	27.4773579	27.4155464	27.7185154	27.2301884
1251	Phosphatidate cytidylyltransferase OS=Rattus norvegicus OX=10116 GN=Cds2 PE=1 SV=1	Cds2	G3V8W2	1.14637111	-0.2634487	18.7831936	18.8023548	18.7604313	19.1680946	19.1377354	19.0138226	19.3428307	19.0734806
1252	Phosphatidylethanolamine-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Pebp1 PE=1 SV=3	Pebp1	P31044	0.44306124	-0.0659556	24.064909	23.8746071	23.9117584	23.8224163	23.90382	24.0695934	23.923357	24.0407429
1253	Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 OS=Rattus norvegicus OX=10116 GN=Ptpmt1 PE=1 SV=1	Ptpmt1	G3V7B6	0.05359156	-0.073494	22.1850109	20.2076244	20.273571	21.1475849	20.8619938	21.1714859	20.7442303	21.3300571
1254	Phosphatidylinositide phosphatase SAC1 OS=Rattus norvegicus OX=10116 GN=Sacm1l PE=1 SV=1	Sacm1l	Q9ES21	0.93319053	0.26605082	19.2076683	18.8809509	18.7993546	19.1588802	19.0371494	18.559494	18.745924	18.6400833
1255	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Rattus norvegicus OX=10116 GN=Inppl1 PE=1 SV=1	Inppl1	Q9WVR3	1.66454731	0.66353273	18.7436008	18.4211807	18.4429817	18.4644184	17.7351589	17.6558857	18.4515324	17.5754738
1256	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Rattus norvegicus OX=10116 GN=Pip4k2c PE=1 SV=1	Pip4k2c	G3V9W5	0.84147671	1.24758077	15.6558475	16.0313263	15.4140453	18.563467	15.26546	15.0233822	14.8403482	15.5451727
1257	Phosphatidylinositol binding clathrin assembly protein, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Picalm PE=1 SV=1	Picalm	A0A0G2JTT	1.3381648	0.43702841	18.540987	18.253727	18.4929733	18.5987225	17.9854927	18.276371	17.6100063	18.2664261
1258	Phosphatidylinositol transfer protein alpha isoform OS=Rattus norvegicus OX=10116 GN=Pitpna PE=1 SV=2	Pitpna	P16446	0.82653445	-0.7330093	16.003355	17.0879803	17.1756458	17.6730919	17.2708607	17.3978405	18.4720364	17.7313728
1259	Phosphatidylinositol transfer protein beta isoform OS=Rattus norvegicus OX=10116 GN=Pitpnb PE=1 SV=3	Pitpnb	D3ZCD4	1.00645338	-1.1335824	15.9709024	18.1575947	18.4588108	17.7951984	18.5019379	19.1660576	18.7551613	18.493679
1260	Phosphofurin acidic cluster sorting protein 1 OS=Rattus norvegicus OX=10116 GN=Pacs1 PE=1 SV=1	Pacs1	F1LPG3	1.22940612	1.09170604	16.3979073	15.2410383	14.8559723	15.9518461	15.2353411	14.801589	13.7836056	14.2594042
1261	Phosphoglucomutase 1 OS=Rattus norvegicus OX=10116 GN=Pgm1 PE=1 SV=2	Pgm1	Q499Q4	0.80413441	-0.2019033	22.2405167	22.2293892	22.1966763	22.6765118	22.5820084	22.4961929	22.6535931	22.4189129
1262	Phosphoglycerate kinase 1 OS=Rattus norvegicus OX=10116 GN=Pgk1 PE=1 SV=2	Pgk1	P16617	0.4789263	-0.0886464	24.7831039	24.6460171	24.663723	24.9968548	24.8072014	24.8894634	24.9082832	24.8393364
1263	Phosphoglycerate mutase 1 OS=Rattus norvegicus OX=10116 GN=Pgam1 PE=1 SV=4	Pgam1	P25113	0.06164439	-0.0220304	23.5967484	23.4815178	23.1525059	23.7088127	23.5800323	23.4335861	23.440918	23.5731697
1264	Phosphoglycerate mutase 2 OS=Rattus norvegicus OX=10116 GN=Pgam2 PE=1 SV=2	Pgam2	P16290	0.75107438	0.21064329	23.9179802	24.2641239	23.9238567	24.4649181	23.9718437	23.8520355	23.9861946	23.918232
1265	Phosphohistidine phosphatase 1 OS=Rattus norvegicus OX=10116 GN=Phpt1 PE=1 SV=1	Phpt1	D3ZP47	0.01059638	0.01579809	18.414341	19.1532612	19.3241749	17.2105179	18.2917175	18.7173405	18.7934914	18.2365532
1266	Phosphoinositide phospholipase C OS=Rattus norvegicus OX=10116 GN=Plcd3 PE=1 SV=1	Plcd3	D4A978	0.1528615	0.1435771	21.0783119	19.9818993	19.8392315	20.3434696	20.3371754	20.1202869	19.5624809	20.6486607
1267	Phospholipase A-2-activating protein OS=Rattus norvegicus OX=10116 GN=Plaa PE=1 SV=3	Plaa	P54319	0.5898447	-0.7406871	15.7015982	17.5315533	18.0178699	18.1006584	18.4230766	17.6374588	18.3741398	17.8797531
1268	Phospholipase B-like 1 OS=Rattus norvegicus OX=10116 GN=Plbd1 PE=2 SV=1	Plbd1	Q5U2V4	0.44969488	-0.1886292	19.3822136	18.669199	19.1789818	19.2587948	19.3751316	19.4270172	19.0007935	19.4407635
1269	Phospholipid hydroperoxide glutathione peroxidase OS=Rattus norvegicus OX=10116 GN=Gpx4 PE=1 SV=3	Gpx4	P36970	0.73822411	0.62762928	20.2486382	20.9154377	20.7967815	20.5644264	18.8994312	20.0974407	20.7159653	20.3019295
1270	Phosphomannomutase OS=Rattus norvegicus OX=10116 GN=Pmm2 PE=1 SV=1	Pmm2	B5DF46	0.40191951	-0.412241	18.2411575	16.8493538	16.9791718	16.8447189	17.2253342	18.1146088	18.1896248	17.0337982
1271	Phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform OS=Rattus norvegicus OX=10116 GN=Phkg1 PE=2 SV=2	Phkg1	P13286	1.36968402	-0.453402	19.9899559	19.6429119	19.8554001	19.7668133	20.2055988	20.1080017	20.7364559	20.0186329
1272	Phosphorylase b kinase regulatory subunit OS=Rattus norvegicus OX=10116 GN=Phka1 PE=1 SV=3	Phka1	F1LLZ7	0.03863611	-0.0591884	18.9725914	18.1144943	18.6589546	17.1419811	18.5344563	18.9181347	17.2952938	18.3768902
1273	Phosphorylase b kinase regulatory subunit OS=Rattus norvegicus OX=10116 GN=Phkb PE=1 SV=1	Phkb	Q5RKH5	2.07121514	0.25355721	21.6644421	21.5995827	21.8416882	21.6889076	21.4677563	21.5173645	21.469553	21.3257179
1274	Phytanoyl-CoA dioxygenase, peroxisomal OS=Rattus norvegicus OX=10116 GN=Phyh PE=1 SV=2	Phyh	P57093	0.45436215	0.32444954	20.5786896	21.5129719	20.4886932	20.1719284	20.7155819	20.0408192	20.2780724	20.4200115
1275	Pitrilysin metallopeptidase 1 OS=Rattus norvegicus OX=10116 GN=Pitrm1 PE=1 SV=1	Pitrm1	A0A0G2K6I	0.1944262	-0.2858665	18.1502972	15.9568453	16.7648602	16.5205326	16.5487843	16.5523224	17.5466671	17.8882275
1276	Plasma kallikrein OS=Rattus norvegicus OX=10116 GN=Klkb1 PE=1 SV=1	Klkb1	P14272	0.47556256	0.21585751	21.9510098	21.7638092	21.221735	21.1541824	21.3063202	21.1776199	21.4580727	21.2852936
1277	Plasma membrane calcium-transporting ATPase 1 OS=Rattus norvegicus OX=10116 GN=Atp2b1 PE=1 SV=3	Atp2b1	P11505	0.23118814	-0.1247535	21.2511959	21.1100445	21.5086308	20.498127	21.2373981	21.1086655	21.2717152	21.2492332
1278	Plasminogen activator inhibitor 1 RNA-binding protein OS=Rattus norvegicus OX=10116 GN=Serbp1 PE=1 SV=2	Serbp1	Q6AXS5	2.16486123	1.79744267	16.9081764	17.856842	17.0049839	16.9337692	14.9368792	15.5865545	14.6314421	16.3591251
1279	Plasminogen OS=Rattus norvegicus OX=10116 GN=Plg PE=2 SV=2	Plg	Q01177	0.01573082	-0.0198884	23.9999352	24.3270721	22.9831543	22.8273106	23.4799232	22.9796143	23.8600712	23.8974171
1280	Platelet factor 4 OS=Rattus norvegicus OX=10116 GN=Pf4 PE=1 SV=1	Pf4	P06765	0.72912365	-1.0214176	19.0894928	19.6381931	17.5176525	16.8302231	18.9170284	19.6484699	18.9959526	19.599781
1281	Platelet glycoprotein 4 OS=Rattus norvegicus OX=10116 GN=Cd36 PE=1 SV=3	Cd36	Q07969	0.99031778	-0.2366614	24.2516479	24.4379997	24.2263889	24.6047459	24.6586189	24.7792454	24.6527691	24.3767948
1282	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Rattus norvegicus OX=10116 GN=Pafah1b1 PE=1 SV=2	Pafah1b1	P63004	0.10911389	-0.0676889	19.3237801	19.3134747	19.5978012	19.7285938	19.7671547	19.7656116	19.7577324	18.9439068
1283	Pleckstrin homology domain-containing family F member 1 OS=Rattus norvegicus OX=10116 GN=Plekhf1 PE=2 SV=1	Plekhf1	Q68FU1	0.26085413	0.17416239	19.9938583	20.4861412	20.223774	20.1272793	19.5839939	20.3548584	19.6196251	20.5759258
1284	Pleckstrin homology-like domain family A member 3 OS=Rattus norvegicus OX=10116 GN=Phlda3 PE=2 SV=1	Phlda3	Q5PQT7	0.2818077	0.3109746	15.1680727	16.3437557	15.1751385	14.8004484	14.6449432	15.4127493	14.4337254	15.752099
1285	Pleckstrin homology-like domain family B member 1 OS=Rattus norvegicus OX=10116 GN=Phldb1 PE=1 SV=1	Phldb1	A0A0G2JV3	0.72490618	0.27224016	22.3031883	22.7255745	22.8288517	22.8166161	22.287159	22.1776047	22.7906075	22.3298988
1286	PNKD, MBL domain-containing OS=Rattus norvegicus OX=10116 GN=Pnkd PE=1 SV=1	Pnkd	M0RBK9	0.9042777	-0.8937163	19.2156506	20.9030018	21.1360264	21.243145	21.328125	21.9573555	21.5422955	21.2449131
1287	Podocalyxin OS=Rattus norvegicus OX=10116 GN=Podxl PE=1 SV=1	Podxl	A0A0G2K2I	1.25819825	-0.6094093	16.9001751	16.6738853	16.07094	16.1243362	16.589695	17.2539864	17.1814899	17.1818027
1288	Poly(rC)-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Pcbp2 PE=1 SV=1	Pcbp2	Q6AYU5	0.56615282	0.21881199	22.6075134	22.3929634	22.127758	22.3498363	22.241478	21.8515663	21.9751244	22.5346546
1289	Poly(rC)-binding protein 4 OS=Rattus norvegicus OX=10116 GN=Pcbp4 PE=4 SV=1	Pcbp4	D3ZCS3	0.11508777	-0.0525584	20.3412476	20.0342102	20.1169262	19.9257641	20.2203045	19.8753033	19.9970818	20.5356922
1290	Polymerase (RNA) I polypeptide C OS=Rattus norvegicus OX=10116 GN=Polr1c PE=1 SV=1	Polr1c	Q5RJK9	2.70741883	0.83934498	16.3868599	16.4879456	16.1580276	16.5595074	15.7208128	15.8220348	15.4713421	15.2207708
1291	Polymerase (RNA) II (DNA directed) polypeptide C, 33kDa OS=Rattus norvegicus OX=10116 GN=Polr2c PE=1 SV=1	Polr2c	Q5EB90	0.87178087	0.24732256	17.7018661	17.3474731	17.2118549	17.186018	17.1893787	16.9085293	17.0815392	17.2784748
1292	Polypyrimidine tract binding protein 1, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ptbp1 PE=1 SV=1	Ptbp1	Q6P736	1.58794834	0.38853598	22.9061966	22.823679	22.7288628	22.8296127	22.388092	22.1145554	22.508543	22.7230167
1293	Polypyrimidine tract-binding protein 3 OS=Rattus norvegicus OX=10116 GN=Ptbp3 PE=1 SV=1	Ptbp3	A0A0G2JV5	0.46001075	0.55735445	18.4300098	17.6848221	17.7926331	17.4124279	15.822567	17.7977448	17.4077358	18.0624275
1294	Popeye domain-containing 2 OS=Rattus norvegicus OX=10116 GN=Popdc2 PE=1 SV=1	Popdc2	Q6P722	1.03371937	0.84784222	17.738039	19.4575748	18.8979702	18.9149475	17.5810299	17.5605297	18.5017223	17.9738808

1295	PPARGC1 and ESRR-induced regulator, muscle 1 OS=Rattus norvegicus OX=10116 GN=Perm1 PE=1 SV=1	Perm1	D3ZH76	0.87035888	0.69034243	19.8972225	18.6613884	19.5949917	19.4972553	18.8323021	18.1633625	19.5173969	18.3764267
1296	PPFIA-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ppfibp1 PE=1 SV=1	Ppfibp1	A0A0G2K78	0.55045809	0.74570322	17.887434	19.9380341	19.1607704	19.9127407	17.6647034	19.1249523	17.8929462	19.2335644
1297	PPFIA-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Ppfibp1 PE=1 SV=1	Ppfibp1	D3ZJW3	0.20037994	0.26157212	15.1192427	16.900177	17.2849674	17.1362934	16.0982475	16.4352837	16.6233902	16.2374706
1298	PRA1 family protein OS=Rattus norvegicus OX=10116 GN=Arl6ip5 PE=1 SV=1	Arl6ip5	A0A0H2UH	0.27545602	-0.0613289	19.948164	20.0231247	19.9280186	20.0553436	20.0396271	20.0425682	20.2716827	19.8460884
1299	Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Pbxip1 PE=1 SV=1	Pbxip1	A2VD12	0.58800563	-0.4995732	18.4192257	18.9826965	17.2822418	17.9633141	18.2978458	18.6370468	19.1373196	18.5735588
1300	Predicted gene 45713 OS=Rattus norvegicus OX=10116 GN=Gm45713 PE=3 SV=1	Gm45713	A0A1W2Q6	0.64067474	0.48375511	20.2941914	20.2988014	19.853735	20.4147472	20.1357803	20.0037651	18.7174721	20.069437
1301	Prelamin-A/C OS=Rattus norvegicus OX=10116 GN=Lmna PE=1 SV=1	Lmna	P48679	0.16954771	-0.4666586	17.8131371	15.71558	17.3234863	20.7670097	18.3787117	18.7075653	17.9496956	18.4498749
1302	Prenylcysteine oxidase OS=Rattus norvegicus OX=10116 GN=Pcyox1 PE=1 SV=1	Pcyox1	Q99ML5	1.32824755	0.3531785	18.4464836	18.3098965	18.0835304	18.0353775	17.8457775	17.8494225	17.6312752	18.1360989
1303	Presenilins-associated rhomboid-like protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Parl PE=1 SV=3	Parl	F1LPN4	0.01848843	0.05703998	15.8236876	16.7238426	16.57967	15.9433498	17.3461304	13.1672649	17.460989	16.8680058
1304	Presequence translocase-associated motor 16 OS=Rattus norvegicus OX=10116 GN=Pam16 PE=1 SV=1	Pam16	D3ZZV1	0.00339159	0.00270081	18.500494	18.3740482	18.5727882	19.2964668	18.4949245	18.4612694	19.1724739	18.6043262
1305	Probable proline--tRNA ligase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pars2 PE=2 SV=1	Pars2	Q5M7W7	1.62402861	1.12145686	16.7679291	17.5921898	17.7560062	16.7580719	16.4768639	16.1327133	16.433836	15.3449564
1306	Probable tRNA N6-adenosine threonylcarbamoyltransferase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Osgepl1 PE=2 SV=1	Osgepl1	Q4V7F3	0.50838364	1.4857204	18.4633732	17.5400047	13.6054335	17.631237	14.869523	15.1526728	13.7769794	17.4979916
1307	Procollagen C-endopeptidase enhancer 1 OS=Rattus norvegicus OX=10116 GN=Pcolce PE=1 SV=1	Pcolce	O08628	0.25972644	0.33423924	17.0847416	16.7364616	15.6909838	15.6688833	15.9310808	14.8861122	16.5037174	16.5232029
1308	Profilin-1 OS=Rattus norvegicus OX=10116 GN=Pfn1 PE=1 SV=2	Pfn1	P62963	0.0209593	0.01736069	22.1783752	22.2483692	21.1445866	22.1478844	21.7264767	21.7705231	21.9831295	22.1696434
1309	Programmed cell death 6-interacting protein OS=Rattus norvegicus OX=10116 GN=Pdcd6ip PE=1 SV=2	Pdcd6ip	Q9QZA2	0.03346481	-0.03334	19.6505089	19.3769627	19.1034737	18.4709663	18.8376789	19.3960876	18.7625198	19.7389851
1310	Prohibitin OS=Rattus norvegicus OX=10116 GN=Phb PE=1 SV=1	Phb	P67779	0.77467503	-0.3856168	24.5659771	25.2290745	25.5676765	25.4665546	25.6083794	25.644516	25.7961655	25.3226891
1311	Prohibitin-2 OS=Rattus norvegicus OX=10116 GN=Phb2 PE=1 SV=1	Phb2	Q5XIH7	0.70391456	-0.3568535	24.5132217	24.9531097	25.3999195	25.4152546	25.5213089	25.420702	25.6700115	25.0968971
1312	Prolargin OS=Rattus norvegicus OX=10116 GN=Prelp PE=2 SV=1	Prelp	Q9EQP5	0.27222624	0.2172513	23.2451687	23.5702877	22.9004517	22.1903515	22.9887409	22.5800934	22.4434128	23.0250072
1313	Proliferation-associated protein 2G4 OS=Rattus norvegicus OX=10116 GN=Pa2g4 PE=1 SV=1	Pa2g4	Q6AYD3	1.43702832	0.68226576	16.9045944	17.8831711	17.2022533	17.7204685	16.949892	16.4157486	16.8397598	16.7760239
1314	Prolyl 4-hydroxylase subunit alpha-1 OS=Rattus norvegicus OX=10116 GN=P4ha1 PE=2 SV=2	P4ha1	P54001	0.41782564	-0.3672957	16.9822369	16.7638111	16.3992825	15.4027863	16.7623901	16.4028778	17.2200794	16.6319523
1315	Prolyl-tRNA synthetase-associated domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Prorsd1 PE=1 SV=1	Prorsd1	B2RZA5	1.1128489	1.21858907	18.9962578	16.9503231	18.329567	17.3000717	17.4798985	16.6044884	15.8871927	16.7302837
1316	Promethin OS=Rattus norvegicus OX=10116 GN=Tmem159 PE=4 SV=1	Tmem159	A0A0G2JSZ	0.09897969	0.13064122	16.6283245	16.5010166	17.3996105	16.4784832	16.9697266	15.3645353	17.323822	16.826786
1317	Propionyl coenzyme A carboxylase, beta polypeptide OS=Rattus norvegicus OX=10116 GN=Pccb PE=1 SV=1	Pccb	Q68FZ8	0.12852146	-0.083498	25.3971462	25.0087738	25.6029682	24.8615627	25.5349808	25.6590271	25.056469	24.9539661
1318	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pcca PE=1 SV=1	Pcca	A0A0G2K40	0.1845216	0.08421707	26.9095421	26.5913563	27.071228	26.5601864	26.9589729	26.8580284	26.5794239	26.3990192
1319	Prosaposin OS=Rattus norvegicus OX=10116 GN=Psap PE=1 SV=2	Psap	F7EPE0	1.28833512	-0.5554905	19.7141762	20.3542442	20.5739231	20.4405632	20.8535957	20.5033875	21.1211605	20.826725
1320	Prostacyclin synthase OS=Rattus norvegicus OX=10116 GN=Ptgis PE=2 SV=1	Ptgis	Q62969	1.54486235	-0.5003047	19.134346	19.4859295	19.3594456	19.1516418	19.8840256	19.3318577	19.915451	20.0012474
1321	Prostaglandin E synthase 2 OS=Rattus norvegicus OX=10116 GN=Ptges2 PE=1 SV=1	Ptges2	D4AE56	1.1032275	-0.5156279	21.1019993	21.7158985	21.909029	21.7935829	22.3363152	22.0095425	22.483429	21.7537346
1322	Prostaglandin E synthase 3 OS=Rattus norvegicus OX=10116 GN=Ptges3 PE=1 SV=2	Ptges3	P83868	1.71317529	1.7994585	18.4763737	19.7755013	19.4384441	18.6823864	18.7246017	16.7780228	16.7893257	16.8829212
1323	Prostaglandin reductase 2 OS=Rattus norvegicus OX=10116 GN=Ptgr2 PE=2 SV=2	Ptgr2	Q5BK81	0.18248791	0.20162153	19.7021866	19.0803242	19.3753052	20.8026104	19.9489956	19.8258133	19.864933	19.5141983
1324	Prostamide/prostaglandin F synthase OS=Rattus norvegicus OX=10116 GN=Prxl2b PE=3 SV=1	Prxl2b	D3ZVR7	0.01322395	0.0214982	18.7265663	18.803215	18.6009331	16.560751	18.2195549	18.0125027	17.96492	18.4084949
1325	Proteasomal ubiquitin receptor ADRM1 OS=Rattus norvegicus OX=10116 GN=Adrm1 PE=1 SV=2	Adrm1	Q9JMB5	0.05599898	-0.077322	19.6237469	18.89431	17.7759914	17.8851776	19.0406895	18.5416374	18.8359642	18.0702229
1326	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 12 OS=Rattus norvegicus OX=10116 GN=Psmd12 PE=1 SV=1	Psmd12	Q5XIC6	0.48631946	0.22974396	20.3910313	20.5949764	19.7425156	20.501482	20.1942368	20.0785465	19.8096218	20.2286243
1327	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 14 OS=Rattus norvegicus OX=10116 GN=Psmd14 PE=1 SV=1	Psmd14	Q4V8E2	0.59589236	0.59393644	18.8691998	18.9333782	18.232523	17.4218216	18.0397835	16.9394226	17.6971951	18.4047756
1328	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 3 OS=Rattus norvegicus OX=10116 GN=Psmd3 PE=1 SV=1	Psmd3	Q5U2S7	1.04138157	0.55188942	20.5226955	20.2110806	19.710043	20.2463913	19.2289467	19.9668694	19.2658234	20.0210133
1329	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 6 OS=Rattus norvegicus OX=10116 GN=Psmd6 PE=1 SV=1	Psmd6	Q6PCT9	0.92311998	0.27504778	21.163826	20.9392395	20.5296307	21.1297817	20.5702133	20.6986866	20.7629833	20.6304035
1330	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 7 (Predicted) OS=Rattus norvegicus OX=10116 GN=Psmd7 PE=1 SV=1	Psmd7	D4AEH3	0.84574433	0.49040508	19.3630047	19.5074863	18.8159676	20.0604095	19.2170773	18.8977547	18.5808887	19.0895271
1331	Proteasome (Prosome, macropain) activator subunit 1 OS=Rattus norvegicus OX=10116 GN=Psme1 PE=1 SV=1	Psme1	Q6P9V7	0.25051881	0.08366776	21.3902721	20.9648476	21.2498569	20.9742851	21.0784492	21.0891209	20.8289127	21.2481079
1332	Proteasome 26S subunit, ATPase 6 OS=Rattus norvegicus OX=10116 GN=Psmc6 PE=1 SV=1	Psmc6	G3V6W6	0.99588634	0.65788269	21.6862679	21.2802486	20.7350559	21.2644253	20.8136005	20.2307739	20.0351582	21.2549343
1333	Proteasome 26S subunit, non-ATPase 8 OS=Rattus norvegicus OX=10116 GN=Psmd8 PE=1 SV=1	Psmd8	F1LMQ3	0.477869	0.34643316	20.2090111	20.4885769	19.4196243	20.0779781	19.5096226	19.7141151	19.2322063	20.3535137
1334	Proteasome activator complex subunit 2 OS=Rattus norvegicus OX=10116 GN=Psme2 PE=2 SV=3	Psme2	Q63798	0.03077753	0.05466747	18.5458126	19.8566093	19.1527748	19.2719364	19.0351715	18.186945	18.6737614	20.7125854
1335	Proteasome subunit alpha type OS=Rattus norvegicus OX=10116 GN=Psma7 PE=1 SV=1	Psma7	A0A0G2K0V	0.0745138	-0.0716038	19.4585991	20.8380852	20.8647804	20.5119133	20.4599075	20.2232285	20.5891151	20.687542
1336	Proteasome subunit alpha type-1 OS=Rattus norvegicus OX=10116 GN=Psma1 PE=1 SV=2	Psma1	P18420	0.37058907	0.26119757	21.5498199	21.4508858	20.6215363	20.5150623	20.8255291	20.5384445	20.573204	21.1553364
1337	Proteasome subunit alpha type-3 OS=Rattus norvegicus OX=10116 GN=Psma3 PE=1 SV=3	Psma3	P18422	0.34393963	0.2907877	19.2174778	18.6843376	17.8086414	18.0871868	18.4340591	18.2783661	18.2934952	17.6285725
1338	Proteasome subunit alpha type-4 OS=Rattus norvegicus OX=10116 GN=Psma4 PE=1 SV=1	Psma4	P21670	0.11386514	-0.2535691	18.1119556	14.3305264	15.9467449	17.0237598	16.4777718	17.0190582	16.1723404	16.7580929
1339	Proteasome subunit alpha type-5 OS=Rattus norvegicus OX=10116 GN=Psma5 PE=1 SV=1	Psma5	P34064	0.91588159	0.37882853	19.4393921	19.4669323	19.1309509	18.7439957	18.8272648	18.688736	18.5877209	19.1622353
1340	Proteasome subunit alpha type-6 OS=Rattus norvegicus OX=10116 GN=Psma6 PE=1 SV=1	Psma6	P60901	0.99065263	0.69976807	18.4317837	18.5518246	18.6348553	19.2203789	18.3169727	17.573288	17.396719	18.7527905
1341	Proteasome subunit beta OS=Rattus norvegicus OX=10116 GN=LOC100360846 PE=3 SV=1	LOC100360	A0A0G2JSL0	0.80186214	0.54872847	18.4643345	18.9143944	19.1811562	19.1548634	18.7216759	18.5919456	17.4937801	18.7124329
1342	Proteasome subunit beta OS=Rattus norvegicus OX=10116 GN=Psmb5 PE=1 SV=1	Psmb5	G3V7Q6	0.01376033	0.01177263	17.9529572	18.9714317	18.6968765	18.5203495	18.2279072	18.1560154	18.8168106	18.8937912
1343	Proteasome subunit beta type-1 OS=Rattus norvegicus OX=10116 GN=Psmb1 PE=1 SV=3	Psmb1	P18421	0.03524137	0.03125048	19.4318695	20.0059566	19.1272888	20.10355	19.752924	20.0833397	19.1294518	19.5779476
1344	Proteasome subunit beta type-10 OS=Rattus norvegicus OX=10116 GN=Psmb10 PE=2 SV=1	Psmb10	Q4KM35	0.28031994	0.24309778	16.8459358	16.8152008	16.9153709	16.3006859	16.5639038	15.6343403	16.4572716	17.2492867
1345	Protein ABHD18 OS=Rattus norvegicus OX=10116 GN=Abhd18 PE=4 SV=3	Abhd18	D4A556	1.49971557	0.33642483	20.8462486	21.1668568	21.0179825	20.6947346	20.6584778	20.6832714	20.4070148	20.6313591
1346	Protein AMBP OS=Rattus norvegicus OX=10116 GN=Ambp PE=1 SV=1	Ambp	Q64240	0.36936095	0.79133391	18.250927	18.3002052	17.1790237	17.6593857	14.3921003	17.8034344	17.9038486	18.1248226
1347	Protein disulfide-isomerase A6 OS=Rattus norvegicus OX=10116 GN=Pdia6 PE=1 SV=1	Pdia6	A0A0G2JSZ5	0.62578908	-0.3275943	20.057209	20.9430828	20.1279144	20.7767563	20.7488174	20.899498	21.0356979	20.5313263
1348	Protein disulfide-isomerase OS=Rattus norvegicus OX=10116 GN=P4hb PE=1 SV=2	P4hb	P04785	0.0149058	-0.0091147	21.7252769	22.1414165	21.4903297	22.3728523	21.9975662	21.7948284	21.9238949	22.050045
1349	Protein disulfide-isomerase OS=Rattus norvegicus OX=10116 GN=Pdia3 PE=1 SV=1	Pdia3	A0A0H2UH	0.31475656	0.14350367	22.8946075	23.544529	23.4678364	22.9404812	22.9051323	23.0585957	22.9919128	23.3177986
1350	Protein ERGIC-53 OS=Rattus norvegicus OX=10116 GN=Lman1 PE=1 SV=1	Lman1	Q62902	0.81605862	-0.3095465	20.7759724	20.8861046	20.6675053	21.3310223	21.2425079	20.9271946	21.5172253	21.2118626
1351	Protein FAM136A OS=Rattus norvegicus OX=10116 GN=Fam136a PE=1 SV=1	Fam136a	B0BN94	0.06780412	0.23507357	16.5196438	17.3332253	17.5196438	14.3871489	17.4847431	17.1174889	13.2008543	17.0162811
1352	Protein FAM162A OS=Rattus norvegicus OX=10116 GN=Fam162a PE=2 SV=1	Fam162a	Q4QQV3	0.98507714	-0.4558969	24.2076054	24.64814	24.6395893	24.7815342	25.0006752	24.8337498	25.5967903	24.669241
1353	Protein FAM210A OS=Rattus norvegicus OX=10116 GN=Fam210a PE=2 SV=1	Fam210a	Q5XIJ4	0.80554769	-0.5053372	20.4926662	21.1974602	21.4892139	21.7627563	21.6434345	21.8577328	22.0843296	21.3779488
1354	Protein fem-1 homolog A OS=Rattus norvegicus OX=10116 GN=Fem1a PE=2 SV=1	Fem1a	Q4V890	1.5737023	0.88928986	20.2436333	20.3480053	19.7619324	19.4043198	18.5943871	19.6181335	18.9816399	19.0065708
1355	Protein kinase C and casein kinase substrate in neurons 2 protein OS=Rattus norvegicus OX=10116 GN=Pacsin2 PE=1 SV=2	Pacsin2	Q9QY17	0.11312634	-0.1041431	19.0787811	20.1671295	19.7191544	20.268322	19.9553566	19.9332275	19.3735428	20.3878326
1356	Protein kinase C and casein kinase substrate in neurons 3 OS=Rattus norvegicus OX=10116 GN=Pacsin3 PE=1 SV=3	Pacsin3	G3V9N7	0.22850112	-0.3263412	20.4133053	20.7344952	19.9207745	19.8098793	22.0838356	20.160902	19.6313286	20.3077526
1357	Protein kinase C substrate 80K-H OS=Rattus norvegicus OX=10116 GN=Prkcsh PE=1 SV=1	Prkcsh	B1WC34	0.16961534	-0.0937886	18.2968941	18.8051758	18.419281	18.8475723	18.6399784	18.6643696	19.1183224	18.3214073
1358	Protein kinase, cAMP-dependent, catalytic, alpha OS=Rattus norvegicus OX=10116 GN=Prkaca PE=1 SV=1	Prkaca	A1L1M0	1.17582158	0.29863119	20.8348389	20.5762138	20.6161594	20.6529617	20.5040054	20.3071899	20.062603	20.6118507
1359	Protein KTI12 homolog OS=Rattus norvegicus OX=10116 GN=Kti12 PE=1 SV=1	Kti12	Q5I0L7	0.16444315	0.15435076	20.1703148	18.9447956	19.4508114	19.0385609	19.5289097	19.6348953	18.6076832	19.2155914
1360	Protein Mpv17 OS=Rattus norvegicus OX=10116 GN=Mpv17 PE=2 SV=1	Mpv17	Q5BK62	0.56450027	-0.5849407	14.6357546	14.7558622	15.7512178	15.9503984	16.0324841	16.5332336	15.9846277	14.8826504
1361	Protein NDRG1 OS=Rattus norvegicus OX=10116 GN=Ndrg1 PE=1 SV=1	Ndrg1	Q6JE36	1.45920537	-0.6643467	16.0846539	16.6181812	16.6945171	15.7831116	17.2752304	16.84762	16.775032	16.9399681
1362	Protein Niban OS=Rattus norvegicus OX=10116 GN=Fam129a PE=1 SV=2	Fam129a	Q9ESN0	0.23243808	-0.2485166	19.4640255	19.5243759	18.5379639	19.0921535	19.5521793	19.6442375	20.0626755	18.3534927
1363	Protein O-GlcNAcase OS=Rattus norvegicus OX=10116 GN=Oga PE=1 SV=1	Oga	A0A0H2UI1	0.85619476	-0.9657369	17.5669384	16.6618938	17.2632084	16.2497292	17.2439804	17.359396	17.6764736	19.3248672
1364	Protein phosphatase 1 regulatory subunit OS=Rattus norvegicus OX=10116 GN=Ppp1r3d PE=1 SV=1	Ppp1r3d	D3ZZ26	0.76261127	0.62214756	21.6997757	21.2755566	21.2949982	20.2482529	20.3600121	21.235075	20.0303802	20.4045258
1365	Protein phosphatase 1K (PP2C domain containing) (Predicted) OS=Rattus norvegicus OX=10116 GN=Ppm1k PE=1 SV=1	Ppm1k	D4A7X5	0.51898037	0.72738504	17.4847736	16.6097221	18.372076	16.4323177	15.9618721	16.1379299	15.9986153	17.8909321
1366	Protein phosphatase 2 (Formerly 2A), regulatory subunit A (PR 65), alpha isoform, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Ppp2r1a PE=1 SV=1	Ppp2r1a	Q5XI34	0.21213732	0.08107567	21.4980068	21.2460518	21.1800175	21.3124695	21.1262379	21.323267	20.9131889	21.5495491

1367	Protein phosphatase 2C, magnesium dependent, catalytic subunit, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Pdp1 PE=1 SV=1	Pdp1	A0A0G2QC	0.40979972	0.71868682	17.4336205	18.6670094	16.4660587	17.9459171	17.9254913	15.1989241	16.7932415	17.7202015
1368	Protein phosphatase 6, regulatory subunit 1 OS=Rattus norvegicus OX=10116 GN=Ppp6r1 PE=1 SV=1	Ppp6r1	A0A0G2JTK	0.54499584	0.63329077	16.9332638	16.6589069	15.8883104	15.9317389	14.735301	16.400631	16.6438675	15.0992575
1369	Protein quaking-like OS=Rattus norvegicus OX=10116 GN=LOC108348175 PE=4 SV=1	LOC108348	A0A0G2JUS	0.46982358	1.02454448	20.0799236	18.9895458	19.2996101	19.1560631	19.3885651	18.9691505	15.5116472	19.5576019
1370	Protein S100-A10 OS=Rattus norvegicus OX=10116 GN=S100a10 PE=1 SV=2	S100a10	P05943	0.73764429	-0.6135969	19.2080097	19.4332733	18.750021	19.9844074	19.7726097	20.8241997	19.9222889	19.3110008
1371	Protein S100-A11 OS=Rattus norvegicus OX=10116 GN=S100a11 PE=3 SV=1	S100a11	Q6B345	1.69728792	-0.5503159	15.314887	15.3066101	15.0025845	15.4476633	15.3989725	15.8841276	15.8957424	16.0941658
1372	Protein S100-A4 OS=Rattus norvegicus OX=10116 GN=S100a4 PE=2 SV=1	S100a4	P05942	0.53642034	0.67206335	17.6802368	18.3993473	16.9083099	19.5985527	17.2134819	17.4457855	17.5624809	17.676445
1373	Protein S100-A6 OS=Rattus norvegicus OX=10116 GN=S100a6 PE=1 SV=3	S100a6	P05964	0.54008935	0.30794334	21.1162357	21.232872	20.6360855	21.8259754	20.9649734	21.0798206	20.6103477	20.9242535
1374	Protein SEC13 homolog OS=Rattus norvegicus OX=10116 GN=Sec13 PE=1 SV=1	Sec13	Q5XFW8	1.07579234	0.23826504	20.6616879	20.97995	20.850481	20.8660374	20.318943	20.6812611	20.6888618	20.7160301
1375	Protein transport protein sec16 OS=Rattus norvegicus OX=10116 GN=Sec16a PE=1 SV=1	Sec16a	D3ZN76	0.2154876	-0.0950789	18.9212456	19.223999	18.6328907	18.4858875	18.9369583	18.7298126	18.9303761	19.0471916
1376	Protein transport protein SEC23 OS=Rattus norvegicus OX=10116 GN=Sec23a PE=1 SV=1	Sec23a	B5DFC3	0.30313237	0.14648247	22.8748722	22.3771248	22.2616196	22.4833183	22.2399197	22.7829723	22.064949	22.323164
1377	Protein transport protein Sec31A OS=Rattus norvegicus OX=10116 GN=Sec31a PE=1 SV=1	Sec31a	G3V699	0.46930294	0.29883051	20.2793255	19.4904995	19.0198479	19.5632172	19.5063953	19.4297047	18.9470367	19.2744312
1378	Protein/nucleic acid deglycase DJ-1 OS=Rattus norvegicus OX=10116 GN=Park7 PE=1 SV=1	Park7	O88767	0.59769002	-0.1441455	22.460762	22.4909019	22.0232124	22.3595524	22.4015675	22.5616093	22.523077	22.424757
1379	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Pcmtd1 PE=1 SV=1	Pcmtd1	D4A629	0.50290349	-0.2913513	19.488863	19.3947353	20.1567612	19.9496365	19.8293934	20.0807228	20.5613117	19.6839733
1380	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Rattus norvegicus OX=10116 GN=Pcmt1 PE=1 SV=2	Pcmt1	P22062	0.07740931	0.06993055	18.7658653	19.6857357	20.1520653	19.7170467	19.379158	19.6034641	19.1971169	19.8612518
1381	Proteolipid protein 2 OS=Rattus norvegicus OX=10116 GN=Plp2 PE=2 SV=1	Plp2	Q6P742	0.71822167	-0.255435	19.3969021	19.7629223	19.4041367	19.7113686	19.7567978	19.4946766	20.187809	19.8577862
1382	Prothrombin OS=Rattus norvegicus OX=10116 GN=F2 PE=1 SV=1	F2	G3V843	1.24010961	-1.1995492	17.9082298	19.8574848	19.166153	17.9756966	19.4395123	20.2748985	20.1813221	19.8100281
1383	Protoporphyrinogen oxidase OS=Rattus norvegicus OX=10116 GN=Ppox PE=1 SV=1	Ppox	D3ZVN7	0.19169587	0.12210464	20.5980301	20.7056446	21.1159897	19.9265022	20.5513	20.4534302	20.3500271	20.5029907
1384	PTC7 protein phosphatase homolog OS=Rattus norvegicus OX=10116 GN=Ptpc7 PE=1 SV=1	Pptc7	D4A520	0.22023772	0.17304754	21.1386223	20.6372318	20.4150486	20.4475403	20.7039509	20.7488308	19.6888542	20.8046169
1385	Purine nucleoside phosphorylase OS=Rattus norvegicus OX=10116 GN=Pnp PE=1 SV=1	Pnp	P85973	0.20593512	0.44067287	18.8995571	18.2579536	18.0752258	21.7042694	19.0266151	18.8298149	18.8210773	18.4968071
1386	Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Pyroxd2 PE=2 SV=1	Pyroxd2	Q68FT3	0.41321707	-0.2830725	21.8968582	21.814661	21.9357109	21.588707	22.8043919	22.3060589	21.781826	21.4759502
1387	Pyridoxal-dependent decarboxylase domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Pdxdc1 PE=1 SV=1	Pdxdc1	G3V6B0	0.05952082	-0.0459714	20.3711262	19.8476582	19.3769341	19.3501549	19.7568474	19.7836628	19.4772854	20.1119633
1388	Pyrophosphatase (inorganic) 2 OS=Rattus norvegicus OX=10116 GN=Ppa2 PE=1 SV=2	Ppa2	D4A830	0.44201026	-0.2422185	20.9706383	20.7822342	21.5822849	21.6179218	21.6293411	21.3809795	21.7261868	21.1854458
1389	Pyrroline-5-carboxylate reductase 3 OS=Rattus norvegicus OX=10116 GN=Pycr3 PE=2 SV=1	Pycr3	Q5PQJ6	0.82232896	0.35680914	22.2635021	22.1161613	21.939682	22.2971134	21.4847488	21.4582653	21.9526997	22.2935085
1390	Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pc PE=1 SV=1	Pc	A0A0G2JTL	1.11680009	0.52451181	24.642868	24.5857601	25.0651226	24.1229706	24.2064133	24.0620174	23.6684647	24.3817787
1391	Pyruvate dehydrogenase E1 component subunit alpha OS=Rattus norvegicus OX=10116 PE=1 SV=3	10116	D4A5G8	0.70920605	0.2010417	25.869812	25.9055634	25.6950073	25.9292145	25.7364445	25.9669456	25.4041023	25.4879379
1392	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pdhb PE=1 SV=1	Pdhb	A0A0G2KA1	0.12146903	0.04399347	25.4164181	25.5999527	25.6387863	25.6220284	25.5166473	25.8731461	25.2886448	25.4227734
1393	Pyruvate dehydrogenase kinase, isoenzyme 4 OS=Rattus norvegicus OX=10116 GN=Pdk4 PE=1 SV=1	Pdk4	G3V778	1.25561087	0.63689661	22.9454422	22.9656277	23.2203426	23.8335438	22.6753559	22.5804596	22.9961586	22.1653957
1394	Pyruvate dehydrogenase phosphatase regulatory subunit OS=Rattus norvegicus OX=10116 GN=Pdpr PE=1 SV=1	Pdpr	D3ZXA6	0.63787566	0.37087774	18.7401695	18.9021435	17.9912395	19.0644855	18.2609558	18.0477467	18.1894474	18.7163773
1395	Pyruvate kinase PKM OS=Rattus norvegicus OX=10116 GN=Pkm PE=1 SV=3	Pkm	P11980	0.01118444	-0.0036402	24.1897564	23.8906841	24.0681686	24.3985004	24.1177883	24.1136456	24.1148586	24.2153778
1396	Quinone oxidoreductase-like protein 2 OS=Rattus norvegicus OX=10116 PE=2 SV=1	10116	B0BNC9	0.41024451	-0.5709763	21.8207397	21.8594494	20.8015614	19.3482876	21.8314075	21.2982388	21.8199139	21.1643829
1397	Rab GDP dissociation inhibitor alpha OS=Rattus norvegicus OX=10116 GN=Gdi1 PE=1 SV=1	Gdi1	P50398	0.14497129	-0.1279483	17.2120762	16.4987431	16.5861645	17.0247135	16.3857441	16.9024143	16.7877693	17.7575626
1398	Rab GDP dissociation inhibitor beta OS=Rattus norvegicus OX=10116 GN=Gdi2 PE=1 SV=2	Gdi2	P50399	0.1897385	0.11118937	22.0248375	21.2111378	21.0271759	21.3009262	21.333725	21.2782307	21.0857391	21.4216251
1399	RAB10, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab10 PE=1 SV=1	Rab10	Q5RKJ9	0.21180891	-0.107306	21.3849239	21.2758007	20.8503437	21.6357994	21.3536835	21.356966	21.7161942	21.1492481
1400	RAB11 family-interacting protein 5 OS=Rattus norvegicus OX=10116 GN=Rab11fip5 PE=1 SV=1	Rab11fip5	A0A0G2K4A	0.01865116	-0.0271668	18.7170506	20.1733036	19.5958824	18.9986572	19.3150978	18.7661953	19.0454712	20.4667969
1401	RAB14, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab14 PE=1 SV=1	Rab14	B0BMW0	3.05053844	-1.3645992	19.4478226	19.6217728	18.8622284	18.7815495	20.4601803	20.767046	20.5369244	20.4076195
1402	RAB22A, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab22a PE=1 SV=1	Rab22a	B0BN19	1.09239039	-0.3494554	19.7520237	20.0829792	20.0974426	19.5474396	20.2315025	20.3080444	20.3984222	19.9397373
1403	Rab28 protein OS=Rattus norvegicus OX=10116 GN=Rab28 PE=2 SV=1	Rab28	Q6IN03	0.12961341	0.21604371	17.4199181	16.1570168	14.7125883	16.2256145	16.2388477	15.1052561	16.4296818	15.8771772
1404	RAB5B, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab5b PE=1 SV=1	Rab5b	A1L1J8	0.16004077	-0.0438814	21.4330578	21.1476345	21.0024624	21.3111038	21.198679	21.1928825	21.3967972	21.2814255
1405	RAB5C, member RAS oncogene family OS=Rattus norvegicus OX=10116 GN=Rab5c PE=1 SV=1	Rab5c	B0BNK1	1.32880242	-0.5265346	18.6598835	18.6468658	18.3463039	18.176012	18.464756	19.1755848	19.0896702	19.2051926
1406	RAC-alpha serine/threonine-protein kinase OS=Rattus norvegicus OX=10116 GN=Akt1 PE=1 SV=1	Akt1	P47196	0.14919942	0.15986633	18.0777912	18.2082806	17.8212833	16.5938301	17.8961544	17.3617764	17.1069431	17.696846
1407	RAF proto-oncogene serine/threonine-protein kinase OS=Rattus norvegicus OX=10116 GN=Raf1 PE=1 SV=1	Raf1	P11345	0.03028505	-0.0391688	20.6119385	19.8628788	18.7118645	19.0361366	19.9461346	19.3953724	19.4759102	19.5620766
1408	Ragulator complex protein LAMTOR1 OS=Rattus norvegicus OX=10116 GN=Lamtor1 PE=1 SV=1	Lamtor1	Q6P791	1.26069826	-0.740591	16.7245045	16.9738903	16.6092987	15.6670856	17.2886829	17.0299606	17.0574932	17.5610065
1409	RALY heterogeneous nuclear ribonucleoprotein OS=Rattus norvegicus OX=10116 GN=Raly PE=1 SV=2	Raly	E9PTI6	0.29834749	-0.2217031	16.8726501	17.8134079	17.5366383	17.9061661	18.1071854	17.4217548	18.1132526	17.3734818
1410	RAN-binding protein 10 OS=Rattus norvegicus OX=10116 GN=Ranbp10 PE=1 SV=2	Ranbp10	D3Z7Z5	0.30909775	0.16080093	17.3375568	16.9228878	17.3245182	16.4887638	16.6134911	16.9662056	16.9982643	16.852562
1411	Rap guanine nucleotide exchange factor 1 OS=Rattus norvegicus OX=10116 GN=Rapgef1 PE=1 SV=3	Rapgef1	F1M8L9	0.68030266	0.97867489	15.8257961	17.25667	15.6408825	15.1452799	16.2237225	14.2154112	14.0148058	15.4999895
1412	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 OS=Rattus norvegicus OX=10116 GN=Raph1 PE=1 SV=2	Raph1	D4ADX8	0.74584814	0.58739614	19.7543621	19.4792233	19.8031178	18.7969704	19.1760559	18.4862499	18.238018	19.583765
1413	RAS guanyl-releasing protein 2 OS=Rattus norvegicus OX=10116 GN=Rasgrp2 PE=1 SV=1	Rasgrp2	P0C643	0.25183447	-0.2055969	21.1096802	21.6705036	21.8846092	22.3598557	21.7108173	21.8914661	22.5735798	21.6711731
1414	Ras homolog family member G OS=Rattus norvegicus OX=10116 GN=Rhog PE=1 SV=1	Rhog	Q32PX6	1.21476246	-0.9801803	17.4002323	18.3537598	16.6421261	17.7164574	18.00214	18.2319889	18.998558	18.8006096
1415	Ras homolog family member T1 OS=Rattus norvegicus OX=10116 GN=Rhot1 PE=1 SV=1	Rhot1	A0A0G2K77	0.44865929	-0.4654112	16.5987892	18.072855	18.2053165	18.3217888	18.1760159	18.4014339	18.7971992	17.6857452
1416	Ras suppressor protein 1 OS=Rattus norvegicus OX=10116 GN=Rsu1 PE=1 SV=3	Rsu1	D4A8F2	0.39058204	0.29863548	22.2386837	22.2030849	20.9332409	22.2686501	21.6846561	21.5387478	21.4420567	21.7836571
1417	RAS-related 2 OS=Rattus norvegicus OX=10116 GN=Rras2 PE=1 SV=1	Rras2	Q5BJU0	0.32193891	-0.2119422	21.4191628	21.7754021	21.057663	22.2192249	21.9046001	22.0728416	21.8712673	21.4705124
1418	Ras-related C3 botulinum toxin substrate 1 OS=Rattus norvegicus OX=10116 GN=Rac1 PE=1 SV=1	Rac1	Q6RUV5	0.38799742	-0.1446729	21.3591156	21.7252064	21.3085537	21.6534424	21.4507885	21.4546394	21.9678364	21.7517452
1419	Ras-related protein Rab-11B OS=Rattus norvegicus OX=10116 GN=Rab11b PE=1 SV=4	Rab11b	O35509	0.85748071	-0.2993503	22.6953869	22.6462803	22.1535206	22.9462643	22.8075733	22.828495	23.0537529	22.9490318
1420	Ras-related protein Rab-12 OS=Rattus norvegicus OX=10116 GN=Rab12 PE=1 SV=3	Rab12	D4A376	0.81828508	-0.5374055	18.2989712	18.7991962	18.4033699	18.71875	18.762207	18.5454311	19.1316586	19.9306126
1421	Ras-related protein Rab-18 OS=Rattus norvegicus OX=10116 GN=Rab18 PE=2 SV=1	Rab18	Q5EB77	1.13933133	-0.6502447	21.7324181	20.8167381	20.394146	21.0417576	21.4157143	21.6793079	21.9184093	21.572607
1422	Ras-related protein Rab-1A OS=Rattus norvegicus OX=10116 GN=Rab1A PE=1 SV=3	Rab1A	Q6NYB7	0.66577686	-0.1495571	23.4007874	22.9320107	23.3005962	23.1838531	23.3744373	23.3445396	23.4412155	23.2552834
1423	Ras-related protein Rab-21 OS=Rattus norvegicus OX=10116 GN=Rab21 PE=2 SV=1	Rab21	Q6AXT5	0.15492233	0.27978039	19.5286961	18.7597866	19.0139694	19.3640823	19.6139584	19.362524	19.68326	16.8876705
1424	Ras-related protein Rab-28 OS=Rattus norvegicus OX=10116 GN=Rab28 PE=2 SV=1	Rab28	P51158	0.2666546	0.26198816	20.9046707	20.2764034	20.1868382	19.9339371	20.0844727	20.6398487	19.0784302	20.4511452
1425	Ras-related protein Rab-2A OS=Rattus norvegicus OX=10116 GN=Rab2a PE=2 SV=1	Rab2a	P05712	1.48308144	-0.4695907	20.1192818	19.9409924	19.92309	19.3605881	20.2821732	20.3966522	20.195858	20.3476315
1426	Ras-related protein Rab-35 OS=Rattus norvegicus OX=10116 GN=Rab35 PE=1 SV=1	Rab35	Q5U316	0.49420261	-0.3177328	20.3295555	19.4315834	19.3133564	19.5772419	19.6918602	19.8701706	20.519762	19.8408756
1427	Ras-related protein Rab-3A OS=Rattus norvegicus OX=10116 GN=Rab3a PE=1 SV=1	Rab3a	P63012	0.23885747	-0.0856771	18.4187145	18.3654251	18.4152927	18.3530045	18.2323265	18.8478088	18.2609291	18.554081
1428	Ras-related protein Rab-5A OS=Rattus norvegicus OX=10116 GN=Rab5a PE=2 SV=1	Rab5a	M0RC99	0.10732583	-0.1021729	18.5329342	18.8579273	18.4844894	17.6157017	18.8844261	17.8490219	18.7451591	18.4211369
1429	Ras-related protein Rab-7a OS=Rattus norvegicus OX=10116 GN=Rab7a PE=1 SV=2	Rab7a	P09527	1.57317655	-0.6422129	20.6817722	20.2866478	20.7484264	20.2601738	20.95294	20.97686	21.6725769	20.9434948
1430	Ras-related protein Rab-8A OS=Rattus norvegicus OX=10116 GN=Rab8a PE=1 SV=2	Rab8a	P35280	0.00612008	-0.005667	16.7098446	16.0549793	15.8799095	15.865489	16.2620335	15.4696331	16.5990696	16.2021542
1431	Ras-related protein Rab-8B OS=Rattus norvegicus OX=10116 GN=Rab8b PE=1 SV=1	Rab8b	P70550	0.94140567	-1.068758	16.9860859	16.1265831	16.2093906	14.6067371	17.1256351	16.2241364	17.6253948	17.2286625
1432	Ras-related protein Ral-A OS=Rattus norvegicus OX=10116 GN=Rala PE=1 SV=1	Rala	P63322	0.47692845	-0.3419514	20.2336674	20.9481945	21.0230865	21.7317734	21.1424751	21.3258457	21.6340084	21.202198
1433	Ras-related protein Ral-B OS=Rattus norvegicus OX=10116 GN=Ralb PE=2 SV=1	Ralb	P36860	0.73858959	-0.4460564	19.1645317	19.2194901	18.6069584	19.1308556	18.783987	19.5163441	20.0417824	19.5639477
1434	Ras-related protein Rap-1A OS=Rattus norvegicus OX=10116 GN=Rap1a PE=1 SV=1	Rap1a	P62836	1.00761545	-0.4259562	20.6184845	20.656126	20.6753063	19.8291569	20.8642101	20.8994236	21.0344086	20.6848564
1435	Ras-related protein Rap-1b OS=Rattus norvegicus OX=10116 GN=Rap1b PE=1 SV=2	Rap1b	Q62636	0.79875268	-0.3168354	21.4340248	22.117548	21.7598705	22.1321793	22.1175442	22.0040894	22.4854965	22.1038342
1436	Ras-related protein R-Ras OS=Rattus norvegicus OX=10116 GN=Rras PE=1 SV=1	Rras	D3Z8L7	0.20001869	0.30580091	18.3608685	19.0689259	18.4191341	18.7612	18.9670525	18.9900284	18.8243771	16.6054668
1437	RBR-type E3 ubiquitin transferase OS=Rattus norvegicus OX=10116 GN=Rnf14 PE=1 SV=1	Rnf14	Q3ZAU6	0.28202559	0.45176554	16.61936	16.9022999	14.8851261	15.9366264	14.4192181	15.9234924	15.4235172	16.7701225
1438	RCG20569, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Rbfa PE=1 SV=1	Rbfa	A0A0G2K1E	0.41214582	0.36297131	19.6432247	18.4910297	19.7220287	19.21591	19.2170315	19.4425144	18.2370281	18.7237339

1439	RCG20603 OS=Rattus norvegicus OX=10116 GN=Serpina3c PE=3 SV=1	Serpina3c	A0A0G2JSK	0.61258217	-0.2773423	21.0444946	21.1454239	21.1343346	21.384985	21.2297783	21.2447453	21.2844105	22.0596733
1440	RCG22622 OS=Rattus norvegicus OX=10116 GN=LOC684270 PE=1 SV=2	LOC684270	M0RAK2	0.21276828	0.71991372	19.1425419	18.8054924	18.4033718	15.0177507	18.5269566	16.7475071	14.5736771	18.6413612
1441	RCG29512 OS=Rattus norvegicus OX=10116 GN=Uqcr11 PE=1 SV=1	Uqcr11	A9UMV7	0.57166471	-0.2459002	21.1196632	21.2380886	22.018116	21.4749432	21.731184	21.7310066	21.7511578	21.6210632
1442	RCG31562, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=Tardbp PE=1 SV=1	Tardbp	I6L9G6	0.3037053	0.26897812	19.0495644	19.1903191	18.9079933	18.1502533	18.7217236	17.7950115	18.5117779	19.1937046
1443	RCG35712, isoform CRA_e OS=Rattus norvegicus OX=10116 GN=Urgcp PE=4 SV=1	Urgcp	A0A096MJ3	1.02462861	0.45026112	24.0960484	24.7367783	23.6456184	24.1857033	23.755785	23.6129398	23.7157021	23.778677
1444	RCG35999, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Smtn PE=1 SV=1	Smtn	D4ABA5	0.41464668	-0.2694714	16.3306465	15.8227739	15.0167837	15.4893684	15.9429407	16.0978565	15.9744091	15.7222519
1445	RCG37250, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Romo1 PE=1 SV=1	Romo1	D4A742	2.18743173	-0.3101144	21.1183891	21.4161758	21.2856617	21.3460865	21.6435394	21.4798222	21.6636486	21.6197605
1446	RCG37273, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Uqcc1 PE=1 SV=1	Uqcc1	Q32Q54	0.08795017	-0.0624685	19.6549377	18.8454456	19.6345978	19.8452492	19.7415028	19.3470402	19.3158512	19.8257103
1447	RCG38820 OS=Rattus norvegicus OX=10116 GN=Upf1 PE=1 SV=3	Upf1	F1LY19	0.14696162	-0.1502614	18.8461971	18.1688976	17.1117573	18.4145031	18.2113285	18.4823818	17.9635792	18.4851112
1448	RCG39700, isoform CRA_d OS=Rattus norvegicus OX=10116 GN=Rab6a PE=1 SV=1	Rab6a	A0A0H2UH	0.01958512	0.0161128	19.2727566	19.1622486	18.7233944	19.8187923	18.7527676	19.5192337	19.2980289	19.3427105
1449	RCG43475 OS=Rattus norvegicus OX=10116 GN=Tomm6 PE=1 SV=1	Tomm6	D3ZJS3	0.49264456	-0.5547154	15.595664	17.1684151	17.0574303	17.78936	17.5877609	17.9782486	17.3273411	16.9363804
1450	RCG44002, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tmem14c PE=1 SV=1	Tmem14c	B0BNJ9	0.19131685	-0.097683	18.4778824	18.9654789	18.1578255	18.4738407	18.8582249	18.6577396	18.6322498	18.3175449
1451	RCG45489, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Stom PE=1 SV=1	Stom	Q5XI04	0.17914692	-0.5304625	17.7742004	16.4465237	18.6042461	18.810957	18.5998859	19.2635765	20.3286343	15.5656805
1452	RCG47744, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=LOC100911440 PE=1 SV=1	LOC100911	A0A0G2K5L	0.77786303	-0.8031631	17.7187786	18.0107155	18.2815208	19.030817	20.0102634	18.7056713	19.4696941	18.0688553
1453	RCG48149, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=LOC100363782 PE=1 SV=1	LOC100363	G3V6H0	0.13997774	-0.036736	23.1113758	22.8931618	22.8762264	23.0447941	23.1279945	22.9460716	23.1737194	22.8247166
1454	RCG48334, isoform CRA_e OS=Rattus norvegicus OX=10116 GN=Rbm14 PE=1 SV=1	Rbm14	M0R9Q1	0.06121427	0.16823673	18.8493919	18.2543793	18.6340179	15.2230759	17.947731	17.6410179	16.229887	18.4692822
1455	RCG53912, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Sphk2 PE=1 SV=1	Sphk2	Q6AYB2	0.42497796	1.11398125	16.1938	17.8651733	19.3813057	16.178648	13.8631344	16.4917679	16.778326	18.0297737
1456	RCG54339, isoform CRA_c OS=Rattus norvegicus OX=10116 GN=LOC687508 PE=4 SV=1	LOC687508	M0R5K3	0.83787264	-0.9748192	21.2428837	21.8563194	19.8424683	22.413784	22.5354557	22.0612545	22.7076263	21.9503956
1457	RCG54610, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Timm50 PE=1 SV=2	Timm50	D3ZJX5	0.44975688	-0.2143488	21.0918369	21.4116287	21.6887722	21.7625999	21.7740097	21.4584694	22.0986557	21.4810982
1458	RCG55135, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Tln1 PE=1 SV=1	Tln1	G3V852	0.35848874	0.18196154	22.8238621	22.2002602	22.1705723	22.4133186	22.4618225	21.8921013	22.0043182	22.521925
1459	RCG56113, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Smyd1 PE=4 SV=1	Smyd1	D4A3D2	0.94371089	0.85767078	23.6687775	23.6213493	24.1545544	22.4804802	22.7925549	22.6834106	21.7978935	23.2206192
1460	RCG57156 OS=Rattus norvegicus OX=10116 GN=Sgcb PE=4 SV=1	Sgcb	A0A0G2K1V	0.24376295	-0.1445284	19.6905861	20.1889286	19.8863411	20.535202	19.8183155	20.5743179	20.2321415	20.2543964
1461	RCG57812, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Slk PE=1 SV=1	Slk	G3V7I8	0.85189292	0.81675243	19.678194	20.573576	19.8289146	18.9133759	18.7292004	19.0020237	18.1806908	19.815136
1462	RCG62056, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Cebpzos PE=1 SV=1	Cebpzos	D3ZL39	0.0811597	0.03373241	18.9103317	19.2616215	19.0517387	19.4684582	19.0011311	18.97645	19.3013821	19.2782574
1463	RCG62531, isoform CRA_g OS=Rattus norvegicus OX=10116 GN=Tpm3 PE=1 SV=1	Tpm3	A0A140TAF	0.28270916	0.34980249	16.9975052	17.3830833	16.9596653	18.62467	17.430109	17.7120113	16.1780968	17.2454967
1464	RCG63041 OS=Rattus norvegicus OX=10116 GN=LOC684509 PE=4 SV=1	LOC684509	M0RB63	0.32066882	-0.2199821	23.1120853	23.7722855	24.0382595	24.154274	24.1151314	23.7411957	24.4223595	23.6781464
1465	Receptor expression-enhancing protein 5 OS=Rattus norvegicus OX=10116 GN=Reep5 PE=1 SV=1	Reep5	B2RZ37	0.65666271	-0.1518226	22.3724003	22.3714199	22.2151909	22.203701	22.5526371	22.444479	22.6134014	22.1594849
1466	Receptor of activated protein C kinase 1 OS=Rattus norvegicus OX=10116 GN=Rack1 PE=1 SV=3	Rack1	P63245	0.20824174	-0.3643899	17.2226601	19.0087261	17.6747112	17.1059628	17.9554729	18.5071392	16.7156448	19.2913628
1467	Regulator of microtubule dynamics protein 1 OS=Rattus norvegicus OX=10116 GN=Rmdn1 PE=1 SV=1	Rmdn1	A0A0G2K16	0.00213994	0.00107336	21.3259335	21.4474792	20.9328766	21.6051846	21.3764725	21.462225	21.0759449	21.3925381
1468	Resistance to inhibitors of cholinesterase 8 homolog A (C. elegans) OS=Rattus norvegicus OX=10116 GN=Ric8a PE=1 SV=1	Ric8a	B1H241	0.268605	0.21384192	16.3916016	15.984396	16.3615875	15.7469501	15.9275627	16.7102528	15.3996172	15.5917349
1469	Reticulocalbin 1 OS=Rattus norvegicus OX=10116 GN=Rcn1 PE=1 SV=1	Rcn1	D3ZUB0	1.52548994	0.79355955	22.1268921	22.1156025	22.1826115	21.8778687	21.4936047	20.4938908	21.4063854	21.7348557
1470	Reticulocalbin-2 OS=Rattus norvegicus OX=10116 GN=Rcn2 PE=1 SV=2	Rcn2	Q62703	1.7373446	0.53209162	22.684742	22.1201305	22.5508308	22.3489971	22.1722622	21.6346188	21.9186687	21.8507843
1471	Reticulon 4-interacting protein 1 OS=Rattus norvegicus OX=10116 GN=Rtn4ip1 PE=1 SV=1	Rtn4ip1	B2GUZ6	1.26394095	0.56046581	22.3478107	22.5457649	21.8485527	22.1677246	21.6669674	22.0084553	21.160635	21.8319321
1472	Reticulon OS=Rattus norvegicus OX=10116 GN=Rtn2 PE=1 SV=1	Rtn2	Q6WN19	1.1217077	-0.3088694	18.907505	18.5296535	18.7046452	18.7674274	19.0233231	19.1761074	19.2439194	18.7013588
1473	Reticulon OS=Rattus norvegicus OX=10116 GN=Rtn4 PE=1 SV=1	Rtn4	F1LQN3	0.67858158	-0.299624	20.5321903	21.3809681	21.114954	21.4500351	21.3148403	21.5109272	21.4687595	21.3821163
1474	Reticulon-3 OS=Rattus norvegicus OX=10116 GN=Rtn3 PE=1 SV=1	Rtn3	Q6RJR6	0.16106125	0.04398108	19.3509846	19.5255566	19.1646175	19.387661	19.0994911	19.3568764	19.4434185	19.3531094
1475	Retinal dehydrogenase 1 OS=Rattus norvegicus OX=10116 GN=Aldh1a1 PE=1 SV=1	Aldh1a1	A0A0H2UH	0.02382952	-0.0341086	20.214962	20.8340092	19.1691685	20.3143635	19.5519428	20.4997215	19.6471825	20.9700909
1476	Retinol dehydrogenase 13 OS=Rattus norvegicus OX=10116 GN=Rdh13 PE=1 SV=1	Rdh13	D3ZFR9	0.70107132	-0.8160334	19.5353508	17.4395523	18.1427212	19.7820358	19.4485874	19.4893341	19.7693443	19.4565277
1477	Retinol dehydrogenase 14 OS=Rattus norvegicus OX=10116 GN=Rdh14 PE=1 SV=1	Rdh14	D3ZUY0	0.08601613	-0.2476845	15.2728367	17.4913406	15.8676291	16.9402905	17.6325741	13.8992586	17.5747356	17.4562664
1478	Rho family-interacting cell polarization regulator 2 OS=Rattus norvegicus OX=10116 GN=Ripor2 PE=1 SV=1	Ripor2	Q7TP54	0.00389047	0.00538731	19.6310654	21.6316166	20.2262535	20.9976311	20.7010975	20.7594185	20.8286037	20.1758976
1479	Rho GDP-dissociation inhibitor 1 OS=Rattus norvegicus OX=10116 GN=Arhgdia PE=1 SV=1	Arhgdia	Q5XI73	0.05626926	0.06262255	20.3452244	20.4033527	19.9849625	19.2451591	19.0996342	20.1148586	20.0840511	20.4296646
1480	Rho GTPase-activating protein 1 OS=Rattus norvegicus OX=10116 GN=Arhgap1 PE=1 SV=1	Arhgap1	D4A6C5	1.17136573	-0.8394146	20.1926746	21.6741142	21.3038864	21.7963581	22.2301064	22.0273228	22.2258415	21.8414211
1481	Rho GTPase-activating protein 17 OS=Rattus norvegicus OX=10116 GN=Arhgap17 PE=1 SV=3	Arhgap17	F1M6X7	0.07074401	-0.2020552	17.3109741	16.6805859	16.3680687	12.9590673	16.2469463	15.2983446	15.8747797	16.7068462
1482	Rho GTPase-activating protein 7 OS=Rattus norvegicus OX=10116 GN=Dlc1 PE=1 SV=1	Dlc1	A0A0G2K9J	0.05470913	0.1122303	14.3616018	16.1136055	16.5190849	16.6901875	14.3529787	16.289217	16.200716	16.3926468
1483	Rho guanine nucleotide exchange factor 1 OS=Rattus norvegicus OX=10116 GN=Arhgef1 PE=2 SV=1	Arhgef1	Q9Z1I6	0.88413679	1.07032943	17.2096729	17.7730789	17.1609058	15.9880486	15.8528004	16.7248917	14.6382475	16.634449
1484	Rho guanine nucleotide exchange factor 2 OS=Rattus norvegicus OX=10116 GN=Arhgef2 PE=1 SV=1	Arhgef2	A0A0G2K0V	0.22067829	0.45660305	17.3771992	17.2184162	16.4609928	15.5833445	14.6209822	15.7716846	16.3441467	18.0767269
1485	Rho guanine nucleotide exchange factor 6 OS=Rattus norvegicus OX=10116 GN=Arhgef6 PE=1 SV=3	Arhgef6	D3ZWQ8	0.13241467	0.3117137	15.0366268	17.7357864	18.2175674	16.5957623	16.1918736	15.5095901	16.5947742	18.0426502
1486	Rho guanine nucleotide exchange factor 7 OS=Rattus norvegicus OX=10116 GN=Arhgef7 PE=1 SV=1	Arhgef7	A0A0G2QCJ	1.00511549	0.53218269	20.5359344	19.7263317	20.5545387	19.5594006	19.4712582	19.5011501	19.4951859	19.7798805
1487	Rho-associated protein kinase OS=Rattus norvegicus OX=10116 GN=Rock2 PE=1 SV=3	Rock2	F1LQT3	0.67264163	0.62693501	17.1730804	17.6954613	17.2021942	18.1498814	17.3729992	16.658226	15.9764996	17.7051525
1488	Ribonuclease inhibitor OS=Rattus norvegicus OX=10116 GN=Rnh1 PE=1 SV=1	Rnh1	A0A0G2K9E	1.11395845	-0.629179	17.8215981	18.1899033	17.9454441	17.9678516	18.7518444	18.5662766	17.8735065	19.2498856
1489	Ribosomal protein L3-like OS=Rattus norvegicus OX=10116 GN=Rpl3l PE=3 SV=2	Rpl3l	D4A9G1	1.11247922	0.63536167	19.7209854	19.7579823	19.0231647	19.7019367	18.7037487	18.8055458	19.6177197	18.5356083
1490	Ribosomal protein S19-like2 OS=Rattus norvegicus OX=10116 GN=Rps19l2 PE=4 SV=1	Rps19l2	A0A0H2UI3	0.85571231	0.33858061	20.2317276	19.9599609	19.4886131	20.2659035	19.5884132	19.4909592	19.6226082	19.8899021
1491	Ribosomal protein S27-like OS=Rattus norvegicus OX=10116 GN=LOC100362987 PE=3 SV=1	LOC100362	M0RA26	0.4236964	0.22210884	20.6847725	20.1272984	19.5937481	20.270443	20.0313873	19.8498497	19.841526	20.0650635
1492	Ribosomal protein S6 kinase OS=Rattus norvegicus OX=10116 GN=Rps6ka3 PE=1 SV=2	Rps6ka3	D3Z8E0	0.23494867	0.48852444	18.5114708	17.2515221	17.1544151	15.2516975	16.7876263	17.2265072	15.0673447	17.1335297
1493	Ribosomal protein S6 kinase OS=Rattus norvegicus OX=10116 GN=Rps6ka4 PE=1 SV=2	Rps6ka4	D3ZSB7	0.22440432	0.40352845	17.9696064	17.2148247	17.3035431	15.5124483	17.2386246	15.1436195	16.7643814	17.2396832
1494	Ribosomal protein S6 kinase OS=Rattus norvegicus OX=10116 GN=Rps6ka5 PE=1 SV=1	Rps6ka5	A0A0G2K36	0.07547897	-0.0350771	21.0354023	20.8113708	21.1133747	21.4907265	21.3391666	21.0586739	21.2461605	20.9471817
1495	Ribosomal protein S6 kinase OS=Rattus norvegicus OX=10116 GN=Rps6kb2 PE=1 SV=1	Rps6kb2	D4AE24	0.08381505	-0.1395676	17.1959972	17.0340118	16.6613159	14.6352835	16.3828812	16.693985	16.2934113	16.7146015
1496	Ribosome-releasing factor 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Gfm2 PE=1 SV=2	Gfm2	F1LMZ4	0.13570241	0.09960461	19.3819942	19.6361675	19.8375797	19.1440945	18.7578049	19.8679829	19.4562359	19.5193939
1497	Ribosyldihydronicotinamide dehydrogenase [quinone] OS=Rattus norvegicus OX=10116 GN=Nqo2 PE=1 SV=3	Nqo2	Q6AY80	0.66463169	-0.7209585	15.4913664	14.7565708	16.0589924	16.635397	15.459795	16.8108463	16.7009277	16.8545914
1498	Ring finger protein 31 OS=Rattus norvegicus OX=10116 GN=Rnf31 PE=1 SV=2	Rnf31	E9PU29	0.97200567	0.51553011	17.2788696	17.6534386	17.3765335	16.4996815	16.8628159	16.7338467	16.7926617	16.3570786
1499	RNA 3'-terminal phosphate cyclase OS=Rattus norvegicus OX=10116 GN=Rtca PE=1 SV=1	Rtca	Q68FS8	0.80747731	0.29060888	23.9338188	24.0807648	23.452486	23.9358978	23.2382603	23.7846642	23.6239815	23.593626
1500	RNA-binding protein, mRNA-processing factor 2 OS=Rattus norvegicus OX=10116 GN=Rbpms2 PE=1 SV=1	Rbpms2	B5DFF2	0.97529223	0.39180565	19.3826962	19.0547886	19.3750057	18.634201	18.9624519	18.6439724	18.4682617	18.8047829
1501	RNA-binding protein, mRNA-processing factor OS=Rattus norvegicus OX=10116 GN=Rbpms PE=1 SV=2	Rbpms	F1M9Y9	0.65962175	0.17727947	18.9311314	19.0381947	18.7287731	18.7610664	18.7846775	18.6299877	18.419796	18.9155865
1502	rRNA 2'-O-methyltransferase fibrillarin OS=Rattus norvegicus OX=10116 GN=Fbl PE=1 SV=2	Fbl	P22509	0.63937498	0.32875252	17.5459461	17.8672543	17.4311447	17.1926041	17.2384338	16.6395969	17.2267742	17.6171341
1503	RT1 class I histocompatibility antigen, AA alpha chain OS=Rattus norvegicus OX=10116 PE=1 SV=2	10116	P16391	0.80782122	-0.6026011	16.7200871	16.9920502	16.3094978	17.6910229	17.0188427	17.2784767	18.0222626	17.8034801
1504	RT1 class I, A2 OS=Rattus norvegicus OX=10116 GN=RT1-A2 PE=1 SV=1	RT1-A2	Q6MGB8	0.94484469	-0.3920283	20.0590744	19.9119911	19.6879711	20.0645046	19.7928257	20.3190327	20.4881191	20.6916771
1505	RUN and FYVE domain-containing 1 OS=Rattus norvegicus OX=10116 GN=Rufy1 PE=1 SV=1	Rufy1	F1LR42	0.09593123	0.13856554	19.6028347	17.7377682	18.9888287	17.7904186	18.5341969	17.7820396	18.2308731	19.0184784
1506	RuvB-like 1 OS=Rattus norvegicus OX=10116 GN=Ruvbl1 PE=1 SV=1	Ruvbl1	P60123	0.16100338	0.36992979	15.5174198	17.3625793	16.9379101	17.6534481	17.6685963	16.7018509	17.2827435	14.3384476
1507	Ryanodine receptor 2 OS=Rattus norvegicus OX=10116 GN=Ryr2 PE=1 SV=2	Ryr2	B0LPN4	0.44747465	-0.0884695	24.0767899	23.9517002	23.9398746	23.7616844	23.9999866	23.9643269	24.1962681	23.9233456
1508	Saccharopine dehydrogenase-like oxidoreductase OS=Rattus norvegicus OX=10116 GN=Sccpdh PE=1 SV=1	Sccpdh	Q6AY30	1.62577757	-0.3752351	21.3861065	21.7837715	21.5943279	21.7314987	22.0472355	21.8726101	22.2260284	21.850771
1509	SAR1 gene homolog A (S. cerevisiae), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Sar1a PE=1 SV=1	Sar1a	Q6AY18	0.10970908	-0.0395794	21.3195419	21.3810482	21.1562366	21.000721	21.2452183	21.2169094	21.0285625	21.5251751
1510	Sarcalumenin OS=Rattus norvegicus OX=10116 GN=Srl PE=1 SV=3	Srl	F1LWG8	0.69065344	0.41992807	27.1314468	27.7296524	26.4777584	27.4503899	26.4458866	27.0161362	26.839035	26.8084774

1511	Sarcoglycan, alpha OS=Rattus norvegicus OX=10116 GN=Sgca PE=1 SV=1	Sgca	D3ZDQ9	0.41672927	-0.2774086	20.1022511	20.600523	19.8340549	21.1362534	20.6751518	20.8846264	20.6492996	20.5736389
1512	Sarcoglycan, delta OS=Rattus norvegicus OX=10116 GN=Sgcd PE=4 SV=3	Sgcd	F1LYS7	0.07744222	-0.041101	20.1623936	20.3437405	19.8966503	20.3836708	20.3131752	20.5552902	20.2712059	19.8111877
1513	Sarcoglycan, gamma OS=Rattus norvegicus OX=10116 GN=Sgcg PE=2 SV=1	Sgcg	Q5XID6	0.07352943	-0.054956	20.9918079	20.9782639	20.2382851	21.4533005	20.8654709	21.218998	20.9997349	20.7972775
1514	Sarcolemmal membrane-associated protein OS=Rattus norvegicus OX=10116 GN=Slmap PE=1 SV=1	Slmap	B5DF63	0.81279544	-0.3121786	22.0543957	21.9958153	21.7200508	22.2172031	22.3221645	21.9484329	22.7279778	22.2376041
1515	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Rattus norvegicus OX=10116 GN=Atp2a2 PE=1 SV=1	Atp2a2	P11507	1.15495066	-0.2825642	28.1572819	28.3518105	28.3255482	28.6390114	28.6854076	28.6191597	28.844141	28.4552002
1516	Sarcospan OS=Rattus norvegicus OX=10116 GN=Sspn PE=4 SV=1	Sspn	D4ABT9	0.4111538	-0.8293569	18.3427601	16.4167347	15.9684725	18.9816971	16.7414341	18.5762405	18.943573	18.7658443
1517	SCO1 cytochrome c oxidase assembly protein OS=Rattus norvegicus OX=10116 GN=Sco1 PE=1 SV=1	Sco1	G3V985	0.39730934	-0.6090293	17.1283855	17.4090576	18.9381008	18.947916	19.0325909	19.10742	19.3821468	17.3374195
1518	Sec1 family domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Scfd1 PE=1 SV=1	Scfd1	Q62991	0.37207695	-0.5979662	16.6875477	18.1597939	17.149292	15.7296124	16.0877361	18.0358753	17.9118824	18.0826168
1519	SECIS binding protein 2, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Secisbp2 PE=1 SV=2	Secisbp2	F1LPQ8	0.04701868	-0.0557966	20.7000446	20.4790897	19.5529404	20.1933746	19.8217735	21.1534328	19.7162895	20.45714
1520	Secretory carrier-associated membrane protein OS=Rattus norvegicus OX=10116 GN=Clk2 PE=1 SV=1	Clk2	A0A0G2K5C	0.8992928	-1.3725288	15.6170416	19.0729656	18.3995628	18.0615044	18.7008514	19.5194435	19.2813416	19.1395531
1521	Secretory carrier-associated membrane protein OS=Rattus norvegicus OX=10116 GN=Scamp2 PE=1 SV=1	Scamp2	Q5U2U4	0.90613415	0.54166794	18.2761345	17.5060444	18.2274704	18.4687042	17.3719406	17.0725441	18.0256538	17.8415432
1522	Sepiapterin reductase OS=Rattus norvegicus OX=10116 GN=Spr PE=1 SV=1	Spr	P18297	0.52351186	-0.4644814	17.5506172	18.3124504	17.4295597	17.3443203	18.2574978	17.382906	17.8496037	19.0048656
1523	Septin-2 OS=Rattus norvegicus OX=10116 GN=Sept2 PE=1 SV=1	37500	Q91Y81	0.00524068	-0.003674	21.2096767	21.1153774	21.3499031	20.3908787	20.9090328	20.8894501	20.9808159	21.3012333
1524	Septin-7 OS=Rattus norvegicus OX=10116 GN=Sept7 PE=1 SV=3	39326	D4A0F5	0.11099514	-0.1183457	20.3550224	20.7864227	19.1742191	19.650404	19.7437267	20.2815037	19.9429226	20.4712982
1525	Septin-9 OS=Rattus norvegicus OX=10116 GN=Sept9 PE=1 SV=1	40057	Q9QZR6	0.57269309	0.43171215	16.5229645	15.9583435	14.9977417	15.6602945	15.7686243	15.0445747	15.2163582	15.3829384
1526	Serine (Or cysteine) peptidase inhibitor, clade B, member 6a OS=Rattus norvegicus OX=10116 GN=Serpinb6a PE=1 SV=1	Serpinb6a	Q6P9U0	0.07770382	0.1898067	16.9304256	16.6269341	16.664835	15.4197445	16.87393	17.3813953	13.8158998	16.8114872
1527	Serine (Or cysteine) peptidase inhibitor, clade C (Antithrombin), member 1 OS=Rattus norvegicus OX=10116 GN=Serpinc1 PE=1 SV=1	Serpinc1	Q5M7T5	0.45123864	0.16374969	21.2619686	21.0373611	20.9251022	20.498373	20.7759247	20.7037468	20.7434063	20.8447285
1528	Serine (Or cysteine) proteinase inhibitor, clade H, member 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Serpinh1 PE=1 SV=1	Serpinh1	Q5RJR9	0.6034397	0.27345848	22.6946335	22.7520485	22.427618	22.1512108	22.1082058	22.6173668	21.8519192	22.3541851
1529	Serine hydrolase-like 2 OS=Rattus norvegicus OX=10116 GN=Serhl2 PE=4 SV=1	Serhl2	D4A071	0.18058363	0.36897278	20.1351452	18.9543743	18.6063251	18.0374546	18.8292599	17.6516113	17.4461269	20.33041
1530	Serine hydroxymethyltransferase OS=Rattus norvegicus OX=10116 GN=Shmt2 PE=1 SV=1	Shmt2	Q5U3Z7	0.02621352	-0.0160565	22.9344769	23.4299107	23.0326042	23.0238266	23.0708122	23.3022747	22.6455803	23.4663773
1531	Serine protease inhibitor A3K OS=Rattus norvegicus OX=10116 GN=Serpina3k PE=1 SV=3	Serpina3k	P05545	0.05553095	-0.1700447	18.423151	17.4058418	16.5567188	18.3812637	15.0292082	18.0372562	19.1120853	19.2686043
1532	Serine protease inhibitor A3N OS=Rattus norvegicus OX=10116 GN=LOC299282 PE=1 SV=1	LOC299282	F1LM05	0.0625434	-0.0406027	21.8206158	21.7129669	21.9331589	21.5496368	21.4969349	21.5136986	21.7512264	22.4169292
1533	Serine protease inhibitor A3N OS=Rattus norvegicus OX=10116 GN=LOC299282 PE=1 SV=1	LOC299282	A0A0G2K9E	0.32471609	-0.2591157	18.9651871	17.5901241	18.402298	17.7266655	18.7715492	18.3626766	18.2821484	18.3043633
1534	Serine protease inhibitor A3N OS=Rattus norvegicus OX=10116 GN=LOC299282 PE=1 SV=1	LOC299282	A0A0G2K1T	0.47672869	0.29083347	17.5569305	17.0766335	17.198637	17.9488735	16.8310242	17.0581112	17.0081329	17.7204723
1535	Serine/arginine-rich splicing factor 2 OS=Rattus norvegicus OX=10116 GN=Srsf2 PE=1 SV=3	Srsf2	Q6PDU1	0.10501221	-0.1248031	15.6147795	15.8256903	14.4847193	15.0482273	14.8859663	14.7577524	15.9784946	15.8504152
1536	Serine/threonine kinase 26 OS=Rattus norvegicus OX=10116 GN=Stk26 PE=1 SV=2	Stk26	F1LXV3	0.61206867	0.42868614	18.4476299	18.6567459	17.3393059	17.8375893	17.3019276	17.7731667	17.5282707	17.9631615
1537	Serine/threonine-protein kinase A-Raf OS=Rattus norvegicus OX=10116 GN=Araf PE=1 SV=1	Araf	P14056	0.21859259	0.17462778	21.3369141	20.249939	20.2745514	20.5215874	20.6437263	20.2420197	19.971777	20.8269577
1538	Serine/threonine-protein kinase MRCK beta OS=Rattus norvegicus OX=10116 GN=Cdc42bpb PE=1 SV=1	Cdc42bpb	A0A0G2KB5	0.00159912	0.00166321	18.4212589	18.5657616	19.2008438	19.7661839	18.7391014	18.988039	19.4245796	18.7956753
1539	Serine/threonine-protein kinase mTOR OS=Rattus norvegicus OX=10116 GN=Mtor PE=1 SV=1	Mtor	P42346	0.19642762	0.12974024	19.7168808	19.3259792	19.1830997	19.2514915	19.3889294	19.0507317	18.7189159	19.7999134
1540	Serine/threonine-protein kinase Nek7 OS=Rattus norvegicus OX=10116 GN=Nek7 PE=2 SV=1	Nek7	D3ZBE5	0.08629333	0.09910488	19.034214	20.8457851	20.5607033	20.5240974	20.2484455	19.9085274	20.2393398	20.1720676
1541	Serine/threonine-protein kinase TNNI3K OS=Rattus norvegicus OX=10116 GN=Tnni3k PE=4 SV=2	Tnni3k	F1LPM9	0.49557528	0.42642641	24.0149994	23.232254	23.663765	22.6096096	23.1727638	22.8805294	22.2936306	23.4679985
1542	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Rattus norvegicus OX=10116 GN=Ppp2r2a PE=2 SV=1	Ppp2r2a	P36876	0.36845134	-0.4460425	16.7500591	15.1207981	15.1207981	16.8202	16.6363239	16.4716568	17.4287796	17.2201195
1543	Serine/threonine-protein phosphatase 2A activator OS=Rattus norvegicus OX=10116 GN=Ptpa PE=1 SV=1	Ptpa	B2RYQ2	1.36188598	1.62110353	18.5819645	18.3979225	17.9194584	17.6374397	16.6393166	14.7881021	17.4004383	17.224514
1544	Serine/threonine-protein phosphatase OS=Rattus norvegicus OX=10116 GN=LOC100362453 PE=3 SV=1	LOC100362	A0A0G2JYA	0.11522717	0.08440638	19.4146767	19.1119804	19.1687469	19.3827438	18.4610748	19.5935917	19.1439457	19.5419102
1545	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Rattus norvegicus OX=10116 GN=Ppp1cb PE=1 SV=3	Ppp1cb	P62142	0.54635068	0.58862638	20.2192001	20.8421345	19.0296516	20.5818481	18.9703255	20.1562557	19.1605473	20.0312004
1546	Serine-threonine kinase receptor-associated protein OS=Rattus norvegicus OX=10116 GN=Strap PE=1 SV=1	Strap	Q5XIG8	0.1867694	-0.4260225	17.5836391	18.2464409	17.2599373	14.3508739	17.3297024	17.4241581	16.626627	17.7644939
1547	Serotransferrin OS=Rattus norvegicus OX=10116 GN=Tf PE=1 SV=1	Tf	A0A0G2QC0	0.30184285	-0.0982709	24.8508453	24.8482494	24.6914139	24.7252102	24.6386509	24.8378372	24.7854462	25.2468681
1548	Serotransferrin OS=Rattus norvegicus OX=10116 GN=Tf PE=1 SV=3	Tf	P12346	0.3082971	0.14160919	20.0605946	19.5364704	19.4279842	19.6849537	19.2802792	19.3502159	19.6496887	19.8633823
1549	Serpin H1 OS=Rattus norvegicus OX=10116 GN=Serpinh1 PE=1 SV=1	Serpinh1	P29457	0.42578496	0.43289185	16.8371487	16.2857494	16.6375141	16.1302929	16.4254951	14.7769184	16.404604	16.5521202
1550	Serum albumin OS=Rattus norvegicus OX=10116 GN=Alb PE=1 SV=1	Alb	A0A0G2JSH	2.75737502	-0.2851872	27.4452991	27.6607056	27.5008774	27.5375404	27.758707	27.8118172	27.8218994	27.8927479
1551	Serum albumin OS=Rattus norvegicus OX=10116 GN=Alb PE=1 SV=2	Alb	P02770	0.11498284	0.21247387	23.9269199	23.7013702	22.9474506	22.0942249	22.7146339	21.5044479	23.7780151	23.8229733
1552	Serum paraoxonase/arylesterase 1 OS=Rattus norvegicus OX=10116 GN=Pon1 PE=1 SV=3	Pon1	P55159	0.08760902	-0.0535769	21.0289707	21.3736477	20.4433784	20.5325451	20.8323765	20.8271255	20.9538631	20.9794846
1553	Seryl-tRNA synthetase 2 (Predicted) OS=Rattus norvegicus OX=10116 GN=Sars2 PE=1 SV=1	Sars2	D3ZM09	0.52650728	-0.1903853	20.8105984	21.0175438	20.7055779	20.9543724	21.3513432	21.2961006	20.790453	20.8117371
1554	Sestrin 1 OS=Rattus norvegicus OX=10116 GN=Sesn1 PE=1 SV=1	Sesn1	A0A0G2K4P	0.06291255	-0.0990777	18.0949135	18.0367641	16.9187679	15.8403912	17.5754757	17.4874935	16.8447914	17.3793869
1555	SET-binding factor 1 OS=Rattus norvegicus OX=10116 GN=Sbf1 PE=1 SV=1	Sbf1	M0RAP5	0.01272676	-0.027808	17.6366081	17.8676872	17.5830536	14.9477663	16.8544998	16.9510002	16.5663109	17.7745361
1556	S-formylglutathione hydrolase OS=Rattus norvegicus OX=10116 GN=Esd PE=2 SV=1	Esd	B0BNE5	0.06264527	-0.0399432	19.3886662	19.190794	19.2968941	18.5514107	19.1198692	19.2101936	18.830595	19.4268799
1557	SH3 domain-binding glutamate-rich protein OS=Rattus norvegicus OX=10116 GN=Sh3bgr PE=1 SV=1	Sh3bgr	D3ZU20	0.42051912	0.55747843	17.8203659	16.8558216	15.8000584	16.3029404	16.7074623	15.8487225	15.1436386	16.8494492
1558	SH3 domain-containing kinase-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Sh3kbp1 PE=1 SV=2	Sh3kbp1	Q925Q9	0.44153221	-0.9887915	18.2225666	18.1372643	17.8384228	14.108799	17.8397465	18.3069725	17.8232059	18.2922935
1559	Short chain dehydrogenase/reductase family 39U, member 1 OS=Rattus norvegicus OX=10116 GN=Sdr39u1 PE=1 SV=1	Sdr39u1	D3ZYY0	0.3145916	0.11442232	21.0374355	20.9697857	20.7078247	21.3627605	20.7432461	20.8659019	20.9114132	21.099556
1560	Short/branched chain-specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Acadsb PE=1 SV=2	Acadsb	A0A0A0MY	0.56089292	0.78866148	21.4779282	21.3638992	20.5816917	20.4067345	20.5763206	18.3938141	20.9910297	20.7144432
1561	Sideroflexin OS=Rattus norvegicus OX=10116 GN=Sfxn3 PE=1 SV=1	Sfxn3	G3V804	0.11546112	-0.1915307	15.6447477	16.1303349	15.1045122	17.1269531	15.5171204	17.4042549	15.5525322	16.2987633
1562	Signal peptidase complex subunit 2 OS=Rattus norvegicus OX=10116 GN=Spcs2 PE=1 SV=1	Spcs2	D3ZD11	1.28981609	-0.5045154	16.2575512	15.8659067	15.4747219	15.7864666	16.1086426	16.6228828	16.527771	16.1434116
1563	Signal recognition particle 54 kDa protein OS=Rattus norvegicus OX=10116 GN=Srp54 PE=2 SV=1	Srp54	Q6AYB5	0.20992542	-0.2445686	15.8897953	14.8226404	14.1507635	14.4098806	15.2933102	14.9027634	14.4207382	15.6345425
1564	Signal recognition particle subunit SRP68 OS=Rattus norvegicus OX=10116 GN=Srp68 PE=1 SV=1	Srp68	B2RYI2	0.68263224	1.06667852	17.4994736	17.8121967	17.2680492	16.040163	15.726553	14.4638042	16.6939678	17.4688435
1565	Signal recognition particle subunit SRP72 OS=Rattus norvegicus OX=10116 GN=LOC108348180 PE=1 SV=2	LOC108348	D4A7R0	0.16910989	0.17695332	17.6907978	19.2248955	18.7454052	18.1285324	18.3651237	18.1553955	17.7427502	18.8185482
1566	Signal transducer and activator of transcription 3 OS=Rattus norvegicus OX=10116 GN=Stat3 PE=1 SV=1	Stat3	P52631	0.73187037	0.41425419	20.9599667	20.5643826	20.4325829	20.7514839	20.4427166	19.9577484	19.7644844	20.8864498
1567	Signal transducer and activator of transcription OS=Rattus norvegicus OX=10116 GN=Stat1 PE=1 SV=2	Stat1	F1M9D6	1.10579298	0.69850016	22.2972431	21.9601555	21.3664055	21.4548817	21.0028496	20.89641	20.6170788	21.7683468
1568	Signal transducer and activator of transcription OS=Rattus norvegicus OX=10116 GN=Stat2 PE=1 SV=1	Stat2	Q5XI26	0.9731381	0.49680471	19.9047585	19.9036083	19.6912479	19.1893845	19.1216087	19.221426	19.6669807	18.6917648
1569	SIK family kinase 3 OS=Rattus norvegicus OX=10116 GN=Sik3 PE=1 SV=2	Sik3	M0RD40	0.53869922	0.30125284	19.2384777	19.2210464	18.916666	18.3403091	18.7510681	18.3897228	18.3691826	19.0015144
1570	Similar to 60S ribosomal protein L23a OS=Rattus norvegicus OX=10116 GN=LOC689899 PE=3 SV=1	LOC689899	D3ZTH8	0.15832526	0.05336332	19.4417477	19.0575714	19.0851688	19.4500027	18.9942627	19.2807808	19.2957306	19.2502632
1571	Similar to 60S ribosomal protein L27a OS=Rattus norvegicus OX=10116 GN=RGD1562402 PE=3 SV=1	RGD156240	A0A0G2K7V	0.19311714	0.11038446	18.3090878	18.7142067	18.5674	19.2936954	18.4751244	18.6951866	18.8080502	18.4644909
1572	Similar to CG3740-PA OS=Rattus norvegicus OX=10116 GN=LOC690000 PE=1 SV=1	LOC690000	D3ZWS2	0.26350227	0.22177935	20.5734234	20.4519329	20.2605572	19.2399635	19.6914005	19.9182148	19.6563225	20.3728218
1573	Similar to RIKEN cDNA 2810055F11 (Predicted) OS=Rattus norvegicus OX=10116 GN=L3hypdh PE=1 SV=1	L3hypdh	D3ZV91	0.55248278	0.31831336	16.8103619	16.873724	17.0538063	17.0519028	16.6509132	16.9061298	17.0693436	15.8901548
1574	Similar to RIKEN cDNA 5730469D23 (Predicted) OS=Rattus norvegicus OX=10116 GN=Uba6 PE=1 SV=1	Uba6	D4A8H3	0.60393587	0.87741089	19.7371502	19.402029	19.6998634	17.1918659	18.4597511	17.5935402	17.6069012	18.8610725
1575	Similar to solute carrier family 25, member 35, isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Slc25a35 PE=1 SV=1	Slc25a35	B0BNI6	0.1771604	0.16484213	16.7265358	16.6212864	17.1722012	15.9282455	16.9848557	16.5385323	15.7555885	16.5099239
1576	Similar to TANK-binding kinase 1 OS=Rattus norvegicus OX=10116 GN=Tbk1 PE=1 SV=1	Tbk1	D4A7D3	0.94868881	0.55728149	19.2780571	19.0383434	19.0232334	18.2473259	18.8500957	17.9343643	18.1350803	18.4382935
1577	Similar to TBC1 domain family, member 8;BUB2-like protein 1;vascular Rab-GAP/TBC-containing (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Tbc1d9b PE=1 SV=2	Tbc1d9b	F1LRL4	0.23229227	0.15784073	22.9439297	23.0754814	22.6954975	22.0086594	22.7471294	22.1291084	22.6589813	22.5569859
1578	Similar to threonine aldolase 1 OS=Rattus norvegicus OX=10116 GN=LOC688286 PE=1 SV=2	LOC688286	M0R6H1	0.12183014	0.07260084	20.5949039	19.7876968	20.6810913	20.6231632	20.4712582	20.1610031	20.348175	20.4160156
1579	Single-stranded DNA-binding protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ssbp1 PE=1 SV=2	Ssbp1	P28042	0.16876797	0.3682878	17.4776936	18.0539856	17.3267841	17.6002865	18.0287018	18.1897564	14.7600412	18.0070992
1580	Sirpa protein OS=Rattus norvegicus OX=10116 GN=Sirpa PE=1 SV=1	Sirpa	Q499T3	0.92005661	-0.5095296	16.6631641	15.9270973	15.6060123	16.3827534	16.7520027	16.4235229	17.0493641	16.3922558
1581	Small integral membrane protein 12 OS=Rattus norvegicus OX=10116 GN=Smim12 PE=3 SV=1	Smim12	D4ACP2	0.16480181	-0.0953875	16.3202705	16.4675331	16.5933056	16.6924057	16.7140789	16.1602821	17.1387863	16.4419174
1582	Small muscular protein OS=Rattus norvegicus OX=10116 GN=Smpx PE=1 SV=1	Smpx	Q925F0	0.17973581	0.11354971	17.9718437	17.9698696	17.1080189	17.6001339	17.6884193	17.3318882	17.3072929	17.8680668

1583	Snta1 protein OS=Rattus norvegicus OX=10116 GN=Snta1 PE=1 SV=1	Snta1	B5DFL0	0.2788997	-0.1211348	20.164402	20.2609177	19.960577	20.1862526	20.0235405	20.7621002	20.118515	20.1525326
1584	Sodium/calcium exchanger 1 OS=Rattus norvegicus OX=10116 GN=Slc8a1 PE=1 SV=3	Slc8a1	Q01728	1.54696462	-0.4304891	21.0595093	21.1834736	20.8271523	21.5250969	21.5615082	21.5927219	21.6681328	21.4948254
1585	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Rattus norvegicus OX=10116 GN=Atp1a1 PE=1 SV=1	Atp1a1	P06685	0.37157235	-0.1050892	25.9518547	26.1506996	26.0298309	26.3443222	26.3421726	26.396759	26.1404133	26.0177193
1586	Sodium/potassium-transporting ATPase subunit alpha-2 OS=Rattus norvegicus OX=10116 GN=Atp1a2 PE=1 SV=1	Atp1a2	P06686	0.12718246	-0.0999217	19.6132889	19.6504955	19.8060017	20.5868454	20.2196941	20.4125042	19.8436947	19.5804253
1587	Sodium/potassium-transporting ATPase subunit alpha-3 OS=Rattus norvegicus OX=10116 GN=Atp1a3 PE=1 SV=2	Atp1a3	P06687	0.84174548	-0.6846213	21.4206715	21.6786804	20.4965229	21.9782391	22.2847195	21.6558189	22.6959343	21.6761265
1588	Sodium/potassium-transporting ATPase subunit beta-1 OS=Rattus norvegicus OX=10116 GN=Atp1b1 PE=1 SV=1	Atp1b1	P07340	0.20549237	-0.0720968	23.9019699	24.0438766	23.8699112	24.3999252	24.158638	24.1448269	24.2630863	23.9375191
1589	Sodium/potassium-transporting ATPase subunit beta-3 OS=Rattus norvegicus OX=10116 GN=Atp1b3 PE=2 SV=1	Atp1b3	Q63377	0.07712113	-0.0395632	20.6099949	19.9319096	20.2912941	19.8379688	20.234684	20.3114414	20.2221851	20.0611095
1590	Solute carrier family 12 member 7 OS=Rattus norvegicus OX=10116 GN=Slc12a7 PE=1 SV=1	Slc12a7	A0A0G2K8S	1.12194201	-0.523541	18.8734093	19.0219059	18.3303509	19.2847233	19.4626637	19.0291824	19.693821	19.4188862
1591	Solute carrier family 2, facilitated glucose transporter member 4 OS=Rattus norvegicus OX=10116 GN=Slc2a4 PE=1 SV=1	Slc2a4	P19357	0.02391876	-0.0099344	19.8753338	19.7040348	19.4257717	19.6253757	19.5142956	19.9577427	19.4996281	19.6985874
1592	Solute carrier family 25 member 12 OS=Rattus norvegicus OX=10116 GN=Slc25a12 PE=1 SV=3	Slc25a12	F1LX07	0.55436898	-0.3342547	24.2942181	24.7083778	24.8523884	25.2561989	25.1655884	24.9915752	25.6220436	24.6689949
1593	Solute carrier family 25 member 13 OS=Rattus norvegicus OX=10116 GN=Slc25a13 PE=1 SV=2	Slc25a13	F1LZW6	0.52915589	-0.2635813	23.2955685	23.6620941	23.7757111	24.2160282	24.0686741	23.8565044	24.3356934	23.7428551
1594	Solute carrier family 25 member 51 OS=Rattus norvegicus OX=10116 GN=Slc25a51 PE=2 SV=1	Slc25a51	Q52KK3	0.47148685	-0.5930395	16.0584221	16.3638287	16.123148	16.1465855	16.9425392	17.2564907	17.725275	15.1398373
1595	Solute carrier family 39 (Zinc transporter), member 14 (Predicted) OS=Rattus norvegicus OX=10116 GN=Slc39a14 PE=1 SV=1	Slc39a14	D3ZZM0	0.65955347	0.33555532	15.5919018	15.1827097	15.3655586	14.86549	15.2967453	15.0319748	14.9435759	14.3911428
1596	Solute carrier family 43, member 3 OS=Rattus norvegicus OX=10116 GN=Slc43a3 PE=1 SV=1	Slc43a3	D4A832	0.94981149	-0.3184791	17.7574043	17.8622932	17.4269295	18.1865158	18.2962494	18.0035858	18.1839733	18.0232506
1597	Sorbin and SH3 domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Sorbs1 PE=1 SV=1	Sorbs1	F1M820	0.3572649	-0.1703186	18.8529205	18.3723469	18.1997318	18.6924973	18.9870625	18.3697891	18.8800449	18.5618744
1598	Sorting and assembly machinery component 50 homolog OS=Rattus norvegicus OX=10116 GN=Samm50 PE=1 SV=1	Samm50	Q6AXV4	1.23085383	-0.4435563	23.2707062	23.71838	23.9627151	23.8866062	24.0465164	24.1547394	24.4611053	23.9502716
1599	Sorting nexin 2 OS=Rattus norvegicus OX=10116 GN=Snx2 PE=1 SV=1	Snx2	B2RYP4	0.032146	-0.0417528	16.4174385	17.8213062	18.0735245	16.9202595	17.323328	17.7010403	16.7237625	17.6514091
1600	Sorting nexin-3 OS=Rattus norvegicus OX=10116 GN=Snx3 PE=1 SV=1	Snx3	Q5U211	1.33274442	0.84150553	18.8408165	19.4207783	19.0439663	18.6742859	18.8542156	17.8933067	17.4900742	18.3762283
1601	Sorting nexin-5 OS=Rattus norvegicus OX=10116 GN=Snx5 PE=1 SV=1	Snx5	B1H267	1.03072157	0.48299503	20.3520756	19.762064	20.1335735	19.7078285	19.7781258	19.7787247	18.9848232	19.4818878
1602	Spartin OS=Rattus norvegicus OX=10116 GN=Spart PE=1 SV=3	Spart	E9PT90	0.45967173	0.31478167	21.0884743	20.8661232	20.4445744	19.7491684	20.1359901	20.0943623	20.1650848	20.4937763
1603	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus OX=10116 GN=Sptan1 PE=1 SV=1	Sptan1	A0A0G2K1Y	0.38791064	-0.2875743	20.9958668	20.7091217	19.8822193	19.9131737	20.2383671	20.808876	20.6163235	20.987112
1604	Spectrin beta chain OS=Rattus norvegicus OX=10116 GN=Sptb PE=1 SV=1	Sptb	A0A140UHX	0.38037959	-0.3937974	23.6111622	24.5162735	23.9466324	23.2470188	23.9896469	25.2813854	23.987299	23.6379452
1605	Spectrin beta chain OS=Rattus norvegicus OX=10116 GN=Sptbn1 PE=1 SV=1	Sptbn1	A0A0G2K8V	0.01004762	-0.0265675	23.3950844	20.9248314	20.5207081	20.9953327	23.265234	21.093029	20.6012497	20.9827137
1606	Spectrin, alpha, erythrocytic 1 OS=Rattus norvegicus OX=10116 GN=Spta1 PE=1 SV=3	Spta1	D4A678	0.67876804	-0.7617784	23.3601952	24.4456692	23.8955822	23.7575188	23.998188	25.7369728	25.1526833	23.6182346
1607	Spermatogenesis-associated 5 OS=Rattus norvegicus OX=10116 GN=Spata5 PE=1 SV=1	Spata5	A0A0G2K0I	0.18588272	0.1219635	21.3555202	20.9999046	21.1246624	21.4104786	21.0273914	20.8066311	21.7946301	20.7740593
1608	S-phase kinase-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Skp1 PE=1 SV=1	Skp1	A0A0G2K4X	0.04565942	0.03179979	21.189476	20.2470398	20.4142036	20.5518456	20.8965511	20.4086609	20.6481857	20.3219681
1609	Splicing factor 3A subunit 2 OS=Rattus norvegicus OX=10116 GN=Sf3a2 PE=2 SV=1	Sf3a2	Q6AXT8	0.13123768	-0.1410744	15.1041727	16.1246071	16.425642	16.0609531	16.6052551	15.2670174	16.1198273	16.2875729
1610	SPRY domain-containing protein 7 OS=Rattus norvegicus OX=10116 GN=Spryd7 PE=2 SV=1	Spryd7	Q5M7T2	0.58266318	-0.9433398	15.4602003	17.7098732	14.8712244	17.6391106	17.2355366	16.9398251	17.8961983	17.3822079
1611	Sqrdl protein OS=Rattus norvegicus OX=10116 GN=Sqor PE=1 SV=1	Sqor	B0BMT9	0.59551624	0.39224815	21.7644844	21.2492199	20.5776024	20.7384262	20.6415386	20.7606735	21.0571136	20.3014145
1612	SRP receptor subunit alpha OS=Rattus norvegicus OX=10116 GN=Srpra PE=1 SV=1	Srpra	Q3KRC3	0.70328174	-0.4327903	17.8384247	17.8747654	18.3325958	18.6925354	18.0652027	18.9866428	18.4642181	18.9534187
1613	Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Snd1 PE=1 SV=1	Snd1	Q66X93	0.22553808	-0.166765	15.796401	15.3852243	14.9580574	15.5795126	15.2408695	16.2969913	15.4507275	15.3976669
1614	STE20/SPS1-related proline-alanine-rich protein kinase OS=Rattus norvegicus OX=10116 GN=Stk39 PE=1 SV=2	Stk39	O88506	1.53690246	1.30041218	20.56777	21.6086178	19.9053898	21.1844654	19.2601051	19.768734	18.9229126	20.1128426
1615	Steroid sulfatase OS=Rattus norvegicus OX=10116 GN=Sts PE=1 SV=1	Sts	G3V9E5	0.06868345	-0.0941629	18.0906048	17.846447	17.9649277	17.2714024	17.9007912	17.2747993	19.1680031	17.20644
1616	STIP1 homology and U-Box containing protein 1, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Stub1 PE=1 SV=1	Stub1	D4A4T0	0.02709389	0.05623102	18.2854004	17.8288059	17.6691189	15.2530289	17.6047554	16.9124565	16.8000412	17.4941769
1617	Stomatin-like protein 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Stoml2 PE=1 SV=1	Stoml2	Q4FZT0	0.41347978	-0.5136886	19.164732	19.5226421	18.5452061	20.6384296	19.8720493	20.2766457	20.660017	19.1170521
1618	Stress-70 protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hspa9 PE=1 SV=1	Hspa9	F1M953	0.19489091	-0.0979548	24.4695549	25.224535	24.6766796	25.0573254	24.8550091	25.0452232	25.1772385	24.7424431
1619	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus OX=10116 GN=Stip1 PE=1 SV=1	Stip1	O35814	0.61983548	0.67710972	19.0085621	18.7450485	17.8507023	18.5090981	16.8937721	18.4054832	17.2807236	18.8249931
1620	Striated muscle-specific serine/threonine-protein kinase OS=Rattus norvegicus OX=10116 GN=Speg PE=1 SV=2	Speg	Q63638	0.36389236	0.26641703	23.5170403	23.3540592	22.4570084	23.6122093	22.5963383	22.8518696	22.9995575	23.4268837
1621	Striatin-3 OS=Rattus norvegicus OX=10116 GN=Strn3 PE=1 SV=2	Strn3	P58405	0.73294247	0.53686428	18.1258621	18.3335629	17.8449116	18.2576332	17.9602757	16.5997982	17.7543106	18.1001282
1622	STT3A, catalytic subunit of the oligosaccharyltransferase complex OS=Rattus norvegicus OX=10116 GN=Stt3a PE=1 SV=1	Stt3a	A0A0G2JWI	1.58919003	1.02293539	17.9044094	18.1086178	18.0532627	18.0928173	17.3727989	16.1955681	16.7437992	17.7551994
1623	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sdhd PE=2 SV=1	Sdhd	Q6PCT8	0.55634975	-0.4346461	20.5226326	21.750721	21.8328094	22.085516	21.7964592	22.125782	22.1952343	21.812788
1624	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sdha PE=1 SV=1	Sdha	Q920L2	0.75633626	-0.3656478	26.549736	27.1597595	27.2563744	27.4201775	27.4503593	27.4866066	27.8059902	27.1056824
1625	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sdhb PE=2 SV=2	Sdhb	P21913	0.79976609	-0.3403649	25.4958286	25.9305649	26.0948601	26.1926594	26.2298985	26.3628998	26.5876427	25.8949318
1626	Succinate dehydrogenase assembly factor 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sdhaf1 PE=3 SV=1	Sdhaf1	B0K036	0.11805926	-0.3632939	18.2089558	17.5837765	13.8147078	18.2934475	16.1283379	17.457449	17.7017651	18.0665112
1627	Succinate dehydrogenase complex subunit C OS=Rattus norvegicus OX=10116 GN=Sdhc PE=1 SV=1	Sdhc	Q641Z9	0.90257988	-0.3414059	22.2514877	22.7556438	23.0134544	22.8684635	23.0693836	22.9824657	23.3276958	22.8751278
1628	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Rattus norvegicus OX=10116 GN=Suclg1 PE=1 SV=1	Suclg1	A0A0H2UH	1.30261287	0.34452438	25.1421909	25.5723763	25.1041355	25.021328	24.7137146	24.8242855	24.8867817	25.0371513
1629	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sucla2 PE=1 SV=1	Sucla2	F1LM47	1.88682224	0.6669302	26.9666901	27.4124317	26.7738552	26.9855385	26.2067089	26.0974121	26.702467	26.4642067
1630	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Suclg2 PE=1 SV=2	Suclg2	F1LPV8	0.21434781	0.11812687	26.3731136	26.4838428	26.1846962	25.7151108	25.9683361	26.2966709	25.7216969	26.2975521
1631	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Rattus norvegicus OX=10116 GN=Oxct1 PE=1 SV=1	Oxct1	B2GV06	0.14554898	0.08964109	27.2511406	27.4923687	26.9738541	26.7299595	27.1930637	27.1416416	26.5275898	27.2264633
1632	Sulfite oxidase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Suox PE=1 SV=2	Suox	Q07116	0.52264196	-0.6342225	17.7080498	17.9548073	18.0063705	15.77598	18.452425	17.630722	18.0100937	17.8888569
1633	Sulfotransferase 1A1 OS=Rattus norvegicus OX=10116 GN=Sult1a1 PE=1 SV=1	Sult1a1	P17988	0.34168559	0.45195293	20.7790108	20.7517452	19.5822449	19.790966	20.0966873	18.590416	19.5767918	20.8322601
1634	Superoxide dismutase [Cu-Zn] OS=Rattus norvegicus OX=10116 GN=Sod1 PE=1 SV=2	Sod1	P07632	0.66118442	-0.2414398	22.7301102	22.938406	23.1698647	23.521841	23.4064312	23.2910671	23.405407	23.2230759
1635	Superoxide dismutase [Mn], mitochondrial OS=Rattus norvegicus OX=10116 GN=Sod2 PE=1 SV=2	Sod2	P07895	1.74425025	-0.4502654	23.5075321	23.7168045	23.7348366	23.6976089	24.0000248	24.2560196	24.3898392	23.8119602
1636	Sushi domain-containing 2 OS=Rattus norvegicus OX=10116 GN=Susd2 PE=1 SV=1	Susd2	A0A0G2K0C	0.17235028	-0.1336365	19.2200699	18.5613308	19.0205631	18.9353752	18.628767	19.6637096	19.3754387	18.6039696
1637	Synaptic vesicle membrane protein VAT-1 homolog OS=Rattus norvegicus OX=10116 GN=Vat1 PE=1 SV=1	Vat1	Q3MIE4	0.68228145	-0.3444319	21.2448959	22.0004959	21.0369549	21.417448	21.8975735	21.535759	22.0709496	21.5732403
1638	Synaptojanin-2-binding protein OS=Rattus norvegicus OX=10116 GN=Synj2bp PE=1 SV=2	Synj2bp	Q9WVJ4	0.40529527	-0.2655716	19.3050537	19.8738041	19.8003998	20.5316124	20.1747913	20.2972488	20.3648281	19.7362881
1639	Synaptophysin-like 1 OS=Rattus norvegicus OX=10116 GN=Sypl1 PE=1 SV=1	Sypl1	Q66H18	0.09448939	0.07424068	19.5399628	20.1843014	19.8806782	19.4730663	19.3150845	20.3815098	19.5257797	19.558672
1640	Syntaxin-12 OS=Rattus norvegicus OX=10116 GN=Stx12 PE=1 SV=1	Stx12	A0A0G2JVB	0.26801833	-0.1641579	20.3501148	19.7876263	19.600811	19.9822407	19.7822552	20.1075115	20.6401691	19.8474884
1641	Syntaxin-7 OS=Rattus norvegicus OX=10116 GN=Stx7 PE=1 SV=4	Stx7	O70257	0.2340437	-0.2902017	17.7287426	17.3504562	18.630909	18.4101677	18.4258347	18.7537785	18.9472847	17.1541843
1642	Syntrophin, basic 1 (Predicted) OS=Rattus norvegicus OX=10116 GN=Sntb1 PE=1 SV=1	Sntb1	D3ZWC6	0.44442967	0.45347929	19.5618763	19.9333076	18.9868927	19.9927826	19.3563232	18.0018826	19.615427	19.6873093
1643	Talin 2 OS=Rattus norvegicus OX=10116 GN=Tln2 PE=1 SV=3	Tln2	D3ZA84	0.14985513	-0.1592617	21.0913601	20.4759293	20.3164806	19.1829224	20.4293346	20.5087147	20.2050438	20.5606461
1644	Target of myb1 homolog (Chicken) OS=Rattus norvegicus OX=10116 GN=Tom1 PE=1 SV=1	Tom1	Q5XI21	0.55768529	0.19067335	20.3070869	19.8008575	19.6047974	19.9584332	19.8775196	19.7501144	19.6080799	19.6727676
1645	Target of myb1-like 2 membrane-trafficking protein OS=Rattus norvegicus OX=10116 GN=Tom1l2 PE=1 SV=1	Tom1l2	A0A0G2K9L	0.1394452	-0.1045747	17.4388065	16.89991	16.3861008	16.6540298	17.1987247	16.5167332	16.8181438	17.2635441
1646	Taste receptor type 1 member 2 OS=Rattus norvegicus OX=10116 GN=Aldh4a1 PE=1 SV=1	Aldh4a1	A0A0G2JVM	0.9619902	0.66678905	25.4903164	25.7778683	25.7210865	24.7065315	24.8081169	24.5042839	24.2708111	25.4454346
1647	Taxilin beta OS=Rattus norvegicus OX=10116 GN=Txlnb PE=1 SV=1	Txlnb	A0A0G2K2T	0.58047915	0.77237272	20.1720371	18.9305553	19.0443783	19.2455883	18.9305058	18.7006378	17.0177345	19.6541901
1648	TBC1 domain family, member 2B OS=Rattus norvegicus OX=10116 GN=Tbc1d2b PE=1 SV=2	Tbc1d2b	D3ZAF7	0.2474381	0.38429666	16.1872959	17.3328362	15.8813162	14.99018	15.538455	14.7925682	16.7677574	15.755661
1649	TBC1 domain family, member 4 OS=Rattus norvegicus OX=10116 GN=Tbc1d4 PE=1 SV=3	Tbc1d4	D3ZGN0	0.69232304	0.47807884	20.7695503	20.1334209	20.0220699	19.6537399	19.319582	19.5931053	19.3853378	20.3684406
1650	T-complex protein 1 subunit alpha OS=Rattus norvegicus OX=10116 GN=Tcp1 PE=1 SV=1	Tcp1	P28480	0.3086004	0.15615177	22.6506138	22.2395515	22.3781013	21.8982201	21.9845352	22.2556953	21.8241062	22.4775429
1651	T-complex protein 1 subunit beta OS=Rattus norvegicus OX=10116 GN=Cct2 PE=1 SV=3	Cct2	Q5XIM9	0.47374982	0.36151743	22.4608421	22.650259	22.0187149	21.5741978	21.5952568	21.9805145	21.2649384	22.4172344
1652	T-complex protein 1 subunit delta OS=Rattus norvegicus OX=10116 GN=Cct4 PE=1 SV=3	Cct4	Q7TPB1	0.73557119	0.83519459	21.3245811	21.6153336	20.7987385	23.2180252	20.6928997	21.381588	20.5017815	21.0396309
1653	T-complex protein 1 subunit epsilon OS=Rattus norvegicus OX=10116 GN=Cct5 PE=1 SV=1	Cct5	Q68FQ0	0.18810486	0.11127329	21.5809422	21.23773	21.2872314	20.7841415	20.923151	21.3794937	20.7468967	21.3954105
1654	T-complex protein 1 subunit eta OS=Rattus norvegicus OX=10116 GN=Cct7 PE=1 SV=1	Cct7	D4AC23	0.31520517	0.2583518	21.2661495	20.6736908	20.0613308	19.9918556	20.3082123	20.2961025	19.7554893	20.5998154

1655	T-complex protein 1 subunit gamma OS=Rattus norvegicus OX=10116 GN=Cct3 PE=1 SV=1	Cct3	Q6P502	1.32915318	0.72754288	22.0594769	22.3033295	21.773941	21.8432846	21.3795509	21.3445816	20.535244	21.8104839
1656	Teashirt zinc finger family member 1 OS=Rattus norvegicus OX=10116 GN=Tshz1 PE=4 SV=1	Tshz1	F1LW29	0.0131533	0.00493526	22.9085197	22.6667442	22.6738605	22.3780098	22.6543064	22.7841129	22.4743404	22.6946335
1657	Tensin 1 OS=Rattus norvegicus OX=10116 GN=Tns1 PE=1 SV=2	Tns1	F1LN42	0.87635439	0.5091815	23.1610699	23.2797394	23.5203838	22.5513535	22.70821	22.61096	22.074131	23.0825195
1658	Tescalcin OS=Rattus norvegicus OX=10116 GN=Tesc PE=4 SV=1	Tesc	D3ZTN1	0.7979585	0.33906841	18.6372261	19.0205116	18.9542027	18.1755447	18.2841034	18.5538692	18.1610851	18.4321537
1659	Tetraspanin OS=Rattus norvegicus OX=10116 GN=Cd63 PE=1 SV=1	Cd63	A0A0G2K0T	0.25180316	-0.8255582	18.6742058	18.7735825	18.3979397	22.0184326	22.1071453	21.9861813	18.9867077	18.086359
1660	Tetraspanin OS=Rattus norvegicus OX=10116 GN=Cd81 PE=1 SV=1	Cd81	Q6P9V1	0.72526379	-0.2231879	20.8530693	21.1950188	21.1803074	21.3389606	21.126255	21.3183937	21.6574516	21.3580074
1661	Tetraspanin OS=Rattus norvegicus OX=10116 GN=Tspan8 PE=2 SV=2	Tspan8	O55158	0.55529348	-0.609447	17.3983345	18.6616058	17.4038391	17.4943161	19.1605034	18.4124413	18.6022377	17.2207012
1662	Tetratricopeptide repeat domain 37 OS=Rattus norvegicus OX=10116 GN=Ttc37 PE=1 SV=3	Ttc37	D3ZL50	0.04204008	-0.0769441	17.3832779	18.4549522	16.5591164	15.714736	16.977314	17.1207161	16.555603	17.7662258
1663	Tetratricopeptide repeat domain 38 OS=Rattus norvegicus OX=10116 GN=Ttc38 PE=1 SV=2	Ttc38	D4ACL2	0.81404361	1.08228445	16.5004063	18.1129074	17.5039654	19.2602768	16.485815	17.664772	16.7491703	16.1486607
1664	Thioredoxin domain containing 13 OS=Rattus norvegicus OX=10116 GN=Tmx4 PE=1 SV=1	Tmx4	G3V912	0.31602472	0.21876001	18.4987698	18.6429234	18.5488663	18.7296486	18.7922649	18.6624756	17.534008	18.5564194
1665	Thioredoxin domain-containing 17 OS=Rattus norvegicus OX=10116 GN=Txndc17 PE=1 SV=1	Txndc17	B0K010	0.12398786	0.22168922	17.7910423	18.0336418	16.0754814	17.6253204	17.8414497	15.6882744	17.7437153	17.3652897
1666	Thioredoxin OS=Rattus norvegicus OX=10116 GN=Txn PE=1 SV=2	Txn	P11232	0.82605753	-0.2164245	20.7284737	21.0046864	20.7910061	21.2557259	21.0776443	21.1349583	21.3190136	21.1139736
1667	Thioredoxin reductase 2, mitochondrial OS=Rattus norvegicus OX=10116 GN=Txnrd2 PE=1 SV=3	Txnrd2	Q9Z0J5	0.00673037	0.00470209	17.768343	17.662241	17.5595474	17.2555561	17.2827682	17.4722977	18.1627331	17.3090801
1668	Thioredoxin-interacting protein OS=Rattus norvegicus OX=10116 GN=Txnip PE=2 SV=1	Txnip	Q5M7W1	0.4086146	0.42067528	21.0021191	19.8495693	20.1674099	19.7005291	19.8404999	19.9962845	18.7786999	20.421442
1669	Thioredoxin-related transmembrane protein 2 OS=Rattus norvegicus OX=10116 GN=Tmx2 PE=2 SV=1	Tmx2	Q5XIK2	0.53963862	-0.1525793	17.7039776	17.448452	17.7758484	17.6724529	17.7900009	17.8726292	18.0384693	17.5099487
1670	Threonine synthase-like 1 OS=Rattus norvegicus OX=10116 GN=Thnsl1 PE=1 SV=1	Thnsl1	E9PTK4	0.38817589	0.3100276	19.1681175	18.6353989	18.8651199	19.4250431	19.1690006	18.3257961	18.0681667	19.2906055
1671	Threonine--tRNA ligase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Tars2 PE=2 SV=1	Tars2	Q68FW7	0.69423356	-0.4380369	19.0481129	19.7409439	19.4377289	19.9978313	19.6014328	20.1882401	20.5464764	19.6406155
1672	Threonyl-tRNA synthetase-like 2 OS=Rattus norvegicus OX=10116 GN=Tarsl2 PE=2 SV=1	Tarsl2	Q5XI17	1.2727547	0.85345078	18.1099815	17.8006268	17.7124577	17.0707664	17.0290127	17.5201435	16.3618431	16.36903
1673	Thrombospondin 1 OS=Rattus norvegicus OX=10116 GN=Thbs1 PE=1 SV=2	Thbs1	M0R979	0.01564005	0.01129436	19.5405235	19.552433	18.8622284	19.3619251	19.3945351	18.8592453	19.2710438	19.7471085
1674	Thymosin beta-4 OS=Rattus norvegicus OX=10116 GN=Tmsb4x PE=1 SV=2	Tmsb4x	P62329	0.07705046	-0.0430379	20.4423466	20.6668949	19.9940586	20.4369011	20.1096325	20.3933449	20.403635	20.8057404
1675	Tissue-type transglutaminase OS=Rattus norvegicus OX=10116 GN=Tgm2 PE=1 SV=1	Tgm2	Q9WVJ6	0.29127723	0.11662817	21.8488064	21.8414612	21.446846	21.529604	21.3259659	21.3805981	21.5920563	21.9015846
1676	T-kininogen 1 OS=Rattus norvegicus OX=10116 GN=Map1 PE=1 SV=2	Map1	P01048	0.1153296	-0.1217756	21.6229115	21.4226875	21.0363026	21.6902275	21.6007481	21.8008842	20.5645027	22.2930965
1677	T-kininogen 2 OS=Rattus norvegicus OX=10116 PE=1 SV=2	10116	P08932	0.03863037	0.07519436	19.7817421	19.245615	18.3342056	17.0540886	18.5865612	18.983984	17.6217289	18.9225998
1678	TPD52-like 1 OS=Rattus norvegicus OX=10116 GN=Tpd52l1 PE=4 SV=1	Tpd52l1	A0A0G2K8N	0.08153744	-0.1729608	19.556694	18.6280384	16.3154755	19.5214481	18.6267338	18.6692505	18.5018539	18.9156609
1679	Trafficking kinesin-binding protein 2 OS=Rattus norvegicus OX=10116 GN=Trak2 PE=4 SV=1	Trak2	A0A0G2K43	0.0804917	0.10548401	19.303587	17.1476212	17.758646	18.4619617	18.242094	18.088253	17.8136921	18.1058407
1680	Trafficking protein particle complex subunit 3 OS=Rattus norvegicus OX=10116 GN=Trappc3 PE=2 SV=1	Trappc3	Q5U1Z2	0.03823323	0.13350654	16.9661026	17.4420681	16.678957	14.2272825	17.2927742	17.2034893	13.2792702	17.0048504
1681	Transaldolase OS=Rattus norvegicus OX=10116 GN=Taldo1 PE=1 SV=2	Taldo1	Q9EQS0	0.11272935	0.23213768	15.927968	15.8359623	15.4713497	17.9442291	15.855648	16.6039715	17.0917263	14.6996126
1682	Transcription factor A, mitochondrial OS=Rattus norvegicus OX=10116 GN=Tfam PE=2 SV=1	Tfam	Q91ZW1	0.78990314	0.34765863	19.2455425	19.3688774	19.4325371	19.416069	18.8030643	19.6179695	19.012495	18.6388626
1683	Transcription intermediary factor 1-beta OS=Rattus norvegicus OX=10116 GN=Trim28 PE=1 SV=2	Trim28	O08629	1.10128045	1.43644404	18.6044636	19.1179295	18.2180099	17.7035656	17.2839794	16.9249382	15.3704729	18.3188019
1684	Transcriptional activator protein Pur-alpha OS=Rattus norvegicus OX=10116 GN=Pura PE=1 SV=3	Pura	F1LPS8	0.31993787	0.34781551	18.316246	17.5532455	17.3507652	17.5216045	16.2558212	17.880312	17.1709023	18.0435638
1685	Transcriptional activator protein Pur-beta OS=Rattus norvegicus OX=10116 GN=Purb PE=1 SV=1	Purb	A0A0G2JUX	0.74376832	0.96614146	18.6799927	18.3625469	17.7433834	18.8668537	17.470417	15.9627523	17.5152645	18.839777
1686	Transferrin receptor protein 1 OS=Rattus norvegicus OX=10116 GN=Tfrc PE=1 SV=1	Tfrc	G3V679	0.53779986	-0.7574656	17.2511005	17.0827293	17.640028	15.0620108	16.9496326	17.0406799	18.1295834	17.9458351
1687	Transforming protein RhoA OS=Rattus norvegicus OX=10116 GN=Rhoa PE=1 SV=1	Rhoa	P61589	0.31775319	-0.1636868	21.6660538	22.4563522	22.1093655	22.6045246	22.3253613	22.268652	22.5564823	22.3405476
1688	Transforming, acidic coiled-coil-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Tacc2 PE=1 SV=1	Tacc2	A0A0G2K59	0.24366987	0.1231122	22.9365234	22.3014793	23.0740795	22.4824505	22.7779446	22.5538769	22.6364594	22.3338032
1689	Transgelin OS=Rattus norvegicus OX=10116 GN=Tagln PE=1 SV=1	Tagln	A0A0G2JWI	0.1645389	-0.5571988	21.0575352	15.4281816	17.5978985	18.6685486	17.8634586	20.2819672	19.0095253	17.8260078
1690	Transgelin-2 OS=Rattus norvegicus OX=10116 GN=Tagln2 PE=1 SV=1	Tagln2	Q5XFX0	0.42286144	-0.7796044	14.9053955	18.3873043	17.2169456	18.3399792	17.7850342	18.1272583	17.9849148	18.0708351
1691	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus OX=10116 GN=Vcp PE=1 SV=3	Vcp	P46462	0.00269797	0.00158787	22.5833664	22.1469288	21.9081306	22.0522537	21.9425297	22.4084816	21.9433155	22.3900013
1692	Transketolase OS=Rattus norvegicus OX=10116 GN=Tkt PE=1 SV=1	Tkt	G3V826	0.48345444	0.88448286	17.3390827	16.3170662	15.5791426	18.9087296	17.2697525	15.7233257	16.2488365	15.3641748
1693	Translation initiation factor eIF-2B subunit beta OS=Rattus norvegicus OX=10116 GN=Eif2b2 PE=1 SV=1	Eif2b2	F7EVX2	0.44163698	0.57409906	20.4560108	19.8260689	19.5417023	18.1534004	19.7917252	18.6050873	18.3177528	18.9662209
1694	Translation initiation factor eIF-2B subunit delta OS=Rattus norvegicus OX=10116 GN=Eif2b4 PE=2 SV=1	Eif2b4	Q63186	0.20837106	-0.5601754	19.6558533	19.5127296	19.3845444	15.4565086	19.122036	19.5628052	18.1176147	19.4478817
1695	Translation initiation factor eIF-2B subunit epsilon OS=Rattus norvegicus OX=10116 GN=Eif2b5 PE=1 SV=2	Eif2b5	Q64350	0.30298386	0.63261127	17.166317	17.7731876	18.126358	15.1580801	16.3250027	17.0781918	14.8493128	17.4409904
1696	Translationally-controlled tumor protein OS=Rattus norvegicus OX=10116 GN=Tpt1 PE=1 SV=1	Tpt1	P63029	0.53389189	-0.4602184	17.5953903	16.5893459	18.3144455	18.137598	18.2466354	18.2070656	17.8452663	18.1786861
1697	Translocon-associated protein subunit delta OS=Rattus norvegicus OX=10116 GN=Ssr4 PE=2 SV=1	Ssr4	Q07984	0.35671511	-0.6820197	18.1313038	14.7512035	16.3881073	18.1865082	17.6548672	17.2541008	17.6366158	17.6396179
1698	Transmembrane 9 superfamily member 2 OS=Rattus norvegicus OX=10116 GN=Tm9sf2 PE=2 SV=1	Tm9sf2	Q66HG5	0.21892165	0.17475939	18.2324314	18.1561375	18.3437614	17.5020905	17.5428429	17.9885292	18.5670605	17.4369507
1699	Transmembrane and coiled-coil domain-containing protein 4 OS=Rattus norvegicus OX=10116 GN=Tmco4 PE=1 SV=2	Tmco4	F1LRM3	0.26212689	0.26538277	17.8777924	17.177145	17.0358219	18.4126148	17.8312378	17.1411438	17.7548599	16.7146015
1700	Transmembrane emp24 domain-containing protein 10 OS=Rattus norvegicus OX=10116 GN=Tmed10 PE=1 SV=2	Tmed10	Q63584	0.66200036	-0.3350115	19.2897224	19.0852451	19.2933083	19.17066	19.5375309	18.8874836	19.9939995	19.7599678
1701	Transmembrane emp24 domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Tmed2 PE=1 SV=1	Tmed2	Q63524	0.15142527	-0.1104641	19.8962688	20.1889935	20.279007	20.7946568	20.3464909	19.8439064	20.7893047	20.6210804
1702	Transmembrane emp24 domain-containing protein 7 OS=Rattus norvegicus OX=10116 GN=Tmed7 PE=1 SV=1	Tmed7	D3ZTX0	0.33028454	-0.195281	19.1739731	18.9077396	18.8780289	19.5933628	19.1542416	18.8942833	19.7293663	19.5563374
1703	Transmembrane emp24 protein transport domain containing 4 (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Tmed4 PE=1 SV=3	Tmed4	G3V6N2	0.02984502	-0.0106983	18.7051163	19.0503502	18.6691723	18.8567734	18.7962894	18.6024914	19.004221	18.9212036
1704	Transmembrane protein 109 OS=Rattus norvegicus OX=10116 GN=Tmem109 PE=2 SV=1	Tmem109	Q6AYQ4	0.32383959	-0.3360162	15.1179667	14.8849316	14.7417955	15.2075653	15.6558027	15.2186079	16.2220383	14.1998749
1705	Transmembrane protein 11, mitochondrial OS=Rattus norvegicus OX=10116 GN=Tmem11 PE=2 SV=1	Tmem11	B0BN86	0.14544335	0.22566223	19.047823	18.8609657	18.9118843	21.2223225	19.0818939	19.0725403	19.6973305	19.2885818
1706	Transmembrane protein 126A OS=Rattus norvegicus OX=10116 GN=Tmem126a PE=2 SV=1	Tmem126a	Q5HZA9	1.45757529	-0.7286305	19.8594646	19.695591	20.2430935	20.6556034	20.9656391	20.9015903	21.1238708	20.3771744
1707	Transmembrane protein 143 OS=Rattus norvegicus OX=10116 GN=Tmem143 PE=1 SV=1	Tmem143	D3ZSD8	2.08439277	-0.7785926	19.244194	19.3280373	19.5069046	19.9101028	20.176363	20.4207439	20.5612698	19.9452324
1708	Transmembrane protein 182 OS=Rattus norvegicus OX=10116 GN=Tmem182 PE=4 SV=1	Tmem182	D3ZZT3	0.8584347	-0.2626615	19.5881214	20.2062492	19.6334629	19.971199	20.1841908	20.1967106	20.0686493	20.0001278
1709	Transmembrane protein 256 OS=Rattus norvegicus OX=10116 GN=Tmem256 PE=1 SV=2	Tmem256	F1LYI7	1.05848716	-0.730289	19.2851315	19.5392036	20.1745834	19.1725445	19.980217	20.6740875	20.8032169	19.6350975
1710	Transmembrane protein 38a (Predicted), isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Tmem38a PE=4 SV=1	Tmem38a	G3V9T4	0.25934898	-0.2133999	17.7676563	18.2191429	18.8671131	18.6938286	18.8332653	18.370594	19.1098061	18.0876751
1711	Transmembrane protein 41B OS=Rattus norvegicus OX=10116 GN=Tmem41b PE=2 SV=1	Tmem41b	Q5FVN2	0.23702197	0.2831049	16.7105484	16.7535458	16.7723675	15.8992119	16.6961117	14.9481182	16.7045898	16.6544342
1712	Transmembrane protein 65 OS=Rattus norvegicus OX=10116 GN=Tmem65 PE=4 SV=1	Tmem65	F1LQZ0	1.71225858	-0.4200463	20.3237572	20.7137699	20.6201439	20.2108192	20.8353806	20.7477474	20.9934177	20.9721298
1713	Transportin 3 OS=Rattus norvegicus OX=10116 GN=Tnpo3 PE=1 SV=2	Tnpo3	D4AAM0	0.19481503	0.13298655	15.3839741	15.5255899	15.5518141	15.6408319	15.1072845	15.8267517	14.7923393	15.8438883
1714	Transthyretin OS=Rattus norvegicus OX=10116 GN=Ttr PE=1 SV=1	Ttr	P02767	0.07070974	0.03448963	19.7423191	20.1273212	19.9167461	19.8145943	19.8500271	19.4395962	20.061058	20.1123409
1715	Triadin OS=Rattus norvegicus OX=10116 GN=Trdn PE=1 SV=3	Trdn	F1LY11	0.57400122	-0.2898569	19.1644077	19.2968407	18.8408661	19.8029518	19.5624008	19.7675552	19.7246189	19.209919
1716	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hadha PE=1 SV=2	Hadha	Q64428	0.25366133	0.07894611	28.0463448	27.6628513	28.0688305	27.8635635	27.9370441	28.0082455	27.7391911	27.641325
1717	Trifunctional enzyme subunit beta, mitochondrial OS=Rattus norvegicus OX=10116 GN=Hadhb PE=1 SV=1	Hadhb	Q60587	0.45468212	0.09777737	27.8385468	27.5061035	27.6750298	27.5813065	27.6502323	27.6770077	27.4619465	27.4206905
1718	Trifunctional purine biosynthetic protein adenosine-3 OS=Rattus norvegicus OX=10116 GN=Gart PE=1 SV=1	Gart	G3V918	0.48693131	0.29656076	21.2197037	21.0647469	20.8036041	20.5589123	20.5143013	21.0357094	19.9917908	20.9189224
1719	Triosephosphate isomerase OS=Rattus norvegicus OX=10116 GN=Tpi1 PE=1 SV=2	Tpi1	P48500	0.38943572	-0.0843549	24.6055508	24.4221668	24.5319405	24.7407494	24.5522823	24.5480404	24.7118378	24.8256664
1720	Tripartite motif protein 29 (Predicted), isoform CRA_a OS=Rattus norvegicus OX=10116 GN=Trim29 PE=4 SV=1	Trim29	A0A0G2K65	0.80276967	-0.4042869	19.2087078	19.6567936	20.1934414	20.1958332	20.0980606	20.4006233	20.2905769	20.0826626
1721	Tripartite motif-containing 25 OS=Rattus norvegicus OX=10116 GN=Trim25 PE=1 SV=3	Trim25	D4A9N5	0.09615316	-0.0701227	19.5926971	18.9243469	19.4079952	18.4583092	19.3671799	19.2038326	19.0088806	19.0839462
1722	Tripartite motif-containing 7 OS=Rattus norvegicus OX=10116 GN=Trim7 PE=4 SV=1	Trim7	D3ZNJ9	0.03822883	-0.0716281	17.2274208	17.674263	17.381424	15.4329433	17.028389	17.7862949	17.3083229	15.8795567
1723	Tripartite motif-containing protein 3 OS=Rattus norvegicus OX=10116 GN=Trim3 PE=1 SV=1	Trim3	O70277	0.22416216	0.33488202	15.9519644	15.1906281	15.3412685	13.4191303	15.0003195	14.1192064	14.305768	15.1381693
1724	Tripartite motif-containing protein 54 OS=Rattus norvegicus OX=10116 GN=Trim54 PE=2 SV=1	Trim54	Q5XIH6	0.84316298	0.76366997	18.9978027	18.8760929	19.0288448	18.1744881	18.3867779	18.1247845	16.8326492	18.6783371
1725	Tripartite motif-containing protein 72 OS=Rattus norvegicus OX=10116 GN=Trim72 PE=1 SV=1	Trim72	A0JPQ4	0.77546063	-0.3221946	23.8704987	24.1371098	23.3332729	24.1004486	24.0153561	24.2846317	24.3784504	24.0516701
1726	Tripeptidyl peptidase I OS=Rattus norvegicus OX=10116 GN=Tpp1 PE=1 SV=1	Tpp1	Q642E6	0.50341753	-1.1239142	19.5713158	19.7884464	19.2914829	15.4974194	19.4036369	19.6743126	19.7580166	19.8083553

1727	tRNA methyltransferase 10 homolog C OS=Rattus norvegicus OX=10116 GN=Trmt10c PE=2 SV=1	Trmt10c	Q5U2R4	0.04643492	-0.0573487	19.2139301	18.8900604	18.9831161	17.580431	19.0296879	18.7587776	18.0789223	19.0295448
1728	tRNA modification GTPase GTPBP3, mitochondrial OS=Rattus norvegicus OX=10116 GN=Gtpbp3 PE=2 SV=1	Gtpbp3	Q5PQQ1	2.92226419	1.31700993	19.8702164	20.442276	20.0328007	20.8379173	19.0442066	19.0794868	19.0261059	18.7653713
1729	tRNA-splicing ligase RtcB homolog OS=Rattus norvegicus OX=10116 GN=Rtcb PE=2 SV=1	Rtcb	Q6AYT3	0.53928425	0.47761202	18.5976868	18.1039963	17.18367	16.9208012	17.1848907	17.5195694	16.9250813	17.2661648
1730	Tropomyosin 1, alpha, isoform CRA_p OS=Rattus norvegicus OX=10116 GN=Tpm1 PE=1 SV=1	Tpm1	A0A0G2JSQ	0.1882949	-0.17156	15.8083019	16.3228645	15.1284466	16.4014854	16.076849	16.4428692	16.3093243	15.5182962
1731	Tropomyosin alpha-1 chain OS=Rattus norvegicus OX=10116 GN=Tpm1 PE=1 SV=3	Tpm1	P04692	1.34938366	-1.4805875	21.0401554	23.6195335	23.0427437	22.9154663	24.0203857	23.7155056	24.2917843	24.5125732
1732	Tropomyosin alpha-3 chain OS=Rattus norvegicus OX=10116 GN=Tpm3 PE=1 SV=2	Tpm3	Q63610	1.11292544	1.47005033	20.0401859	19.2942371	19.6698589	20.1641407	19.1387596	18.6158562	16.374342	19.1592636
1733	Troponin I, cardiac muscle OS=Rattus norvegicus OX=10116 GN=Tnni3 PE=1 SV=2	Tnni3	P23693	0.97197491	-0.9204798	19.8042679	21.5459232	21.3722019	20.620285	21.3777485	21.2200832	22.0193996	22.4073658
1734	Troponin T, cardiac muscle OS=Rattus norvegicus OX=10116 GN=Tnnt2 PE=1 SV=2	Tnnt2	P50753	1.56759698	-1.4449606	18.718504	20.729723	20.6596699	20.1035786	21.3211498	21.2865238	21.3731976	22.0104465
1735	Tryptophan--tRNA ligase, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Wars PE=1 SV=2	Wars	Q6P7B0	0.27673319	0.32423687	19.4366398	19.0391026	17.933363	18.0385685	18.3344212	18.1421509	17.5807133	19.093441
1736	TSC22 domain family protein 4 OS=Rattus norvegicus OX=10116 GN=LOC102550456 PE=1 SV=1	LOC1025504	A0A0G2K1V	0.17086391	0.60749102	16.1981182	16.3247242	14.0344486	20.4751053	15.5741911	16.6154709	15.71	16.7027702
1737	Tubulin alpha chain OS=Rattus norvegicus OX=10116 GN=Tubal3 PE=1 SV=2	Tubal3	F1LUM5	0.30859619	-0.1441331	19.6762104	19.0876694	19.2029266	18.7452831	19.2606239	19.3486748	19.2529831	19.4263401
1738	Tubulin alpha-1A chain OS=Rattus norvegicus OX=10116 GN=Tuba1a PE=1 SV=1	Tuba1a	P68370	0.52272954	-0.4217916	23.3275928	22.7032719	22.5786762	21.6488457	22.900116	23.0653248	22.6686611	23.311451
1739	Tubulin alpha-1B chain OS=Rattus norvegicus OX=10116 GN=Tuba1b PE=1 SV=1	Tuba1b	Q6P9V9	0.38510333	-0.1774435	26.4143238	25.999382	25.7875805	25.6559658	26.006588	26.0454216	26.0317593	26.4832573
1740	Tubulin alpha-1C chain OS=Rattus norvegicus OX=10116 GN=Tuba1c PE=1 SV=1	Tuba1c	Q6AYZ1	0.33714802	-0.3086843	21.6439095	20.7502022	19.878933	20.4908257	20.9179401	20.9328041	20.7552166	21.3926468
1741	Tubulin alpha-4A chain OS=Rattus norvegicus OX=10116 GN=Tuba4a PE=1 SV=1	Tuba4a	Q5XIF6	0.11239705	-0.0484033	29.1004848	28.6355515	28.4672318	28.5695553	28.8034592	28.6102333	28.623457	28.929287
1742	Tubulin alpha-8 chain OS=Rattus norvegicus OX=10116 GN=Tuba8 PE=2 SV=1	Tuba8	Q6AY56	0.00248511	0.00195169	24.993103	23.9216423	24.3344078	24.0868568	24.4200439	24.224411	24.0795937	24.6041546
1743	Tubulin beta chain OS=Rattus norvegicus OX=10116 GN=Tubb1 PE=1 SV=1	Tubb1	M0R8B6	0.47646615	-0.6167669	19.2013054	19.1144485	17.0475636	17.5022697	18.420845	18.8036861	18.7275009	19.3806229
1744	Tubulin beta chain OS=Rattus norvegicus OX=10116 GN=Tubb4a PE=1 SV=1	Tubb4a	B4F7C2	0.08430311	0.13627625	13.4575987	14.6358719	14.6620197	15.9616652	14.9652929	15.0654707	13.882349	14.2589378
1745	Tubulin beta chain OS=Rattus norvegicus OX=10116 GN=Tubb4b PE=1 SV=2	Tubb4b	G3V7C6	0.28586657	-0.11163	29.7305565	29.3957043	29.2645817	29.0493393	29.5090981	29.2859955	29.4322205	29.6593876
1746	Tubulin beta chain OS=Rattus norvegicus OX=10116 GN=Tubb6 PE=1 SV=1	Tubb6	Q4QQV0	1.10508481	-0.8902674	20.1096687	20.2839775	20.0528526	19.6972885	21.0152969	19.8478737	21.047802	21.7938843
1747	Tubulin beta-2A chain OS=Rattus norvegicus OX=10116 GN=Tubb2a PE=1 SV=1	Tubb2a	P85108	0.11980391	0.0516634	22.7706337	22.5423203	22.2278805	22.4058838	22.7569981	22.2793827	22.2763271	22.4273567
1748	Tubulin beta-2B chain OS=Rattus norvegicus OX=10116 GN=Tubb2b PE=1 SV=1	Tubb2b	Q3KRE8	0.75620484	-0.3286715	23.4176273	23.2143078	22.9722385	22.501215	23.3545895	23.3000126	23.1860867	23.5793858
1749	Tubulin beta-3 chain OS=Rattus norvegicus OX=10116 GN=Tubb3 PE=1 SV=1	Tubb3	Q4QRB4	0.41586629	0.45597792	21.4319305	21.7866497	20.3590088	20.0550079	20.8987255	20.2686901	19.8284073	20.8128624
1750	Tubulin beta-5 chain OS=Rattus norvegicus OX=10116 GN=Tubb5 PE=1 SV=1	Tubb5	P69897	0.36649978	-0.225965	25.4894161	25.1829147	25.019659	24.4886932	25.3448715	24.8133869	25.3201523	25.6061325
1751	Tubulin folding cofactor D OS=Rattus norvegicus OX=10116 GN=Tbcd PE=1 SV=3	Tbcd	F1M1D5	1.32338974	-0.6849179	16.7123814	16.8254547	15.7385406	16.0315266	16.9011574	17.167038	17.1376991	16.8416805
1752	Tubulin gamma-1 chain OS=Rattus norvegicus OX=10116 GN=Tubg1 PE=2 SV=1	Tubg1	P83888	0.06528341	0.03253412	19.9580498	19.3098927	19.4480591	19.7249985	19.5498333	19.3905926	19.5014286	19.869009
1753	Tubulin-specific chaperone cofactor E-like protein OS=Rattus norvegicus OX=10116 GN=Tbcel PE=1 SV=1	Tbcel	Q5PQJ7	0.00479368	-0.0035639	17.4829502	16.8889885	16.8682041	16.6396427	17.2787094	16.8330936	16.5553665	17.2268715
1754	Tumor protein D52 OS=Rattus norvegicus OX=10116 GN=Tpd52 PE=1 SV=1	Tpd52	A0A0G2K86	0.68117839	0.42378426	18.9451447	18.3039112	18.9694176	18.7648621	17.6634045	18.7714252	18.6929665	18.1604023
1755	Tumor protein D54 OS=Rattus norvegicus OX=10116 GN=Tpd52l2 PE=1 SV=1	Tpd52l2	Q6PCT3	0.45355615	0.25824451	20.8724308	21.1368313	20.4595509	20.4790535	20.4272289	20.0587864	21.0095901	20.4192829
1756	Tyrosine-protein kinase OS=Rattus norvegicus OX=10116 GN=Jak1 PE=1 SV=1	Jak1	G3V9W2	0.07846578	0.14878464	19.9214325	19.0496445	17.4301796	18.5674286	17.9492378	17.8805923	18.7655964	19.77812
1757	Tyrosine-protein phosphatase non-receptor type 11 OS=Rattus norvegicus OX=10116 GN=Ptpn11 PE=1 SV=4	Ptpn11	P41499	0.7141292	0.65246773	18.1645489	17.1027489	18.0576897	16.7444401	16.1307716	16.7826977	17.3722649	17.1738224
1758	Tyrosine-protein phosphatase non-receptor type OS=Rattus norvegicus OX=10116 GN=Ptpn3 PE=1 SV=2	Ptpn3	F1LQQ5	0.80099115	1.08293724	18.7494469	17.325573	17.7958431	15.6643963	16.6666679	16.408844	15.776968	16.3510303
1759	Tyrosine--tRNA ligase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Yars2 PE=2 SV=1	Yars2	Q5I0L3	1.55924396	0.71403313	20.9026871	20.4212914	20.5817013	20.0870209	20.0947704	19.6619072	19.3319416	20.0479488
1760	Ubiquilin 2 OS=Rattus norvegicus OX=10116 GN=Ubqln2 PE=1 SV=1	Ubqln2	D4AA63	1.09424551	-0.4964752	16.7946587	17.0469303	16.3725071	17.1595764	17.2463169	17.3784752	17.7504921	16.9842892
1761	Ubiquinol-cytochrome c reductase, complex III subunit X OS=Rattus norvegicus OX=10116 GN=Uqcr10 PE=1 SV=1	Uqcr10	A0A0G2K8C	1.52330282	-0.3576531	24.6026306	24.6132507	25.0024433	24.920557	25.0708141	25.2898331	25.2339344	24.9749126
1762	Ubiquinol-cytochrome-c reductase complex assembly factor 2 OS=Rattus norvegicus OX=10116 GN=Uqcc2 PE=2 SV=1	Uqcc2	B5DFN3	0.38785867	-0.4925189	18.5627594	17.2191429	17.6261978	19.2799091	17.8062954	19.1503391	18.6573448	19.0441055
1763	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial OS=Rattus norvegicus OX=10116 GN=Coq6 PE=2 SV=1	Coq6	Q68FU7	1.25287705	0.52980375	21.4942932	21.5715523	21.2757263	21.0883331	20.7841911	21.3696384	20.4398174	20.7170429
1764	Ubiquinone biosynthesis O-methyltransferase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Coq3 PE=2 SV=2	Coq3	Q63159	0.1807487	0.07172441	24.5086994	24.4053249	24.2823658	24.5046177	24.6587543	24.2983437	24.4797001	23.9773121
1765	Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Rattus norvegicus OX=10116 GN=Coq9 PE=1 SV=2	Coq9	Q68FT1	1.43710643	0.67346859	25.1649075	24.64188	24.7994194	24.6977539	24.3192711	24.5828571	23.5371265	24.1708317
1766	Ubiquitin carboxyl-terminal hydrolase 4 OS=Rattus norvegicus OX=10116 GN=Usp4 PE=1 SV=1	Usp4	B2GUZ1	1.31358173	0.86784005	17.5690804	16.8204365	16.2057877	17.1876316	16.4817524	15.5573626	16.263464	16.008997
1767	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus OX=10116 GN=Uchl3 PE=1 SV=2	Uchl3	D4ABI6	1.0425516	0.39805079	18.0642452	18.7102108	18.6893005	18.0323601	18.066494	18.033268	17.7988987	18.0052528
1768	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus OX=10116 GN=Usp13 PE=2 SV=2	Usp13	D3ZDI9	0.61417008	1.40741825	18.5762215	17.1301212	16.2806797	16.1037655	16.9674606	12.9709015	15.6647015	16.8580513
1769	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus OX=10116 GN=Usp5 PE=1 SV=1	Usp5	D3ZVQ0	0.93135296	0.50963783	20.57967	20.8460884	21.151247	20.8635292	20.1830006	20.656517	19.717041	20.8454247
1770	Ubiquitin protein ligase E3A OS=Rattus norvegicus OX=10116 GN=Ube3a PE=1 SV=2	Ube3a	F1M7B8	1.10076807	0.40551043	23.4269638	22.8583527	22.6988182	22.6730461	22.4240704	22.4778557	22.3970432	22.7361698
1771	Ubiquitin protein ligase E3C (Fragment) OS=Rattus norvegicus OX=10116 GN=Ube3c PE=1 SV=1	Ube3c	A0A1B0GW	0.57745465	0.46625566	20.5025387	20.5516605	20.5506821	19.4074688	20.0171089	19.4047565	19.3347626	20.3906994
1772	Ubiquitin protein ligase E3C OS=Rattus norvegicus OX=10116 GN=Ube3c PE=1 SV=3	Ube3c	D3ZHB7	0.3406401	0.26265287	18.8172855	18.6118546	18.4022293	18.4369984	18.3280048	17.6683578	18.0605106	19.1608829
1773	Ubiquitin thioesterase OTUB1 OS=Rattus norvegicus OX=10116 GN=Otub1 PE=1 SV=1	Otub1	B2RYG6	0.19566688	0.21498919	20.1054363	19.3719311	18.775959	19.8982372	19.5185604	18.7998447	18.8441277	20.1290741
1774	Ubiquitin-40S ribosomal protein S27a OS=Rattus norvegicus OX=10116 GN=Rps27a PE=1 SV=2	Rps27a	P62982	0.17610004	0.07787657	24.0190964	23.5823841	23.5816936	23.4172554	23.7198982	23.3937187	23.3626137	23.8126926
1775	Ubiquitin-conjugating enzyme E2 D3 OS=Rattus norvegicus OX=10116 GN=Ube2d3 PE=2 SV=1	Ube2d3	P61078	0.03835565	0.0921526	17.5426979	17.2847595	17.5083122	20.0102673	19.5695591	17.3223324	17.5783386	17.5071964
1776	Ubiquitin-conjugating enzyme E2 N OS=Rattus norvegicus OX=10116 GN=Ube2n PE=1 SV=1	Ube2n	Q9EQX9	0.64021078	0.18728018	23.3246746	23.2741718	23.1606102	23.5371494	23.0635643	23.3712578	22.8480663	23.2645969
1777	Ubiquitin-conjugating enzyme E2 V1 OS=Rattus norvegicus OX=10116 GN=LOC100912618 PE=1 SV=1	LOC100912(	D3ZFY8	0.58646585	-0.4953971	19.5753002	18.3389111	18.6407604	19.7513428	19.1171818	19.6265182	19.482029	20.0621738
1778	Ubiquitin-conjugating enzyme E2M OS=Rattus norvegicus OX=10116 GN=Ube2m PE=1 SV=1	Ube2m	D3ZNQ6	0.07735352	0.04607296	18.4166279	18.2462769	18.0696449	18.8428421	18.4509792	18.0765839	18.1833038	18.680233
1779	Ubiquitin-like modifier-activating enzyme 1 OS=Rattus norvegicus OX=10116 GN=Uba1 PE=1 SV=1	Uba1	Q5U300	0.19728681	0.13186073	21.2970219	21.4436302	21.166441	21.1670017	21.1076851	21.282671	20.4643326	21.6919632
1780	Ubiquitin-like modifier-activating enzyme 2 OS=Rattus norvegicus OX=10116 GN=Uba2 PE=1 SV=3	Uba2	F1LS72	1.10622317	0.62228537	19.7024498	19.7089176	19.2432442	18.5009918	18.5620937	18.6546783	18.573307	18.8763828
1781	Ubiquitin-like modifier-activating enzyme 5 OS=Rattus norvegicus OX=10116 GN=Uba5 PE=1 SV=1	Uba5	Q5M7A4	2.28360024	0.76676607	21.7441483	21.8703861	21.5079231	21.361084	20.699316	21.2145252	20.5894241	20.9132118
1782	Ubiquitin-like modifier-activating enzyme ATG7 OS=Rattus norvegicus OX=10116 GN=Atg7 PE=2 SV=1	Atg7	Q641Y5	0.554866	0.3197751	18.5462818	18.8016014	18.5925827	17.8179588	18.1518898	18.5254803	17.7402	18.0617542
1783	Ubiquitin-like protein 4A OS=Rattus norvegicus OX=10116 GN=Ubl4a PE=2 SV=1	Ubl4a	B2GV38	0.02714747	-0.0686336	20.2506905	19.2389374	16.9202862	17.0563602	18.2922192	18.0666676	18.1469421	19.2349796
1784	Ubiquitin-specific peptidase 24 OS=Rattus norvegicus OX=10116 GN=Usp24 PE=1 SV=2	Usp24	F1LSM0	0.94140309	1.15938854	19.1716976	19.4355164	18.251667	18.0599728	18.2173004	16.800684	16.548811	18.7145042
1785	Ubiquitin-specific peptidase 47 OS=Rattus norvegicus OX=10116 GN=Usp47 PE=1 SV=1	Usp47	A0A0G2JUX	0.56512826	-0.1676331	21.0146198	21.4811497	20.930645	21.0073795	21.1981373	21.1862926	21.4406052	21.2792912
1786	Ubiquitin-specific peptidase 9, X-linked OS=Rattus norvegicus OX=10116 GN=Usp9x PE=1 SV=1	Usp9x	A0A0G2K2C	0.71393335	0.31476831	18.9327869	19.272459	18.5167561	18.7264004	18.9497967	18.4744549	18.279623	18.4854546
1787	UBX domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Ubxn1 PE=3 SV=2	Ubxn1	Q499N6	0.1051343	0.06389856	18.3204899	17.4075947	17.471283	17.5126648	17.4349537	17.6856365	17.7058926	17.6299553
1788	UMP-CMP kinase OS=Rattus norvegicus OX=10116 GN=Cmpk1 PE=1 SV=1	Cmpk1	A0A0G2JTN	1.21650135	0.42300749	20.2940273	20.2849216	19.7901058	19.9156075	19.6037941	19.4159374	19.5501232	20.0227776
1789	Unc-45 myosin chaperone B OS=Rattus norvegicus OX=10116 GN=Unc45b PE=4 SV=1	Unc45b	A0A096MJB	0.69958051	0.12074518	23.6890926	23.5787907	23.6122379	23.8929176	23.6315861	23.4397697	23.5880699	23.6306324
1790	Uncharacterized protein (Fragment) OS=Rattus norvegicus OX=10116 PE=1 SV=3	10116	F1LWK7	0.77785252	-0.5030167	15.3282442	14.828558	14.7660646	15.0400372	15.2098694	16.205904	15.7006283	14.8585691
1791	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=Apoll11a PE=4 SV=2	Apoll11a	F1M512	0.10595251	0.11611128	16.9076405	16.2762737	16.8587532	17.2292614	16.8040562	15.6943817	16.9934998	17.315546
1792	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=Gbp1 PE=4 SV=2	Gbp1	D3ZKU6	0.28859791	0.74778748	18.7681179	18.2770443	16.7551098	18.1537266	15.8114996	15.544198	17.8168526	19.7902985
1793	Uncharacterized protein OS=Rattus norvegicus OX=10116 GN=L1td1 PE=1 SV=2	L1td1	M0R3X5	1.20130584	-0.6541095	17.6750145	18.2267056	18.4038162	18.3740082	19.2013664	18.5007648	19.241827	18.3520241
1794	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	10116	D3Z874	0.51555188	0.56377602	20.518755	19.6061954	19.5236607	19.2819939	20.061636	19.5475674	18.0830173	18.9832802
1795	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	10116	D4A8Y1	0.51099192	-1.1095257	19.1108589	16.0811882	16.1201954	15.149353	17.3850441	18.6387024	16.4622536	18.4136982
1796	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=1	10116	F1LPW0	0.45551318	-0.7389872	16.954771	17.260376	14.3506517	16.8561974	16.4417133	17.5109329	16.815239	17.6100597
1797	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	10116	M0RCH6	0.8884174	-1.1265097	16.0102348	18.4313812	18.293541	18.7279873	18.5871887	19.1561203	19.2111778	19.0146961
1798	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=2	10116	M0R6W5	0.07032026	-0.0441875	17.7714748	17.0562725	17.2071075	16.7815685	17.4855423	17.2359276	17.1116295	17.1600742

1799	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	10116	F1LTJ5	0.53095089	0.30406618	20.1108704	20.0482979	19.1417675	19.3280315	19.3707905	19.2209454	19.2056217	19.615345
1800	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=1 SV=3	10116	F1M7L9	0.03026733	0.02557182	19.3550053	19.1220818	18.658865	19.1909294	18.7875004	19.4279137	18.4904213	19.5187588
1801	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	10116	M0R5J4	0.07382479	-0.0462809	25.0638943	25.1965313	25.4547405	25.6154575	24.9070568	25.3988476	25.3865089	25.8233337
1802	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	10116	D4A5L9	0.78429466	-0.2610106	23.3058929	23.6907997	23.9771442	23.9986782	23.9249744	24.0635929	24.0450134	23.9829769
1803	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	10116	D4A6W6	0.94864653	1.77954221	18.4209747	19.5376778	18.8594322	20.216095	18.8317966	18.3141422	17.8397789	14.9302931
1804	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	10116	M0RCY2	0.17842066	-0.1008048	19.5781097	19.9219437	19.2291775	19.9640865	19.8187981	19.9244099	19.3723927	19.9809361
1805	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	10116	A0A0G2K6L	0.40872325	0.41946745	18.8759136	19.0444431	17.3856735	18.9790421	17.8423367	17.9047489	18.0679035	18.7922134
1806	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	10116	A0A0G2K3I	1.92876866	-0.4966736	19.5077896	19.4056816	19.0845394	19.5025425	19.653059	20.1165466	19.8090439	19.9085979
1807	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=1	10116	D3ZZN4	0.30567229	0.26695752	15.2439461	15.3855867	14.7145863	16.1084881	15.1635151	14.4544649	15.5358963	15.2309008
1808	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=3 SV=3	10116	D3ZM33	1.75575082	0.51028633	20.8757362	20.4890957	20.2659931	20.7933159	19.8893871	20.1237221	20.1771851	20.1927013
1809	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	10116	A0A0G2K3Z	0.66515721	0.1314106	23.1560364	23.118187	22.9232121	22.898283	22.7485695	22.9323406	22.8252354	23.0639305
1810	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	10116	D3ZJD3	1.08454724	0.42888403	23.4660816	23.1243916	22.952137	22.541605	22.7954979	22.4720001	22.6043606	22.4968204
1811	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	10116	D3Z9G3	0.77538751	0.54888821	18.6721249	18.8685093	17.9635277	18.73283	17.2655125	17.8641815	18.4900761	18.421669
1812	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=1	10116	F1M6F4	0.43821147	-0.3566813	19.7847519	19.5358257	18.2244415	18.755228	19.3497467	19.4274044	19.6067982	19.3430233
1813	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	10116	D3ZPL5	0.20580038	0.12213182	20.7653465	20.8207188	21.074234	21.5449352	20.6100445	21.1262035	21.2531147	20.7273445
1814	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	10116	D3ZX87	0.97770989	1.29584026	19.7268257	18.6796265	18.2170582	19.3475571	16.5784855	18.8875675	18.5297794	16.7918739
1815	Uncharacterized protein OS=Rattus norvegicus OX=10116 PE=4 SV=2	10116	M0R3K7	0.44845822	0.41096735	16.5174294	16.1148262	15.5671387	17.3675938	15.5818071	16.108963	15.9026899	16.3296585
1816	Unconventional myosin-Ib OS=Rattus norvegicus OX=10116 GN=Myo1b PE=1 SV=1	Myo1b	Q05096	0.39376439	-0.6077685	18.9988651	18.3553562	18.7899933	16.0737095	18.76861	18.6525612	18.4798183	18.7480087
1817	Unconventional myosin-Ic OS=Rattus norvegicus OX=10116 GN=Myo1c PE=1 SV=2	Myo1c	Q63355	1.0922253	-0.514257	23.3108101	22.5653992	22.547102	22.6642399	23.3546314	22.9334965	23.147686	23.708765
1818	UPF0598 protein C8orf82 homolog OS=Rattus norvegicus OX=10116 PE=2 SV=1	10116	Q642A4	0.14834116	-0.119637	19.5123711	18.1447182	18.6289616	18.6856384	18.6064148	19.1076546	18.7219563	19.0142117
1819	UPF0729 protein C18orf32 homolog OS=Rattus norvegicus OX=10116 PE=3 SV=1	10116	B1WC88	0.05238904	-0.1007299	17.5476761	16.0055237	17.8038845	17.6904926	17.7447014	17.5103226	18.3288841	15.8665886
1820	Up-regulated during skeletal muscle growth protein 5 OS=Rattus norvegicus OX=10116 GN=Atp5md PE=1 SV=1	Atp5md	Q9JJW3	0.52888954	-0.2542019	24.5525379	25.1783543	25.3953838	25.3821507	25.287178	25.5888824	25.5027161	25.1464577
1821	Uridine monophosphate synthetase OS=Rattus norvegicus OX=10116 GN=Umps PE=1 SV=1	Umps	Q4QQS7	0.2893077	0.29439831	16.1454754	16.7978058	17.1063175	16.1598721	15.8364868	15.6278667	16.3681259	17.199398
1822	Uridine-cytidine kinase OS=Rattus norvegicus OX=10116 GN=Uck1 PE=1 SV=1	Uck1	B5DF24	0.15361882	-0.3139291	17.6594467	17.7944031	17.3315353	14.5193863	17.1608505	16.8853989	17.1142387	17.3999996
1823	Uridine-cytidine kinase OS=Rattus norvegicus OX=10116 GN=Uck2 PE=3 SV=1	Uck2	A0A0G2JX0	1.01565515	1.19914603	17.354372	17.156353	16.7404861	16.5305405	16.8330383	14.4821053	15.0510645	16.6189594
1824	UTP--glucose-1-phosphate uridylyltransferase OS=Rattus norvegicus OX=10116 GN=Ugp2 PE=1 SV=1	Ugp2	Q4V8I9	0.88310459	0.21799898	20.3769989	20.6306248	20.3211861	20.1512451	20.1819038	19.9314461	20.2313595	20.2633495
1825	Utrophin OS=Rattus norvegicus OX=10116 GN=Utrn PE=1 SV=1	Utrn	A0A0G2JW6	0.46993314	-0.1799159	19.8868446	19.5160294	19.7959957	19.801075	20.3010998	19.6298122	20.0545578	19.7341385
1826	Vacuolar protein sorting 13 homolog C OS=Rattus norvegicus OX=10116 GN=Vps13c PE=1 SV=2	Vps13c	D4A4K4	1.29582663	0.25438738	22.6462135	22.623064	22.4809036	22.6642284	22.413887	22.185276	22.2068481	22.5908489
1827	Vacuolar protein sorting 13 homolog D OS=Rattus norvegicus OX=10116 GN=Vps13d PE=1 SV=1	Vps13d	D3ZKC6	0.20548551	0.16953945	17.8559093	16.5758781	16.8730507	17.5014954	17.3840637	16.7124901	17.1601982	16.8714237
1828	Vacuolar protein sorting 4 homolog B OS=Rattus norvegicus OX=10116 GN=Vps4b PE=1 SV=1	Vps4b	Q4KLL7	0.51176915	-0.6101451	16.7860966	18.2324219	18.9627247	18.7214928	18.2740707	19.1419945	18.448122	19.279129
1829	Vacuolar protein sorting-associated protein 16 homolog OS=Rattus norvegicus OX=10116 GN=Vps16 PE=1 SV=1	Vps16	Q642A9	0.67169785	0.97593236	17.6965141	17.0603638	16.2281857	16.382431	16.5661335	15.8982801	14.1281414	16.8712101
1830	Vacuolar protein sorting-associated protein 28 homolog OS=Rattus norvegicus OX=10116 GN=Vps28 PE=1 SV=1	Vps28	A0A0H2UH	0.19791381	0.26139832	18.3376141	18.3102188	16.9638271	17.1120987	17.9031124	16.3437347	17.8396664	17.5916519
1831	Vacuolar protein sorting-associated protein 33B OS=Rattus norvegicus OX=10116 GN=Vps33b PE=2 SV=1	Vps33b	Q63616	0.90597798	0.73111582	19.2815228	18.009079	18.3750095	19.7685661	18.0519085	18.2576962	18.2051353	17.9949741
1832	Vacuolar protein sorting-associated protein 35 OS=Rattus norvegicus OX=10116 GN=Vps35 PE=1 SV=1	Vps35	G3V8A5	0.16885824	0.11613321	20.0638046	20.1640224	19.9754448	19.108139	19.8266907	19.907238	19.4115601	19.7013893
1833	Vacuolar protein sorting-associated protein 4A OS=Rattus norvegicus OX=10116 GN=Vps4a PE=1 SV=1	Vps4a	F7F1Y3	0.1136702	-0.1763015	20.8080921	20.1829071	18.4853458	20.1161423	20.2776337	19.9437523	19.3447838	20.7315235
1834	Vacuolar protein-sorting-associated protein 36 OS=Rattus norvegicus OX=10116 GN=Vps36 PE=1 SV=1	Vps36	B1H248	0.33468864	0.4768343	21.3050995	21.6208935	20.6535053	23.1411648	20.9824276	21.7090492	20.4452477	21.6766014
1835	Vacuolar-sorting protein SNF8 OS=Rattus norvegicus OX=10116 GN=Snf8 PE=1 SV=1	Snf8	Q5RK19	0.178359	0.32723212	18.2078266	18.070879	17.0312386	16.359293	18.0289097	15.9599123	16.282093	18.0893936
1836	Valine--tRNA ligase OS=Rattus norvegicus OX=10116 GN=Vars PE=2 SV=2	Vars	Q04462	0.01345613	-0.0280299	17.2408676	16.6439629	15.6814861	14.7123938	15.8282032	16.8022346	14.9932394	16.7671528
1837	Vanin 1 OS=Rattus norvegicus OX=10116 GN=Vnn1 PE=1 SV=1	Vnn1	Q4KLZ0	1.54470321	-0.4844036	21.3404789	21.8169613	21.3470173	21.7341309	21.8693314	22.0450916	22.3621826	21.8995972
1838	Very-long-chain enoyl-CoA reductase OS=Rattus norvegicus OX=10116 GN=Tecr PE=1 SV=1	Tecr	Q64232	0.2113822	-0.3065577	19.1062622	16.9956417	17.2849712	19.062252	18.2700748	18.7487049	18.4583721	18.1982059
1839	Vesicle-associated membrane protein 3 OS=Rattus norvegicus OX=10116 GN=Vamp3 PE=1 SV=1	Vamp3	P63025	0.90915537	0.58531141	19.9796352	19.9264717	20.0205193	20.9169445	19.2902393	19.6654892	20.2492275	19.297369
1840	Vesicle-associated membrane protein-associated protein A OS=Rattus norvegicus OX=10116 GN=Vapa PE=1 SV=3	Vapa	Q9Z270	1.10269316	-0.339467	21.1739101	21.2107468	21.307579	21.6336021	21.7368889	21.439106	21.9844532	21.5232582
1841	Vesicle-associated membrane protein-associated protein B OS=Rattus norvegicus OX=10116 GN=Vapb PE=1 SV=3	Vapb	Q9Z269	0.07942394	-0.0513716	19.9218273	19.9350357	20.0019875	20.6952915	20.1935997	19.9449329	20.5805511	20.0405445
1842	Vesicle-trafficking protein SEC22b OS=Rattus norvegicus OX=10116 GN=Sec22b PE=1 SV=3	Sec22b	Q4KM74	0.51310823	-0.3496222	17.7157516	18.5966568	17.7493038	17.2246723	18.3940277	18.0905075	17.8389263	18.361412
1843	Vimentin OS=Rattus norvegicus OX=10116 GN=Vim PE=1 SV=1	Vim	G3V8C3	0.15956081	0.28174829	20.1068192	20.0064926	19.9366264	22.6964111	20.6296082	20.2240124	20.2332516	20.5324841
1844	Vinculin OS=Rattus norvegicus OX=10116 GN=Vcl PE=1 SV=1	Vcl	A0A0G2K8V	1.0047252	0.32167006	23.3680515	22.8661098	22.7731133	23.2099934	22.8042297	22.7444153	22.4906025	22.8913403
1845	Vitamin D-binding protein OS=Rattus norvegicus OX=10116 GN=Gc PE=1 SV=3	Gc	P04276	1.81789773	-0.8751531	19.0915508	18.7133541	19.8556881	19.4004955	20.225975	19.9598331	20.3715763	20.0043163
1846	Vitronectin OS=Rattus norvegicus OX=10116 GN=Vtn PE=1 SV=1	Vtn	Q3KR94	0.02537444	0.01814842	22.2721043	22.8384895	22.1945515	22.0473518	21.9285126	22.1629105	22.4733372	22.7151432
1847	Voltage-dependent anion-selective channel protein 1 OS=Rattus norvegicus OX=10116 GN=Vdac1 PE=1 SV=4	Vdac1	Q9Z2L0	1.18725741	-0.4043565	26.7944832	27.2576733	27.3650036	27.4673595	27.5177765	27.6051159	27.9141006	27.4649525
1848	Voltage-dependent anion-selective channel protein 2 OS=Rattus norvegicus OX=10116 GN=Vdac2 PE=1 SV=2	Vdac2	P81155	1.40345721	-0.4081697	25.5957928	26.0573196	26.1061916	26.1506977	26.2497272	26.3860512	26.6331234	26.2737789
1849	Voltage-dependent anion-selective channel protein 3 OS=Rattus norvegicus OX=10116 GN=Vdac3 PE=1 SV=1	Vdac3	A0A0G2JSR	1.30203634	-0.3586383	24.1390972	24.4865627	24.5028687	24.6049843	24.8095798	24.7709713	25.0515957	24.5359192
1850	Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Rattus norvegicus OX=10116 GN=Cacna2d1 PE=1 SV=1	Cacna2d1	A0A0G2K7E	1.9764234	-0.68648	17.7417336	18.6528168	18.2212105	18.1921997	18.9029961	18.9459057	18.8448181	18.8601608
1851	von Willebrand factor A domain-containing 8 OS=Rattus norvegicus OX=10116 GN=Vwa8 PE=1 SV=1	Vwa8	A0A0G2K3V	2.93049676	0.72262573	24.2445564	23.7714386	24.1035957	24.0532207	23.4652157	23.4155712	23.1271439	23.2743778
1852	VPS18 CORVET/HOPS core subunit OS=Rattus norvegicus OX=10116 GN=Vps18 PE=1 SV=1	Vps18	B5DFJ4	0.15941816	0.22540426	18.3357162	16.3195858	16.655777	17.6011734	17.3329659	16.1714764	17.0291862	17.4770069
1853	V-type proton ATPase subunit B, brain isoform OS=Rattus norvegicus OX=10116 GN=Atp6v1b2 PE=1 SV=1	Atp6v1b2	P62815	0.35926896	0.56343365	17.7715836	17.8152504	15.5206823	18.0064869	16.4985352	17.1656837	15.8650484	17.3310013
1854	V-type proton ATPase subunit OS=Rattus norvegicus OX=10116 GN=Atp6v0d1 PE=1 SV=1	Atp6v0d1	Q5M7T6	0.88839662	-0.4705014	17.8279305	17.9816437	16.8299179	17.7879658	18.032568	17.9541798	18.1243248	18.198391
1855	WASH complex subunit 4 OS=Rattus norvegicus OX=10116 GN=Washc4 PE=1 SV=1	Washc4	D4A7I6	0.35285392	-0.4333754	15.1010704	16.1266079	16.6620502	17.410656	16.7588997	16.6635799	17.3115482	16.2998581
1856	WD repeat-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Wdr1 PE=1 SV=3	Wdr1	Q5RKI0	0.63395425	0.17200089	20.5181541	20.424902	20.4097862	20.0086689	20.1673679	20.2744579	19.9918022	20.2398796
1857	WD repeat-containing protein 26 OS=Rattus norvegicus OX=10116 GN=Wdr26 PE=3 SV=2	Wdr26	F1LTR1	1.43274618	1.44752812	18.8436527	18.28825	18.256916	17.6386833	18.0772038	16.7375164	16.6940403	15.7286291
1858	WD repeat-containing protein 7 OS=Rattus norvegicus OX=10116 GN=Wdr7 PE=1 SV=1	Wdr7	Q9ERH3	0.09906143	0.10253382	17.9654293	18.2699776	16.7599545	18.0231266	17.51507	17.3693905	17.570816	18.1530762
1859	WW domain binding protein 2, isoform CRA_b OS=Rattus norvegicus OX=10116 GN=Wbp2 PE=1 SV=1	Wbp2	G3V721	0.47834082	0.98816156	17.4242439	17.1840858	15.2533436	18.0148907	16.9725571	13.8551826	16.3155441	16.7806339
1860	Zinc finger CCCH-type-containing 7B OS=Rattus norvegicus OX=10116 GN=Zc3h7b PE=1 SV=1	Zc3h7b	A0A0G2K21	0.32216781	-0.2615461	16.8238335	16.8172092	16.7378788	16.4384689	17.0095482	17.2404976	17.5799885	16.0335407
1861	Zinc finger protein 438 OS=Rattus norvegicus OX=10116 GN=Zfp438 PE=1 SV=1	Zfp438	A0A0G2JU0	0.33970497	-0.1974416	19.5798664	19.9223843	19.7029514	20.3320065	20.1186829	19.8044262	20.5938911	19.8099747
1862	Zinc finger, C3HC-type-containing 1 OS=Rattus norvegicus OX=10116 GN=Zc3hc1 PE=1 SV=1	Zc3hc1	A0A140UHX	1.00505327	0.33026004	15.7337313	15.6477642	15.3474264	15.5001326	15.5305843	15.1443758	14.8580408	15.3750134
1863	Zinc finger, HIT type 6 OS=Rattus norvegicus OX=10116 GN=Znhit6 PE=1 SV=1	Znhit6	B1WC05	1.11862292	0.5437746	18.8755016	18.326458	17.821331	18.3247147	17.6269684	18.0357552	17.5012054	18.0089779
1864	Zinc finger, SWIM-type-containing 8 OS=Rattus norvegicus OX=10116 GN=Zswim8 PE=1 SV=1	Zswim8	A0A0G2K9R	0.196944	0.43792081	17.3292465	14.6811886	16.3799858	14.7272739	16.9521885	14.3848629	14.547739	15.4812212
1865	Zyxin OS=Rattus norvegicus OX=10116 GN=Zyx PE=1 SV=1	Zyx	D4A7U1	0.21803557	-0.257762	16.2332497	15.1801281	15.8585825	14.8159504	14.8757544	15.6021137	16.4051991	16.2358913