Adiposity and fat loss in cancer:
Exploring the prognostic significance and underlying mechanisms of adipose alterations in cancer

by

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Abstract

During cancer progression, many patients will experience some degree of wasting of both muscle and adipose tissue. However, little is-known about adipose tissue alterations after a cancer diagnosis. Therefore, this research was conducted to first understand the prognostic significance of adipose tissue in cancer survival, secondly to assess alterations that occur in adipose tissue after cancer diagnosis, and lastly to investigate molecular mechanisms associated with these alterations. The first objective was to determine the association between adiposity and mortality risk after a cancer diagnosis in a large cohort of gastrointestinal and renal cell carcinoma patients (n=1746). High adiposity independently associated with lower mortality risk, irrespective of cancer type. Among adipose tissue depots, subcutaneous adipose tissue appeared to be protective against mortality in cancer patients suggesting varying importance of body fat distribution in conferring risk. Low subcutaneous adiposity independently associated with increased mortality (HR: 1.26; 95% CI: 1.11-1.43; $p<0.001$) and shorter survival compared to patients with high subcutaneous adiposity. Although the presence of severe muscle depletion decreased the survival of cancer patients, its effect was more pronounced in patients with low subcutaneous adiposity. Secondly, we determined the intensity and time course of changes in adipose tissue in advanced cancer patients in the year preceding death. Our work demonstrated adipose tissue can be either gained or lost in the year preceding death. Visceral adipose tissue loss occurred further away from death and preceded subcutaneous loss. As death approaches, the majority of patients lose fat; however, gain of adipose tissue was observed further away from death; suggesting that early interventions may be more effective at maintaining adipose tissue. While evidence is emerging regarding the effect of tumor on adipose tissue, much less is known about drug-related mechanisms of adipose atrophy. To address mechanisms underlying adipose atrophy during the

clinical course of cancer, a pre-clinical model was used. Rats bearing Ward Colon Carcinoma were fed a semi-purified diet with or without fish oil (2.3% w/w) initiated at the same time as chemotherapy. Rats were-euthanized before chemotherapy, after 1-cycle, or 2-cycles of chemotherapy and periuterine adipose tissue was isolated. Healthy rats with no tumor, no chemotherapy, served as a reference group. Larger adipocytes (3993.7 ± 52.6μm^2) in tumour-bearing animals compared to the reference group (3227.7 ± 36.7μm^2; $p<0.001$) associated with diminished expression of proteins involved in lipolysis and mitochondrial fatty acid oxidation pathways. However, chemotherapy treatment decreased size of adipocytes (2243.9 ± 30.4μm^2; $p<0.001$). Evaluation of proteomic profile suggested that altered mitochondrial dysfunction could be the major reason for adipose atrophy in rats following chemotherapy ($p<0.001$). Mitochondrial dysfunction was associated with decreased expression of proteins involved in ATP generation, β-oxidation, and lipogenesis. Dietary fish oil fed at 2% w/w was not effective in maintaining adipose tissue pathways altered by chemotherapy. This study contributes to gaps in knowledge around the importance of adipose tissue on survival as well as how altered adipose tissue function contributes to atrophy of adipose tissue in cancer.

Preface

Chapter 1. Part of this chapter has been published as two review manuscripts as 1. "*Evidence and mechanisms of fat depletion in cancer*", Maryam Ebadi, Vera C Mazurak, Nutrients 2014 Nov 19; 6(11):5280-5297 and 2. "*Potential biomarkers of fat loss as a feature of cancer cachexia*", Maryam Ebadi, Vera C Mazurak, Mediat Inflamm 2015;2015:820934". I conducted a literature review of all studies in the published literature with an objective to assess fat mass or mechanisms of fat loss in experimental and human models. I was responsible for critically reviewing the papers, compiling the data tables, drafting and writing the manuscript with ongoing discussions with Dr. Mazurak and subsequent revisions by Dr. Mazurak.

Chapter 3. This chapter was prepared in a paper format and submitted to British Journal of Cancer as "*Subcutaneous adiposity is an independent predictor of mortality in cancer patients",* Maryam Ebadi, Lisa Martin, Sunita Ghosh, Catherine J. Field, Richard Lehner, Vickie E. Baracos, Vera C. Mazurak. I retrieved and compiled the data from CT scans, performed statistical analysis and drafted the paper; Dr. Sunita Ghosh was involved in data analysis; Lisa Martin contributed to data collection; Dr. Vera C Mazurak assisted with the study conception, compilation of data and writing of manuscript; Dr. Vickie E. Baracos supervised CT image analysis, assisted with the compilation and analysis of the data, revising the manuscript; Dr. Catherine J. Field and Dr. Richard Lehner contributed to critically revising the manuscript. This study was approved by the University of Alberta Research Ethics Board, "M*olecular mechanisms of cachexia"*, No. *ETH21709*.

Chapter 4. This chapter has been published as part of a manuscript entitled "*Loss of visceral adipose tissue precedes subcutaneous adipose tissue and associates with n-6 fatty acid content*", Maryam Ebadi, Vickie E. Baracos, Oliver F Bathe, Lindsy E Robinson, Vera C Mazurak, Clin

Nutr. 2016 Feb 24. pii: S0261-5614(16)00071-6. I conducted the research, analyzed data and wrote the paper; Dr. Mazurak assisted with writing of manuscript; Dr. Oliver F Bathe, provided the samples, and contributed to revising the manuscript; Dr. Lindsy E Robinson conducted adipokine analysis and contributed to revising the manuscript; Dr. Vickie E. Baracos supervised CT data acquisition and contributed to revising the manuscript. This study was approved by the University of Alberta Research Ethics Board, "*Molecular mechanisms of cachexia"*, No. *ETH21709*.

Chapter 5. This chapter is written in a manuscript format and part of this chapter will be prepared for submission to the BMC Cancer. I was responsible for performing the fatty acid analysis, quantitative image analysis using ImageJ software, gene expression experiments, proteomic and statistical analysis, and drafting the manuscript. Liquid chromatography-mass spectrometry was conducted by Jack Moore at the Alberta Proteomics and Mass Spectrometry Facility. Dr. Richard Fahlman helped with proteomics data analysis. Dr Vera C. Mazurak, Dr. Catherine J. Field and Dr. Richard Lehner provided critical input. Abha Dunichand-Hoedl and Kait St. Pierre assisted with animal care and sample collection at necropsy. This animal study was approved by the University of Alberta Research Ethics Board, "*Nutritional modulation of antineoplastic therapy*", No. AC12200.

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List of abbreviations

5-FU	5-fluorouracil
ABCD2	ATP binding cassette subfamily D member 2
ACAA1	Acetyl-CoA acyltransferase 1
ACADM	Acyl-CoA dehydrogenase, C-4 to C-12 straight chain
ACC	Acetyl-CoA carboxylase
ACLY	ATP-citrate lyase
ACN	Ammonium bicarbonate/acetonitrile
ADRB1	ß1-adrenoceptor
AIN-76	American Institute of Nutrition-76
ATGL	Adipose triglyceride lipase
BIA	Bioelectrical impedance
BMI	Body mass index
cAMP	Cyclic adenosine monophosphate
CAT	Catalase
c/EBP	CCAAT-enhancer-binding protein
CGI-58	Comparative gene identification-58
CI	Confidence interval
CIDE	Cell death-inducing DNA fragmentation factor- alpha-like effector
CIDEA	Cell death-inducing DNA fragmentation factor-alpha-like effector-a
CO1	Control diet + 1-cycle chemotherapy
CO2	Control diet + 2-cycles chemotherapy
COX4I1	Cytochrome c oxidase subunit 4I1
COX5A	Cytochrome c oxidase subunit Va
COX6c	Cytochrome c oxidase subunit VIc
CPT2	Carnitine palmitoyltransferase 2
CPT-11	Irinotecan
CT	Computed tomography
DEXA	Dual-energy X-ray absorptiometry
DGAT	Diacylglycerol acyltransferase
DHA	Docosahexaenoic acid
DLAT	Dihydrolipoamide S-acetyltransferase
ECHS1	Enoyl-CoA hydratase, short chain, 1, mitochondrial
ECI1	Enoyl-CoA delta isomerase 1
EPA	Eicosopentaenoic acid
FAS	Fatty acid synthase
FFMI	Fat-free mass index
FMI	Fat mass index
FO	Fish oil

FO1	Fish oil diet + 1-cycle chemotherapy
FO2	Fish oil diet + 2-cycles chemotherapy
G6PD	Glucose-6-phosphate dehydrogenase
GEE	Generalized estimating equations
GI	Gastrointestinal
GPAT	Glycerol-3-phosphate acyltransferase
GPD1	Glycerol-3-phosphate dehydrogenase
GPX1	Glutathione peroxidase 1
GPX3	Glutathione peroxidase 3
GST	Glutathione S-transferase
H & E	Haematoxylin and Eosin
HR	Hazard ratio
HSD17B10	Hydroxysteroid (17-beta) dehydrogenase 10
HSL	Hormone sensitive lipase
HU	Hounsfield unit
IDH	Isocitrate dehydrogenase
IL-6	Interleukin-6
IPA	Ingenuity Pathway Analysis
L3	Third lumbar vertebra
LC-MS/MS	Liquid chromatography-mass spectrometry
LPL	Lipoprotein lipase
LXR	Liver X receptor
MCP-1	Monocyte chemotactic protein-1
MCP2	Mitochondrial pyruvate carrier 2
MDH2	Malate dehydrogenase 2
MRI	Magnetic resonance imaging
MT-CO2	Cytochrome c oxidase subunit II
MUFA	Monounsaturated fatty acid
NDUFs	NADH dehydrogenase (ubiquinone) subunits
OXPHOS	Oxidative phosphorylation
Pbe	Peroxisomal bifunctional enzyme
PDH	Pyruvate dehydrogenase
PDHA1	Pyruvate dehydrogenase alpha 1
PDHB	Pyruvate dehydrogenase beta
PGC-1α	Peroxisome proliferator-activated receptor-gamma coactivator-1 alpha
PG-SGA	Patient-Generated Subjective Global Assessment
PGD	Phosphogluconate dehydrogenase
PL	Phospholipids
PPARγ	Peroxisome proliferator-activated receptor gamma
PRDX	Peroxiredoxin

PRDX2	Peroxiredoxin 2
PRKACA	Protein kinase cAMP-activated catalytic subunit alpha
PS	Performance status
PUFA	Polyunsaturated fatty acid
REF	Reference
RT-PCR	Real-time PCR
SAT	Subcutaneous adipose tissue
SATI	Subcutaneous adipose tissue index
SCD	Stearoyl-CoA desaturases
SCP-2	Sterol carrier protein 2
SD	Standard deviation
SDH	Succinate dehydrogenase
SFA	Saturated fatty acid
SLC25A1	Solute carrier family 25 Member 1
SLC2A4 (Glut-4)	Solute carrier family 2 member 4
SMI	Skeletal muscle index
SREBP-1c	Sterol regulatory element binding protein-1c
STAT3	Signal transducer and activator of transcription-3
TATI	Total adipose tissue index
TG	Triglyceride
TNF-α	Tumor necrosis factor alpha
TUM	Tumour
UCP-1	Uncoupling protein-1
UCP-2	Uncoupling protein-2
VAT	Visceral adipose tissue
VATI	Visceral adipose tissue index
VLCAD	Acyl-CoA dehydrogenase, and very long chain
ZAG	Zinc-alpha2-glycoprotein

Chapter 1: Introduction and literature review*

1.1 Adipose tissue in health

Adipose tissue is an active secretory organ, composed mainly of adipocytes, and non-adipocyte cells such as blood vessels, immune cells, pre-adipocytes, fibroblasts and endothelial cells (Ibrahim, 2010). Mature adipocytes contain a large lipid droplet with a phospholipid monolayer, and peripherally located nucleus (Fujimoto & Parton, 2011). Adipose tissue is involved in energy homeostasis by synthesis and storage of fat in the form of triglyceride (TG) and hydrolysis of TG. Adipose tissue also synthesizes and secretes proteins called adipokines that regulate glucose metabolism, insulin sensitivity, angiogenesis, appetite, inflammation and fat metabolism (Ali et al., 2013).

1.1.1 Types of adipose tissue

White adipose tissue and brown adipose tissue are the two major types of adipose tissue in the body. White adipose tissue can take on lipid-burning characteristics of brown adipose tissue through stimuli including cold exposure, peroxisome proliferator-activated receptor γ (PPARγ) agonist or β-adrenergic stimulation to become brite (brown in white) or beige adipocytes. Brown adipose tissue is found in newborns, hibernating animals and supraclavicular areas in adult humans [reviewd in (Lo & Sun, 2013)]. Brown adipocytes, compared to white adipocytes, are smaller, and contain several lipid droplets with higher number of mitochondria to produce heat (Cedikova et al., 2016; Lo & Sun, 2013). Recently, pink adipocytes that produce and secrete milk, have been identified in the mammary gland of mice during pregnancy and

* Parts of this chapter have been published as review manuscripts in the Nutrients and Mediators of Inflammation. A copy of Mediators of Inflammation manuscript is attached in Appendix B.

lactation. These adipocytes are derived from subcutaneous adipose tissue (SAT) (Giordano et al., 2014).

Two main depots of white adipose tissue exist in body including visceral adipose tissue (VAT) and SAT. VAT is located inside the abdominal muscular wall (around abdominal viscera in mesentery and omentum) and SAT is located under the skin (Ibrahim, 2010; Porter et al., 2009). SAT constitutes about 80% of whole body fat, whereas, VAT comprises 10-20% of total fat in men and 5-8% in women (Wajchenberg et al., 2002). Besides differences in anatomic location, other characteristics such as adipocyte size, lipolytic capacity, insulin response and adipokine secretion varies between these two depots, which can cause functional and metabolic variations (Bjorntorp, 2000; Fain et al., 2004; Garaulet et al., 2001; Hellmer et al., 1992). Insulin resistant adipocytes that reside in VAT are more sensitive to catecholamine-induced lipolysis than SAT (Bjorntorp, 2000) and VAT is an active producer of cytokines such as interleukin 6 (IL-6), tumour necrosis factor alpha (TNF-α) and monocyte chemotactic protein 1 (MCP-1)(Fain et al., 2004; Harman-Boehm et al., 2007). Compared to SAT, elevated VAT lipolysis in the presence of catabolic hormones, facilitates direct delivery of free fatty acids to liver and consequently, can cause elevated hepatic TG deposition (Girard & Lafontan, 2008; Hellmer et al., 1992).

1.1.2 Adipose tissue fatty acid composition

Fatty acid composition of adipose tissue is altered by dietary intake especially for polyunsaturated fatty acids (PUFAs) and is also influenced by endogenous metabolism of fatty acids (Baylin et al., 2002; Hodson et al., 2008). Dietary fatty acids or fatty acids synthesized by fatty acid synthase (FAS) in the cytosol can undergo elongation or/and desaturation by endoplasmic reticulum enzymes (Guillou et al., 2010). Fatty acid elongation into long chain fatty

acids (>C18) and very long chain fatty acids (>C20) requires the enzymatic activity of very-long-chain fatty acids (ELOVL) family (Guillou et al., 2010). Conversion of saturated into mono-unsaturated fatty acids requires rate-limiting enzymes called stearoyl-CoA desaturases (SCD). SCD-1 is the major isoform of SCD family in adipose tissue and liver (Ntambi & Miyazaki, 2004). Fatty acids are then incorporated into TG, phospholipids (PLs) and cholesteryl esters (Ntambi & Miyazaki, 2004).

The major fatty acids in humans are 16:0, 16:1, 18:0, 18:1, and 18:2n-6 constituting more than 90% of TG in adipose tissue whereas the main fatty acids in adipose tissue PLs are 16:0, 18:0, 18:1, 18:2n-6, 20:4n-6 (Field et al., 1985). Alterations in dietary fatty acid intake is reflected in the composition of fatty acids in stored TGs and membrane PLs (Clandinin et al., 1985; Field et al., 1985) The composition of adipocytes influences their function with PUFAs conferring greater membrane fluidity, and permeability (Fickova et al., 1998a; Flachs et al., 2009). Higher proportions of PUFAs in membrane PLs may be related to membrane-associated functions such as phosphate transport across the inner mitochondrial membrane, glucose transport, insulin receptor functions and the activity of membrane-bound enzymes, transporters, receptors, as well as prostaglandin production (Kiechle & Jarett, 1983; Spector & Yorek, 1985).

1.1.3 Lipid synthesis, mobilization and utilization in adipose tissue

Lipids stored in adipocytes are not only metabolic fuels, but also provide substrate for membrane synthesis, cell signaling, and lipid mediators (Welte, 2015). Perilipin and cell death-inducing DNA fragmentation factor-α-like effector (CIDE) protein families are lipid associated proteins that regulate lipid droplet growth and TG deposition in adipocytes (Wu et al., 2014). Three CIDE family proteins, known in mammals are CIDEA, CIDEB and CIDEC/FSP27 in

mice and humans (Guilherme et al., 2008). CIDEA is expressed in both white and brown adipocytes in mice (Abreu-Vieira et al., 2015) but its function in human and mice is opposite. While increased expression of CIDEA in mice associated with TG deposition and larger adipocytes (Guilherme et al., 2008; Gummesson et al., 2007; Reynolds et al., 2015), low expression of CIDEA in humans associates with obesity and larger adipocytes (Nordstrom et al., 2005).

Various transcriptional factors regulate expression of genes involved in controlling lipid metabolism. Transcriptional factors such as liver X receptor (LXR), and sterol regulatory element binding protein-1c (SREBP-1c) are important regulators of *de novo* lipogenesis (Strable & Ntambi, 2010). SREBP-1c also activates the expression PPARγ, a ligand- activated transcription factor involved in adipocyte adipogenesis and lipogenesis (J. B. Kim, Wright et al., 1998) as well as regulating the expression of lipoprotein lipase (LPL) (Laplante et al., 2003).

Adipose tissue metabolism and whole body fat mass are regulated through two major pathways: lipolysis (fat breakdown) and lipogenesis (fat synthesis) (Ali et al., 2013). These two pathways are controlled in adipocytes by short and long term signals. Hormones in blood provide short term signals, for example, lipolysis is inhibited by insulin. Long term regulation is facilitated by alterations in size and number of adipocytes (Ali et al., 2013). An overview of lipid metabolism inside adipose tissue is summarized in Figure 1-1. Table 1-1 summarizes several molecules involved in regulating adipose tissue lipid metabolism.

Adipogenesis is a highly regulated process that encompasses preadipocyte proliferation and differentiation into mature adipocytes. Adipogenesis is followed by lipogenesis to store lipids in fat cells. Fatty acid synthesis occurs through *de novo* lipogenesis from acetyl-CoA and by subsequent TG synthesis (esterification of fatty acids to glycerol-3-posphate within the

endoplasmic reticulum), synthesized fat stores within lipid droplet of adipocytes (Ali et al., 2013; Lo & Sun, 2013).

De novo lipogenesis involves fatty acids synthesis from 2-carbon precursors (Donnelly et al., 2005). Enzymes involved in *de novo* lipogenesis including ATP-citrate lyase (ACLY), acetyl-CoA carboxylase (ACC), FAS, SCD-1, and glycerol-3-phosphate acyltransferase (GPAT) are SREBP-1c target enzymes (Horton, Shimomura et al., 1998; Ntambi et al., 2002). Fatty acids derived from *de novo* lipogenesis as well as fatty acids taken up by the tissue are used to synthesize TG. Uptake of fatty acids into adipose tissue, liberated by LPL-hydrolysis of TGs in lipoproteins, or free fatty acids bound to albumin is facilitated by membrane proteins such as fatty acid translocase FAT/CD36 (Goldberg et al., 2009). Fatty acids activated by acyl-CoA synthase, as an acyl-CoAs, are subsequently incorporated into TG by diacylglycerol acyltransferases (DGATs) (Harris et al., 2011). TG synthesis is an energy consuming process; mitochondrial activity is crucial for TG synthesis as it is the major source for the production of ATP, and acetyl-CoA [(Kusminski & Scherer, 2012); (Figure 1-1)].

Lipolysis involves the hydrolysis of stored TG into fatty acids and glycerol under the control of lipases. Hormone sensitive lipase (HSL) and adipose triglyceride lipase (ATGL) are major enzymes that contribute to TG breakdown in adipose tissue. HSL activity is regulated by hormones, such as catecholamines, insulin and glucagon, through a cAMP-mediated process (Jaworski et al., 2007; Jocken & Blaak, 2008). Catecholamines stimulate lipolysis, whereas insulin has anti-lipolytic functions (Holm, 2003). Binding of hormones to G-protein-coupled receptors results in up-regulation of adenylate cyclase, which leads to an increase in intracellular cyclic adenosine monophosphate (cAMP) concentrations. cAMP stimulates a protein kinase A which in turn phosphorylates perilipin 1 and activates HSL (Jaworski et al., 2007; Jocken &

Blaak, 2008). Phosphorylated HSL translocates from the cytosol to the surface of lipid droplets to induce lipolysis. Although HSL has an ability to completely hydrolyze TG, it has a higher activity on diacylglycerol (Kraemer & Shen, 2002). ATGL catalyzes the first step in TG hydrolysis. ATGL activation requires interaction with coactivator comparative gene identification-58 (CGI-58), a lipid droplet-associated lipase cofactor (Figure 1-1). CGI-58 attaches to perilipin 1 in basal (unphosphorylated) conditions; however, phosphorylation of perilipin 1 by PKA disassociates CGI-58 from perilipin 1, making it available for ATGL activation (Lass et al., 2011).

Liberated fatty acids are used for energy production mainly in peripheral tissues or are incorporated into membrane lipids or used to produce lipid mediators (Viscarra & Ortiz, 2013). Activated fatty acids in the form of acyl-CoA, enter mitochondrial β-oxidation via carnitine palmitoyltransferase-1 to produce acetyl-CoA. Generated acetyl-CoA enters the Krebs cycle, and subsequently NADH and $FADH_2$ generated by both fatty acids β-oxidation and Krebs cycle transfer to oxidative phosphorylation for ATP synthesis (Eaton, 2002). Infrequently, liberated fatty acids could be esterified into TG (Edens et al., 1990). Therefore, mitochondria plays a central role in adipose tissue metabolism by regulating major pathways including energy demanding lipogenesis, fatty acid β-oxidation and re-esterification inside adipocytes (Kusminski & Scherer, 2012). Considering the importance of mitochondria in regulating lipid homeostasis, mitochondrial dysfunction associates with impairment in adipocyte differentiation, ATP and TG synthesis (Lu et al., 2010) as well as suppressed β-oxidation (J. A. Kim et al., 2008).

1.1.4 Long chain n-3 PUFAs to improve adipose tissue metabolism and function

Considering the importance of adipose tissue fatty acid composition on its metabolism and function, fish oil derived long chain n-3 PUFAs, eicosapentaenoic acid (20:5, n-3; EPA), and docosahexaenoic acid (22:6, n-3; DHA) have been studied *in vitro* and *in vivo* to improve various aspects of metabolism. However, the majority of the research in this area has been conducted in animal or cell models (Baillie et al., 1999; Barber et al., 2013; Fickova et al., 1998; H. K. Kim et al., 2006; M. Kim et al., 2015; Leray et al., 1993; D. S. Lin & Conner, 1990; Murali et al., 2014; Wang et al., 2010) and translating pre-clinical data into clinical studies to apply optimal dose and duration is challenging. Endpoints in intervention studies are different and the majority of findings are derived from obesity models. The dose of EPA and DHA applied, duration of intervention as well as macronutrient composition, quantity and fatty acid profile of the background diet limit comparability between studies. Clinical research is usually limited to measuring circulating metabolites such as plasma TG, cholesterol, adipokines such as leptin, adiponectin or inflammatory markers due to the invasiveness of tissue biopsies and these are not typically performed in vulnerable populations.

Experimental studies suggest that adipose tissue stores only a small proportion of EPA and DHA which are typically located in PLs [reviewed in (Puglisi et al., 2011; Todorcevic & Hodson, 2015)]. Short term intervention with EPA and DHA may influence adipose tissue fatty acid composition. Dietary intervention with EPA and DHA in the form of fish oil for 1 week was enough to cause changes in adipose lipid composition in Wistar rats. Two groups of rats were fed isocaloric diets (21.4g/100g lipid) with either n-3 PUFAs (3.49g EPA+ 1.99g DHA/100g diet) or n-6 PUFAs, mainly linoleic acid (8.08g linoleic acid/100g diet)] for 1 week. Rats fed a diet containing EPA and DHA exhibited smaller adipocytes in their adipose tissue concurrent with

higher content of n-3 PUFAs in PL fraction of adipose tissue compared to the n-6 group. However, proportions of EPA and DHA in adipose tissue PLs were not reported in this study (Fickova et al., 1998). Incorporation of long chain n-3 PUFAs into adipose tissue TGs may require longer duration interventions. Significant increases in proportions of these fatty acids in adipose tissue TG have been reported after 2 weeks of intervention with EPA and DHA at the dose of 19g purified fish oil/100g diet (3.02g EPA + 1.79g DHA/100g diet) in male Wistar rats. EPA and DHA proportions increased from 0.2% to 4.5% and from 0.6 to 3.9% of total fatty acids, respectively by 2 weeks of EPA and DHA intervention reaching steady state after 4-weeks of intervention (Leray et al., 1993). Two months of fish oil feeding (10g/100d diet containing 1.6g EPA + 1.1g DHA/100g diet) in rabbits resulted in 2.2 and 4.9% fold increase in the proportion of EPA and DHA in stored TGs. Rabbits fed diet for 4 months showed a similar adipose fatty acid composition demonstrating the steady state for adipose tissue composition was reached after 2 months (D. S. Lin & Conner, 1990). Although 1 week of intervention with EPA and DHA has an ability to moderately increase the content of long chain n-3 PUFAs in PLs, incorporation of long chain n-3 PUFAs into adipose tissue TGs requires a longer time to reach steady state. However, a range of 4 weeks (Leray et al., 1993; Raclot & Groscolas, 1994) to 2 months (D. S. Lin & Conner, 1990) has been reported in animal studies as the time required to reach steady state.

Deposition and mobilization of PUFAs from adipose tissue differs between EPA and DHA. While EPA, DHA are mainly incorporated into sn-2 position in PLs, the distribution of EPA and DHA in TGs follows a different pattern. Four weeks of feeding diet supplemented with EPA and DHA in rats showed 57% of n-3 fatty acids in sn-3 position of TGs. Majority (more than 60%) of EPA was stored in sn-3 position. DHA, however, was equally stored in sn-2 (48%)

and sn-3 positions (Leray et al., 1993). DHA is preferentially stored in adipose tissue over EPA whereas EPA is preferentially released (Raclot & Groscolas, 1994) and oxidized over DHA (D. S. Lin & Conner, 1990).

Comprehensive reviews of cellular and molecular effects of long chain n-3 PUFAs on adipose tissue metabolism suggest several metabolic effects of these fatty acids in a study may be related to altering membrane fluidity and associated functions, anti-inflammatory actions, diminished lipogenesis and storage capacity of adipose tissue, prevention of adipocyte growth, improved adipokine production, induction of mitochondrial biogenesis and subsequent elevation in fat oxidation inside various tissues including adipose, muscle and liver as well as decreased fatty acids uptake in adipose tissue [reviewed in (Flachs et al., 2009; Todorcevic & Hodson, 2015)]. Smaller adipocytes have been observed following intervention with EPA and DHA, which may relate to pre-adipocyte proliferation, diminished fat synthesis and storage or elevation in the breakdown of stored fat. However, it should be noted that majority of these mechanistic findings come from studies using cell-lines that may not be representative of human adipose tissue metabolism and also it does not consider existing cross talk between adipose tissue and other tissues. Moreover, inconsistencies exist in cell line studies might be related to the differences in cell line types and stages, EPA and DHA concentration, duration of incubation times (Todorcevic & Hodson, 2015). Better understanding of the mechanisms by which EPA and DHA may affect adipose tissue metabolism and function is necessary in order to apply this intervention to prevent or treat some metabolically associated diseases.

Major gaps remain regarding the effect of EPA and DHA or EPA vs. DHA on adipose tissue metabolism in humans. Although, plasma phospholipid appears to reach steady state by 4 weeks of supplementation with 2g DHA/day (Arterburn et al., 2006) or 2g EPA/day (Braeckman

et al., 2014) in humans, the saturation of these fatty acids in adipose tissue has not been reported in humans. A 6-week double-blind randomized clinical trial of 2g fish oil supplementation (640mg EPA and 480 mg DHA) reported a small but significant increase (EPA: 0.01%, DHA: 0.03% increase) in the proportions of EPA and DHA in gluteal adipose tissue of the group consuming fish oil compared to the baseline. No changes, however, were observed in the control subjects who received 2g olive oil (Gammelmark et al., 2012). Differences in study designs as well as poor compliance may have contributed to the discrepant results in clinical studies. Inconsistency in the literature regarding the effect of EPA and DHA on adipose tissue may be due to limited number of participants, varying supplementation duration, dose, proportions of dietary EPA and DHA, the type of fat depot assessed as well as other confounding factors such as age, gender, health status and adiposity [reviewed in (Flachs et al., 2009; Todorcevic & Hodson, 2015)]. Lack of a robust method for body fat mass assessment was another limitation of some of human studies.

1.2 Adipose tissue in cancer

In pathophysiological conditions like cancer, alterations in production of adipokines, and lipid metabolites associates with alterations in adipose tissue mass, function and consequently affects whole body lipid metabolism. On the other hand, alterations in lipid metabolism in adipose tissue can promote tumour progression by providing lipids as source of energy, signaling transduction, or for membrane biosynthesis, required for tumour cell growth, proliferation and survival (Santos & Schulze, 2012). Therefore, due to the important role of adipose tissue in regulating whole body lipid metabolism as well as tumour metabolism, attention needs to be directed toward the prognostic significance of adipose tissue at the time of cancer diagnosis and alterations in adipose tissue during cancer progression.

1.2.1 Prognostic significance of adipose tissue in cancer survival

The association between obesity and increased cancer incidence is well established (Calle & Kaaks, 2004; Prieto-Hontoria et al., 2011), but the relationship between fat mass and cancer survival is much less clear. "Obesity paradox" refers to the condition in which obese patients experience longer survival compared to non-obese patients after a diagnosis of a disease [reviewed in (Prado et al., 2015)]. In the majority of published studies, the obesity paradox has been evaluated based on body mass index (BMI). Considering the role of adipose tissue in regulating whole body lipid metabolism and limitations of using BMI to assess body compartments, prognostic significance of adiposity should be evaluated based on adiposity index rather than BMI. However, discrepant methods of assessing obesity such as BMI, anthropometric measurements such as circumferences, bioelectrical impedance (BIA) as well as direct body composition assessment methods limit the ability to interpret and compare studies (Prado et al., 2015). Moreover, some covariates such as severe muscle depletion or fat infiltration into muscle, have not been taken into account in multivariate models.

Body composition is assessed in cancer patients using a variety of methods including BIA, dual-energy X-ray absorptiometry (DEXA), magnetic resonance imaging and computed tomography (CT) scan analysis (Fabbro et al., 2010). In an oncologic population, CT images are a routine part of treatment and are available from patient records as a chart review. CT image analysis has emerged as the gold standard for body composition assessment in cancer patients due to its ability to discriminate and quantify muscle, adipose tissue and organs (Fabbro et al., 2010). The third lumbar is used as a standardized landmark, as muscle and adipose tissue areas in a single CT image at the third lumbar correlate well with whole body muscle and fat mass (Shen et al., 2004).

Little is known about the effect of obesity on cancer mortality. Recently published work by Gonzalez et al., (2014) showed that obesity paradox exists in cancer patients only if BMI is used as a measure of adiposity. Median survival was significantly longer ($P<0.001$) in obese (31 months) and overweight (32 months) cancer patients compared to the normal (24 months) and low BMI (6 months) patients. Using BIA in this group of 175 cancer patients, severe muscle depletion (sarcopenia) was associated with increased mortality even in patients with high fat mass index (FMI). Therefore, although BMI defined obesity associated with better survival in cancer patients, body composition assessment using BIA demonstrated a survival advantage of higher fat mass in the absence of low muscle mass (Gonzalez et al., 2014). However, various limitations apply to this study as cut-offs for fat-free mass index (FFMI) and FMI were derived from non-cancer hospitalized patients (Kyle et al., 2005). Moreover, these cut-offs were associated with length of hospital stay but not with survival, which was the primary outcome in that study. Another limitation was that BMI was considered along with FFMI and FMI in multivariate Cox regression analysis. BMI and FMI are correlated, therefore, BMI should not be considered as a variable predicting survival in multivariate analysis to avoid an overestimating model due to the collinearity between these two variables. Lastly, an inappropriate selection of a reference group (BMI <18.5 kg/m^2), in multivariate model limits the interpretation of results in this study (Winkels et al., 2014).

Using CT image analysis in 1473 gastrointestinal and lung cancer patients with 966 deaths and a median survival of 16.7 months, overweight and obese patients experienced longer survival compare to normal and low BMI category patients. Weight loss (>8%), severe muscle loss and fat infiltration into muscle (low muscle radiodensity) were associated with lower survival. Overall, higher BMI was protective in the absence of these contributing factors. BMI

<20 was associated with lower survival either in the presence or absence of these conditions (Martin et al., 2013).

When considering VAT and SAT as components of total adipose tissue (TAT), studies have yielded inconsistent results in regard to the importance of each depot in conferring longer survival. The main reason for this discrepant result may be variation in adiposity markers used (index, area, ratio, percentage) and lack of well-established survival associated cut-offs. Moreover, the distribution of fat differs between genders with men showing greater visceral adiposity (Wajchenberg et al., 2002), therefore, gender specific cut-offs should establish to assess the association between different depots and survival in cancer patients.

CT image analysis in 1257 patients with different stages of hepatocellular carcinoma was conducted to determine the effect of body composition variables on survival. BMI was not an independent predictor of survival in multivariate analysis. Among adiposity markers including visceral adipose tissue index (VATI), subcutaneous adipose tissue index (SATI) and VAT/SAT ratio, only VAT/SAT ratio associated with mortality as a continuous variable. VAT/SAT >1.33 in male and >0.93 in female were considered as visceral adiposity. Compared to the patients in low visceral adiposity group, high visceral adiposity associated with 35% increase in mortality risk after adjusting for confounding variables including BMI, sarcopenia, age, gender, alcohol consumption, smoking and diabetes (Fujiwara et al., 2015).

On the contrary, it has been reported that visceral obesity associates with better survival in 2187 advanced renal cell carcinoma. Sex-specific median of visceral fat area and visceral to subcutaneous fat ratio were used to categorize patients into high and low visceral adiposity groups. Ratio of visceral to subcutaneous fat area did not show any significant association with

survival whereas mortality risk increased by 65% in patients with low visceral fat area compared to the high visceral adiposity group (HR: 1.65, 95% CI: 1.11-2.46; p=0.01) (Lee et al., 2015). On the other hand, a recent study (Antoun et al., 2015) in 127 metastatic prostate cancer patients showed that high subcutaneous adiposity is an indicator of better prognosis. Due to the lack of valid established cut-offs, median values of VATI and SATI were included in multivariate analysis. Among body composition parameters, only SATI but not BMI, VATI or muscle mass, was an independent predictor of survival. In low subcutaneous adiposity group, the median survival was 15 months (95% CI: 9-18) compared to 18 months in patients with high subcutaneous adiposity (95% CI: 13-30) (Antoun et al., 2015).

Several gaps remain regarding prognostic significance of adiposity in cancer survival. Recognizing that BMI is not a good indicator of adiposity, specific adiposity markers such as total, visceral, and subcutaneous area, index or ratio have been applied in previous studies. However, VAT to SAT ratio may not be a good indicator as it may lead to the misclassification of patients. This ratio would be similar in people with high adiposity, with large amounts of both visceral and subcutaneous and in people with low adiposity who have small amounts of both visceral and subcutaneous (Rickles et al., 2013). In conclusion, considering different adiposity variables in multivariate analysis, lack of covariates associated with survival of cancer patients in Cox regression analysis as well as lack of valid cut-offs limit the ability to interpret and compare studies.

1.2.2 Adipose atrophy in cancer

As cancer progresses, the majority of cancer patients experience some degree of cancer-related wasting of both muscle and fat (K. C. Fearon, 2008). However, little is known about the

importance of fat loss in cancer because the majority of studies of cancer-associated wasting typically focus on muscle. Potential links between fat loss and poor outcomes have been identified that recognize fat loss to be a poor prognostic factor in advanced cancer independent of a patient's body weight (Fouladiun et al., 2005; Murphy et al., 2010). In the majority of human studies evaluating fat loss in cancer, severe wasting is defined as ≥ 5% weight loss over 3 months or ≥10% within the previous 6 months. Weight loss does not necessarily reflect the severity of cancer-associated wasting but is the first outcome measurement typically reported in studies of cancer.

1.2.2.1 Longitudinal assessment of adipose tissue over the cancer trajectory

Body composition analysis using BIA has demonstrated lower body fat (% or kg) in weight-losing patients compared to weight-stable cancer patients (Agustsson et al., 2007; D. X. Cao et al., 2010; Dahlman et al., 2010; Ryden et al., 2008), healthy controls (Zuijdgeest-van Leeuwen et al., 2000a), or non-malignant controls (Cao et al., 2010; Ryden et al., 2008). When DEXA was applied to malnourished palliative cancer patients, no differences were observed in absolute fat mass (kg) during follow-up (4-62 months) (Fouladiun et al., 2005). However, the relative change (percentage of change from initial values) revealed a loss of fat concurrent with a marginal increase in lean mass during cancer progression (Fouladiun et al., 2005). As DEXA quantifies regional lean body mass, this study raised the possibility that patients may not have been gaining skeletal muscle per se but rather lean mass in internal organs such as the liver and spleen which has been reported as patients approach death in a subsequent study (Lieffers et al., 2009).

With respect to types of fat, volumes of TAT, VAT and SAT were calculated in newly diagnosed treatment-naive gastrointestinal cancer patients (Agustsson et al., 2012). Weight-

losing groups were separated into two groups, those with and without gastrointestinal obstruction that interfered with food intake. Weight-losing groups were compared to weight-stable cancer patients. Deterioration in nutritional status was confirmed by higher Patient-Generated Subjective Global Assessment (PG-SGA) score in the weight-losing patients with gastrointestinal obstruction. Both BIA and CT analysis indicated that total fat mass (kg), visceral and abdominal subcutaneous volumes were lower in weight-losing patients compared to the weight-stable group. The weight-losing patients with gastrointestinal obstruction reported losing approximately two times more weight but VAT volume was greater compared to weight-losing group without gastrointestinal obstruction (Agustsson et al., 2012). This study applied CT scans taken at one point in time; therefore, intensity of loss over time cannot be determined, however, a lower amount of VAT was observed in the weight-losing group who did not have altered food intake.

Approaching death, the intensity of tissue loss increases and patients experience the greatest and most accelerated rate of loss (Fouladiun et al., 2005; Lieffers et al., 2009; Murphy et al., 2010; Ogiwara et al., 1994). Analysis of sequential CT images in 34 advanced colorectal cancer patients revealed that the greatest changes in body composition occur starting at 4.2 months from death (Lieffers et al., 2009). One month from death, liver and spleen mass increase whereas skeletal muscle and fat mass decrease (Lieffers et al., 2009). A study by Murphy et al. quantified fat mass in 108 colorectal and lung cancer patients with at least 2 abdominal CT images in the last 500 days of life. Beginning 7 months prior to death, both VAT and SAT mass were being lost in cancer patients, reaching intensities of 10kg of fat loss/100 days (Murphy et al., 2010). A recent study in pancreatic cancer patients suggested that the rate of VAT loss, rather than the absolute amount, may be an important indicator of survival (Di Sebastiano et al., 2013).

Patients with at least two abdominal CT scans between diagnosis and death, receiving surgery (62%) or chemotherapy (88%) during cancer progression, were selected for this study. Rate of change (%change/100d) for SAT was similar to VAT but a change in VAT was significantly correlated with survival in cancer patients. The presence of co-morbidities such as diabetes and anaemia may have accelerated loss of VAT (Di Sebastiano et al., 2013). In another study, weight-losing gastrointestinal cancer patients exhibited significantly lower VAT and SAT mass three months prior to death compared to the benign controls, and with weight-losing patients having smaller visceral and subcutaneous area compared to weight-stable cancer patients (Ogiwara et al., 1994). To our knowledge, at present, no other studies exist regarding the pattern of fat loss in cancer and further studies are needed to establish the timeline and pattern of fat mass alterations in different adipose tissue depots during cancer progression. Further, the majority of studies assessing fat mass focus on gastrointestinal cancer patients so there is a gap in knowledge related to other malignant tumours.

While the majority of human studies focus on weight-losing vs. weight-stable patients, less is known about the effect of cancer treatments, which may also induce alterations in fat mass. For example, cancer surgery contributes to weight loss. Six months after surgery, weight is reduced from baseline due to the catabolic response to the operation (Adams, 1967; Bachmann et al., 2008; Liedman et al., 1997) and stabilizes after 12 months (Bachmann et al., 2008). Adams reported that weight loss occurs rapidly in the 3 months following surgery (Adams, 1967). Body composition assessment before, 6 and 12 months after gastrectomy, measured from total body potassium and water, indicated 40% of fat mass was lost during the 6 months following surgery (Liedman et al., 1997). Intra-abdominal and subcutaneous adipose tissue mass were assessed before and after surgery using CT scans in pancreatic cancer patients during early stages of

disease progression. Fat loss from the intra-abdominal depot was greater than from the abdominal subcutaneous region following surgery (Haugen et al., 2011). Therefore, surgical procedures may contribute to weight and fat loss due to the catabolic and inflammatory response to the surgery.

Fat loss or gain after chemotherapy may depend on the tumour type, drug type, dose and overall response to chemotherapy. Following at least one cycle of chemotherapy treatment (cisplatin, 5-fluorouracil and/or epirubicin), patients with locally advanced oesophagogastric cancers lost an average of 1.3 ± 3.2 kg (6%) fat mass (Awad et al., 2012). In advanced pancreatic cancer patients, a multivariate survival analysis revealed that VAT loss (determined from CT pre- and post-chemoradiation) but not muscle loss was significantly related to shorter survival (Dalal et al., 2012).

Three months after chemotherapy initiation, testicular cancer patients who received 3 or 4 cycles of cisplatin-based chemotherapy had significantly higher VAT volume without changes in SAT (Willemse et al., 2014). However, 9 months later, both VAT and SAT increased significantly, suggesting a capacity to rebuild lost adipose tissue (Willemse et al., 2014). A recent study applied CT imaging to understand the loss and gain of muscle and adipose tissue during the year preceding death to reveal that anabolic potential does exist, as some patients gained muscle and adipose tissue, but were only capable of doing this >3 months prior to death (Prado et al., 2013). These results will initiate further research aiming to define the appropriate time to initiate nutritional intervention to preserve both muscle and fat tissue.

Fat loss may precede the loss of lean tissues and blocking of lipolysis prevents muscle loss in experimental studies. Lung carcinoma or melanoma cells were injected subcutaneously to induce wasting in mice. Fat loss occurred prior to muscle loss, at early stages of tumour growth,

at an intensity that was greater than muscle loss (Das et al., 2011a). White adipose tissue browning, which has been proposed to contribute to fat loss in cancer, occurred before skeletal muscle wasting in mouse models of cancer wasting (Petruzzelli et al., 2014). To support experimental results, a summary of clinical studies indicating that fat loss occurs prior to the muscle loss are presented in Table 1-2. The only patient group in which this question has been addressed is patients with newly diagnosed gastrointestinal cancers. However, in all studies that have addressed this question to date, changes in adipose tissue were observed in absence of changes in lean tissues. The majority of these studies use BIA and DEXA for body composition assessments which are limited in ability to provide a direct estimate of muscle mass; further studies are needed to confirm that these findings are attributable to muscle loss or other lean body mass loss. Only one study used CT scans to assess body composition in gastrointestinal cancer patients and that study showed no difference in abdominal muscle volume between weight-losing and weight-stable cancer patients. However, CT images were assessed at only one time point in that study (Agustsson et al., 2012). Adipose depletion may occur more rapidly than muscle during disease progress. Advanced pancreatic cancer patients lost both VAT and SAT over time, and the rate of change (%change/100d) in total adipose tissue (-40.4 ± 25.4%/100d) was greater than muscle (-3.1 ± 12.0%/100d). No significant differences in adipose tissue mass were observed between patients who were or were not receiving chemotherapy (Tan et al., 2009).

1.2.2.2 Adipose tissue morphological alterations in cancer

Analysis of adipose tissue morphology and body composition has revealed body fat depletion in human and animal models of cancer [reviewed in (Ebadi & Mazurak, 2014)]. Morphological characterization of adipose tissue in experimental models indicates alterations in

size and shape of adipocytes as well as extracellular matrix remodeling of the tissue (Agustsson et al., 2007; Batista et al., 2012; Bertevello & Seelaender, 2001; Bing et al., 2006; Dahlman et al., 2010; Machado et al., 2004; Ryden et al., 2008). The murine adenocarcinoma (MAC16) causes diminished adipocyte size with increased mitochondrial density, and elevated adipose tissue fibrosis in tumour-bearing mice, compared to pair-fed and control animals (Bing et al., 2006). The Walker 256 carcinoma, a well-established cancer wasting model, affects adipose tissue in a time and depot-dependent manner (Batista et al., 2012; Bertevello & Seelaender, 2001; Machado et al., 2004). Fourteen days after Walker 256 tumour injection, size of mesenteric adipocytes increased whereas adipocyte size of retroperitoneal, and epididymal adipose tissue was decreased (Batista et al., 2012; Bertevello & Seelaender, 2001). In support of these experimental studies, reduction in fat cell volume has been reported in weight-losing gastrointestinal cancer patients (Agustsson et al., 2007; Dahlman et al., 2010; Ryden et al., 2008). Weight-losing patients exhibited smaller adipocytes compared to weight-stable controls (Agustsson et al., 2007; Dahlman et al., 2010; Mracek et al., 2011; Ryden et al., 2008) and non-cancer patients (Ryden et al., 2008) but total body fat cell number was not altered (Dahlman et al., 2010; Ryden et al., 2008).

A recent study in 11 weight-losing gastrointestinal cancer patients demonstrated morphological remodeling in adipose tissue by diminished size of adipocytes, elevated fibrosis (increased collagen amounts) and elevated number of infiltrated macrophages around fibrotic areas compared to 9 weight-stable cancer patients and 7 non-cancer controls. An increased number of macrophages were identified by CD68 as macrophage specific marker. Presence of inflammatory cells was confirmed by elevated mRNA expression of MCP-1 and CD68 in SAT of the patients (Batista et al., 2016). Collectively, the few studies that exist suggest adipose tissue

remodeling occurs in a neoplastic state as evidenced by altered adipocyte size and reduced lipid storage capacity as well as fibrosis and elevated collagen content.

1.2.3 Mechanisms for adipose depletion in cancer

Human and experimental models have been used to study the mechanisms of fat loss in cancer. Animal models are necessary to elevate our understanding of cancer-associated wasting. However, each model may represent only some aspects of human cancer-associated wasting and choice of animal model is based on research objectives. For example, the MAC16 adenocarcinoma induces severe wasting in the absence of anorexia and is suitable to study wasting related to the tumour produced factors rather than food intake. YAH-130, on the other hand, induces wasting and anorexia accompanied by inflammation (Bennani-Baiti & Walsh, 2011). A variety of animal models with various tumours, used to investigate cancer-associated wasting, presents obstacle in our current understanding of human cancer-associated wasting. Therefore, the result of studies investigating the mechanisms underlying fat loss in cancer should be interpreted with caution as each specific tumour type, in various stages of growth, can affect various adipose tissue depots in a different manner.

Overall, elevated energy expenditure, decreased food intake and alterations in circulating levels of hormones including insulin, leptin, catecholamines, as well as elevated catabolism due to the tumour presence (high energy demands of tumour, inflammatory mediators produced by tumour) and tumour-host interactions are factors contributing to wasting in cancer (Tisdale, 2002). However, reduced food intake alone does not explain decreased body weight or/and fat mass in cancer patients and cancer-associated wasting cannot be completely reversed by elevated nutritional intake (K. Fearon et al., 2011). In advanced cancer patients, during 4-62 months follow-up, body weight and fat mass decreased. Despite providing nutritional support to patients

who had baseline calorie intake less than 90% of their energy requirement, body weight and fat mass did not increase (Fouladiun et al., 2005). Therefore, factors other than nutrient intake may contribute to fat loss in cancer. Increased lipolytic activity, evidenced by elevated fasting plasma glycerol and free fatty acids is a driver of fat loss in advanced cancer patients (Agustsson et al., 2007; Ryden & Arner, 2007; Zuijdgeest-van Leeuwen et al., 2000a) but the underlying causes of elevated lipolysis are not known. Other mechanisms including decreased lipogenesis (Lanza-Jacoby et al., 1984; Lopez-Soriano et al., 1996), impairment in adipogenesis (Batista et al., 2012; Bing et al., 2006), elevated fat oxidation (Dahlman et al., 2010; Laurencikiene et al., 2008; Zuijdgeest-van Leeuwen et al., 2000a), and decreased lipid deposition (Briddon et al., 1991; Lopez-Soriano et al., 1995; Lopez-Soriano et al., 1997; Notarnicola et al., 2012; Thompson et al., 1981) have also been attributed to fat loss in cancer (Figure 1-2).

1.2.3.1 Elevated lipolysis

Elevated lipolysis is one of the main causes of fat loss in cancer (Agustsson et al., 2007; Cao et al., 2010; Dahlman et al., 2010; Jeevanandam et al., 1986; S. Klein & Wolfe, 1990a; Zuijdgeest-van Leeuwen et al., 2000a), however the specific mechanisms contributing to lipolysis have not been clearly defined. Animal studies suggest that HSL-induced lipolysis is elevated in early stages of wasting (Kliewer et al., 2015) whereas ATGL plays a more important role in adipose tissue loss in advanced stages (Das et al., 2011a; Tsoli et al., 2014). In mice bearing lung carcinoma or melanoma cells, lower body weight, decreased fat and muscle mass and elevated lipolysis were observed in tumour group compared to the controls. In HSL deficient mice, the tumour reduced body weight and fat mass due to elevated ATGL activity. However, in ATGL deficient mice, the tumour did not induce elevated lipolysis and there was no significant difference in weight and fat mass between control and tumour group. Fat preservation in ATGL

deficient mice, prevented muscle loss in tumour-bearing animals (Das et al., 2011). Consistent with these findings, a recent study in mice bearing the Colon-26 carcinoma revealed lower fat mass and higher lipolysis in tumour-bearing mice compared to control mice. Increased lipolysis was induced by ATGL rather than the PKA/HSL pathway during late stages of cancer wasting. ATGL protein levels increased in tumour-bearing mice, however, no changes were observed in ATGL mRNA expression suggesting post-translational modifications (Tsoli et al., 2014).

Elevated expression of HSL mRNA (Agustsson et al., 2007; Cao et al., 2010; Thompson et al., 1993) and protein (Agustsson et al., 2007; Cao et al., 2010) has been reported in adipose tissue of weight-losing cancer patients compared to weight-stable patients. Higher mRNA expression of HSL in SAT was associated with higher serum free fatty acids in cancer patients, however, no significant differences were observed in mRNA expression of LPL, FAS, insulin and TNF-α in adipose tissue of cancer patients compared to controls (Thompson et al., 1993). These results are supported by a study that reported HSL mRNA and protein over-expression in weight-losing cancer patients compared to weight-stable cancer patients, explained the elevated adipose atrophy in cancer (Agustsson et al., 2007). The ratio of plasma glycerol/body fat (index of *in vivo* lipolysis) was two fold higher in weight-losing cancer patients. Culture of adipocytes from the same patients revealed no difference in basal lipolysis (glycerol release to the media) between groups. However, incubation of adipocytes with catecholamines and natriuretic peptides resulted in higher glycerol in the media in weight-losing group suggesting that the adipocytes were more sensitive to the same amount of stimuli, and therefore more catabolic. There was no significant difference in plasma levels of catecholamines and natriuretic peptides between groups (Agustsson et al., 2007). An explanation of the lack of difference in plasma hormone levels could be that lipolytic effects of hormones are elevated at the receptor level, evidenced by elevated β1-

adrenoceptor (ADRB1) expression on adipocyte membranes in weight-losing gastrointestinal cancer patients (Cao et al., 2010). Consequently, higher HSL expression and activity, which positively correlated with ADRB1 expression, were associated with higher plasma glycerol/fat mass and free fatty acids/fat mass (Cao et al., 2010). Therefore, lipolysis can be elevated in cancer patients due to increased expression of receptors on adipocyte membranes and their response to lipolytic effects of hormones, rather than elevated levels of mediators.

In a study by Agustsson et al. (Agustsson et al., 2007), elevated HSL mRNA and protein expression contributed to the increased lipolysis. No significant difference in mRNA expression of ATGL was observed between weight-losing cancer patients and controls; however, protein expression was not measured in this study (Agustsson et al., 2007). Das and Hoefler (2013) reported that ATGL mRNA expression may not translate to enzyme activity as its function is regulated via post-translational modifications. In another study, Das et al. reported higher ATGL and HSL activity in VAT of weight-losing cancer patients compared to non-cancer and cancer patients without weight loss (Das et al., 2011). Therefore, not only mRNA expression but also protein expression and/or activity of these enzymes need to be determined in adipose tissue to investigate mechanisms that underlie elevated lipolysis.

1.2.3.2 Elevated fat oxidation

The majority of studies suggest elevated lipolysis as a reason for fat loss in cancer; and consequently, increased fatty acid oxidation could be a tentative approach to utilize surplus fatty acids. By increasing fatty acid oxidation within adipose tissue, liberated fatty acids are oxidized and are not be released or re-esterified into TG. Up-regulation of transcriptional factors involved in mitochondrial fat oxidation such as peroxisome proliferator-activated receptor-gamma

coactivator 1 alpha (PGC-1α), and uncoupling protein 2 (UCP-2) have been demonstrated in animal models of cancer (Bing et al., 2006). No differences were observed in mRNA expression of PPARα, PGC-1α, and carnitine palmitoyltransferase-1 in mice bearing Colon-26 carcinoma compared to controls. However, mRNA expression of peroxisomal bifunctional enzyme, specific for peroxisomal fatty acid oxidation, was higher in tumour-bearing mice (Tsoli et al., 2014).

Zuijdgeest-van Leeuwen et al. (Zuijdgeest-van Leeuwen et al., 2000a) reported higher lipolysis accompanied reduced food intake in weight-losing cancer patients compared to healthy weight-stable adults. Whole body lipolysis and fatty acid oxidation were higher in cancer patients compared to healthy subjects, even after adjusting for food intake. However, this heterogeneous population of cancer patients had varying degrees of weight loss (5.3-25% /6months) and were at different stages in the disease trajectory (1-180 months since diagnosis) (Zuijdgeest-van Leeuwen et al., 2000a). Enhanced fat oxidation was reflected by a decreased respiratory quotient (Dahlman et al., 2010; Laurencikiene et al., 2008), higher expression of genes related to energy and fatty acid metabolism pathways such as Krebs cycle, oxidative phosphorylation, and fatty acid degradation have been reported in weight-losing cancer patients (Dahlman et al., 2010). In support of this, mRNA levels of CIDEA, which encodes for the protein that mediates oxidation of excess fatty acids rather than glucose in humans, was increased in SAT of weight-losing patients. Also, weight-losing patients had lower plasma TGs, and lower respiratory quotient indicating elevated fatty acid oxidation (Laurencikiene et al., 2008). In pancreatic cancer patients, CIDEA expression was higher in intra-abdominal adipose tissue compared to subcutaneous in early stages of tumour progression. CT image analysis of these same patients revealed that patients were losing intra-abdominal fat at a greater rate than subcutaneous (Haugen et al., 2011).

1.2.3.3 White adipose tissue browning in cancer

Excess fatty acids from enhanced lipolysis are oxidized by mitochondria to produce energy. However, the appearance of brown adipocytes within the white adipose tissue can dissipate energy of substrate oxidation as heat by uncoupling fatty acid oxidation from ATP production by uncoupling protein-1 (UCP-1) (Harms & Seale, 2013). Recently, studies have reported that white adipose tissue browning can contribute to adipose atrophy in cancer by enhancing white fat thermogenesis (Kir et al., 2014; Petruzzelli et al., 2014). Small adipocytes with large nuclei were observed during early stages of wasting in subcutaneous adipose tissue of mouse models of lung and pancreatic cancer. Multi-locular cells interspersed in the white adipose tissue, resembling brown adipocytes, positively stained for UCP-1 (Petruzzelli et al., 2014). White adipose tissue browning was associated with increased expression of brown fat markers including UCP-1, PGC-1α, and PPARγ in tumour-bearing mice compared to the controls (Kir et al., 2014; Petruzzelli et al., 2014). β-adrenergic signaling, inflammatory cytokines like IL-6, (Petruzzelli et al., 2014) and tumour-derived parathyroid hormone-related protein (Kir et al., 2014) can mediate white adipose browning by inducing expression of thermogenic genes. Blocking of these mediators might help to prevent adipose atrophy in cancer (Kir et al., 2014; Petruzzelli et al., 2014).

A recent study in Colon 26-murine model of cancer (Kliewer et al., 2015) investigated alterations in adipose tissue in early stages of wasting. Less than 10% weight loss and moderate loss of adipose tissue (34-42%) was observed in tumour-bearing animals compared to the control group. Lipid utilization evaluated as respiratory exchange ratio showed that 70% of total energy came from fat in tumour group while this ratio was only 48% in control group. HSL-induced lipolysis was elevated in early stages of wasting in this model whereas ATGL was involved in fat

loss in advanced stages of wasting (Tsoli et al., 2014). Markers of thermogenesis were elevated in brown adipose tissue but not in white adipose tissue, and were associated with elevated energy expenditure. Although fatty acid oxidation increased in white adipose tissue, no changes in expression of genes involved in white adipose tissue browning was reported. Therefore, white adipose tissue browning may not occur prior to severe loss of adipose tissue. It was concluded in this study that mechanisms underlying fat loss differs between early and late stages of adipose tissue wasting, therefore, identifying these mechanisms would help to define interventions to maintain adipose tissue in cancer (Kliewer et al., 2015). Collectively, lipolysis, increased fatty acid oxidation and elevated white adipose tissue thermogenesis play important roles in adipose tissue depletion in cancer. The relevance and incorporation of white adipose browning remains to be characterized in humans.

1.2.3.4 Lipogenesis and lipid deposition

Despite the importance of lipolysis in fat loss in cancer, fat depletion can also occur when lipogenesis is limited in white adipose tissue. In rats bearing the Yoshida AH-130 ascites hepatoma, decreased adipose tissue lipogenesis is accompanied by an increase in liver lipogenesis and hypertriglyceridemia (Lopez-Soriano et al., 1996). Decreased lipogenesis was accompanied by lower activities of FAS, citrate cleavage enzyme, and malic enzyme in rats bearing a mammary adenocarcinoma during late phases of tumour progression (Lanza-Jacoby et al., 1984). Deterioration in lipid synthesis capacity of epididymal adipose tissue was observed in MAC16 bearing rats, evidenced by decreased mRNA levels of important lipogenic enzymes such as ACC, FAS, SCD-1 and GPAT (Bing et al., 2006). Increased lipolysis and decreased lipogenesis has been reported in male Japanese white rabbits bearing the VX2 tumour cells compared to food-restricted animals. Body weight reduction and fat loss occurred before any

decrease in food intake (Ishiko et al., 1999).

LPL mediates fatty acid uptake in adipose tissue by hydrolysis of TG in very-low-density lipoproteins and chylomicrons. Numerous animal studies suggest reduced LPL activity in cancer (Lanza-Jacoby et al., 1984; Lopez-Soriano et al., 1995; Lopez-Soriano et al., 1996; Lopez-Soriano et al., 1997). Reduction in adipose tissue LPL activity in tumour-bearing mice to levels observed in food restricted animals was associated with impaired lipid deposition, fat loss, reduced breakdown of plasma lipoproteins and increased circulating lipid concentrations (Thompson et al., 1981). Decreased adipose tissue LPL activity was associated with hypertriglyceridemia during early stages of tumour growth in Lewis rats bearing a mammary adenocarcinoma (Lanza-Jacoby et al., 1984). Decreased fat content and LPL activity in white adipose tissue was accompanied by increasing circulating TGs, and body weight loss induced by the Yoshida AH-130 ascites hepatoma in rats (Lopez-Soriano et al., 1995; Lopez-Soriano et al., 1996; Lopez-Soriano et al., 1997). In mice bearing MAC16, plasma TG levels decreased during cancer progression, regardless of the amount of weight loss. At early stages, plasma free fatty acids decreased and LPL activity increased; however, at advanced stages of tumour, LPL activity decreased (Briddon et al., 1991).

While the majority of studies have utilized animal models to investigate lipogenesis and LPL activity during cancer progression, the few human studies that exist have reported decreased mRNA expression and activity of LPL and FAS in visceral adipose tissue in proximity to a tumour compared to distal adipose tissue in colorectal cancer patients (Notarnicola et al., 2012). Decreased FAS activity in adipose tissue and elevated activity in tumour cells might be important for tumour cell growth (Notarnicola et al., 2012). No changes were observed in lipogenesis, assessed by radioactive glucose incorporation into total lipids, in adipocytes isolated

from cancer patients' SAT compared to controls (Ryden et al., 2008). Lower plasma TG and higher glycerol and free fatty acids have been observed in weight-losing cancer patients (Dahlman et al., 2010; Ogiwara et al., 1994; Ryden et al., 2008) but the activity or expression of LPL was not determined in these studies.

Overall, these studies suggest elevated lipolysis and decreased lipogenesis in adipose tissue in cancer. However, limited number of human studies exists because of the cancer type, stage and fat depot from where an adipose biopsy can be obtained. Moreover, biological differences between animal and humans limit extrapolating results between pre- and clinical studies. Further studies are required to determine the lipogenesis capacity and fatty acid uptake by adipose tissue in various groups of cancer patients at different stages during disease trajectory.

1.2.3.5 Adipogenesis

Fat loss may arise from impairment in adipose tissue development and capacity for fat synthesis and storage. A reduction in mRNA levels of adipogenic transcription factors including PPARγ, c/EBPα, SREBP-1c in epididymal adipose tissue of mice bearing MAC16 tumour was associated with diminished adipocyte size (Bing et al., 2006). Expression of adipogenic factors including C/EBPα, SREBP-1c and PPARγ were reduced in rats bearing the Walker256 tumour during early stages of wasting. Smaller adipocytes were observed during late stages of wasting which supports a reduction in expression of adipogenic genes (Batista et al., 2012). Lower expression of adipogenic factors such as C/EBPα, Reverba, Per2 and PPARγ has been reported in mice bearing the Colon-26 carcinoma (Tsoli et al., 2014). More research in both animal and human models is required to demonstrate the possible alterations in adipogenesis during cancer

progression which has not been a focus in the research of adipose atrophy in cancer until recently.

1.2.3.6 Factors contributing to fat loss in cancer

Local adipokines produced by adipose tissue, circulating cytokines, and lipid mobilizing factors are collectively involved in adipose atrophy in cancer [reviewed in (Batista, Peres et al., 2012; Bing, 2011)]. Proinflammatory cytokines, such as interleukin-1 beta (IL-1β), TNF-α, IL-6 produced by the tumour or host tissue leads to both systemic and local inflammation in cancer (Bing & Trayhurn, 2009; W. W. Lin & Karin, 2007). Plasma levels of inflammatory cytokines are elevated in cancer (Tan et al., 2008) and are thought to promote adipose atrophy in animal and human models of cancer-associated wasting (Bing, 2011).

Overall, evidence would suggest that inflammatory cytokines are involved in adipose tissue depletion in cancer (Bing, 2011; Das & Hoefler, 2013; Tisdale, 2009); however, plasma concentrations may represent the presence of a tumour rather than cancer-associated adipose atrophy per se (Batista et al., 2013). It is also necessary to consider that the ability of cytokines to evoke cancer-associated wasting depends on tumour type, stage and the complex response within a network of mediators, rather than a single cytokine (Argiles et al., 2012; Tisdale, 2005). On the other hand, a major gap remains related to comparison of local inflammatory markers in both visceral and subcutaneous depots. Therefore, assessing whether depot-specific differences in inflammatory cytokines transcription may contribute to inflammatory factors production and subsequent alterations in fat mass would be of great value.

1.2.4 Adipose tissue fatty acid composition in cancer

Alterations in adipose tissue fatty acid metabolism in conditions like cancer may alter adipose tissue fatty acid composition and subsequently, lead to the changes in the production of lipid metabolites and carcinogenic mediators (Murff et al., 2009), which may also affect adipose tissue function and mass. Therefore, characterizing fatty acid composition of adipose tissue helps to enhance understanding of aberrations of adipose tissue metabolism in cancer. There are few data on adipose tissue fatty acid composition in cancer (Neoptolemos et al., 1988; Schoen et al., 1996; Zhu et al., 1995), and the effect of tumour or treatments such as chemotherapy on fatty acid composition is not clear. No differences in the fatty acid composition of either VAT and SAT between advanced cancer and control groups have been reported in previous studies (Schoen et al., 1996). A significant correlation between VAT and SAT fatty acid content was observed in 19 patients undergoing exploratory laparotomy. Fourteen subjects underwent subsequent surgery for colorectal cancer. No consistent pattern for one site compared to the other was observed and the variability in fatty acid content was greater between individuals rather than between depots within the same individual, likely reflecting the influence of diet on both VAT and SAT composition (Schoen et al., 1996). On the other hand, higher levels of 16:1n-9, 20:3n-6 and 22:5n-3 and lower proportion of 18:3n-3 were observed in SAT of newly diagnosed colorectal cancer patients compared to control subjects with benign disease which may collectively be related to both endogenous lipid synthesis and exogenous lipid sources (Cottet et al., 2015). Therefore, not only dietary changes of cancer patients but also presence of the tumour and associated changes in adipose tissue metabolism may affect fatty acid metabolism inside the tissue.

1.3 Nutritional interventions to prevent cancer-associated wasting

Among specific dietary supplements applied to prevent wasting in cancer, long chain n-3 PUFAs; EPA and DHA (Xue et al., 2009) have received major attention. Supplementation with fish oil containing EPA and DHA prevents weight and muscle loss and improves response to chemotherapy in animal models (Xue et al., 2009) and cancer patients (Murphy et al., 2011a; Murphy et al., 2011b). Although there have been few clinical studies investigating nutritional intervention approaches within the scope of treatment, supplementing with fish oil containing EPA and DHA in advanced cancer patients has been shown to stabilize the weight of patients. Efficacy of chemotherapy treatment was improved when patients supplemented with fish oil containing EPA and DHA during treatment for non-small cell lung cancer (Murphy et al., 2011a). Although EPA and DHA intervention has shown beneficial effect on tumour growth, body weight, muscle mass, food intake and response to the treatment in pre and clinical studies, limited data exist regarding the effect of EPA and DHA on adipose tissue in cancer and it would seem important to clarify if supplementation with EPA and DHA, concurrent with chemotherapy treatment, would help to restore altered adipose tissue metabolism caused by tumour and cancer treatment.

1.3.1 Effect of EPA and DHA on adipose tissue in cancer

Little is known about the influence of EPA and DHA on adipose tissue atrophy in cancer. Emerging evidence suggests that EPA and DHA may attenuate fat loss in cancer wasting (Russell & Tisdale, 2005; Tisdale & Dhesi, 1990). EPA intervention (0.5g/kg body weight) in NMRI mice bearing the MAC-16 tumour, maintained body weight and preserved both skeletal muscle and adipose tissue. Dexamethasone stimulated lipolysis in 3T3-L1 adipocytes showed that adipose tissue preservation by EPA was associated with downregulation of zinc-alpha2-

glycoprotein (ZAG) as a lipid-mobilizing factor in adipose tissue (Russell & Tisdale, 2005). Moreover, EPA inhibits tumour-induced lipolysis by decreasing intracellular cAMP levels in incubated mice epididymal adipocytes (Tisdale & Beck, 1991). However, isolated adipocytes from NMRI mice incubated with ZAG and EPA showed that the lipolysis inhibiting effect of EPA might be related to direct inhibition of adenylate cyclase activity rather than indirect reduction in the levels of intracellular cAMP (Price & Tisdale, 1998).

EPA enriched PLs, containing 42% EPA, and 6.8% DHA (% of n-3 PUFAs), were extracted from starfish and administered intragastrically into mice bearing sarcoma 180. Fourteen days of intervention (100mg/kg/d) prevented weight and adipose tissue loss. Elevation in serum levels of IL-6, TNF-α and mRNA expression of ATGL, HSL, ZAG in adipose tissue was inhibited by oral EPA treatment. Reduction in the expression of LPL, PPARγ, SREBP-1c induced by tumour was not observed in EPA-administrated animals. EPA also inhibited TNF-α induced lipolysis in 3T3-L1 adipocytes. In summary, EPA administration preserved adipose tissue in tumour-bearing animals through anti-lipolytic pathways (Du et al., 2015).

Effect of short term (7 days) supplementation with EPA (6 g/d) on inhibition of lipolysis was investigated in 17 weight losing cancer patients of mixed tumour types and 16 healthy subjects. In comparison to the placebo group (olive oil), EPA showed no significant effect on lipolysis, and oxidation in healthy nor in cancer groups. It was concluded that the effect of longer supplementation period should be investigated to identify the mechanisms by which EPA can prevent weight loss in cancer (Zuijdgeest-Van Leeuwen et al., 2000).

So far, few cell-lines, pre-clinical and clinical studies have investigated the effect of EPA and DHA on adipose tissue in tumour-bearing state alone or concurrent to the treatment. Overall,

a major gap remains regarding underlying mechanisms by which EPA and DHA may help to maintain adipose tissue. As higher doses of EPA and DHA are typically applied in pre-clinical studies, physiological doses and duration remain to be elucidated in human studies. It still remains to be clarified if higher pharmacological doses of EPA and DHA have the ability to maintain adipose tissue. Finally, indirect effects of EPA and DHA on adipose tissue should be considered in neoplastic states by affecting tumour growth and tumour derived mediators that affect adipose tissue.

1.4 Summary

Patients with advanced cancer frequently suffer weight and fat loss. While little is known about the effect of tumour on adipose tissue, much less is known on the mechanisms contribute to adipose atrophy in patients undergoing chemotherapy. Alterations in adipose tissue fat metabolism including changes in expression of genes involved in fat synthesis, storage, mobilization or oxidation, browning of white adipose tissue, adipocyte development, and elevated inflammatory signaling may have a role in fat loss in cancer patients. Collectively, a major gap remains in our understanding of the effect of tumour and chemotherapy treatment on adipose tissue in cancer. Factors including tumour type, cancer stage, response to treatment should be considered in interpretation of the results.

Due to various roles of adipose tissue in controlling human metabolism, further identification of mechanisms of fat loss in cancer would help to identify fat-losing cancer patients that would benefit from early therapeutic interventions which could improve survival. Therefore, the prognostic significance of adiposity at the time of diagnosis require further investigation to clarify if excess fat or prevention of fat loss might be beneficial for the survival

of patients. Studies have recently emerged reporting supplementation with fish oil containing EPA and DHA to prevent weight loss, fat loss and improve response to chemotherapy in cancer; thus demonstrating the importance of developing effective interventions to maintain adipose tissue mass and function in cancer.

Tables

Table 1-1. Adipose tissue molecules involved in lipid metabolism with their functional roles

Molecules	Description	Pathway	Role in adipose tissue
ACC	Acetyl coenzyme A carboxylase	Fatty acid synthesis	Carboxylation of acetyl-CoA to malonyl-CoA
ACL	ATP citrate lyase	Fatty acid synthesis	Formation of acetyl-CoA from citrate and CoA
ATGL	Adipose triglyceride lipase	TG degradation	Hydrolysis of stored TG
CGI-58	Comparative gene identification-58	TG degradation	Facilitates ATGL-mediated lipolysis
CIDE	DNA fragmentation factor-α-like effector	TG enlargement	Lipid droplet associated proteins regulating growth and TG deposition in adipocytes
CPT-1α	Carnitine palmitoyltransferase I	Fatty acid oxidation	Fatty acid entry into mitochondria
DGAT	Diacylglycerol acyltransferase	TG synthesis	Terminal step in TG synthesis from diacylglycerol and acyl CoA
FAS	Fatty acid synthase	Fatty acid synthesis	Synthesis of C16:0 from acetyl-CoA and malonyl-CoA
FAT/CD36	Fatty acid translocase	Fatty acid uptake	Mediates long chain fatty acids uptake into adipocytes
GPAT	Glycerol-3-phosphate acyltransferase 1	TG synthesis	Catalyzes the initial step in glycerolipid biosynthesis
HSL	Hormone-sensitive lipase	TG degradation	Hydrolysis of stored TG, with higher affinity for diacylglycerol
LPL	Lipoprotein lipase	Fatty acid metabolism	Hydrolysis of circulating lipoproteins

PGC-1α	Peroxisome proliferator-activated receptor gamma coactivator 1-alpha	Fatty acid metabolism	Co-operate with transcriptional factors to regulate mitochondrial biogenesis, and glucose/fatty acid metabolism
PPARγ	Peroxisome proliferator-activated receptor γ	Fatty acid/TG metabolism	Regulates adipocyte differentiation, fatty acid synthesis and storage in adipose tissues
SCD-1	Stearoyl-CoA desaturase 1	Fatty acid synthesis	Biosynthesis of monounsaturated fatty acids from saturated fatty acids
SREBP-1c	Sterol regulatory element-binding protein 1c	Fatty acid/TG synthesis	Regulates expression of genes involved in lipogenesis
UCP-1	Uncoupling Protein **1**	Mitochondrial Oxidative phosphorylation	Dissipate energy of substrate oxidation as heat by uncoupling fatty acid oxidation from ATP production

Abbreviations: TG, Triglyceride; ATP, Adenosine triphosphate

Table 1-2. Articles reporting fat and lean tissue loss in newly diagnosed cancer patients

Reference	Subjects[1]	Cancer Type	Study design	Body composition assessment	Results
Fouladiun et al. (2005)	Malnourished patients (n=132; 66±3years) advanced cancer with malnutrition (T4N1M1)	GI (n=123) Breast (n=1) Melanomas (n=2) Other (n=6), followed for 6-42 months	Longitudinal	DEXA	Whole body fat loss was related to shorter survival Body fat loss more intense and pronounced compared to lean tissue
Agusstson et al. (2007)	Weight stable cancer patients (n= 11), Weight-losing cancer patients with (n=8) and without (n=7) malnutrition	Surgical GI cancer	Cross-sectional	BIA	No differences in lean body mass between groups Higher lipolysis in weight-losing patients
Dahlman et al. (2010)	Weight-losing cancer patients (n=13), Weight-stable cancer (n=14)	Surgical GI cancer	Cross-sectional	BIA	Lower body fat mass but similar lean body mass between weight-losing and weight-stable patients
Ryden et al. (2008)	Weight-losing cancer patients (n=13), Weight stable cancer patients (n=10), Controls (n=5)	Surgical GI cancer	Case-control	BIA	No difference in lean body mass between groups Elevated lipolysis with no changes in lipogenesis

Agustsson et al. (2012)	Weight-losing cancer patients without (n=13) and with gastrointestinal obstruction (n=10), Weight stable- cancer (n=17)	Surgical GI cancer	Cross-sectional	BIA, CT	No changes were observed in lean mass Visceral fat volume was lower in weight-losing cancer group compared to weight stable

1 No patients received chemotherapy or radiotherapy
Abbreviations: GI, Gastrointestinal; DEXA, Dual-energy X-ray absorptiometry; BIA, Bioelectrical impedance; CT, Computed tomography

Figures

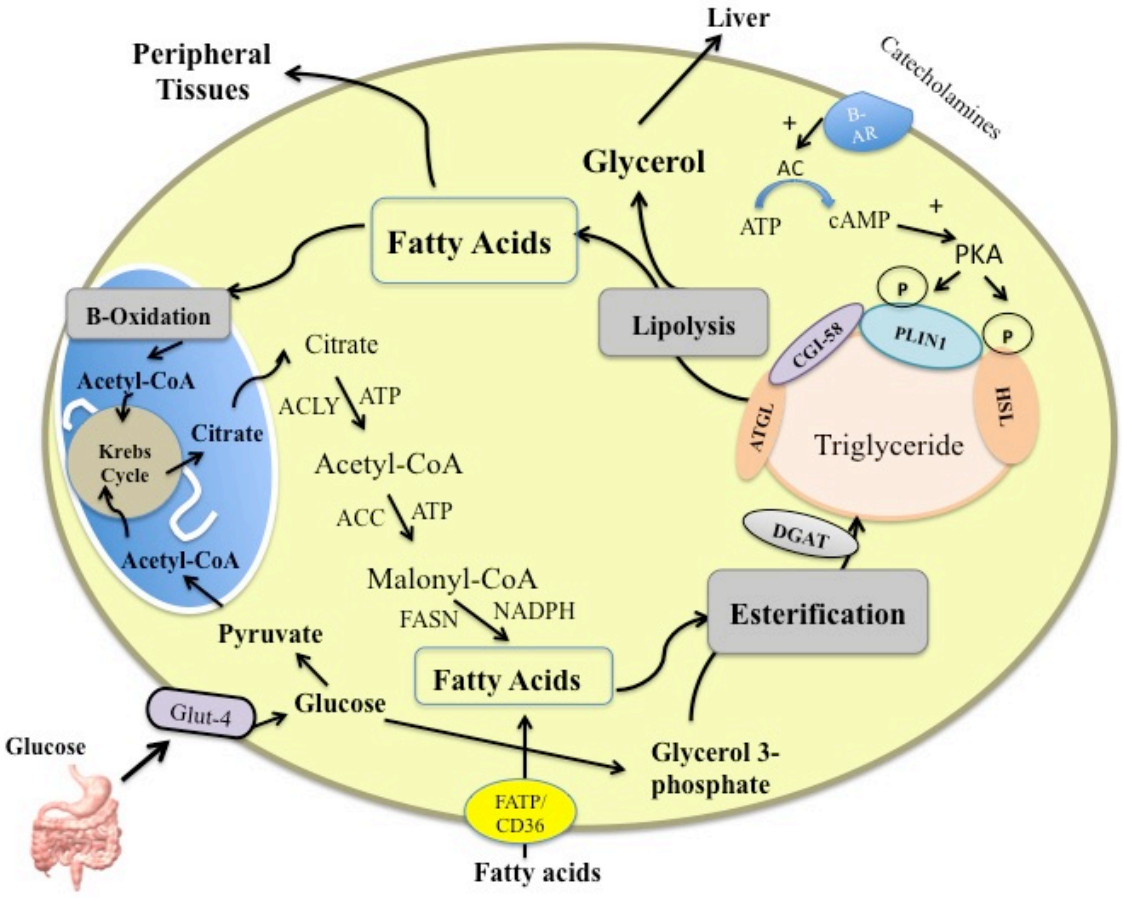


Figure 1-1. Overview of lipid metabolism inside adipose tissue.

Adipose tissue metabolism is regulated through two major pathways: lipolysis (breakdown of triglycerides to fatty acids and glycerol) and lipogenesis. Fatty acid synthesis occurs through *de novo* lipogenesis from acetyl-CoA and by subsequent TG synthesis (esterification of fatty acids with glycerol), synthesized fat stores within lipid droplet of adipocytes. Fatty acids liberated by lipolysis of stored TG can be released into plasma or enter mitochondrial β-oxidation to produce energy. Abbreviations: ATP, Adenosine triphosphate; ACLY, ATP citrate lyase; ACC, Acetyl-CoA carboxylase; FAS, Fatty acid synthase; NADPH, Nicotinamide adenine dinucleotide phosphate; AC, Adenylyl cyclase, β-AR, beta-adrenergic receptors; PKA, protein kinase A; ATGL, Adipose triglyceride lipase; HSL, Hormone-sensitive lipase, PLIN1, Perilipin 1; CGI-58, Comparative gene identification-58, DGAT, Diacylglycerol acyltransferase

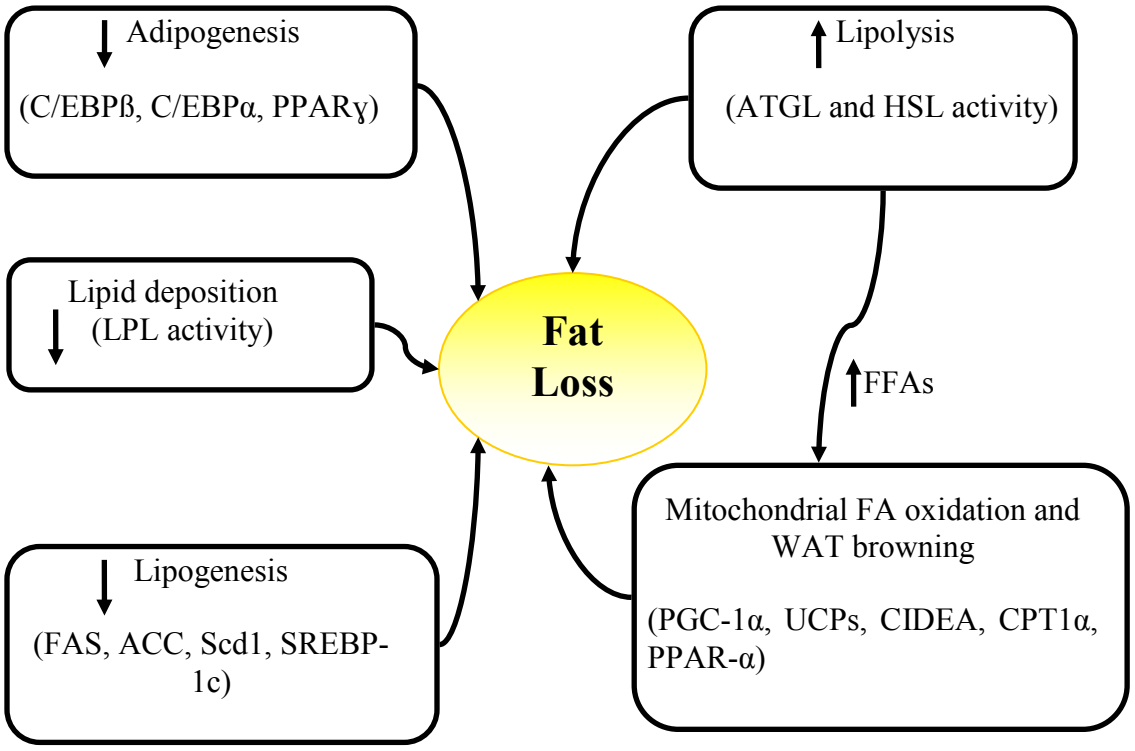


Figure 1-2. Summary of mechanisms and specific genes involved in adipose atrophy in cancer.

Increased lipolytic activity, elevated fat oxidation, white adipose browning, decreased lipogenesis, impairment in adipogenesis, and decreased lipid deposition have been attributed to fat loss in cancer. Abbreviations: WAT, White adipose tissue; FFAs, Free fatty acids; ATGL, Adipose triglyceride lipase, HSL, Hormone sensitive lipase; PGC-1α, Peroxisome proliferator-activated receptor-gamma coactivator 1 alpha; UCPs, Un-coupling proteins; CIDEA, Cell death-inducing DFFA (DNA fragmentation factor-alpha)-like effector A, CPT1α, Carnitine palmitoyltransferase; PPARγ, Peroxisome proliferator-activated receptor gamma, C/EBPα, CCAAT-enhancer-binding proteinα; LPL, Lipoprotein lipase; FAS, Fatty acid synthase, ACC, Acetyl-CoA carboxylase; Scd1, Stearoyl-CoA desaturase, SREBP-1c, Sterol regulatory element binding protein-1c

Chapter 2: Research plan

2.1 Rationale

The majority of cancer patients experience some degree of adipose atrophy during the disease trajectory (Fearon, 2008). Recently, potential links between fat loss and poor outcomes have been identified indicating shorter survival and reduced quality of life in cancer patients who are losing fat independent of BMI (Murphy et al., 2010). However, the independent prognostic significance of adipose tissue at the time of cancer diagnosis in predicting survival is not clear. The majority of studies have used BMI as an index of adiposity to predict the survival of cancer patients. Considering the limitations of BMI in assessing body fat [reviewed in (Buss, 2014; Kok et al., 2004; Noori et al., 2010)], the effect of adiposity on cancer survival requires evaluation based on the adiposity index, assessed by gold standard techniques such as computed tomography, rather than BMI. Moreover, in spite of the divergent behavior of adipose tissue depots, the importance of visceral and subcutaneous adiposity in cancer survival has not been characterized.

A recent work in advanced cancer patients reported adipose tissue to be gained or lost in the year preceding death (Prado et al., 2013). As death approaches, the majority of patients lose fat with many experiencing losses of up to 0.1kg of fat mass per day (Murphy et al., 2010). Fat loss occurs from both VAT and SAT depots [reviwed in (Ebadi & Mazurak, 2014)]; however the patterns of changes of VAT and SAT have not been demonstrated and little is known regarding the fluctuations throughout the cancer trajectory within and between depots. Metabolic differences between VAT and SAT (Garaulet et al., 2001; Wajchenberg, 2000) would suggest a requirement to investigate depot- specific pattern of loss rather than TAT loss. Gain, or maintanace, of adipose tissue has been observed further away from death, mainly at 9 and 6

months prior to death (Prado et al., 2013). This period of time may present an appropriate time to initiate interventions to improve outcome of cancer patients.

As cancer progresses, patients often receive treatments, such as chemotherapy which further exacerbates an already dysregulated metabolic state. While evidence is emerging regarding the effect of tumor on adipose tissue, much less is known about drug-related mechanisms contributing to adipose atrophy. Therefore, identification of mechanisms by which tumor and cancer treatments, such as chemotherapy, affect adipose tissue are required to develop appropriate therapeutic interventions to prevent further fat depletion. Studies have recently emerged reporting fish oil supplementation prevents weight loss and improve response to chemotherapy (Murphy et al., 2011a; Murphy et al., 2011b; Tisdale & Dhesi, 1990; Xue et al., 2009) It would seem important to clarify if fish oil supplementation, concurrent with chemotherapy treatment, also helps to prevent alterations in adipose tissue metabolism induced by tumor and chemotherapy.

The overall objective of this research is to enhance understanding of adipose tissue alterations that occur after a cancer diagnosis until death and consists of three complementary objectives: 1) To investigate the prognostic significance of adiposity in cancer survival; 2) To assess the intensity and time course of changes in TAT, VAT and SAT of advanced cancer patients in the year preceding death; 3) To investigate the effect of a tumor and alterations that occur after chemotherapy initiation, when animals are provided a control or fish oil diets, on adipose tissue, in an experimental model of colorectal cancer.

2.2 Objectives and hypotheses

2.2.1 The association between adiposity and survival after a cancer diagnosis

Objectives:

i) To determine whether there is level of sex-specific adiposity (total, visceral and subcutaneous) that associates with mortality risk in a model that accounts for known prognostic variables in cancer.

ii) To investigate whether a high level of adiposity has an independent effect on survival and to compare the median survival between high vs. low adiposity.

iii) To determine whether visceral or subcutaneous adiposity significantly contributes to the survival advantage of total adiposity in cancer.

iv) To compare the overall survival of high and low adiposity patients in the presence and absence of low muscle mass.

Hypothesis:

It was hypothesized that low adiposity is associated with increase mortality risk. Subcutaneous adiposity compared to visceral, would associate with longer survival in cancer patients. However, presence of low muscle mass is expected to shorten survival in cancer patients, regardless of amount and location of fat.

This objective was investigated in chapter 3.

2.2.2 Intensity and time course of alterations in adipose tissue in advanced cancer patients

Objectives:

i) To compare changes in adipose tissue cross sectional areas in visceral and subcutaneous depots at mean time points corresponding to 9, 6, 3 and 1 months before death in advanced colorectal and cholangiocarcinoma cancer patients.

ii) To estimate and compare the proportions of patients experiencing loss, gain or stability of TAT, VAT and SAT depots between 9, 6, 3 and 1 months prior to death.

Hypothesis:

It was hypothesized a progressive loss of adipose tissue occurs within the last months preceding death. It was also hypothesized that VAT would precede, and be lost at a greater intensity than SAT.

This objective was investigated in chapter 4.

2.2.3 Adipose tissue alterations in an animal model of colorectal cancer

Objectives

Fischer 344 rats bearing the Ward colorectal carcinoma receiving chemotherapy [irinotecan (CPT-11) + 5-fluorouracil (5-FU)] has been developed to represent as much as possible, the same doses, cycles, and level of toxicity observed clinically in humans diagnosed with colorectal cancer. We used this model to:

i) Evaluate and compare the morphology, fatty acid composition, lipogenic gene expression and the proteome profiles of periuterine adipose tissue of healthy rats (reference) to rats bearing the Ward colorectal carcinoma on a control diet (Tumour- bearing).

ii) Evaluate and compare the morphology, fatty acid composition, lipogenic gene expression and the proteomic* profiles of periuterine adipose tissue of rats bearing the Ward colorectal carcinoma on a control diet to rats bearing the Ward colorectal carcinoma undergoing either 1- or 2-cycles of chemotherapy (CPT- 11 + 5-FU) on a control diet.

iii) Evaluate and compare the morphology, fatty acid composition, lipogenic gene expression and the proteomic* profiles of periuterine adipose tissue in rats receiving 1- and 2- cycles of chemotherapy (CPT-11 + 5-FU) consuming a control diet, to rats consuming a diet containing fish oil initiated at the same time of chemotherapy.

* Proteomic analysis was conducted only after 2-cycles of chemotherapy but not in rats undergoing 1-cycle of chemotherapy.

Hypothesis 1

It was hypothesized that compared to healthy-no tumour- rats (reference), rats bearing the Ward colorectal tumor will exhibit:

i) Lower body weight, adipose tissue weight (%body weight) and smaller adipocytes.

ii) Lower proportion of total n-3 fatty acids, EPA, and DHA in adipose TG and PL fractions.

iii) Decreased mRNA expression of genes involved in lipogenesis.

iv) Diminished expression of proteins involved in lipid synthetic pathways.

Hypothesis 2

It was hypothesized that compared to tumour-bearing rats, rats receiving 1-cycle or 2-cycles of chemotherapy fed a control diet will exhibit:

i) Lower body weight, adipose tissue weight (%body weight) and smaller adipocytes.

ii) Lower proportion of total n-3 fatty acids, EPA, and DHA in adipose TG and PL fractions.

iii) Decreased mRNA expression of genes involved in lipogenesis.

iv) Reduced expression of proteins in the pathways that contribute to lipid accumulation in adipose tissue.

v) While alterations will be evident subsequent to one cycle, a greater effect will be observed on all assessments after the second cycle.

Hypothesis 3

It was hypothesized that compared to rats receiving 1- or 2-cycles of chemotherapy on a control diet, rats receiving 1- or 2- cycles of chemotherapy on a fish oil diet will exhibit:

i) Smaller adipocytes.

ii) Higher proportion of total n-3 fatty acids, EPA, and DHA in adipose TG and PL fractions.

iii) Rats fed fish oil diets will maintain adipose tissue function by attenuating chemotherapy-induced alterations in adipose tissue.

Chapter 3. Subcutaneous adiposity is an independent predictor of mortality in cancer patients*

3.1 Introduction

Adipose tissue is an active metabolic tissue, involved in regulating whole body metabolism. Previous studies have shown fat loss to be a poor prognostic factor in advanced cancer independent of body weight (Murphy et al., 2010). However, the prognostic significance of adiposity, at the time of cancer diagnosis, on mortality is not clear.

The "obesity paradox" refers to obese patients experiencing longer survival after a diagnosis of a disease and has been described in some wasting associated diseases such as cancer, cardiovascular disease, diabetes, and renal diseases [reviewed by (Prado et al., 2015)]. While some studies have shown an association between obesity and poor survival (Dignam et al., 2006; Doria-Rose et al., 2006; Kasenda et al., 2014; Meyerhardt et al., 2003), others have reported obesity, compared to low or healthy BMI (kg/m^2), to be associated with lower mortality after a cancer diagnosis (Hakimi et al., 2013; Hughes, 2013; Martin et al., 2013; Schlesinger et al., 2014). Previous studies addressing the obesity paradox have primarily used BMI as an assessment of body composition. BMI does not provide an appropriate assessment of body composition as it does not differentiate between fat and fat-free mass or different fat depots. Adipose tissue and skeletal muscle are 2 major body compartments with different functions, therefore, the concept of the 'obesity paradox" needs to be investigated based on the independent prognostic significance of fat and muscle rather than the BMI. Moreover, individual variability in adiposity (Noori et al., 2010), especially visceral adiposity (Kaneko et al., 2015; Kuk et al., 2005) exists within each BMI category. Recently studies have applied CT imaging to deal with

* A version of this chapter has been submitted for publication in British Journal of Cancer.

the controversial concept of the obesity paradox. In an oncologic population, CT images are a routine part of treatment and are available from patient records as a chart review (Fabbro et al., 2010). CT image analysis has emerged as the gold standard for body composition assessment in cancer patients due to its ability to discriminate and quantify muscle as well as VAT and SAT (Fabbro et al., 2010; Shen et al., 2004a). VAT and SAT differ in anatomic location, endocrine function, adipokine secretion, and lipolytic activity [reviewed previously (Ibrahim, 2010; Wajchenberg, 2000)]. Variability in regional adipose tissue distribution by sex (Wajchenberg, 2000) and within each category of BMI (Kaneko et al., 2015; Kuk et al., 2005), as well as divergent behavior of adipose depots (Ebadi et al., 2016; Wajchenberg, 2000) demonstrates the need to understand the importance of visceral and subcutaneous adiposity in cancer survival.

Recently, Martin et al. (Martin et al., 2013) reported that BMI ≥25 kg/m^2 in both sexes was associated with longer survival using sex-specific cutoffs in a large cohort of cancer patients. However, survival advantage of obesity was diminished in the presence of concurrent conditions including weight loss, sarcopenia (severe muscle depletion) and low muscle radiodensity (fat infiltrated muscle). Considering BMI limitations in predicting adiposity, sex-specific values associated with mortality for adipose tissue are required to evaluate the effect of low muscle mass on survival of high adiposity patients.

Studies assessing the effect of adiposity, either visceral or subcutaneous, on cancer survival have yielded inconsistent results (Fujiwara et al., 2015; Kaneko et al., 2015; Lee et al., 2015; Rickles et al., 2013). Small sample sizes, lack of cancer-specific cut offs associated with survival, exclusion of conventional or body composition variables associated with survival in multivariate analysis as well as focusing on short or long term mortality as an outcome contribute to inconsistent results. Previous studies have applied cut-offs derived from renal cell

carcinoma patients in an Asian population (Kaneko et al., 2015; Lee et al., 2015) that may not be generalizable to all cancer populations or to non-Asians. Moreover, adipose tissue distribution differs by sex (Wajchenberg, 2000), which demonstrates the need to apply sex- specific cut offs. Therefore, a major gap remains regarding the role of adipose tissue in cancer survival, which led us to explore the independent prognostic significance of adipose tissue in predicting mortality as well as the importance of visceral and subcutaneous adiposity in estimating cancer mortality in a large cohort of cancer patients. Survival advantage of adiposity in the presence and absence of sarcopenia was also evaluated. It was hypothesized that higher adiposity, especially subcutaneous adiposity, as defined by CT images would be associated with the lowest mortality risk in cancer patients, but that the presence of sarcopenia would decrease the survival advantage of high adiposity.

3.2 Methods

3.2.1 Patients

The study was performed in accordance with the institutional research ethics board. Alberta Cancer Board Research Ethics Board (Edmonton, Alberta, Canada) reviewed and approved this study. Our site encompasses patients in Northern Alberta, Canada. Data regarding cancer site, morphology, clinical and demographic characteristics for each of the subjects were collected from the Alberta Cancer Registry. We extracted data from gastrointestinal or respiratory cancer patients' initial visit to medical oncology before receiving any treatment, between January 2004 and January 2007 (n=1473). Patient's baseline characteristics for gastrointestinal and respiratory tract cancers were reported in detail in Martin et al. 2013 (Martin et al., 2013). CT scans for this study were taken within 30 days of patient's initial assessment. Metastatic renal cell carcinoma patients (n=273) treated with sunitinib between March 2005-

2012 at the Cross Cancer Institute (Edmonton, Alberta, Canada) were also included in this study. For these patients, CTs within a median of 26 days (95% CI: 12-63 days) from the start of the treatment were used to represent baseline body composition. Self-reported height, weight, and performance status (PS) were collected using the Patient-Generated Subjective Global Assessment.

3.2.2 CT image analysis

All participants had body composition measured using secondary analysis of images retrieved from the patient clinical record. Adipose tissue cross-sectional areas measurement was conducted by analyzing CT scans at the 3rd lumbar vertebra (L3). The third lumbar was selected as a standardized landmark, as adipose tissue areas in a single CT image at L3 correlate well with whole body fat mass (Mourtzakis et al., 2008). Regression equations for VAT have not been developed for cancer populations; however, VAT cross sectional area at L3 strongly correlate with whole-body VAT volume in healthy populations (Shen et al., 2004b). Two consecutive transverse CT images extending from L3 to the iliac crest were assessed using Slice-O-Matic (V4.2; Tomovision, Montreal, QC, Canada). Adipose tissue cross-sectional areas were calculated by using standard Hounsfield Unit (HU) thresholds of -29 to 150 HU for skeletal muscle (SM), -150 to -50 HU for VAT (Miller et al., 1998) and -190 to -30 HU for SAT (Mitsiopoulos et al., 1998). Tissue cross-sectional areas (cm^2) were calculated by summing the given tissue pixels and multiplying by the pixel surface area. Mean tissue areas for 2 consecutive images were calculated; the mean CV of paired images was 2.7% for adipose tissue areas. VAT and SAT cross sectional areas were summed to estimate TAT areas. The cross-sectional areas of skeletal muscle, total adipose tissue, visceral adipose tissue and subcutaneous adipose tissue were normalized for the patient height to calculate indexes (cm^2/m^2) for skeletal muscle (SMI), total

adipose tissue (TATI), visceral adipose tissue (VATI) and subcutaneous adipose tissue (SATI). Mean muscle radiation attenuation (HU) was reported as muscle radiodensity which correlates with TG content of the muscle (Aubrey et al., 2014).

3.2.3 Statistical analysis

Descriptive statistics are presented as mean ± SD for continuous variables and percentage for categorical variables. The comparison between study groups were conducted using independent t-test and Pearson χ^2 test for continuous and categorical variables, respectively. Overall survival was defined as the time from diagnosis to the date of death or date of last contact of August 2010 for 1473 gastrointestinal and respiratory tract cancer patients. For 273 metastatic renal cell carcinoma patients, time from the start of sunitinib treatment to the date of death or date of last contact (March 2012) were defined as survival time. Patients alive at the time of the last contact were censored at the date last known to be alive. Univariate and multivariate analysis to determine mortality Hazard Ratios (HR) were conducted using Cox proportional hazard models to identify significant predictors of mortality. Variables significant at $p< 0.10$ level in the univariate analysis were selected to be entered in the multivariate model. Results were reported as HRs and 95% confidence intervals (CIs). Factors known to correlate with mortality of cancer patients (Martin et al., 2013) including age, sex, cancer type, stage, performance status as well as body composition variables including lumbar SMI, muscle radiodensity and TATI or VATI and SATI were included in the analysis.

Cut-off values for lumbar SMI and muscle radiodensity were derived from Martin et al. (2013) established cut-offs in gastrointestinal and respiratory cancer patients (Martin et al., 2013). For SMI, values below 41 cm^2/m^2 in females of all BMI categories and SMI values below

43 cm^2/m^2 in males with a BMI <25 and SMI <53 cm^2/m^2 in male with a BMI ≥25 associated with shorter survival and were considered as sarcopenic groups. Muscle radiodensity of <33 HU in patients with a BMI ≥25 and <41 in those with a BMI <25 associated with shorter survival (Martin et al., 2013).

Sex specific adiposity values associated with the lowest mortality risk were determined by examining the continuous variable on the basis of quartiles using the first quartile as the reference group in a fully adjusted multivariate model. Following, adjunct quartiles with similar risk of death (non statistically significant different hazard ratios indicated by non-significant p-value in Cox model) were pooled together and statistically significant values that provide satisfactory discrimination of mortality risk between patients were determined for each sex. Kaplan-Meier curves were plotted to estimate survival over time and the log-rank test were used to compare the difference between survival curves. Pearson correlation test was conducted to assess whether there was a significant relationship between adiposity and muscle radiodensity. Analyses were performed using IBM SPSS Statistic Software 21 (SPSS for Windows, version 21.0, SPSS, Chicago, IL). P values <0.05 was considered as a significant difference.

3.3 Results

Patient characteristics are summarized in Table 3-1. The most common cancer was colorectal (42% of cancer types in both sexes) with the majority of patients in stage IV (62.5% in men and 59% in women). Patients were followed until death (n=1207) or censoring (the date last known to be alive; n=555). The median overall survival of the cohort was estimated to be 16.7 months (95% CI, 15.4 to 18.1) and the median follow-up of censored patients was 24.8 months (95% CI, 20.8 to 28.8). Fifty-three percent of the population were overweight or obese. Men had higher BMI and SMI than women (Table 3-1). Although TATI did not differ between males and

females, fat distribution differed between sexes, with men having greater visceral adiposity and women having more subcutaneous fat (Table 3-1).

High adiposity, characterized by TATI ≥107.7 cm^2/m^2 in male and ≥102.2 cm^2/m^2 in females, were the values that associated with the lowest mortality risk. In order to find mortality associated values, VATI and SATI were separately divided into quartiles and in fully-adjusted models, visceral adiposity of VATI of 52.9 cm^2/m^2 in males and 51.5 cm^2/m^2 in females were defined as VATI values that discriminate between high and low risk patients. SATI ≥50 cm^2/m^2 in males and ≥42 cm^2/m^2 in females, defined as high subcutaneous adiposity, were set as values associated with the lowest mortality (Table 3-2).

To evaluate the independent prognostic significance of adiposity in predicting mortality, a fully adjusted cox proportional hazard analysis was performed based on mortality-associated values reported in Table 3-2. The following variables associated with mortality risk in patients: age, cancer type, stage, PS, TATI, SMI and muscle radiodensity in the univariate analysis (Table 3-3). Compared with the reference group with high adiposity, patients with low adiposity, had a significant increase in mortality risk after adjustment for major predictors of survival (HR: 1.26; 95% CI: 1.11 to 1.41; $p<0.001$) (Table 3-3). Patients with high adiposity survived 19.8 months (95% CI, 17.6 to 22) while the median survival in low adiposity group was 14.0 months (95% CI, 12.4 to 15.6; $p=0.001$).

In order to investigate the importance of fat depots in predicting cancer mortality, in the next step, multivariate analysis was repeated including all of the same variables presented in Table 3-3 and VATI and SATI rather than TATI. In multivariate analysis, including both VATI and SATI, only subcutaneous adiposity significantly associated with survival (Table 3-4). Compared to the high SATI group, low SATI was an independent predictor of increased

mortality in multivariate analysis (HR: 1.26; 95% CI: 1.11 to 1.43; p<0.001) (Table 3-4). Subsequently, we used a Kaplan-Meier model to estimate survival probability based on subcutaneous adiposity, revealing longer median survival in patients with high SATI (19.3 months; 95% CI, 17.6 to 21.0) compared to the patients with low SATI (13.1 months; 95% CI, 11.4 to 14.7) (Figure 3-1; p<0.001). The trend for high VATI patients to have a longer median survival time (19.7 months; 95% CI, 17.1 to 22.3) compared to those with a lower VATI (15.1 months; 95% CI, 13.6 to 16.5) was not significant (Table 3-4; p=0.08).

To investigate the prognostic significance of different depots, patients were categorized into one of 4 phenotypes according to categories of high and low VATI and SATI (Table 3-5). Having low SATI was associated with the shortest survival with the highest mortality risk. Patients with both high SATI and VATI had the best survival advantage with a median survival of 20.4 months (Table 3-5). Therefore, the diminished survival in patients with high visceral adiposity concurrent with low subcutaneous adiposity suggests high visceral adiposity may not be protective alone and indicates the importance of high subcutaneous adiposity.

Low subcutaneous adiposity was more prevalent in male patients with low BMI (Table 3-6). No significant difference was observed between low and high SATI patients regarding cancer stage and performance status. Mean SMI was significantly higher in those with greater subcutaneous adiposity (48.1 ± 10 cm^2/m^2) compared to the low SATI group (45.8 ± 8.6 cm^2/m^2, p<0.001) (Table 3-6). Despite having higher SMI, patients with high subcutaneous adiposity had significantly lower muscle radiodensity compared to the patients with low SATI (31.6 ± 9.2 vs 38.7 ± 8.4, p<0.001) (Table 3-6). Among patients with high subcutaneous adiposity, 62% exhibited low muscle radiodensity. The association between adiposity and muscle radiodensity was investigated and a moderate, but highly significant, inverse association was observed

between the muscle radiodensity, and visceral adipose adiposity ($r=-0.43$, $p<0.001$) and subcutaneous adiposity ($r= -0.44$, $p<0.001$; Figure 3-2).

We did not include weight loss in our model, as the data was not available for metastatic renal cell carcinoma patients. However, in subgroup analysis of 1176 respiratory tract and colorectal cancer patients for whom weight loss was available, we observed that adiposity remained as an independent predictor of mortality in the presence of weight loss (Table 3-7). Low adiposity independently associated with elevated mortality risk (HR: 1.18; 95% CI: 1.01 to 1.37; $p= 0.03$) in a multivariate model adjusted for age, cancer type, stage, performance status, skeletal muscle index, muscle radiodensity and weight loss.

Presence of sarcopenia decreased the median survival within each 4-adiposity phenotypes (Table 3-8). However, no significant difference in median survival was observed between sarcopenic and non-sarcopenic patients with concurrent high visceral and subcutaneous adiposity. The shortest median survival was observed in patients with a low VATI and SATI regardless of whether patients were sarcopenic or not. The effect of sarcopenia, however, was more pronounced in patients with low SATI. Therefore, in the presence of sarcopenia, the longest survival was observed in patients with high subcutaneous adiposity.

3.4 Discussion

In this retrospective, large cohort study investigating the prognostic significance of adiposity in cancer mortality, low adiposity was as an independent predictor of increased mortality risk and shorter survival after adjusting for known prognostic variables including age, cancer type, stage, performance status, skeletal muscle index and muscle radiodensity. To our knowledge, this is the largest study assessing the association between adipose depots and cancer mortality. In order to determine whether different adipose depots, visceral or subcutaneous,

associated with mortality risk in cancer patients, two different measures of adiposity, VATI and SATI were included in multivariate analysis. Our data demonstrates that cancer patients with lower subcutaneous adiposity are at greater risk of mortality and that patients with a high SATI experienced a significantly longer median survival time compared to those with a lower SATI. Moreover, having high VATI, without high subcutaneous adiposity increases mortality risk. This result is consistent with Antoun et al. who reported that a high amount of SAT independently and significantly associates with longer survival in 120 prostate cancer patients (Antoun et al., 2015). Controversy remains regarding the association between visceral adiposity and cancer survival as VAT is reported to be associated with poorer survival in patients with hepatocellular carcinoma (Fujiwara et al., 2015) or with better prognosis (Kaneko et al., 2015; Lee et al., 2015) in advanced renal cell carcinomas. Adiposity variables such as VAT/SAT ratio have been applied in previous studies (Fujiwara et al., 2015). We observed that in patients with high or low levels of both VATI and SATI, the ratio remains constant; therefore, VAT/SAT ratio is not a precise indicator of adiposity.

VAT and SAT distribution differs between males and females. These depots are also metabolically different as VAT produces more inflammatory cytokines such as IL-6, TNF-α and other adipokines (Fain et al., 2004; Harman-Boehm et al., 2007). Higher responsiveness of VAT to lipolytic factors as well as direct delivery of adipokines and free fatty acids to the liver, links VAT to a pro-inflammatory state that can affect liver metabolism and whole body homeostasis (Girard & Lafontan, 2008). SAT, on the other hand, is the main producer of leptin (Ebadi et al., 2016) that exerts some metabolic benefits on insulin sensitivity, glucose and lipid metabolism (Porter et al., 2009; Tran et al., 2008). These metabolic differences demonstrate the necessity to

evaluate cancer mortality based on visceral and subcutaneous adiposity rather than total adiposity.

Considering the limitations of using BMI as an indicator of adiposity, an adiposity index is the preferred method. However, controversy remains regarding prognostic significance of adipose tissue in cancer, as adiposity cut-points associated with survival in cancer are unknown. The majority of previously published studies used median or sex specific median to evaluate the adiposity association with survival. However, optimized sex-specific cut off values, less prone to bias, are required. Therefore, in the current study, sex-specific mortality-associated values were determined on the basis of quartiles in a fully adjusted model to overcome the limitations of dichotomizing continuous variables just by median, as reviewed by Mallett et al. (Mallett et al., 2010).

Potential explanations for the protective effects of high adiposity have not been clearly identified. Excess adipose tissue in obese cancer patients may provide fuel to bridge the gap between decreased energy intake and elevated requirements as hypothesized by Hughes (Hughes, 2013). Obese patients, if diagnosed at earlier stages, may receive better medical care [reviewed by (Prado et al., 2015)]. Signals produced by adipose tissue, such as leptin, associates with better prognosis and longer survival in colorectal cancer patients (Ogino et al., 2009). Lower mRNA expression of fatty acid synthase and acetyl-CoA carboxylase, enzymes involved in fatty acid production as an energy substrate, have been observed in the tumor of obese renal cell carcinoma patients (Hakimi et al., 2013).

There was a moderate but highly significant inverse association between muscle radiodensity and adiposity in this study. Fat accumulation in the muscle (low muscle radiodensity) might be related to the various factors such as elevated transportation and uptake of

fatty acid into muscle or increased availability of lipids (Miljkovic & Zmuda, 2010). On the other hand, enlarged fat mass associates with elevated release of fatty acids which might be considered as one of the potential sources contributing to the low muscle radiodensity (Boden, 2008). Although low adiposity and low muscle radiodensity were both independent predictors of mortality in this study, it may be appropriate to undertake further statistical analysis in order to assess the effect of various interactions between muscle radiodensity with adiposity on the survival of cancer patients.

In conclusion, lower adiposity independently associates with increased mortality risk after adjustment for major known predictors of mortality in cancer patients. Among adipose tissue depots, SAT appears to hold prognostic value over VAT. When a combination of adiposity and sarcopenia was considered, presence of sarcopenia associated with shorter survival in all adiposity cancer patients. However, effect of sarcopenia on survival was more pronounced in patients with low subcutaneous adiposity. Therefore, high adiposity in the absence of sarcopenia appears to be protective body composition phenotype, associates with survival advantage. Interventions to promote muscle anabolism and maintain adipose tissue should be considered in clinical settings to improve survival of cancer patients.

Tables

Table 3-1. Patient characteristics by sex at baseline

	Male (n=1047)	Female (n=715)	
Characteristics	**n (%)**	**n (%)**	**P**
Age, years			
Mean ± SD	64.4 ± 11.0	64.6 ± 11.3	0.8*
Cancer site			<0.001#
Colon/rectum	439 (42)	301 (42)	
Respiratory Tract	229 (22)	207 (29)	
Pancreas	69 (7)	75 (10)	
Esophageal	16 (1)	7 (1)	
Stomach	33 (3)	18 (3)	
Other GI	18 (2)	19 (3)	
Kidney	243 (23)	88 (12)	
Cancer stage			0.22#
I	35 (3)	35 (5)	
II	134 (13)	88 (12)	
III	224 (21)	169 (24)	
IV	654 (63)	423 (59)	
ECOG PS			0.72#
0	201 (19)	139 (19)	
1	468 (45)	313 (44)	
2	207 (20)	133 (19)	
3	158 (15)	115 (16)	
4	13(1)	14 (2)	
BMI, kg/m^2	26.3 ± 4.7	25.3 ± 5.9	<0.001*
BMI category, kg/m^2			<0.001#
<20.0	72 (7)	124 (18)	
20.0-24.9	356 (35)	263 (37)	
25.0-29.9	406 (39)	184 (26)	
≥30.0	195 (19)	134 (19)	
SMI, cm^2/m^2	51.4 ± 8.7	41.1 ± 7.0	<0.001*
Muscle radiodensity, HU	34.7 ± 9.0	34.0 ± 10.2	0.12*
TATI, cm^2/m^2	111.3 ± 59.1	112.6 ± 72.7	0.69*
VATI, cm^2/m^2	57.0 ± 36.4	34.6 ± 27.6	<0.001*
SATI, cm^2/m^2	54.3 ± 29.7	77.9 ± 50.3	<0.001*

Continuous variables are presented as mean ± SD. * Independent t-test for continuous and # Pearson $\chi 2$ test for categorical variables comparison. Abbreviations: BMI, Body mass index; ECOG PS, Eastern Cooperative Oncology Group performance status; HU, Hounsfield unit; SD, Standard deviation; SMI, Skeletal muscle index; TATI, Total adipose index; SATI, Subcutaneous adipose index; VATI, Visceral adipose index

Table 3-2. Sex specific adiposity values associated with the lowest mortality risk

Adiposity variable	Male	Female
TATI, cm^2/m^2	≥107.7	≥102.2
VATI, cm^2/m^2	≥52.9	≥51.5
SATI, cm^2/m^2	≥50	≥42

Values to predict mortality were determined by examining adiposity as a continuous variable on the basis of quartile using the first quartile as the reference group in fully adjusted models. Groups with similar risk of death were pooled together and values that provide satisfactory discrimination of mortality risk between patients were determined for each sex. Patients with adiposity indexes below these values are considered low adiposity (total, visceral and subcutaneous) associated with increased mortality risk. Abbreviations: TATI, Total adipose index; SATI, Subcutaneous adipose index; VATI, Visceral adipose index

Table 3-3. Median survival, and multivariate analysis by conventional and body composition parameters for overall mortality

				Univariate			Multivariate		
Characteristics	**No. of patients**	**No. of deaths**	**Median (95% CI)**	**Coefficient (SE)**	**HR (95% CI)**	**P**	**Coefficient (SE)**	**HR (95% CI)**	**P**
Sex									
Female	715	482	15.6 (13.7-17.5)						
Male	1047	725	17.2 (15.3-19.0)	0.06 (0.06)	1.10 (.95-1.20)	0.27			
Age, years				0.01 (0.003)	1.01(1.00-1.01)	<0.001	0.008 (0.003)	1.008 (1.002-1.01)	0.01
Cancer site									
Colon/rectum	740	358	30.7 (27.5-33.9)						
Respiratory Tract	436	383	9.4 (7.7-11.2)	1.04 (0.07)	2.83 (2.44-3.27)	<0.001	0.95 (0.08)	2.59 (2.23-3.01)	<0.001
Pancreas	144	126	5.4 (3.8-7.0)	1.37 (0.10)	3.94 (3.21-4.84)	<0.001	1.16 (0.11)	3.16 (2.58-3.93)	<0.001
Esophageal	23	16	17.5 (9.6-25.5)	0.66 (0.26)	1.93 (1.17-3.18)	<0.001	0.59 (0.26)	1.80 (1.09-2.98)	0.02
Stomach	51	41	11.3 (6.7-16.0)	0.90 (0.16)	2.46 (1.78-3.40)	<0.001	0.79 (0.17)	2.20 (1.59-3.05)	<0.001
Other GI	37	23	20.6 (3.4-37.8)	0.46 (0.21)	1.59 (1.04-2.42)	0.03	0.38 (0.22)	1.46 (0.96-2.23)	0.08
Kidney	331	260	17.7 (14.4-21.0)	0.43 (0.08)	1.54 (1.31-1.81)	<0.001	-0.18 (0.09)	0.83 (0.69-1.00)	0.05
Cancer stage									
I	70	21	37.2 (22.2-52.3)						
II	222	61	52.4 (42.2-62.6)	-0.27 (0.25)	0.76 (0.46-1.25)	0.29	0.03 (0.26)	1.03 (0.62-1.69)	0.92
III	393	209	29.0 (23.6-34.4)	0.26 (0.23)	1.3 (0.83-2.03)	0.25	0.35 (0.23)	1.42 (0.90-2.23)	0.13
IV	1077	916	10.3 (9.1-11.4)	1.06 (0.22)	2.9 (1.88-4.47)	<0.001	1.35 (0.22)	3.85 (2.48-5.97)	<0.001
ECOG PS									
0	340	196	28.4 (22.7-34.1)						
1	781	491	22.2 (19.6-24.6)	0.17 (0.08)	1.18 (1.0-1.40)	0.04	0.30 (0.09)	1.36 (1.14-1.61)	<0.001
2	340	257	11.1 (8.6-13.7)	0.64 (0.09)	1.90 (1.58-2.29)	<0.001	0.66 (0.10)	1.93 (1.59-2.34)	<0.001
3	273	241	4.4 (3.2-5.6)	1.34 (0.10)	3.82 (3.16-4.63)	<0.001	1.26 (0.10)	3.53 (2.9-4.30)	<0.001
4	28	22	2.4 (0-5.7)	1.24 (0.22)	3.46 (2.22-5.38)	<0.001	1.37 (0.24)	3.91 (2.46-6.23)	<0.001
TATI									
High	881	572	19.8 (17.6-22.0)						
Low	881	635	14.0 (12.4-15.6)	0.25 (0.06)	1.26 (1.11-1.41)	<0.001	0.23 (0.06)	1.26 (1.12-1.41)	<0.001
SMI									
Non-sarcopenic	998	652	19.6 (17.6-21.7)						
Sarcopenic	746	539	14.0 (12.4-15.6)	0.22 (0.06)	1.25 (1.12-1.40)	<0.001	0.01 (0.06)	1.01 (0.9-1.14)	0.86
Muscle radiodensity									
High	746	444	20.4 (17.5-23.3)						
Low	998	738	13.7 (12.1-15.3)	0.34 (0.06)	1.41 (1.25-1.59)	<0.001	0.28 (0.07)	1.33 (1.17-1.51)	<0.001

TATI ≥107.7 cm^2/m^2 in male and ≥102.2 cm^2/m^2 in females were defined as high TATI. Cut-off values for SMI and muscle radiodensity were derived from established cut-offs in gastrointestinal and respiratory cancer patients (Martin et al., 2013). Median survival estimated using Kaplan-Meier method. HRs and P values calculated using Cox proportional hazard model. Abbreviations: ECOG PS, Eastern Cooperative Oncology Group performance status; TATI, Total adipose tissue index; SMI, Skeletal muscle index; HR, Hazard ratio; CI, Confidence interval

Table 3-4. Median survival and mortality hazard ratios (95% CI) for visceral and subcutaneous adiposity

Body composition variables	No. of patients	No. of deaths	Median (95% CI)	Coefficient (SE)	HR (95%CI)	P
VATI						
High	703	462	19.7 (17.1-22.3)			
Low	1059	745	15.1 (13.6-16.5)	0.23 (0.06)	1.13 (0.99-1.28)	0.08
SATI						
High	1068	710	19.3 (17.6-21.0)			
Low	694	497	13.1 (11.4-14.7)	0.12 (0.07)	1.26 (1.11-1.43)	<0.001
SMI						
Non-sarcopenic	998	652	19.6 (17.6-21.7)			
Sarcopenic	746	539	14.0 (12.4-15.6)	0.01 (0.06)	1.01 (0.89-1.14)	0.88
Muscle radiodensity						
High	746	444	20.4 (17.5-23.3)			
Low	998	738	13.7 (12.1-15.3)	0.30 (0.07)	1.36 (1.19-1.54)	<0.001

Adjusted for Age, Cancer type, Stage, Performance status

VATI ≥52.9 cm^2/m^2 in male and ≥51.5 cm^2/m^2 in females were defined as high VATI. SATI ≥50 cm^2/m^2 in males and ≥42 cm^2/m^2 in females were defined as high SATI. Cut-off values for lumbar SMI and muscle radiodensity were derived from established cut-offs in gastrointestinal and respiratory cancer patients (Martin et al., 2013). Median survival estimated using Kaplan-Meier method. HRs and P values calculated using Cox proportional hazard model. Abbreviations: VATI, Visceral adipose index; SATI, Subcutaneous adipose index; SMI, Skeletal muscle index; HR, Hazard ratio; CI, Confidence interval

Table 3-5. Median survival and mortality hazard ratios (95% CI) according to 4-adiposity phenotypes in a fully adjusted model

4-adiposity phenotypes	No. of patients	No. of deaths	Median (95% CI)	Coefficient (SE)	HR (95% CI)	P
High VATI High SATI	564	377	20.4 (17.5-23.2)			
Low VATI Low SATI	555	412	12.6 (10.7-14.4)	0.35 (0.08)	1.42 (1.23-1.65)	<0.001
High VATI Low SATI	139	85	15.7 (12.1-19.2)	0.24 (0.12)	1.27 (1.00-1.62)	0.05
Low VATI High SATI	504	333	17.6 (15.6-19.6)	0.12 (0.08)	1.14 (0.97-1.32)	0.13

Adjusted for Age, Cancer type, Stage, Performance status, SMI and Muscle radiodensity
VATI ≥52.9 cm^2/m^2 in male and ≥51.5 cm^2/m^2 in females were defined as high VATI. SATI ≥50 cm^2/m^2 in males and ≥42 cm^2/m^2 in females were defined as high SATI. Median survival estimated using Kaplan-Meier method. HRs and P values calculated using Cox proportional hazard model. Abbreviations: VATI, Visceral adipose index; SATI, Subcutaneous adipose index; HR, Hazard ratio; CI, Confidence interval

Table 3-6. Characteristics of patients with high and low subcutaneous adiposity

	Low subcutaneous adiposity (n=694)	**High subcutaneous adiposity** (n=1068)	**P**
Sex, n (%)			<0.001#
Male	516 (74)	531 (50)	
Female	178 (26)	537 (50)	
Age, years	64 ± 12	64 ± 11	0.68*
Cancer site, n (%)			<0.001#
Colon/rectum	296 (43)	444 (42)	
Respiratory Tract	187 (27)	249 (23)	
Pancreas	70 (10)	74 (7)	
Esophageal	14 (2)	9 (1)	
Stomach	29 (4)	22 (2)	
Other GI	12 (2)	25 (2)	
Kidney	86 (12)	245 (23)	
Cancer stage, n (%)			0.40#
I	25 (4)	45 (4)	
II	81 (12)	141 (13)	
III	147 (21)	246 (23)	
IV	441 (63)	636 (60)	
ECOG PS, n (%)			0.70#
0	128 (18)	212 (20)	
1	302 (44)	479 (45)	
2	141 (20)	199 (19)	
3	110 (16)	164 (15)	
4	13 (2)	14 (1)	
BMI, Kg/m^2	22.3 ± 3.0	28.2 ± 4.9	<0.001*
TATI, cm^2/m^2	61.0 ± 37.8	144.8 ± 57.1	<0.001*
SATI, cm^2/m^2	30.4 ± 12.6	85.6 ± 38.4	<0.001*
VATI, cm^2/m^2	30.6 ± 29.0	59.1 ± 33.8	<0.001*
SMI, cm^2/m^2	45.8 ± 8.6	48.1 ± 10	<0.001*
Muscle radiodensity (HU)	38.7 ± 8.4	31.6 ± 9.2	<0.001*

Continuous variables are presented as mean ± SD. * Independent t-test for continuous and # Pearson $\chi 2$ test for categorical variables comparison. Abbreviations: ECOG PS, Eastern Cooperative Oncology Group performance status; BMI, Body mass index; TATI, Total adipose index; SATI, Subcutaneous adipose index; VATI, Visceral adipose index; SMI, Skeletal muscle index; HU, Hounsfield unit

Table 3-7. Median survival and mortality hazard ratios (95% CI) for body composition variables in 1176 colorectal and respiratory tract cancer patients

Body composition variables	No. of patients	No. of Deaths	Median (95% CI)	Coefficient (SE)	HR (95%CI)	P
TATI						
High	564	327	21.5 (18.1-24.9)			
Low	612	414	15.9 (14.1-17.7)	0.16 (0.08)	1.18 (1.01-1.37)	0.03
Weight loss,%						
< 8	716	436	20.2 (18.1-22.3)			
≥ 8	460	302	15.6 (12.5-18.8)	0.30 (0.08)	1.35 (1.16-1.58)	<0.001
SMI						
Non-sarcopenic	707	422	21.8 (19.1-24.6)			
Sarcopenic	469	319	15.5 (13.3-17.6)	0.09 (0.08)	1.09 (0.94-1.27)	0.26
Muscle radiodensity						
High	516	283	23.5 (19.7-27.3)			
Low	660	458	15.1 (13.1-14.1)	0.18 (0.08)	1.20 (1.02-1.41)	0.02

Adjusted for Age, Cancer type, Stage, Performance status

TATI ≥107.7.0 cm^2/m^2 in male and ≥102.2 cm^2/m^2 in females was defined as high adiposity. Cut-off values for lumbar skeletal muscle index, muscle radiodensity and weight loss were derived from established cut-offs in gastrointestinal and respiratory tract cancer patients (Martin et al., 2013). Median survival estimated using Kaplan-Meier method. HRs and P values calculated using Cox proportional hazard model. Abbreviations: TATI, Total adipose index; SMI, Skeletal muscle index, HR, Hazard ratio; CI, Confidence interval

Table 3-8. Effect of sarcopenia on median overall survival in high and low visceral and subcutaneous adiposity patients

4-adiposity phenotypes	SMI	No. of patients	No. of events	Median Survival, months (95% CI)
High VATI High SATI	non-sarcopenic	359	232	21.8[a] (17-26.7)
	Sarcopenic	200	140	18.5[ae] (13.7-23.4)
Low VATI Low SATI	non-sarcopenic	289	204	14.2[b] (11.3-17.1)
	Sarcopenic	260	202	10.7[c] (8.6-12.9)
High VATI Low SATI	non-sarcopenic	86	47	22.7[a] (16-29.4)
	Sarcopenic	51	36	12.8[cd] (5.7-20)
Low VATI High SATI	non-sarcopenic	264	169	20.1[a] (17-23.2)
	Sarcopenic	235	161	16.4[de] (13.8-19)

VATI ≥52.9 cm^2/m^2 in male and ≥51.5 cm^2/m^2 in females were defined as high VATI. SATI ≥50 cm^2/m^2 in males and ≥42 cm^2/m^2 in females were defined as high SATI. Sarcopenia was defined using Martin et al., established cut-offs in gastrointestinal and respiratory tract cancer patients (Martin et al., 2013) as values below 41cm^2/m^2 in females of all BMI categories and SMI values below 43 cm^2/m^2 in male with a BMI <25 and SMI <53 cm^2/m^2 in male with a BMI ≥25. Different superscripts indicate significant differences ($p<0.05$) determined by log-rank test. Median survival estimated using Kaplan-Meier method. Abbreviations: VATI, Visceral adipose index; SATI, Subcutaneous adipose index; SMI, Skeletal muscle index; CI, Confidence interval

Figures

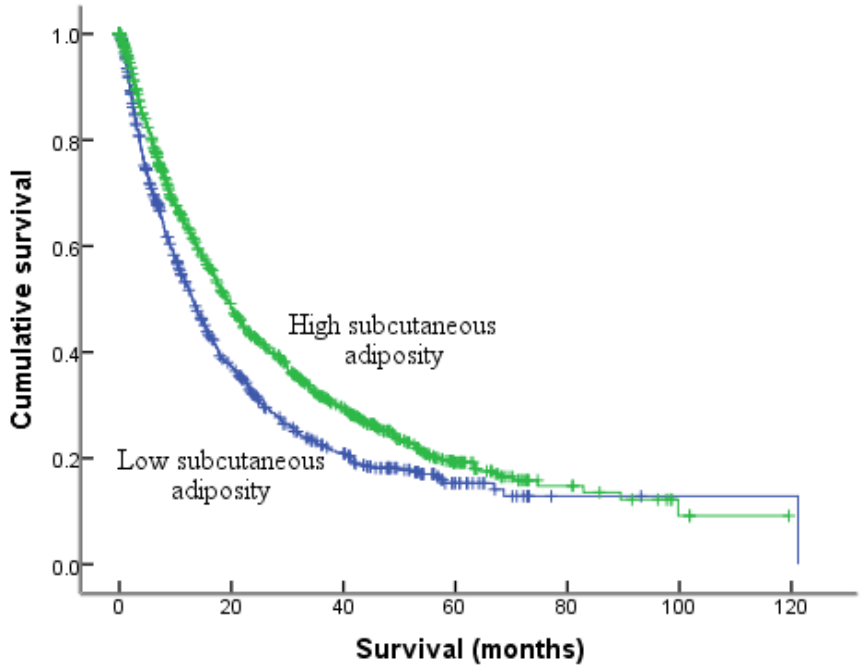


Figure 3-1. Kaplan-Meier survival curves in patients with high versus low subcutaneous adiposity.

Kaplan-Meier curves were plotted to estimate survival over time and the log-rank test were used to compare the difference between survival curves. Green line represents high and blue line is the low subcutaneous adiposity.

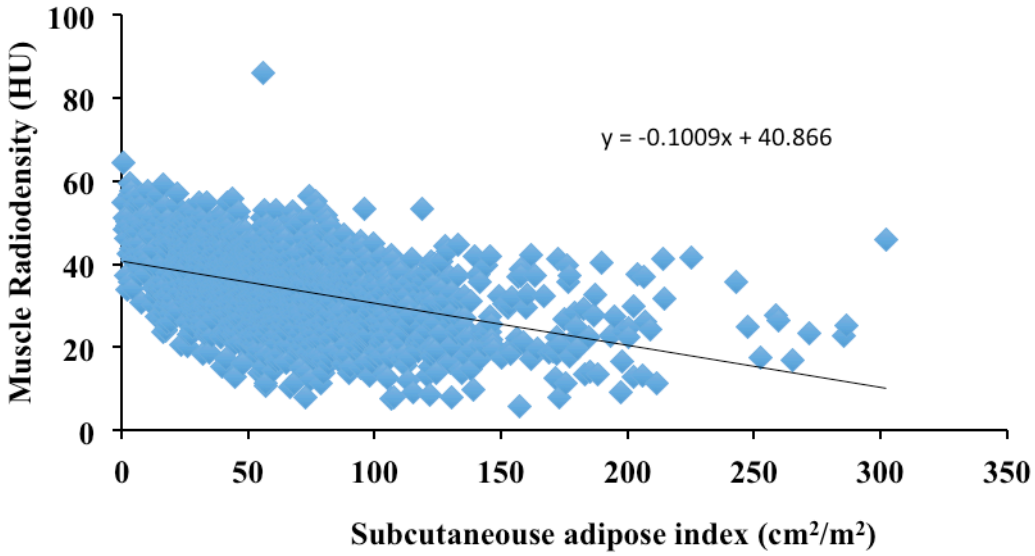


Figure 3-2. Relationship between subcutaneous adipose index and muscle radiodensity.

Pearson correlation test revealed highly significant ($r=-0.43$; $p<0.001$) inverse association between muscle radiodensity and subcutaneous adiposity.

Chapter 4. Loss of visceral adipose tissue precedes subcutaneous adipose tissue loss*

4.1 Introduction

Body composition assessment using CT images in patients with advanced cancer reveals accelerated loss of adipose tissue as cancer progresses (Lieffers et al., 2009; Prado et al., 2013). Approaching death, patients experience the most intense losses (Fouladiun et al., 2005; Lieffers et al., 2009; Murphy et al., 2010). Fat loss has been reported to be an important predictor of the length of survival (Fouladiun et al., 2005; Murphy et al., 2010), independent of patient's body weight.

Studies suggest divergent behaviours of different adipose tissue depots. Animal studies indicate that cancer can affect adipose tissue in a time and depot dependent manner (Batista et al., 2012; Bertevello & Seelaender, 2001). No significant changes were observed in adipocyte size 7 days after Walker 256 tumour injection, however, after 14 days, adipocyte size of retroperitoneal, and epididymal adipose tissue was decreased. Mesenteric adipose tissue was not lost and size of mesenteric adipocytes increased after 14 days (Batista et al., 2012). Studies performed in humans reveal that fat loss occurs in both VAT and SAT depots; however, the intensity of loss and the type of fat being lost (VAT vs. SAT) have not been consistently demonstrated and little is known regarding alterations throughout the cancer trajectory. VAT and SAT differ in anatomic location, endocrine function, lipolytic activity, response to insulin and cytokine production [reviewed previously (Ibrahim, 2010; Wajchenberg, 2000)]. Catecholamines have greater effects on lipolysis of VAT compared to SAT (Hellmer et al., 1992) and the location of VAT enables direct delivery of free fatty

* A version of this chapter has been published in the Clinical Nutrition. A copy of this paper is attached in Appendix C.

acids to liver. Therefore, increased lipolytic activity in VAT may lead to more free fatty acids reaching the liver which exacerbates an already dysregulated metabolic state in cancer (Hellmer et al., 1992). This divergent behaviour demonstrates the necessity to understand the depot specific pattern of loss using validated body composition assessment tools.

CT image analysis has emerged as the gold standard for body composition assessment in cancer patients (Fabbro et al., 2010). Retrospective analysis of serial CT images analysis in colorectal cancer patients (Lieffers et al., 2009) as well as quantitative analysis of CT images in a cohort of patients with advanced solid tumours (Prado et al., 2013) showed fat loss increases exponentially in the year preceding death with the greatest loss of adipose tissue occurring within 3 month prior to death (Prado et al., 2013). While there was a general trajectory involving loss of adipose tissue, tissue stability and even gain of adipose tissue can occur during some periods at >3 months prior to death (Prado et al., 2013). However, these previous studies have focused on TAT. A major gap remains regarding the specific behaviour of VAT and SAT in cancer patients which led us to explore the intensity and time course of changes in VAT and SAT cross sectional areas in a retrospective cohort of advanced cancer patients during the year preceding death. In this study, we hypothesized that that the intensity of VAT and SAT loss increase as death approaches. It was also hypothesized that VAT loss would precede SAT. Identifying types of fat being lost from adipose tissue may help to define the onset of wasting and to design interventions to circumvent wasting.

4.2 Materials and methods

4.2.1 Patient population

This study was approved by the Alberta Cancer Board Research Ethics Board (Edmonton, Alberta, Canada). Our site encompasses patients in northern Alberta, Canada. Data regarding cancer site, morphology, clinical and demographic characteristics for each of the subjects were collected from the Alberta Cancer Registry. The sampling of patients occurred between 2001 and 2004 for colorectal cancer and between 1997 and 2007 for cholangiocarcinoma. Loss of adipose tissue is noticeable approaching the end of life and to take advantages of repeated measures, we focused on colorectal and cholangiocarcinoma cancer patients with ≥4 CT images in the year preceding death. Colorectal and cholangiocarcinoma patients were not different in sex distribution, age at death, survival time, and tumour morphology and body composition features (ie, muscle and adipose tissues) at the same time to death (Prado et al., 2013).

Date of death rather than the date of diagnosis, was selected as the point of departure for this analysis to capture patients at a similar time in disease trajectory. Changes in VAT, SAT and TAT cross-sectional areas were calculated as the absolute change between two consecutive CT images (i.e., CT_2-CT_1). Date of CT_1 (CT closer to death) was subtracted from the date of death to define the time to death. Longitudinal quantitative analysis of CT images for changes in VAT, SAT and TAT cross sectional areas were evaluated for mean time points categorized into 9 (220-365d), 6 (140-219d), 3 (60-139d) and 1 (0-59d) month before death.

Using absolute values of changes in cross sectional areas in this cohort, TAT categories for loss, gain and stable changes were defined based on a previous report by Prado et al. (Prado et al., 2013). As 14.7 cm^2 total adipose cross sectional area at L3 is equal to 1 kg of whole body fat mass (Shen et al., 2004a), TAT changes were categorized as stable if the values were -14.7<

stable <14.7 cm^2 in the period of assessment. For VAT an SAT, changes between -3 and +3 cm^2 were considered stable as the minimum detectable change of CT measurements is 3 cm^2 (Mourtzakis et al., 2008).

4.2.2 CT image analysis

In an oncologic population, CT images are a routine part of treatment and are available from patient records as a chart review. All participants in this study had body composition measured using secondary analysis of images that were retrieved from the patient clinical record. Adipose tissue cross sectional area measurement was conducted by analyzing CT scans at L3. The third lumbar was selected as a standardized landmark, as adipose tissue areas in a single CT image at L3 correlate well with whole body fat mass (Mourtzakis et al., 2008; Shen et al., 2004a). Regression equations for VAT have not been developed for cancer populations; however, VAT cross sectional area at L3 strongly correlate with whole-body VAT volume in healthy populations (Shen et al., 2004b). Two consecutive transverse CT images extending from L3 to the iliac crest were assessed using Slice-O-Matic (V4.2; Tomovision, Montreal, QC, Canada). Adipose tissue cross-sectional areas were calculated by using standard Hounsfield unit thresholds of -150 to -50 for VAT (Miller et al., 1998) and -190 to -30 for SAT (Mitsiopoulos et al., 1998). Tissue cross-sectional areas (cm^2) were calculated by summing the given tissue pixels and multiplying by the pixel surface area. Mean tissue areas for 2 consecutive images were calculated; the mean CV of paired images was 2.7% for adipose tissue areas. VAT and SAT cross sectional areas were summed to estimate TAT areas. Regression Equations were used to estimate whole body fat mass (Shen et al., 2004a) as follows:

Whole body FM (kg) = [0.068 * (total adipose at L3 (cm^2))] + 4.142; r^2 = 0.927 (Shen et al., 2004a)

4.2.3 Statistical analysis

In this longitudinal study, demographic and whole body fat mass data are expressed as mean ± SD whereas longitudinal changes of VAT, SAT and TAT are reported as mean ± SEM. Generalized estimating equations (GEE) was used to analyze the longitudinal changes of VAT, SAT and TAT cross sectional area. A bonferroni test was used for post-hoc analysis of the data. In this study, GEE was preferred to repeated-measures ANOVA for analyze of longitudinal data due to the presence of missing CTs for some data points. GEE provides unbiased results where the number of measurements for each individual may differ. Categorical variables are reported as proportions and differences in proportions between gaining, losing and stable groups were compared using Chi-square test. Statistical analyses were performed using SPSS (SPSS for Windows, version 22.0, SPSS, Chicago, IL) and a difference was considered to be statistically significant if the p value was less than 0.05.

4.3 Results

All patients had stage IV colorectal cancer or cholangiocarcinoma with a mean age of 57 years and median 13 months to death (Table 4-1). There were no differences in demographics between patients within each diagnosis ($p>0.05$). Variation in TAT cross sectional area at L3 ranged from 5.1 cm^2 to 858.9 cm^2. Whole body fat mass on average was 27 ± 2 kg at nine months which decreased to 21 ± 2 kg by 1 month prior to death ($p=0.02$; Figure 4-1). On average, loss of TAT occurred at all time-points but the intensity of loss increased as patients approach death (Figure 4-2). Nine months from death, 42% of patients were losing fat (Mean TAT cross sectional area change = -0.2 ± 13cm^2) whereas within one month of death, fat wasting was observed in 78% of patients (-60.1 ± 9.2cm^2, $p=.001$) (Figure 4-2).

Although the overall adipose tissue was lost, mean change in cross sectional area of TAT hide the fact that some patients were gaining adipose tissue. Stratification of patients into adipose tissue stable, losing and gaining groups showed that some patients experienced tissue stability or gain at some time-points, primarily further from death. Nearly half the patients were gaining adipose tissue at 9 months (46%) whereas only 10% were gaining adipose tissue at 1 month (Table 4-2).

Assessment of TAT cross sectional area changes during cancer trajectory can mask what is occurring specifically in each depot. Data reveals divergent behaviour between VAT and SAT depots. No significant differences in TAT, VAT or SAT cross sectional area were observed between 3 and 6 months. Intensity of VAT loss was not significantly different at times close to death compared to 9 and 6 months (Figure 4-2). Loss of SAT was at its lowest intensity 9 months from death, with 62% of patients experiencing gains in SAT during this time period. Loss of SAT was more prevalent as death approaches (Figure 4-2). One month before death, mean VAT and SAT changes were respectively -24.5 ± 4.9 cm^2 and -34.5 ± 5.2 cm^2 (p=0.05). Nine months before death, mean change in cross sectional area of VAT was -7.9 ± 6.8 cm^2 whereas, mean change in cross sectional area of SAT was 7.4 ± 7.7 cm^2 (p=0.03; Figure 4-2), suggesting different behaviour of VAT and SAT further away from death in this group.

Variability in VAT and SAT behaviour is exemplified by two cancer patients of the same age, sex, and BMI who are losing approximately the same amount of TAT. Patient 1 was losing TAT at the intensity of -55.5 cm^2 nine months prior to death, patient 2 was losing TAT at -49.9 cm^2. However, patient 1 lost -80.4 cm^2 of VAT and gained 24.9 cm^2 of SAT whereas patient 2 lost -33.8 cm^2 of VAT and -16.1 cm^2 of SAT. Mean time to death was 11 months and 18 months,

respectively for patient 1 and patient 2. This example illustrates the variability expected among cancer populations for adipose tissue changes during the last year of life.

To further elucidate depot specific behaviours, patients were classified into groups according to whether they were experiencing loss or gain of VAT and SAT. As illustrated in Figure 4-3, nine months before death, 39% of patients were gaining both VAT and SAT while 25% were experiencing VAT loss concurrent with SAT gain. Within one month from death, however, the majority of patients (86%) were experiencing loss of both VAT and SAT. There was a clear downward trend in the percentage of patients who were gaining SAT, which decreased from 62% to 10% over the study period.

4.4 Discussion

Adipose tissue can be gained or lost in the year preceding death. As death approaches, the majority of patients lose fat with many experiencing what would be considered high intensity of loss. Gain or stability of adipose tissue was observed at 9 and 6 months prior to death. This might be considered as an appropriate timing to start early and proper interventions to preserve fat or prevent further fat depletion and consequently, to improve survival of cancer patients. We observed that changes in different fat depots did not necessarily coincide. Therefore, assessment of depot behaviour rather than TAT per se, may be a better indicator of alterations in adipose tissue, especially further away from death as changes in TAT masks what occurs specifically in each depot. Moreover, the underlying physiologic changes leading to alterations in each depot may vary, and this will require further interrogation.

Previous studies have reported greater fat loss from the intra-abdominal depot than abdominal subcutaneous regions in cancer patients (Agustsson et al., 2012; Haugen et al., 2011). Intra-abdominal and SAT mass were assessed before and after surgery using CT scans in

pancreatic cancer patients during early stages of disease progression. Fat loss from the intra-abdominal depot was greater than from the abdominal subcutaneous region following surgery (Haugen et al., 2011). However, this is the first study assessing changes in VAT and SAT cross sectional areas in a year preceding death using longitudinal CT images. Focusing on gain or loss of each depot specifically, intensity of VAT loss remains constant throughout the disease progression whereas SAT is more likely to be gained further way from death. Therefore, further away from death, behaviour of VAT and SAT are divergent whereas close to death, marked loss occurs from both depots. Identifying the time course of changes and the intensity of VAT and SAT change over the disease trajectory may help to define the onset of wasting.

Elevated catabolism due to the tumour presence, decreased food intake and tumour-host interactions are factors contributing to wasting in cancer (Tisdale, 2002). These factors can cause abnormalities in lipid metabolism which may also lead to fat loss. Increased lipolysis, decreased lipogenesis and adipogenesis, elevated oxidation of free fatty acids, and potentially white adipose thermogenesis contribute to altered lipid metabolism in advanced cancer patients and can lead to fat loss in cancer [Reviewed in (Ebadi & Mazurak, 2014)]. It was speculated by Prado et al. (Prado et al., 2013) that various factors such as response to cancer treatment, management and treatment of cancer-associated pain and symptoms may lead to adipose stability or gain.

Longitudinal CT imaging to describe changes in adipose tissue in advanced cancer patients is a major strength of this study. CT imaging, as a gold standard method, has the ability to precisely quantify adipose depots. Moreover, this is the first study assessing the timeline and intensity of changes in different adipose tissue depots during cancer progression. Therefore, we can conclude that VAT loss occurs at greater intensity and precedes SAT loss in the disease trajectory. We acknowledge that our results need to be confirmed in larger population of cancer

patients; however, the pattern of change in VAT and SAT areas during cancer progression was remarkable even with a small number of patients. These results verifies the need to initiate further research aiming to define the appropriate time to initiate proper interventions to preserve adipose tissue in cancer.

Tables

Table 4-1. Patient characteristics

Patients characteristics	Colorectal	Cholangiocarcinoma
Patients (n)	29	17
Male (%)	67	63
Median time to death at diagnosis (months)	11.5 (6, 24)	16.0 (6, 91)
*Age (y)	55.5 ± 11.2	58.0 ± 7.3
*[a] BMI (kg/m^2)	25.0 ± 6.5	25.9 ± 5.0

*Mean ± SD

[a] BMI information was available for 23 colorectal and 15 Cholangiocarcinoma patients

Table 4-2. Proportions of patients of losing, gaining or stable in total adipose tissue at 9, 6, 3 and 1 months prior to death

Group	Mean Time to Death (months)				
	9	**6**	**3**	**1**	**P-value***
TAT Loss (%)	42	50	55	78	0.048
TAT Gain (%)	46	22	12	10	0.016
TAT Stable (%)	12	28	33	12	0.040
P-value**	0.026	0.049	0.004	<0.001	

Changes between CTs were categorized as loss or gain if the values were $x \geq 14.7$ cm^2 and stable if the values were -14.6 $cm^2 > x < 14.6$ cm^2. *Chi square test was used to compare proportions of patients between 9 (n=42), 6 (n=40), 3(n=46) and 1 (n=34) month prior to death. ** Chi square test was used to compare proportions of losing, gaining and stable patients within each time point. Abbreviations: TAT, Total adipose tissue

Figures

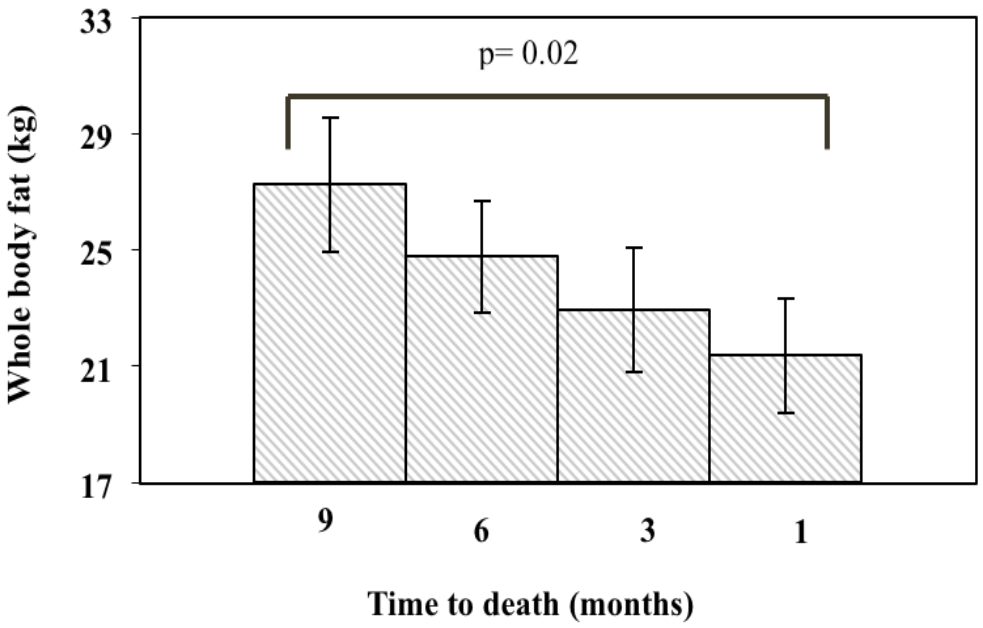


Figure 4-1. Estimated whole body fat mass (kg) at 9, 6, 3 and 1 months prior to death.

Significant reduction in whole body fat mass at 1 month before death compared to 9 month ($p<0.05$). Whole body fat mass (kg) was estimated using (Shen et al., 2004a).

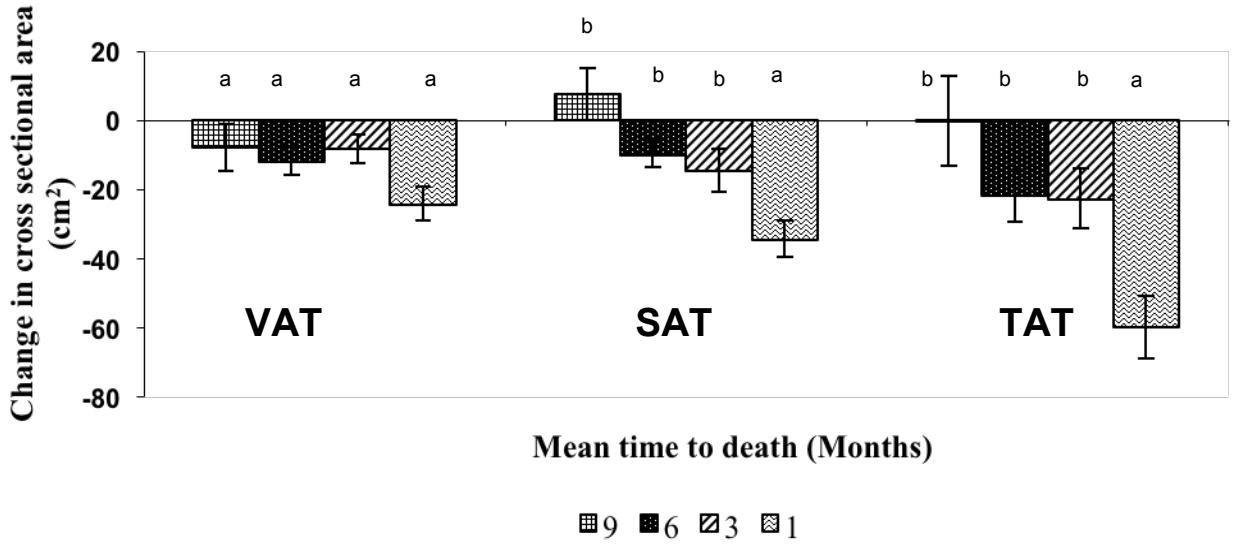
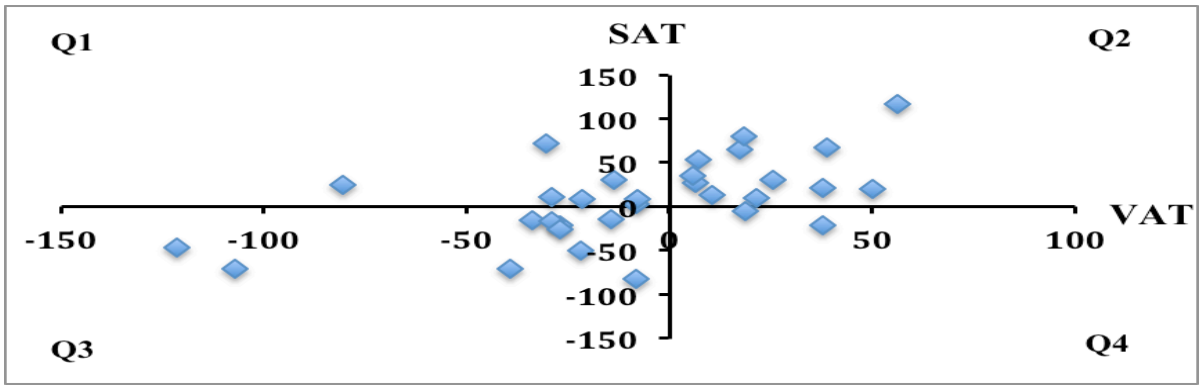


Figure 4-2. Pattern of change for each depot at 9 (n=42), 6 (n=40), 3(n=46) and 1 (n=34) months prior to death.

Data are presented as Mean ± SEM, Generalized Estimating Equations (GEE), different superscripts for each depot are significantly different ($p < 0.05$). Abbreviations: VAT, Visceral adipose tissue; SAT, Subcutaneous adipose tissue; TAT, Total adipose tissue

A: 9 months to death



B: 1 month to death

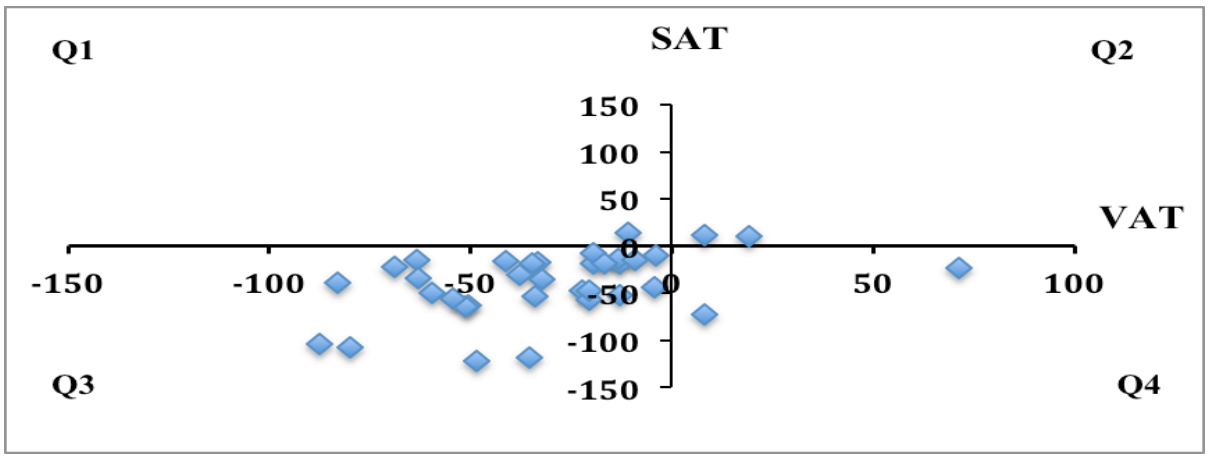


Figure 4-3. Scatter plot displays the distribution of VAT and SAT losing and gaining patients at 1 and 9 months prior to death.

In both graphs, the y-axis represents the changes in SAT cross sectional area and the X-axis represent the changes in VAT cross sectional area which were divided into quadrants (Q1, Q2, Q3, and Q4) to reveal the loss or gain of the depot as follows: Q1, VAT Loss, SAT gain; Q2, VAT gain, SAT gain; Q3, VAT Loss, SAT Loss; Q4, VAT gain, SAT Loss.
A: 9 months to death; Q1(25% of patients), Q2 (39% of patients), Q3 (29% of patients), Q4 (7% of patients). The Chi-square P-value when comparing the four quartiles was significant (0.02).
B: 1 month to death; Q1(3% of patients), Q2 (6% of patients), Q3 (86% of patients), Q4 (6% of patients). The Chi-square P-value when comparing the four quartiles was significant (0.002).
Abbreviations: VAT, visceral adipose tissue; SAT, subcutaneous adipose tissue

Chapter 5. Adipose tissue alterations in an animal model of colorectal cancer

5.1 Introduction

Human and animal studies have revealed adipose atrophy in a variety of cancer types [reviewed in (Ebadi & Mazurak, 2014)]. Accelerated loss of adipose tissue is associated with shorter survival, reduced quality of life, and impaired response to anti-cancer treatments (Murphy et al., 2010; Murphy et al., 2011a; Murphy et al., 2011b). On the other hand, studies have reported that adipose depletion may precede and occur more rapidly than muscle loss during cancer progression [reviewed in (Ebadi & Mazurak, 2014)]. However, identification of molecular mechanisms by which the tumour and cancer treatments, such as chemotherapy, affect adipose tissue are required to develop appropriate therapeutic interventions to prevent fat depletion.

A comprehensive review of literature on fat loss in cancer indicated that mechanisms such as elevated lipolysis, decreased lipogenesis, impairment in adipogenesis, elevated fat oxidation, and decreased lipid deposition contribute to adipose atrophy in cancer [reviewed in (Ebadi & Mazurak, 2014)]. Although elevated lipolysis has been the focus of the majority of previous studies (Agustsson et al., 2007; D. X. Cao et al., 2010; Dahlman et al., 2010; Jeevanandam et al., 1986; Klein & Wolfe, 1990; Zuijdgeest-van Leeuwen et al., 2000), adipose atrophy can also occurs when lipogenesis is limited in white adipose tissue. Diminished lipid synthesis capacity of adipose tissue, evidenced by decreased mRNA levels of key enzymes such as ACC, FAS, SCD-1, LPL, DGAT-2 as well as lower expression of PPARγ, a key regulator of adipose tissue lipid metabolism, has been observed in previous studies (Bing et al., 2006; Ishiko et al., 1999; Lanza-Jacoby et al., 1984; Lopez-Soriano et al., 1996; Tsoli et al., 2014). While

little is known about the effect of tumour on adipose tissue, much less is known about chemotherapy-induced adipose tissue alterations.

It has been observed that n-3 PUFAs; EPA (C20:5n-3) and DHA (C22:6n-3) have the potential to attenuate cancer-associated wasting. Supplementation with EPA and DHA in the form of fish oil in advanced cancer patients has been shown to stabilize the weight of patients, improve chemotherapy efficacy and prevent muscle loss (Murphy et al., 2011a; Murphy et al., 2011b). A limited number of studies investigating the effect of long chain n-3 PUFAs on adipose tissue in animal models of cancer have shown fish oil to be effective in preventing adipose atrophy and attenuating weight loss (Du et al., 2015; Price & Tisdale, 1998; Russell & Tisdale, 2005). However, a major gap remains regarding the effect of fish oil supplementation on adipose tissue composition and function in the neo-plastic state and within the scope of treatment.

The animal model used in this study was developed to represent the same doses, cycles and levels of toxicity observed clinically in human colorectal cancer patients. This study aimed to assess the effect of a tumour and chemotherapy on periuterine adipose tissue fatty acid composition, morphology and expression of genes involved in lipogenesis in rats undergoing one or two cycles of chemotherapy. In order to gain global knowledge of adipose tissue alterations in neoplastic state, as well as to understand the effect of anti-neoplastic treatment on adipose tissue, proteomic analysis was performed. In this study, our focus is on proteins that are altered in response to chemotherapy following 2-cycles of chemotherapy, a clinically relevant time point. We hypothesized that chemotherapy would decrease adipocyte size and expression of proteins involved in lipid synthetic pathways in adipose tissue. Secondly, the effect of dietary fish oil on chemotherapy-induced alterations in adipose tissue was investigated. It was hypothesized that dietary fish oil intervention, concurrent with chemotherapy treatment, would reverse tumour and

chemotherapy induced depleted adipose tissue n-3 PUFAs and improve pathways of lipid synthetic. The results of this work will provide a basis to plan interventions aimed at improving adipose tissue composition and function that are altered by tumour and chemotherapy which could be effectively translated to clinical practice.

5.2 Material and methods

5.2.1 Animal model

All animal experiments were approved by the Institutional Animal Care Committee and performed in accordance with the Canadian Council on Animal Care Guidelines for the Care and Use of Laboratory Animals. Female Fisher 344 rats (Charles River Laboratories, St. Constant, Quebec, Canada) were received at 150-180g, 11 to 12 weeks of age and were held two per cage. All cages were kept in a room with controlled temperature (21–22°C), a reverse light–dark cycle (12/12h) and with food and water available ad libitum.

5.2.2 Experimental design

The experimental design is outlined in Figure 5-1. Rats serving as reference group (REF; n=8) did not undergo tumour injection or chemotherapy treatment but were handled similar to the experimental groups. Tumour-bearing rats (TUM; n=8) were injected with tumour, received no chemotherapy and were on control diet. The Ward colorectal carcinoma, provided by Dr. Y. Rustum (Department of Cancer Biology, Chair, Director of Institute Core Resources, Roswell Park Cancer Institute, Buffalo, NY (S. Cao & Rustum, 2000), was implanted subcutaneously in the left flank of the rats under light anaesthesia. The size of the tumour was measured using callipers and calculated by multiplying the length, width, and height. Tumour volume (cm^3) was

estimated by multiplying the length × width × height × 0.5 (Girit et al., 2008) and subsequently was converted to mass assuming a tumour density of 1.0 g/cm^3 (Jensen et al., 2008).

Two weeks following implantation of the tumour, when the implants grew to approximately 2.3 cm^3 (or 1.2% of body weight), rats received irinotecan (CPT-11 + 5-FU) combination regimens, a first-line chemotherapy of patients with advanced colorectal cancer, for 1 or 2 cycles. The first cycle of chemotherapy (cycle 1) consisted of CPT-11 (50mg/Kg BW/d s.c.) administered on day 0 and 5-FU (50mg/Kg BW/d s.c) administered on day 1. The second chemotherapy cycle (cycle 2) consisted of the same drug regime occurring one week after cycle 1 (day 7 and 8). Subcutaneous injection of atropine (1mg/kg) was given prior to each CPT-11. On day 0 (reference, tumour), day 7 (1-cycle chemotherapy) and day 14 (2-cycles chemotherapy), animals were anesthetized with carbon dioxide followed by decapitation. Rats that underwent 1 or 2 cycles of chemotherapy on control diet were assigned as (CO1; n=8) and (CO2; n=8), respectively. Fish oil fed rats receiving 1 and 2 cycles of chemotherapy were designated as (FO1; n=8) and (FO2; n=8) groups. The periuterine adipose tissue was excised, weighed and immediately snap frozen in liquid nitrogen and stored at -80°C for subsequent measurements or fixed in formalin.

5.2.3 Diet

Animals consumed control diet during the two-week period of tumour growth, until chemotherapy initiation at which time they were randomized to remain on control diet or began a diet containing EPA and DHA in the form of fish oil (2% w/w). Composition of experimental diets (control and fish oil diets) is presented in Table 5-1. Diets were a modified American Institute of Nutrition-76 (AIN-76), casein-based diet with fat-source omitted (Harlan Tekland, Madison, WI, USA). The control and fish oil diet were formulated to be isonitrogenous and

isocaloric and are representative of some North American diets supplying 40% of energy as fat, 40% as carbohydrates and 20% as protein (Table 5-1). The polyunsaturated to saturated fat (P/S) ratio in both diets was 0.35. The added fish oil (2.3g fish oil/100g diet; Table 5-1) contained 51% EPA and 21% DHA of total fatty acids (Ocean Nutrition Canada). The fish oil diet was prepared weekly and stored at -20°C under vacuum, with α–tocopherol as an antioxidant.

5.2.4 Body weight and food intake

Body weight and food intake were measured every other day prior to chemotherapy initiation. After treatment initiation, animals were followed daily by measuring body weight and food intake. Body weight at baseline (day 0) was set to 100 and subsequent changes during chemotherapy were expressed as relative body weight (%). Food intake was reported as gfood /100g body weight/day. Relative food intake during chemotherapy was reported as a percentage change from baseline (the mean food intake prior to chemotherapy).

5.2.5 Adipose tissue morphometry

Haematoxylin and Eosin (H & E) histological stain was used to provide information with regards to alterations in tissue morphology such as the formation of crown-like structures (adipocyte surrounded by macrophages), or changes in adipocyte cell size (Berry et al., 2014). In this study, periuterine adipose tissue samples were fixed in 10% formalin for 24h, dehydrated in absolute ethanol, cleared in xylene then embedded in paraffin and cut into 5µm sections. Sections were stained with Harris haematoxylin, counterstained with eosin, viewed at 20X magnification, and images were obtained with light microscopy (Olympus Qlmaging micropublisher camera). Adipocyte size was determined by measuring cross-sectional areas of 300 cells in 5 random fields from 5 rats/group using Image J software (National Institutes of

Heath, alth, http://rsbweb.nih.gov/ij). A hemacytometer was used as a calibrator for measuring the size of adipocytes.

5.2.6 Real-time-PCR

Total RNA was isolated from 50mg ground tissue powder using an RNeasy Lipid Tissue Mini Kit (Qiagen) according to the manufacturer's instructions and stored at −80°C. RNA concentration was quantified spectrophotometrically (NanoDrop 1000; NanoDrop Technologies, Boston, MA), and the quality was assessed using the Agilent Bioanalyzer 2100 (Agilent Technologies, Palo Alto, CA, USA). Real-time (RT)-PCR was performed using Applied Biosystems (Foster City, CA, USA) reagents and instruments. All first-strand cDNA samples were synthesized from 750ng total RNA per 20µL reaction using the High Capacity cDNA reverse transcription kit (Applied Biosystems) on a GeneAmp PCR 9700 thermal cycler and then diluted 1:10 with nuclease-free water. PCR was performed with 10µL TaqMan® Fast Advanced Master Mix (Life Technologies, Carlsbad, CA), 1µL of a TaqMan® probe and primer set, 7µL of NFH2O and 2µL diluted cDNA in a 20µl final reaction mixture. Pre-designed TaqMan® probes and primer sets (Life Technologies, Carlsbad, CA) with a 6-carboxyfluorescein phosphoramidite (FAM™) label on the 5' end were used which contained the following assays: fatty acid synthase (Rn00569117_m1), acetyl-CoA carboxylase alpha (Rn00573474_m1), stearoyl-Coenzyme A desaturase 1 (Rn00594894_g1), peroxisome proliferator-activated receptor gamma (Rn00440945_m1), peroxisome proliferator-activated receptor gamma, coactivator 1 alpha (Rn00580241_m1), sterol regulatory element binding transcription factor 1 (SREBP-1c) (Rn01495769_m1), ribosomal protein large P0 (Rn03302271gH), diacylglycerol acyltransferase 2 (Rn01506787m1), lipoprotein lipase (Rn00561482_m1), cell death-inducing DFFA-like effector a (Rn04181355_m1).

qRT-PCR reactions were amplified on an Applied Biosystems 7900HT Fast Real-Time PCR System using SDS 2.3 software for 10 min at 95°C, followed by 95°C for 15 sec and 1 min at 60°C for 40 cycles. Reactions were done in duplicate and the obtained threshold cycle (CT) values were plotted against the log template amount of the cDNA. The cycle number at which the reaction crossed an arbitrarily-placed threshold was determined for each gene and the relative target mRNA expression was described using the equation $2^{-\Delta\Delta CT}$ where $\Delta CT = (CT_{target} - CT_{RPLP0})$, thereby normalizing the data to the endogenous control mRNA of RPLP0 (Livak & Schmittgen, 2001).

5.2.7 Proteomics

Proteomics analysis was conducted on 3 animals from reference (control fed), tumour (control fed) and 2-cycles chemotherapy (both control and fish oil fed) groups. Frozen periuterine adipose tissue was ground in liquid nitrogen, mixed with 10XRIPA (Pierce Biotechnology, Rockford, IL, USA) lysis buffer containing 0.22% Beta glycerophosphate, 10% Tergitol-NP40, 0.18% Sodium orthovanadate, 5% Sodium deoxycholate, 0.38% EGTA, 1% SDS, 6.1% Tris, 0.29% EDTA, 8.8% Sodium chloride, 1.12% Sodium pyrophosphate decahydrate (), supplemented with protease and phosphatase inhibitors (Invitrogen Corporation, Frederick, MD, USA) in a 1:3 ratio for homogenization. The homogenate was then centrifuged at 12000g for 20 min at 4°C and the supernatant fraction was transferred into new tubes (repeat this step until the supernatant was clear), stored at -80°C prior to analysis. Protein concentration was quantified using Pierce bicinchoninic acid (BCA) Protein Assay (Thermo Scientific, Rockford, IL, USA). Bovine serum albumin was used as a standard and the absorbance was read by spectrophotometry at 562nm. Tissue homogenate was standardized for protein content based on the sample with the lowest protein content and 95 micrograms of total protein, in duplicates

(repeated loading of the same sample), were loaded on 4–20% Mini-PROTEAN® TGX™ Precast Protein Gels (Bio-Rad, Hercules, CA). Gels were run at 200V constant until the dye was seen at the bottom of the gel. Each gel lane was cut, digested and analyzed using liquid chromatography-mass spectrometry (LC-MS/MS) at the Alberta Proteomics and Mass Spectrometry Facility (APM). Briefly, excised gel bands were de-stained twice in ammonium bicarbonate/acetonitrile (ACN) (50:50), reduced (10mM β–mercaptoethanol 100mM AmBic), alkalated and digested with trypsin. Following trypsin digestion (6ng/µl, 16h, RT), peptides were extracted from the gel firstly using 97% water/2% ACN containing 1% formic acid and secondly with a 1:1 mixture of extraction buffer and acetonitrile.

Nanoflow HPLC (Easy-nLC II, Thermo Scientific) coupled to the LTQ XL-Orbitrap hybrid mass spectrometer (Thermo Scientific) was used to ionized the tryptic peptides resolved in 25% ACN and 1% v/v formic acid. Peptide mixtures injection flow rate was 3000 nL/min, with the resolved rate kept at 500nL/min using 60 min linear acetonitrile gradients from 0% to 45% v/v aqueous acetonitrile in 0.2% v/v formic acid. Data were obtained in a data-dependent manner in the Orbitrap spectra with a resolution of 60000 and the collision induced dissociation was used to fragment ten most intense multiply charged ions, recorded in the linear ion trap. Data were analyzed by Proteome Discoverer 1.3 (Thermo Scientific) and searched using SEQUEST (Thermo Scientific) against the Rattus norvegicus protein database. A precursor mass tolerance of 10ppm and a fragment mass tolerance of 0.8Da were considered in search parameters.

5.2.8 Ingenuity pathway analysis (IPA)

IPA is a web-based analysis tool that enables identification of canonical pathways, biological process, molecular and cellular functions, molecular networks, upstream regulators in a set of molecules of interest. Differentially expressed proteins (>1.5 fold change with a p-value

<0.05) were uploaded into IPA software (Ingenuity Systems; Mountain View, CA, USA) and the significant canonical pathways, molecular and cellular functions, and upstream regulators were generated based on the known data in the literature. The significance was calculated using Fisher Exact test with the p-value <0.05.

5.2.9 Adipose tissue fatty acid analysis

Frozen adipose tissue was homogenized in a 1.6 ml calcium chloride [CaCl2; 0.025%] solution with glass beads [0.5 mm diameter; FastPrep ®-24, MP Biomedicals, Santa Ana, CA, USA] in 20 sec intervals for 1 min. Lipids were extracted using modification of the Folch procedure (Neoptolemos et al., 1988), by adding chloroform/methanol (2:1,vol/vol) to each tube. Layers were separated after an overnight store at 4°C. The bottom layer containing lipids was transferred into a second clean tube and the original tube was washed with chloroform/methanol/water (C/Me/H2O; 86:14:1, v/v), and vortexed. After layers separation, the bottom layer was added to the second tube, and dried down under nitrogen gas.

Thin layer chromatography chromatography (TLC) plates (G plated, Silica Gel, 20 x 20 cm, 250 microns, Analtech Inc., Newark, DE) was used to isolate triglyceride and phospholipids. Briefly, plates were prepared in chloroform wash in G tank and then dried in oven 110℃ for one hour. Solvent (80:20:1 petroleum ether/ diethyl/ethyl ether/acetic acid [glacial; HAC]) was added to the developmental chamber lined with Whatman filter paper and allowed to equilibrate for one hour. Chloroform/methanol (2:1) was added to each dried tube, vortexed and samples were spotted on plates in duplicate. Spotted plates were run in a solvent system until the solvent mixture reached ~1.5 cm from the top of the plate. Dried plates were sprayed with 0.1% 8-anilino-1- naphthalenesulfonic acid (ANSA) to visualize the PL and TG bands under ultraviolet light. Bands were scraped and added to clean methylation tubes.

Thin layer chromatography was followed by saponification and methylation for TG and direct methylation for PL containing tubes. To saponify TGs, 1ml of KOH in methanol (0.5N) was added to TG tubes and left in heating block for 1 hour at 110℃. Both PL and TG tubes were methylated using 1 ml boron triflouride (14%; in methanol) and 2 ml hexane. Tubes were heated in heating block for 1 hour. Once tubes cooled at room temperature, 1 mL of double distilled water (ddH_2O) was added. Tubes were vortexed and refrigerated at 4°C overnight to allow for separation. The top layers were transferred to gas liquid chromatography (GLC) glass vial and dried under nitrogen. After adding 200 µL hexane to each dried vials, entire volume was pipetted into glass inserts, placed into GLC vials, capped well and stored at -20℃ until analysis with gas liquid chromatography.

Fatty acid methyl esters were separated by an automated gas-liquid chromatograph (Vista 8400 autosampler, Varian CP-3400). The system used a bonded phase fused silica capillary column, BP20:25mm X 0.25 OD SGE product. Helium was used as the carrier gas at a flow rate of 2.6 ml/minute using a splitless injector. These conditions separate saturated, monounsaturated and polyunsaturated fatty acids from 12 to 24 carbon chain lengths by comparison with known standards. Proportions of saturated (SFA), monounsaturated (MUFA), PUFA, n-6 and n-3 fatty acids were calculated.

5.2.10 Statistical analysis

Data were reported as mean ± SEM and parametric or non-parametric statistic tests were chosen according to data distribution. One-way ANOVA with Bonferroni post-hoc comparisons was used to compare between groups when data was normally distributed. Non-normally distributed data were analyzed by Kruskal-Wallis non-parametric test followed by Dunn's Multiple comparison test. A two-way repeated measure ANOVA for time and type of diet

(repeated measure on food intake and body weight following chemotherapy initiation) was performed. Statistical analyses were performed using SPSS (SPSS for Windows, version 22.0, SPSS, Chicago, IL) and a difference was considered to be statistically significant if the p value was less than 0.05.

5.3 Results

5.3.1 Food intake

Food intake was markedly reduced for the first 3 days following chemotherapy treatment. Following the first day of each cycle of chemotherapy, food intake decreased in all groups, recovering to baseline by the end of the cycle (Figure 5-2). Relative food intake (%); was significantly different between control and fish oil fed groups on days 4, 6, 7, 10 and 12 ($P<0.05$). During the first cycle of chemotherapy, mean food intake in fish oil group was 4.4 ± 0.2 g/100gBW (equivalent to 84.3mg EPA + DHA/day), and in the second cycle was 3.5 ± 0.3 g/100gBW (equivalent to 64.5mg EPA + DHA/day).

5.3.2 Body weight and tumour volume

Tumour-free body weight was reduced during chemotherapy cycles (Figure 5-3). Following the first day of the first cycle of chemotherapy, both fish oil and control fed groups exhibited a significant decrease in body weight from baseline (Figure 5-3), followed by restoration of body weight by the end of cycle-1. The same pattern of weight loss was observed during the second cycle but with a greater decrease in body weight during the first 3 days post chemotherapy initiation. Percent change of body weight from baseline at day 1 (the second day of the first cycle) was -2.6% ± 0.4 and -2.1% ± 0.4 in control fed and fish oil fed rats, respectively and after the second cycle (day 8) was -4.0% ± 1.2 in control and to -4.2% ± 0.8 in

fish oil fed rats. There were no significant differences in relative body weight change in fish oil fed animals compared to control fed animals during both 1- and 2-cycles of chemotherapy (Figure 5-3). There were no significant differences in relative tumour volumes in fish oil fed animals compared to control fed animals during both 1- and 2-cycles of chemotherapy. However, the ratio of relative tumur volume to the relative body weight was significantly higher in control fed animas compared to the fish oil fed animals during the first ($p=0.02$) but not the second cycle of chemotherapy (Giles, 2014).

5.3.3 Adipose tissue weight

Periuterine adipose tissue weight, as a percentage of tumour free body weight, was significantly higher in the tumour ($p=0.001$) group compared to the reference group. No change in adipose tissue weight was observed after 1 cycle of chemotherapy. However, following 2 cycles of chemotherapy, in control and fish oil groups, adipose tissue weight was less than the tumour group ($p= 0.005$ and $p=0.010$, respectively; Figure 5-4A).

5.3.4 Histological characteristics

We examined whether the reduction in pre-uterine adipose mass following chemotherapy was detectable at the microscopic level. Examples of adipocytes stained with hematoxylin and eosin (H&E) from reference, tumour, and chemotherapy groups (both control and fish oil diets) are presented in Figure 5-4C. Adipocytes were surrounded with a thin rim of cytoplasm in which nuclei are compressed into the peripheral rim. Larger adipocytes, determined by cell cross sectional area, were observed in tumour group compared to the other groups (Figure 5-4B). Tumour-bearing animals ($3993.7 \pm 52.6 \mu m^2$) had larger adipocytes than the reference group ($3227.7 \pm 36.7 \mu m^2$; $p < 0.001$). Chemotherapy decreased the size of adipocytes after the first

cycle with greater reduction during the second cycle of chemotherapy. In rats undergoing 2-cycles of chemotherapy, adipocytes were smaller in fish oil fed animals (2243.9 ± 30.4μm^2) compared to the control fed animals (2772.3 ± 33.0μm^2; $p<0.001$) (Figure 5-4B).

5.3.5 mRNA expression of genes involved in lipid metabolism in adipose tissue

mRNA expression of several key genes involved in lipogenesis as well as major transcriptional factors expressed in adipose tissue including PPARγ, SREBP-1c and PGC-1α were assessed. The tumour alone had no significant effect on the expression of transcriptional factors nor the genes regulating lipogenic proteins. However, mRNA expression of CIDEA, a lipid droplet-associated protein, was 2-fold higher in tumour-bearing animals compared to the reference animals.

After the first cycle of chemotherapy, control fed animals had reduced expression of all genes assessed, with the exception of LPL which was significantly decreased only after cycle 2. Expression of all genes remained significantly low after the second cycle (Figure 5-5). Fish oil fed animals had significantly lower expression of all the genes following 1 cycle of chemotherapy, with the exception of PGC-1α which was similar to the tumour-bearing animals (Figure 5-5). After 2 cycles of chemotherapy, fish oil fed animals, exhibited decreased mRNA expression of SREBP-1c, PPARγ, FAS, ACC, DGAT-2 and SCD-1. However, 2 weeks of fish oil feeding during chemotherapy restored the chemotherapy induced reduction in the expression of LPL, PGC-1α and CIDEA, to the levels of tumour-bearing animals. No significant differences were observed between control fed and fish oil fed animals undergoing chemotherapy, with the exception of CIDEA which was significantly higher after 2 cycles of chemotherapy in fish oil fed animals compared to control fed animals.

5.3.6 Proteomics results

We first evaluated the influence of the tumour on global protein expression in adipose tissue (Appendix 4). In general, proteins involved in fatty acid β-oxidation such as hydroxysteroid (17-beta) dehydrogenase 10 (HSD17B10), enoyl-CoA hydratase, short chain, 1, mitochondrial (ECHS1), enoyl-CoA delta isomerase 1 (ECI1) were down- regulated in tumour-bearing animals (p-value< 0.001). Proteins involve in mitochondrial anti-oxidant systems such as glutathione peroxidase 1 (GPX1), glutathione peroxidase 3 (GPX3), peroxiredoxin 2 (PRDX2) were also down regulated. Expression of protein kinase cAMP-activated catalytic subunit alpha (PRKACA), involved in phosphorylation and activation of various proteins such as HSL, was decreased by 6 fold. Expression of two transporters, ATP binding cassette subfamily D member 2 (ABCD2), involved in transport of very long chain acyl-CoA into peroxisomes and sterol carrier protein 2 (SCP-2), responsible for fatty acid and phospholipid transport and involved in oxidation of very long chain fatty acids in peroxisomes were up regulated (6 and 2 fold) compared to the reference animals (Table 5-2).

Next, we evaluated the impact of chemotherapy on adipose tissue protein expression (Appendix D). Similar to what was observed for gene expression, major changes in protein expression occurred after chemotherapy in both control and fish oil fed animals. A total of 124 and 122 proteins were differentially expressed in control fed and fish oil fed animals after 2 cycles of chemotherapy compared to the tumour, respectively. Of these proteins, 112 in control fed and 102 in fish oil fed were down-regulated whereas 12 and 20 proteins in control fed and in fish oil fed were up-regulated, respectively. Mapping each protein accession number to IPA identified 57 canonical pathways ($p<0.05$). The top canonical pathways identified in both groups are presented in Table 5-3. Overall, chemotherapy induced alterations in protein expression in

mitochondria-linked pathways involved in glucose and lipid metabolism. Mitochondrial dysfunction was manifested by reduction in proteins involved in ATP production as well as increased oxidative stress. Reduced ATP production may result from inhibition of protein complexes involved in oxidative phosphorylation such as ATP synthase subunits, succinate dehydrogenase (SDH), NADH dehydrogenase (ubiquinone) subunits (NDUFs), Coenzyme Q – cytochrome c reductase subunits (UQCRC1, UQCRC2, UQCRFS1) and pyruvate dehydrogenase (PDH). Low levels of pyruvate dehydrogenase complex (PDHC) evidenced by down regulation of pyruvate dehydrogenase alpha 1 (PDHA1), dihydrolipoamide S-acetyltransferase (DLAT), pyruvate dehydrogenase beta (PDHB) would be expected to reduce acetyl-CoA biosynthesis. Moreover, there was a reduction in expression of proteins involved in mitochondrial antioxidant systems such as cytochrome c oxidase subunit Va (COX5A), cytochrome c oxidase subunit 4I1 (COX4I1), cytochrome c oxidase subunit VIc (Cox6c) and cytochrome c oxidase subunit II (MT-CO2), and reactive oxygen species scavenging enzymes such as peroxiredoxin (PRDX), glutathione S-transferase (GSTM5, GSTZ1) and catalase (CAT) (Table 5-3).

Proteins involved in pathways related to fatty acid metabolism including fatty acid biosynthesis (ACYL, FAS, ACC) and fatty acid β-oxidation were down regulated. LXR target proteins, ACC and FAS were down regulated by 7 and 8 fold respectively after 2 cycles of chemotherapy in control fed chemotherapy group compared to the tumour group. There was a 8 and 6 fold reduction in protein expression of ACC and FAS, respectively in fish oil fed animals after 2 cycles of chemotherapy. The expression of glycerol-3-phosphate dehydrogenase (GPD1) was also suppressed. Cytoplasmic GPD1 connects glycolysis to lipid biosynthesis by converting dihydroxyacetone phosphate to glycerol-3-phosphate. There was a reduction in the expression of enzymes that generates NADPH for fatty acid biosynthesis including glucose-6-phosphate

dehydrogenase (G6PD), phosphogluconate dehydrogenase (PGD), malate dehydrogenase 2 (MDH2), Isocitrate dehydrogenase (IDH1, IDH2, IDH3A). On the other hand, enzymes implicated in fatty acid β-oxidation such as carnitine palmitoyltransferase 2 (CPT2), acetyl-CoA acyltransferase 1 (ACAA1), enoyl-CoA hydratase (ECH), enoyl-CoA delta isomerase 1 (ECl1), acyl-CoA dehydrogenase, C-4 to C-12 straight chain (ACADM) and acyl-CoA dehydrogenase, and very long chain (VLCAD) were also down regulated. Chemotherapy also caused reduction in protein expression of other molecules including hormone-sensitive lipase (HSL), solute carrier family 2 member 4 [SLC2A4 (GLUT4)], solute carrier family 25 Member 1 (SLC25A1), involved in citrate transport across inner mitochondrial membrane and mitochondrial pyruvate carrier 2 (MCP2), necessary for pyruvate transport across a mitochondrial membrane. Molecules in other major metabolic pathways including glycolysis, pentose phosphate pathway, gluconeogenesis were also down-regulated (Table 5-3).

Mapping proteins into IPA revealed that the most significant molecular and cellular function for differentially expressed proteins associated with lipid metabolism including fatty acid metabolism, accumulation of lipid, synthesis of lipid, β-oxidation of fatty acid and, synthesis of acyl-coenzyme A (p-value: 1.14E-02 - 3.80E-14). Top highly activated and inhibited upstream regulators predicted by IPA in control and fish oil fed animals following 2 cycles of chemotherapy are summarized in Table 5-4. The 5-top upstream regulators predicted to be inhibited were PGC-1α, PPARγ, PPARα, MYC and SERBP-1c. The chemical drug, 5-FU, was predicted to be activated with highly significant positive z score. Finally, the effect of dietary intervention on protein expression was assessed and no significant differences in proteins involved in lipid metabolism was observed between control fed and fish oil fed animals undergoing 2-cycles of chemotherapy.

5.3.7 Fatty acid composition of periuterine adipose tissue

5.3.7.1 Triglyceride fatty acids

The fatty acid composition of TG in periuterine adipose tissue are shown in Table 5-5. The most abundant fatty acids in TG fraction were 18:1n-9> 18:2n-6> 16:0> 18:0. The tumour had no effect on TG fatty acid composition of adipose tissue in comparison to the reference group. Chemotherapy significantly decreased 18:3n-3 proportions in adipose tissue after each cycle of chemotherapy for both control and fish oil fed animals. All animals that received 2 cycle of chemotherapy (control and fish oil fed) had reduced proportions of 16:0 and 16:1 compared to the tumour group. In fish oil fed rats undergoing 2-cycles of chemotherapy, proportion of 18:0 and 20:4n-6 in adipose tissue TG fatty acids were higher and lower, respectively, compared to tumour group.

Proportion of total n-3 PUFAs, was significantly lower after 2 cycles of chemotherapy in control fed animals compared to tumour and fish oil fed animals. Rats provided fish oil had significantly higher proportion of 20:5 n-3 compared to the control fed animals after both 1 and 2 cycles of chemotherapy. However, proportion of DHA in TG fatty acids were higher in fish oil fed animals only after 2-cycles of chemotherapy compared to the other groups. The ratio of n-6/n-3 fatty acids was significantly higher in control fed rats after both 1 and 2 cycles of chemotherapy compared to the tumour group ($p<0.001$). Only, after 2-cycles of chemotherapy, control fed animals exhibited a higher ratio of n-6/n-3 in adipose tissue TG fatty acids compared to fish oil fed group ($p= 0.01$).

5.3.7.2 Phospholipid fatty acids

The fatty acid composition of PL in periuterine adipose tissue is shown in Table 5-6. The

presence of a tumour increased the proportions of SFAs and decreased proportions of C16:1, C18:1 and C18:3n-3 in PL which did not change after either 1 and 2 cycles of chemotherapy in both control and fish oil fed animals. There was no significant difference in the proportion of SFAs, MUFAs and n-6 PUFAs between control and fish oil fed groups after both 1 and 2 cycles of chemotherapy.

Fish oil feeding significantly increased PL total n-3 fatty acids compared to tumour-bearing rats. Rats receiving 2 weeks of fish oil intervention tended ($p=0.08$) to have a greater proportion of n-3 PUFAs compared to rats on the fish oil containing diet for one week. The reduction in EPA and DHA that was observed in control fed animals given chemotherapy, was prevented by fish oil feeding. The ratio of n-6/n-3 fatty acids was significantly lower in fish oil fed rats after both 1 and 2 cycles of chemotherapy compared to both tumour and chemotherapy receiving rats in control diet groups. Therefore, higher proportions of total n-3 fatty acids and a decreased n-6/n-3 ratio, after both 1- and 2- cycles of chemotherapy in adipose tissue of fish oil fed rats compared to control fed rats, were attributable to the greater proportions of EPA and DHA.

5.4 Discussion

Lipid metabolism in the neoplastic state has been minimally investigated and even less is known about the effect of anti-cancer treatments, which may also induce alterations in adipose tissue. The current study investigated the effect of tumour and chemotherapy (5-FU + CPT-11) on the periuterine adipose tissue composition and function in a pre-clinical model resembling the clinical course for humans with colorectal cancer. Based on observations from tumour-bearing animals and those receiving chemotherapy in this study, we propose that inhibition of proteins

involved in mitochondrial fatty acid oxidation and HSL-mediated lipolysis contributes to larger adipocytes in tumour-bearing animals, whereas reduced expressed proteins involved in fatty acid synthesis and re-esterification concurrent with down regulation of proteins in mitochondria-linked metabolic pathways would explain the observation that adipocytes shrink in size after chemotherapy treatment. Figure 5-6 summarizes proposed alterations in adipose tissue metabolism in rats undergoing two-cycles of chemotherapy.

Protein identification by LC-MS-based quantitative proteomics enables comprehensive elucidation of protein function and associated pathways that might be altered in health and disease (Hochstrasser et al., 2002). Protein expression profiling in this study was a practical approach to determine crucial metabolic pathways altered in adipose tissue in the presence of tumour or anti-cancer treatments. The larger adipocytes observed in the tumour-bearing animals could be explained by the proteomics data which revealed inhibition of proteins involved in fatty acid β-oxidation and lipolysis. Elevated CIDEA expression and diminished PRKACA, which phosphorylates and activates HSL, suggests that lipolysis was inhibited in tumour-bearing animals. If fat is not being mobilized, adipocytes with larger lipid droplets would be expected. This finding is consistent with previous studies reporting larger lipid droplets, diminished lipolysis and elevated TG storage capacity of adipose tissue concurrent with CIDEA overexpression in adipose tissue (Christianson et al., 2010; Reynolds et al., 2015). However, no significant changes in the lipogenic pathway were detected in tumour group compared to the reference animals.

The presence of a tumour has a significant effect on PL but not TG fatty acid composition. There were greater proportions of SFAs and reduction in MUFAs within the PL fraction of adipocytes. Elevated transportation of very long chain acyl-CoA into peroxisomes,

evident by elevated protein expression of ABCD2 and SCP2, involved in oxidation of very long chain fatty acids, concurrent with inhibited mitochondrial fatty acid β-oxidation may lead to the greater proportion of saturated fatty acid. This finding is in line with previous studies indicating accumulation of saturated fatty acids with mitochondrial fatty acid oxidation enzymes deficiency (Modre-Osprian et al., 2009). Changes in membrane PL composition alters membrane fluidity and affects physiological functions such as glucose transport, insulin signalling and membrane-bound enzymes activity, transporters, and receptors (Clandinin et al., 1985; Fickova et al., 1998; Spector & Yorek, 1985). Dietary interventions might enable membrane PL fatty acid composition to be altered in such a way to preserve function of adipose tissue and prevent further alterations by anti-cancer treatments.

It seems that chemotherapy-derived factors are mainly responsible for the alterations in adipose tissue lipid metabolism contributing to diminished adipocyte size observed following chemotherapy delivery. Loss of adipose tissue in chemotherapy receiving animals associated with significant alterations in global protein expression. Ingenuity pathway analysis revealed down-regulation of numerous proteins involved in mitochondrial function, as well as glucose and lipid metabolism in periuterine adipose tissue of rats undergoing 2 cycles of chemotherapy. However, the most pronounced alterations occurred in pathways contributing to the mitochondrial energy regulation and fatty acid metabolism. Canonical pathway analysis revealed chemotherapy-induced mitochondrial dysfunction, evidenced by down-regulation of large number of proteins involved in mitochondrial electron transport chain, fatty acid β-oxidation, and the Krebs cycle (Figure 5-6). Moreover, proteins associated with glucose metabolism pathways such as glycolysis, gluconeogenesis, and pentose phosphate were also down-regulated as a consequence of chemotherapy treatment.

Diminished expression of proteins involved in Krebs cycle associates with down-regulation of pathways involved in the generation of substrates for Krebs cycle. Acetyl-CoA produced by fatty acid β-oxidation or derived from pyruvate (glycolysis) in mitochondria is a source for fatty acid synthesis (Laliotis et al., 2010). In this study, mitochondrial dysfunction associated with decreased expression of proteins involved in acetyl-CoA production and consequently, reduction in lipogenic enzymes protein expression such as FAS, ACC. Our results are also consistent with previous studies showing decreased expression of PPARγ, SREBP-1c, C/EBPα, FAS, LPL concurrent with diminished TG content of the adipocytes by inhibition of mitochondrial oxidative phosphorylation (OXPHOS) activity (Lu et al., 2010). On the other hand, mitochondrial impairment associates with decline in oxidative phosphorylation and ATP production [reviewed in (Kusminski & Scherer, 2012)]. ATP produced in mitochondria is necessary for energy demanding lipogenic pathway (Lu et al., 2010). Overall, diminished acetyl-CoA availability, decreased NADPH generation by pentose phosphate and ATP production limits fatty acid biosynthesis through lipogenic pathway.

De novo lipogenesis is one of the major pathways associated with fatty acid metabolism in adipose tissue and consequently affect adipocyte composition and size. There was a reduction in expression of lipogenic enzymes such as ACYL, ACC, FAS and SCD-1 in rats receiving chemotherapy. Protein expression of GLUT4 was also decreased, suggesting less glucose is available for glycolysis, and less substrate available for lipogenesis. Rats with lower adipose tissue expression of lipogenic genes exhibited lower proportions of palimitate, the primary product of FAS, in stored TG.

Mitochondrial electron transport chain is a main source for the generation of reactive oxygen species. Suppression of antioxidant system such as glutathione, cytochrome c and

enzymes like catalase, glutathione-peroxidase and scavengers, damages OXPHOS activity and induce oxidative stress [reviewed in (Kusminski & Scherer, 2012)]. Elevated mitochondrial oxidative stress not only associates with intracellular lipids oxidation but also cause damage to lipids, proteins and DNA (Curtis et al., 2010). It also down regulates PPARγ expression (Furukawa et al., 2004) and by impairing OXPHOS exacerbates mitochondrial dysfunction (Curtis et al., 2010). Therefore, inhibition of mitochondrial antioxidant enzymes by chemotherapy could promote increased oxidative stress.

Chemotherapy decreased food intake for 3 days; however, food intake recovered by the end of each cycle. Reduced food intake and glucose availability associates with elevated fatty acid β-oxidation as a response to negative energy balance (Bruss et al., 2010; Thupari et al., 2004). In this study, however, we observed inhibited expression of proteins involved in fatty acid β-oxidation, therefore, chemotherapy drugs likely contributed to the observed alterations. Reduced HSL-mediated lipolysis and subsequently, decreased fatty acid availability may reduce substrate available for not only mitochondrial fatty acid β-oxidation but also as a ligand for PPARγ. Reduced PPARγ expression, consequently, associates with decreased expression of PARγ-target genes (ACC, FAS, SCD-1). Further studies are required to elucidate whether PPARγ agonist may help to maintain chemotherapy-altered adipose tissue metabolism. On the other hand, inhibited HSL-mediated lipolysis might be the consequence of down-regulated proteins in mitochondrial β-oxidation. Whether decreased lipogenesis and lipid storage capacity of adipose tissue by chemotherapy is a compensatory mechanism for inhibited HSL-mediated lipolysis, or is the consequence of mitochondrial impairment and inhibited mitochondria-linked pathways, remains uncertain, although the mitochondrial dysfunction of these animals is more plausible due to impaired OXPHOS and reduced PGC-1α mediated mitochondrial biogenesis.

Decreased expression of proteins involved in OXPHOS as well as decreased expression of PGC-1α reflect impaired mitochondrial function and biogenesis, respectively, however, alterations in mitochondria number, morphology and mitochondrial DNA (MtDNA) content could be explored in future studies.

Chemotherapy led to depletion of n-3 PUFAs, stored in adipose tissue TG and to a lesser extent, PLs. Two weeks of fish oil intervention significantly increased n-3 PUFA in periuterine adipose tissue, compared to the chemotherapy treated animals on control diet. Fish oil intervention also restored the mRNA expression of some genes of interest (LPL, PGC-1α, and CIDEA) to the levels of tumour-bearing animals. Fish oil feeding has been reported to increase the mRNA expression of PGC-1α, major regulator of mitochondrial biogenesis (Puigserver et al., 1998). Rats receiving 1 and 2 weeks of fish oil intervention concurrent with chemotherapy treatment was able to restore PGC-1α mRNA expression. However, adipose tissue mitochondrial function was not maintained, probably due to the post translational regulation of PGC-1α. Therefore, based on some effects of fish oil intervention, observed in two weeks in this animal model, we speculate that 2 weeks of fish oil intervention with the current doses may cause alterations in mRNA synthesis but not able to induce regulation at the level of translation into proteins. Fish oil used in this study contained EPA/DHA with the ratio of 2:1, however, it is unclear if both EPA and DHA or EPA vs. DHA might be in involved in modifying adipose tissue metabolism. In summary, although fish oil could improve metabolism in muscle of these rats (unpublished data), adipose tissue was not a major target of fish oil in this study. Given the major role of mitochondria in regulation adipose tissue function, future investigations are warranted to determine the effect of various duration of fish oil intervention, containing different ratios of EPA and DHA, in maintaining not only mitochondrial biogenesis but also function.

Alterations in adipose tissue mitochondrial function and related lipid metabolic pathways may associate with impaired lipid storage capacity of tissue, resulting in ectopic fat accumulation in peripheral tissues and consequently, exacerbate the dysregulated whole body lipid and glucose mtabolism. Although reduced expression of proteins involved in mitochondrial function, lipogenesis and β-oxidation are occurring as a consequence of chemotherapy treatment and contributing to diminished size of adipocytes, many details remain to be explored. Therefore, metabolic adaptations to mitochondrial impairment may contribute to diminished lipid storage capacity of adipose tissue. In other words, adipose tissue was not able to efficiently oxidize fatty acids to provide energy to maintain energy demanding pathways like lipogenesis inside the tissue. Future studies should deeply investigate alterations in other metabolic pathways inside adipose tissue including lipolysis and adipogenesis, as well as local adipose inflammation in neoplastic state and in response to anti-cancer treatments. This study also proposes the need for further studies to assess the effect of early interventions to maintain adipose tissue mitochondrial function in order to maintain adipose tissue mass and function in cancer.

Tables

Table 5-1. Composition of the experimental diet

Ingredient	Control diet	Fish oil diet
Constant portion (80% w/w of diet)		
Modified AIN-76 basal mix (g/100g of diet):		
Casein	22.7	22.7
DL-Methionine	0.3	0.3
Corn Starch	25.5	25.5
Sucrose	20.4	20.4
Vitamins (AIN-76)	1.2	1.2
Minerals (AIN-76)	4.1	4.1
Inositol	0.6	0.6
Choline Bitartrate	0.2	0.2
Cellulose	5.0	5.0
Variable portion (20% w/w of diet)		
Fatty acid composition:	58.7	59.9
Saturated fatty acids	17.3	14.3
Monounsaturated fatty acids	20.6	22.5
Polyunsaturated fatty acids	(18.6)	(13.6)
Total n-6	(2.0)	(8.9)
Total n-3	(0.0)	(5.1)
EPA	(0.0)	(2.1)
DHA		

Diets were isocaloric and isonitrogenous. The variable lipid portion allowed the addition of fish oil (2.3g/100g diet) to the diet of fish oil group. A gas liquid chromatography showed that each gram of fish oil contains 360mg EPA, and 180mg DHA. Fish oil (12.4 mg of EPA + DHA/g diet) (DSM, formerly Ocean Nutrition Canada, Nova Scotia) was added to AIN-76 basal-diet. Abbreviations: AIN, American Institute of Nutrition; DHA, Docosahexaenoic acid; EPA, Eicosapentaenoic acid

Table 5-2. Lipid metabolism proteins differentially expressed in tumour-bearing animals compared to the reference animals

Accession	Gene	Protein	Fold change
P14604	ECHS1	Enoyl-CoA hydratase, short chain, 1, mitochondrial	-1.9
P23965	ECI1	Enoyl-CoA delta isomerase 1	-1.6
P04041	GPX1	Glutathione peroxidase 1	-2.0
P23764	GPX3	Glutathione peroxidase 3	-2.2
O70351	HSD17B10	Hydroxysteroid (17-beta) dehydrogenase 10	-1.6
P35704	PRDX2	Peroxiredoxin 2	-1.7
P27791	PRKACA	Protein kinase cAMP-activated catalytic subunit alpha	-6.3
Q9QY44	ABCD2	ATP binding cassette subfamily D member 2	6.3
P11915	SCP2	Sterol carrier protein 2	2.0

Table 5-3. Top Canonical pathways identified using IPA, exhibited in periuterine adipose tissue of rats undergoing two cycles of chemotherapy (control and fish oil feeding) compared to tumour-bearing animals

Pathway	P-value	Ratio	Molecules
Two cycles of chemotherapy (Control diet) vs. Tumour			
Mitochondrial Function	5.01E-14	0.1	SDHB, NDUFA9, ATP5O, MT-CO2, PDHA1, PRDX3, PARK7, NDUFV2, UQCRC2,CAT, COX5A, UQCRFS1, VDAC1,UQCRC1, MAOA, GPX3, GSTMS
Gluconeogenesis	7.94E-13	0.3	ENO1, ENO3, PGAM1, ALDOA, GAPDH, ME1, MDH2, ALDOC
Glycolysis	4.90E-09	0.2	ENO1, ENO3, PGAM1, ALDOA, GAPDH, ALDOC
Oxidative Phosphorylation	1.26E-08	0.1	SDHB, NDUFA9, NDUFV2, UQCRC2, ATP5O, COX5A, UQCRFS1, MT-CO2, UQCRC1
Krebs Cycle	1.74E-07	0.2	SDHB, CS, IDH3A, IDH2, FH, MDH2
Acetyl-CoA Biosynthesis (Pyruvate Dehydrogenase Complex)	6.31E-06	0.4	PDHA1, DLAT, PDHB
TR/RXR Activation	2.09E-05	0.1	ENO1, FAS, ACACA, PCK1, ME1, THRSP
Pentose Phosphate Pathway	2.09E-05	0.3	PGD, TKT, PGLS
Fatty Acid β-oxidation	3.24E-05	0.1	ECHS1, ACAA1, SCP2, IVD, CPT2, ACADVL
Two cycles of chemotherapy (Fish oil diet) vs. Tumour			
Mitochondrial Dysfunction	3.98E-21	0.1	SDHA, SDHB, NDUFA9, Cox6c, ATP5A1, MT-CO2, PDHA1, NDUFS1, PRDX3, ATP5B, NDUFV2, CAT, UQCRC2, COX5A, UQCRFS1, CYCS, VDAC1, UQCRC1, ATP5F1, COX4I1
Oxidative Phosphorylation	1.26E-18	0.1	SDHA,NDUFS1,SDHB,NDUFA9,NDUFV2,ATP5B ,Cox6c,ATP5A1,UQCRC2,COX5A,UQCRFS1, CYCS,MT-CO2,UQCRC1,ATP5F1,COX4I1
Gluconeogenesis	7.94E-15	0.4	ENO1, ENO3, PGAM1, ALDOA, GAPDH, ME1, MDH1, MDH2, ALDOC

Krebs Cycle	3.162E-11	0.3	SDHA, SDHB, CS, IDH3A, IDH2, MDH1, FH, MDH2
Glycolysis	4.27E-09	0.2	ENO1, ENO3, PGAM1, ALDOA, GAPDH, ALDOC
Fatty Acid β-oxidation	2.09E-08	0.2	ECHS1, ACAA1, SCP2, IVD, ACADM, ECI1, CPT2, ACADVL
TR/RXR Activation	1.26E-06	0.1	ENO1, FAS, ACACA, PCK1, ME1, FGA, THRSP
Acetyl-CoA Biosynthesis (Pyruvate Dehydrogenase Complex)	5.75E-06	0.4	PDHA1, DLAT, PDHB
LXR/RXR Activation	6.03E-05	0.0	ECHS1, APOH, FAS, ACACA, FGA, CLU

The ratio is calculated based on the numbers of proteins in a given pathway divided by total numbers of proteins that make up that pathway in IPA. P-value calculated by Fisher's exact test. Abbreviations: TR, Thyroid hormone receptor; RXR, Retinoid X receptor; LXR, Liver X receptor

Table 5-4. Highly activated and inhibited upstream regulators predicted by IPA in control and fish oil fed animals following 2 cycles of chemotherapy

Upstream regulator	Molecular Type	Predicted activation state	Control Diet 2-cycles		Fish Oil Diet 2-cycles		Target molecules in differentially expressed dataset
			Activation Z-score*	P-value of overlap	Activation Z-score*	P-value of overlap	
PPARGC1A	Transcription regulator	Inhibited	-4.379	2.17E-19	-4.892	7.85E-27	ACACA, ACADVL, ACAT1, ATP5O, CAT, COX5A, CS,DLAT, FASN, IDH3A, MDH2, ME1, MT-CO2, NDUFV2, PCK1, PDHA1, PGAM1, PRDX3, SLC2A4,UQCRFS1
PPARγ	Ligand-dependent nuclear receptor	Inhibited	-4.06	1.629E-23	-4.08	1.28E-22	ACAA1, ACACA, ACLY, ATP5O, CAT, CPT2, CS, DLAT, FABP1, FASN, FDPS, GAPDH, GPD1,GPT, IDH1, IVD, KRT18, LIPE, ME1, MGLL, PC, PCK1, PDHB, PYGL, RPSA, SCP2, Slc25a1, SLC2, TKT
PPARα	Ligand-dependent nuclear receptor	Inhibited	-2.97	4.41E-16	-3.40	9.42E-25	ACAA1, ACACA, ACADVL, ACAT1, ACAT2, CAT, CPT2, CS, DBI, FABP1, FASN, FDPS, GPD1, GPT, MGLL,MT-CO2, PC, PCK1, PRDX6, SCP2, SLC2A4, UQCRC1
MYC	Transcription regulator	Inhibited	-2.61	2.27E-12	-2.71	7.88E-12	ACACA, ACAT1, AK2, ALDOA, CANX, CAPNS1, CPT2, DBI, ENO1, FABP1, FASN, GAPDH, GCSH, GPT, HSPE1, IDH1, IDH2, LUM, NDRG2, PCK1, PDHA1, PGAM1, PHB, PHB2, PRDX3, SLC25A5, TKT
SREBF1	Transcription regulator	Inhibited	-2.13	7.82E-09	-2.49	2.88E-11	ACACA, ACLY, ALDOC, DBI, FASN, FDPS, GPX3, IDH1, PCK1, THRSP, UQCRFS1

MAP4K4	Kinase	Activated	3.44	8.13 E-13	3.44	6.00E-13	ACACA, ACADVL, ACLY, DLAT, FASN, IVD, MGLL, PGAM1, SCP2, SLC2A4, UQCRC1, UQCRFS1
5-Fluorouracil	Chemical drug	Activated	3.21	1.30E-11	3.21	9.22E-12	ALDOA, ATP5O, CANX, CAPNS1, ECHS1, FDPS, GAPDH, HSPE1, IDH2, NDUFV2, PSMA7, RPS8, SLC25A5, UQCRC2

Z>2 and Z<-2 predict activation and inhibition of the upstream regulator, respectively. The p-value indicates the significance of the overlap between the molecules targeted by the upstream regulator in the IPA database and the experimental dataset. Abbreviations: PPARγ, Peroxisome proliferator-activated receptor gamma; PPARα, Peroxisome proliferator-activated receptor alpha; PPARGC1A, Peroxisome proliferator-activated receptor gamma coactivator 1-alpha; SREBF1 (SREBP1c), Sterol regulatory element binding transcription factor 1; MAP4K4, Mitogen-activated protein kinase kinase kinase kinase 4

Table 5-5. Fatty acid composition of triglyceride in periuterine adipose tissue of Fischer 344 rats

Fatty acids (%total)	REF	TUM	Control Diet		Fish oil Diet	
			1- Cycle	2- Cycles	1- Cycle	2- Cycles
C16:0	20.6 ± 0.5^{a}	19.7 ± 0.3^{a}	20.0 ± 0.4^{a}	17.9 ± 0.7^{b}	19.2 ± 0.4^{ab}	18.2 ± 0.4^{b}
C16:1	3.9 ± 0.2^{a}	3.6 ± 0.1^{a}	3.4 ± 0.2^{ab}	2.6 ± 0.3^{c}	3.0 ± 0.1^{bc}	2.5 ± 0.2^{c}
C18:0	6.0 ± 0.3^{a}	6.9 ± 0.2^{ab}	6.7 ± 0.1^{ac}	7.9 ± 0.4^{bd}	7.4± 0.2^{bce}	8.1 ± 0.2^{de}
C18:1	41.3 ± 2.1	42 ± 1	41.3 ± 0.6	44.3 ± 0.9	42.2 ± 0.6	43.9 ± 0.7
C18:2n6	22.3 ± 1.6	22.0 ± 0.7	23.4 ± 0.5	22.5 ± 0.4	23 ± 0.4	22.1 ± 0.6
C18:3n3	1.6 ± 0.1^{a}	1.7 ± 0^{a}	1.3 ± 0^{c}	1.2 ± 0.1^{c}	1.3 ± 0^{c}	1.1 ± 0.1^{c}
C20:4n6	0.8 ± 0.1^{a}	0.7 ± 0^{a}	0.6 ± 0^{ab}	0.6 ± 0^{ab}	0.6 ± 0^{ab}	0.5± 0.0^{b}
C20:5n3	ND^{a}	ND^{a}	ND^{a}	ND^{a}	0.1 ± 0^{b}	0.2 ± 0.1^{b}
C22:6n3	0.4 ± 0.1^{a}	0.4 ± 0^{a}	0.3 ± 0^{a}	0.3 ± 0^{a}	0.4 ± 0^{a}	0.5 ± 0^{b}
ΣSFA	28.3 ± 0.3	28.2 ± 0.2	28.3 ± 0.3	27.3 ± 0.3	28.1 ± 0.2	27.9 ± 0.2
ΣMUFA	45.7 ± 2	46.1 ± 1	45.2 ± 0.6	47.4 ± 0.7	45.7 ± 0.6	46.9 ± 0.7
Σn-6/n-3	11.2 ± 0.6^{a}	10.3 ± 0.2^{a}	13.6 ± 0.5^{bc}	14.7 ± 0.7^{b}	12.3 ± 0.3^{bc}	11.7 ± 1^{ac}
Σn-6	23.8 ± 1.7	23.4 ± 0.8	24.7 ± 0.5	23.7 ± 0.4	24.3 ± 0.4	23.2 ± 0.7
Σn-3	2.2 ± 0.3^{a}	2.3 ± 0.1^{a}	1.8 ± 0.1^{bc}	1.6 ± 0.1^{b}	2.0 ± 0.0^{ac}	2.1 ± 0.2^{a}

Triglyceride fatty acids in periuterine adipose tissue of Fischer 344 rats bearing the Ward colorectal carcinoma receiving 1- or 2- cycles of chemotherapy and fed either a fish oil or control diet. Healthy rats were used a reference for comparison (REF). Mean ± SEM, Kruskall test was used to determine significant differences between groups. Different superscripts indicate significant differences between groups ($p<0.05$); (n=6-8/group). Abbreviations: SFA, Saturated fatty acids; MUFA, Monounsaturated fatty acids; PUFA, Polyunsaturated fatty acids; REF, Healthy; TUM, Tumour-bearing; ND, not determined

Table 5-6. Fatty acid composition of phospholipids in periuterine adipose tissue of Fischer 344 rats

Fatty acids (%total)	REF	TUM	Control Diet		Fish oil Diet	
			1- Cycle	2- Cycles	1- Cycle	2- Cycles
C16:0	26.4 ± 1.4	26.2 ± 2	28.8 ± 1.3	29.4 ± 1.4	26.7 ± 1.1	28.8 ± 0.9
C16:1	3.0 ± 0.1^{a}	1.6 ± 0.2^{b}	1.4 ± 0.1 ^{b}	1.5 ± 0.2^{b}	1.4 ± 0.1^{b}	1.5 ± 0.1^{b}
C18:0	22.3 ± 0.6^{a}	30.3 ± 1.1^{b}	29.2 ± 1.1^{b}	30.1 ± 1.4^{b}	30 ± 1^{b}	29 ± 1.1^{b}
C18:1	26.3 ± 1.4^{a}	17.0 ± 1.5^{b}	16.9 ± 1.5^{b}	16.1 ± 1.2^{b}	17.6 ± 1.5^{b}	17.4 ± 1.2^{b}
C18:2n6	13.4 ± 0.6	12.4 ± 0.8	12.2 ± 0.8	11.6 ± 0.6	12.7 ± 0.6	11.4 ± 0.4
C18:3n3	0.8 ± 0 ^{a}	0.2 ± 0^{b}	0.2 ± 0.1^{b}	0.2 ± 0^{b}	0.2 ± 0^{b}	0.2 ± 0.1^{b}
C20:4n6	5.4 ± 0.6	8.3 ± 0.7	7.6 ± 0.5	7.03 ± 0.5	6.8 ± 0.7	6.5± 0.8
C20:5n3	0.1 ± 0^{a}	ND^{a}	ND^{a}	ND^{a}	0.5 ± 0^{b}	0.7 ± 0.1^{b}
C22:6n3	0.8 ± 0.1^{a}	0.5 ± 0^{ab}	0.3 ± 0^{b}	0.3 ± 0^{b}	0.6± 0^{a}	0.8 ± 0.1^{a}
ΣSFA	49.9 ± 1^{a}	57.9 ± 2.3^{b}	59.2 ± 1.8^{b}	61 ± 1.9^{b}	58.0 ± 1.6^{b}	59.1 ± 1.1^{b}
ΣMUFA	29.4 ± 1.3^{a}	19.2 ± 1.6^{b}	19.2 ± 1.6^{b}	18.3 ± 1.4^{b}	19.6 ± 1.5^{b}	19.6 ± 1.3^{b}
Σn-6/n-3	11.1 ± 0.5^{ab}	16.1 ± 0.5^{ac}	21.0 ± 1.6^{c}	18.6 ± 1.2^{c}	9.8 ± 0.4^{bd}	7.7 ± 0.7^{d}
Σn-6	18.9 ± 0.6^{a}	21.5 ± 1.1^{a}	20.6 ± 0.8^{a}	19.5 ± 0.8^{a}	20.3 ± 1.2^{a}	18.7 ± 1.1^{a}
Σn-3	1.7 ± 0.1^{ab}	1.3 ± 0.1^{bc}	1.0 ± 0.1^{c}	1.1 ± 0.1^{c}	2.1 ± 0.1^{a}	2.6 ± 0.3^{a}

Phospholipid fatty acids in periuterine adipose tissue of Fischer 344 rats bearing the Ward colorectal carcinoma receiving 1- or 2- cycles of chemotherapy and fed either a fish oil or control diet. Healthy rats were used a reference for comparison (REF). Mean ± SEM, Kruskall test was used to determine significant differences between groups. Different superscripts indicate significant differences between groups ($p<0.05$); (n=6-8/group). Abbreviations: SFA, Saturated fatty acids; MUFA, Monounsaturated fatty acids; PUFA, Polyunsaturated fatty acids; REF, Healthy; TUM, Tumour-bearing; ND, not determined

Figures

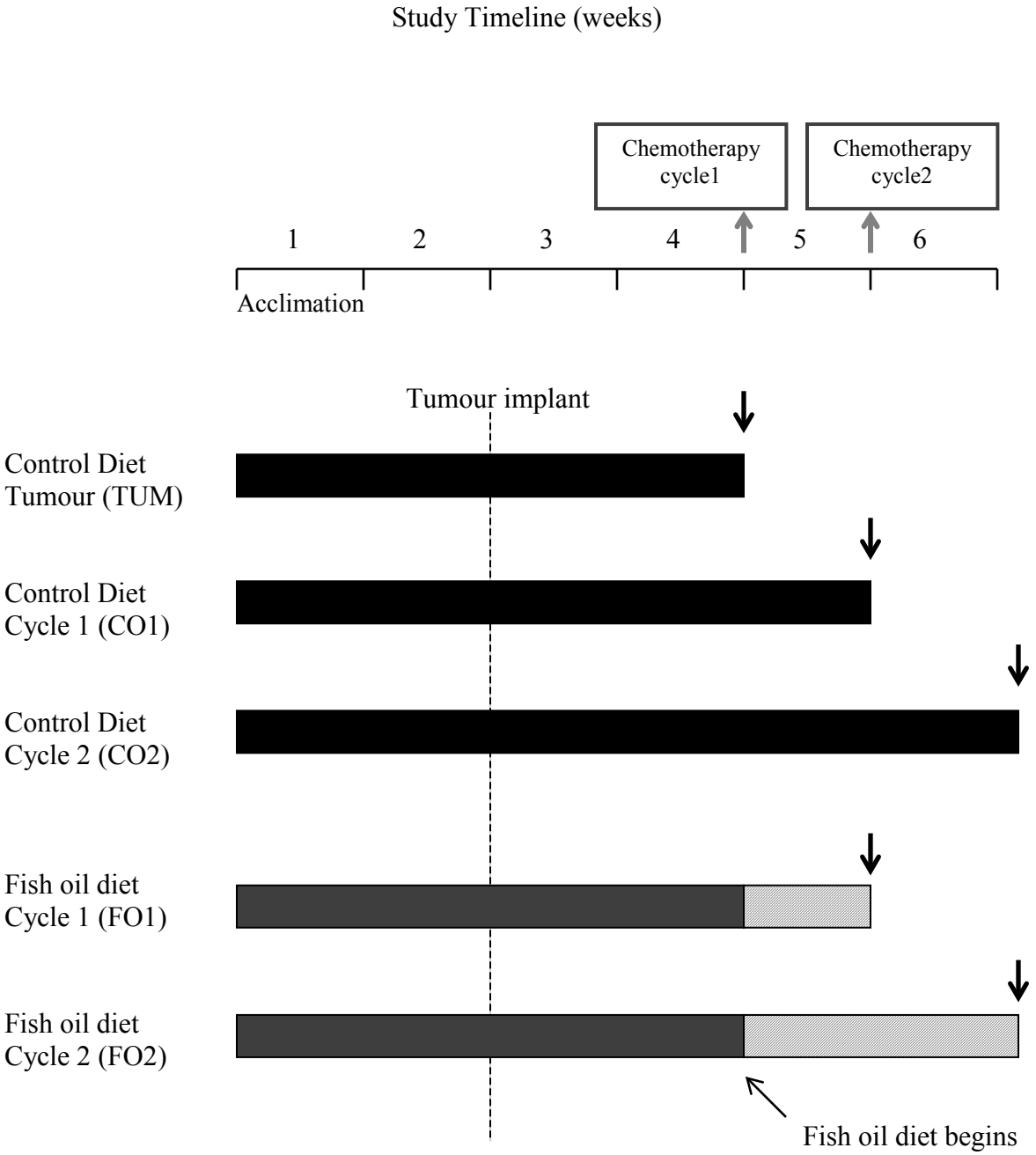


Figure 5-1. Experimental study design

The start day of chemotherapy cycle-1 (week 5); the first day of chemotherapy cycle-2 (week 6).
Hash bar represents duration of fish oil feeding.
🡻 End of each bar represents the day that animals were euthanized.
Reference animals did not undergo tumour injection or chemotherapy treatment but were handled similar to experimental groups.

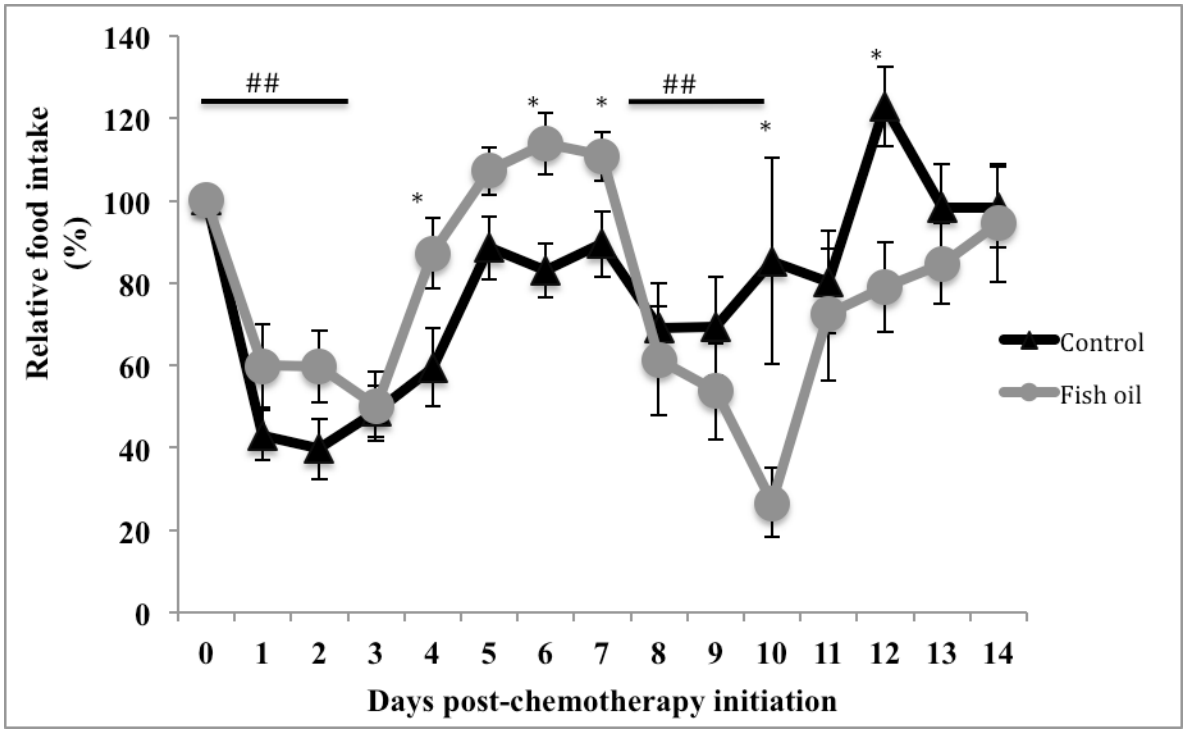


Figure 5-2. Relative food intake (%) compared to the baseline (Day 0, mean food intake prior to chemotherapy) in control fed and fish oil fed rats bearing the Ward colorectal carcinoma during chemotherapy.

Values represent mean ± SEM. The x-axis represents days after chemotherapy initiation. Day 0 represents the first day of the first cycle of chemotherapy (n=14 in control and n=15 in fish oil group), and day 7, representing the first day of the second cycle of chemotherapy (n=7 in each group). *Significant difference between fish oil fed and control fed animals during chemotherapy; determined by two-way repeated measure ANOVA. ##Significant differences between day 0 and days 1-3 of the first cycle or between day 7 and days 8-10 of the second cycle of chemotherapy evaluated by two-way repeated measure ANOVA ($p<0.05$).

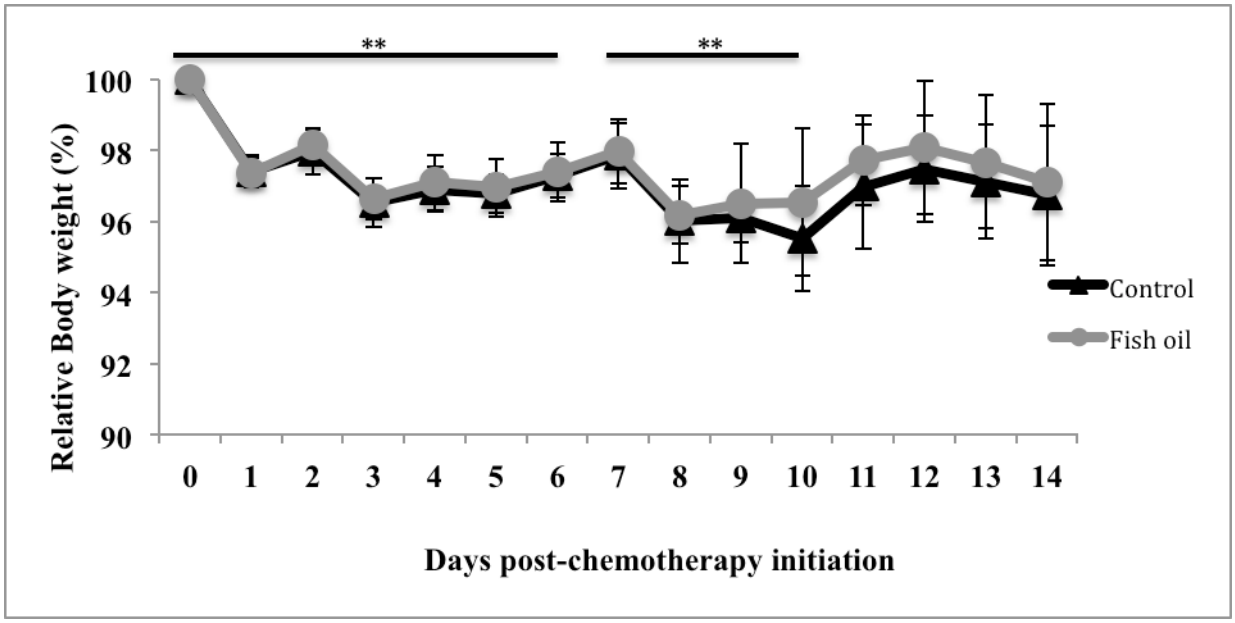


Figure 5-3. Relative body weight (%) compared to baseline (Day 0) in control fed and fish oil fed rats bearing the Ward colorectal carcinoma during chemotherapy.

Values represent mean ± SEM. The x-axis represents days after chemotherapy initiation. Day 0 represents the first day of the first cycle of chemotherapy (n=14 in control and n=15 in fish oil group), and day 7, represents the first day of the second cycle of chemotherapy (n=7 in each group). **Significant difference between day 0 (baseline) and days 1-6 or between day 7 and days 8-10 following chemotherapy initiation evaluated by two-way repeated measure ANOVA ($p<0.05$).

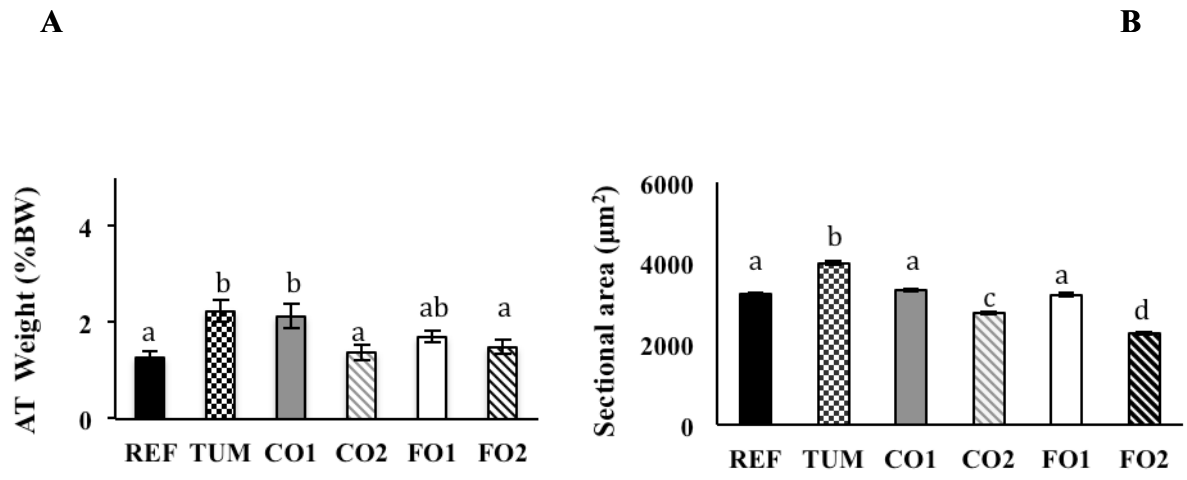
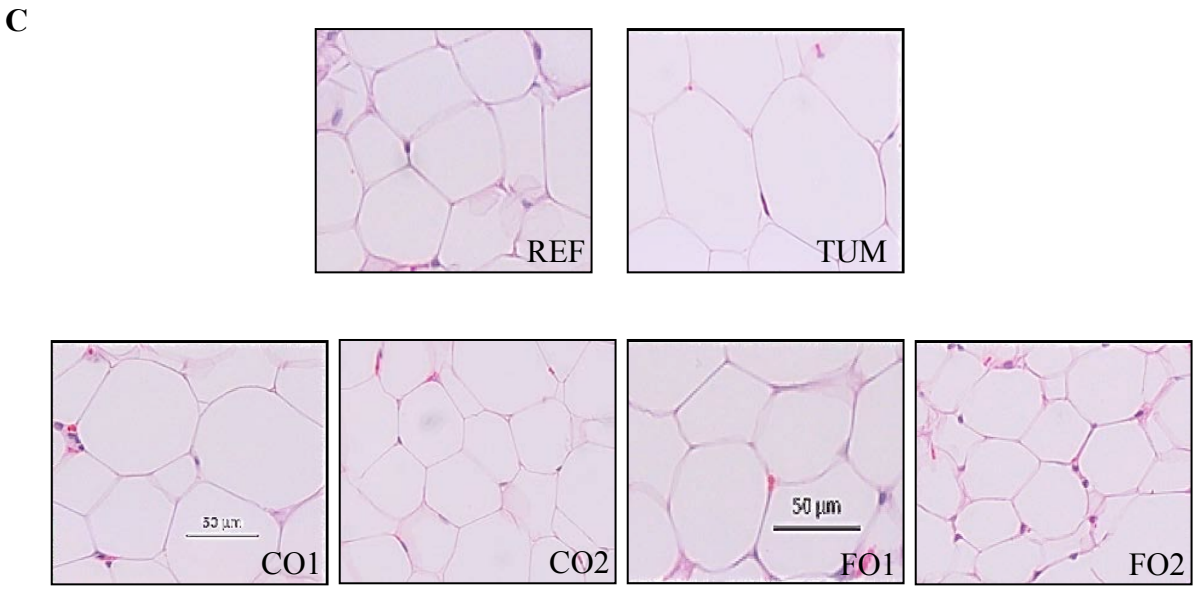
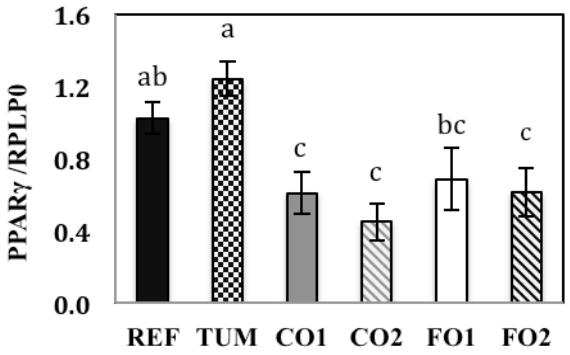


Figure 5-4. Periuterine adipose tissue weight and morphological characteristics.

Periuterine adipose tissue weight (%BW) (A) and morphometric analysis of adipocyte cross sectional area (µm2) (B) in Fischer 344 rats.Values are mean ± SEM, different superscripts indicate significant differences ($p<0.05$) determined by Kruskal–Wallis test for periuterine adipose tissue weight (n=7-8/group) and one way ANOVA for cross sectional area (1500 cells/group; 5 animals/group). C) Example images of periuterine adipocytes stained with hematoxylin and eosin (magnification 20X) from Reference, Tumour, and chemotherapy groups either on control or fish oil diets. Bar= 50µm. Abbreviations: REF, Reference; TUM, Tumour; CO1, Control diet + 1-cycle; CO2, Control diet + 2-cycles; FO1, Fish oil diet + 1-cycle; FO2, Fish oil diet + 2-cycles

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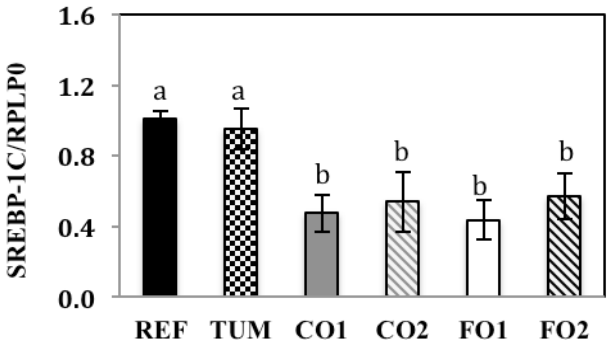
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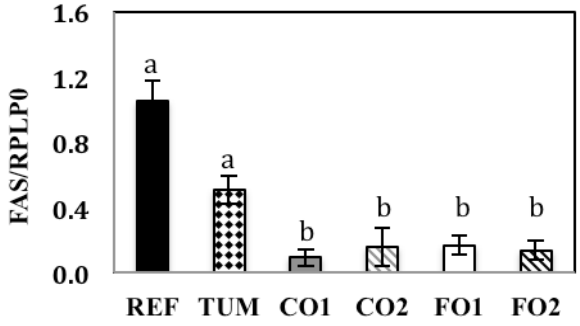
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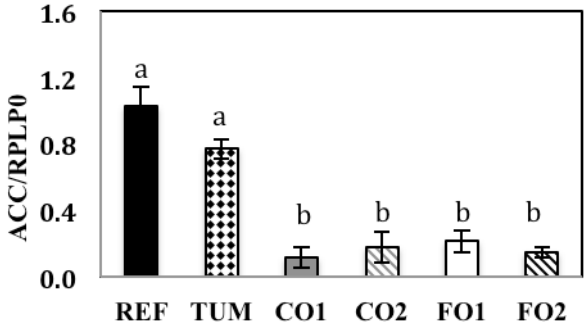
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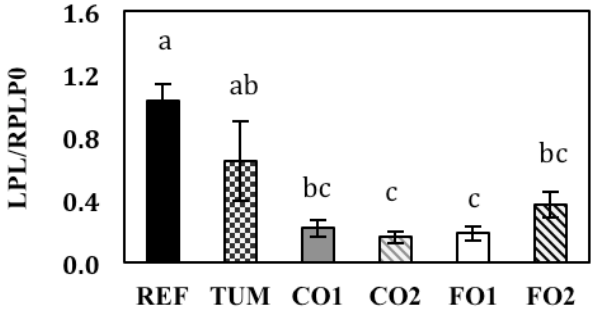
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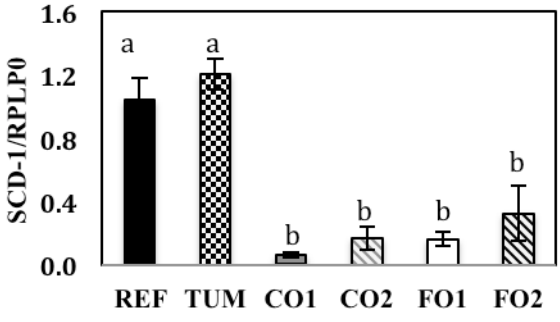
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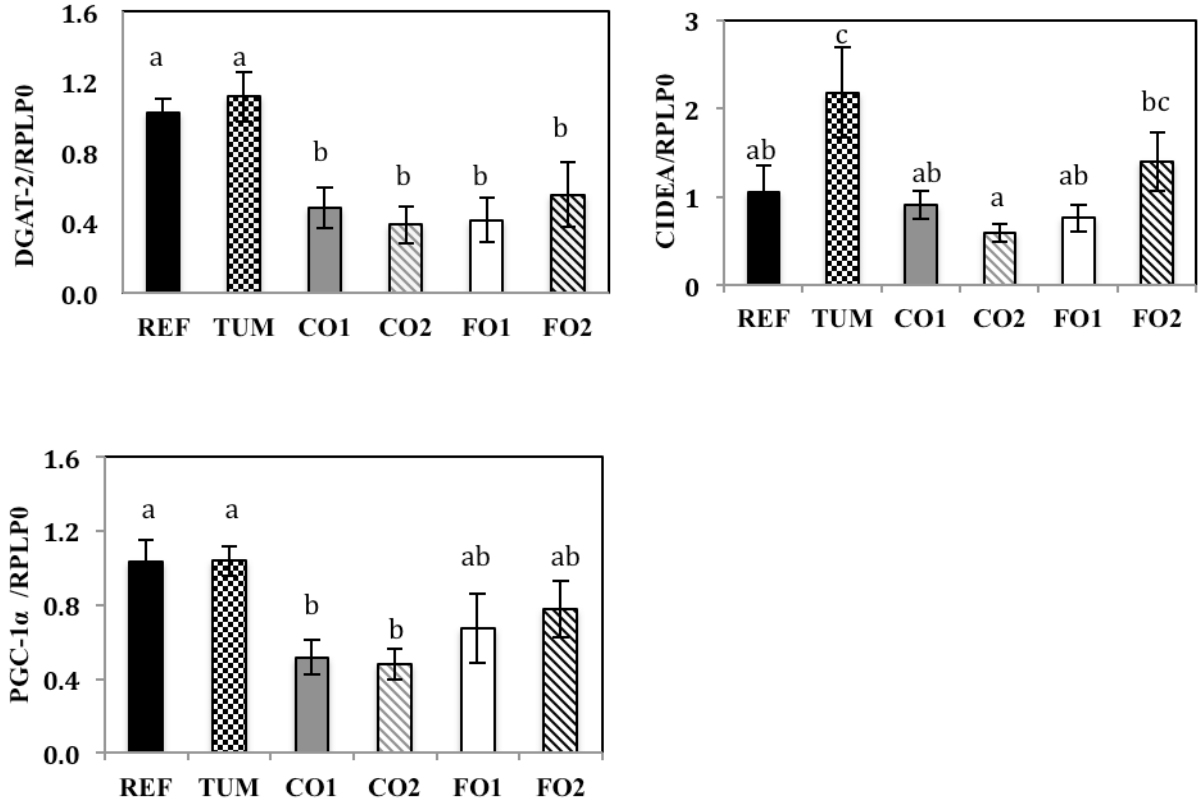

Figure 5-5: Relative mRNA levels of genes encoding various lipogenic enzymes assessed using Real-time PCR.

The mRNA levels of the target genes included FAS, ACC, SCD-1, DGAT-2 as well as LPL, PPARγ, SREBP-1c, PGC-1α and CIDEA were normalized to the expression of RPLP0 and are shown as mean ± SEM. Results are fold change of gene expression relative to the reference group; different superscripts indicate significant differences ($p<0.05$) determined by Kruskal–Wallis Test; (n=6-8/group). Abbreviations: REF, Reference; TUM, Tumour; CO1, Control diet + 1-cycle; CO2, Control diet + 2-cycles; FO1, Fish oil diet + 1-cycle; FO2, Fish oil diet + 2-cycles

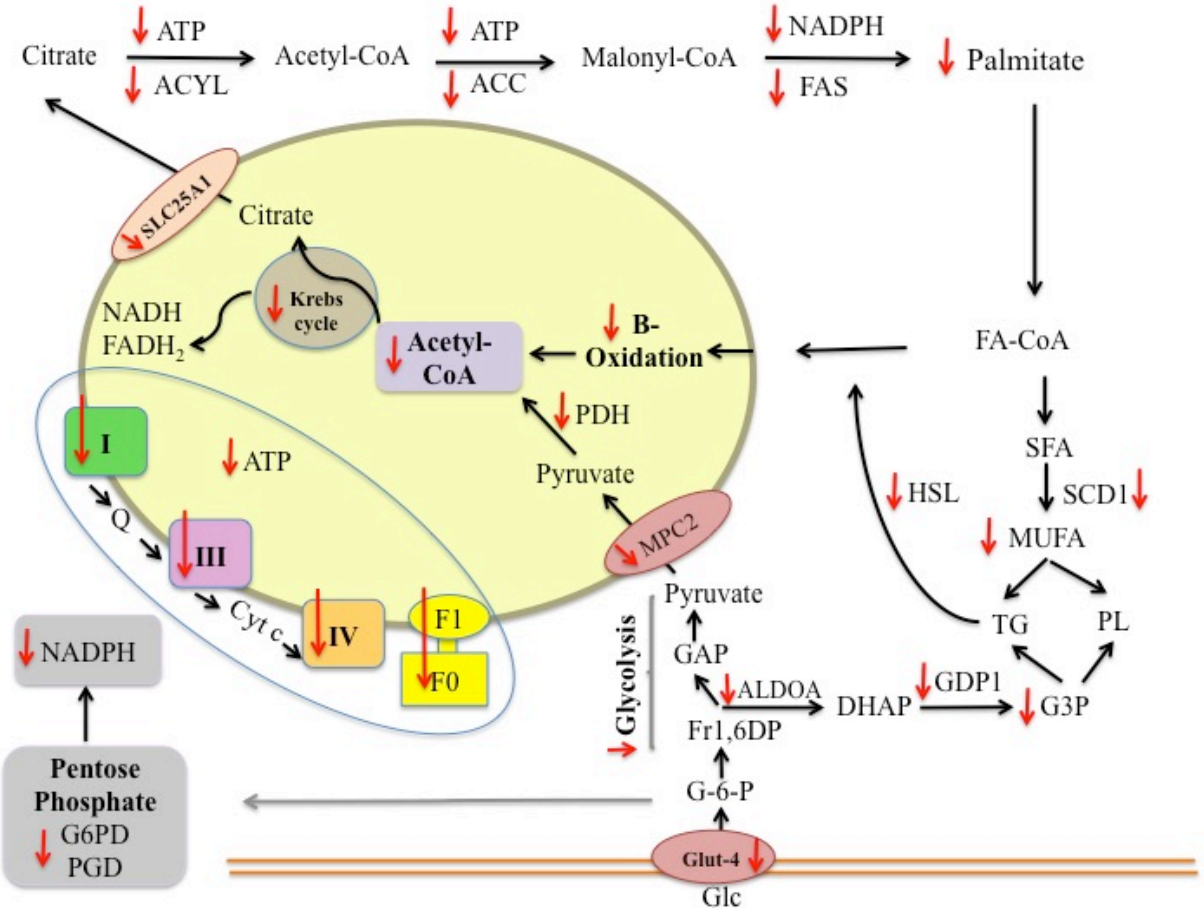

Figure 5-6. Schematic diagram summarizing adipose tissue alterations in rats undergoing 2-cycles of chemotherapy.

Many pathways within adipose tissue are altered in response to chemotherapy, which are mainly related to mitochondrial function. Mitochondrial dysfunction associates with decreased ATP generation, fatty acid β-oxidation, Krebs cycle and acetyl-CoA production inside mitochondria. There was also a reduction in the expression of proteins in other metabolic pathways such as glycolysis, pentose phosphate, lipogenesis as well as decreased glucose uptake. Red arrows indicate reduced expression of proteins. Abbreviations: GLUT4, Glucose transporter-4; G-6-P, Glucose 6-phosphate; Fr 1,6-DP, Fructose 1,6-diphospate; GAP, Glyceraldehyde3-P; DHAP, Dihydroxyacetone phosphate; GDP1, Glyceraldehyde-3-phosphate dehydrogenase; G3P, Glycerol-3-phosphate; TG, triglyceride; PL, Phospholipid; MUFA, Monounsaturated fatty acid; SCD1, Stearoyl-coenzyme A desaturase 1; FA, Fatty acid; HSL, Hormone-sensitive lipase; MPC2, Mitochondrial pyruvate carrier 2; SLC25A1, Solute carrier family 25 member 1; G6PD, Glucose-6-phosphate dehydrogenase; PGD, 6- phosphogluconate dehydrogenase; ACYL, ATP citrate lyase; ACC, Acetyl-coenzyme A carboxylase; FAS, Fatty acid synthase

Chapter 6. Final discussion

6.1 Introduction

Adipose tissue, as one of the major body composition compartments, plays an important role in mediating human metabolism, not only by storing fat but also by its secretory function. Therefore, this research was conducted to first understand the prognostic significance of adipose tissue in cancer survival, secondly to assess alterations that occur in adipose tissue after cancer diagnosis, and lastly to investigate molecular mechanisms associated with these alterations. This discussion summarizes key findings of studies presented in the previous chapters and makes recommendations for future research.

6.2 The association between body composition variables and survival after a cancer diagnosis

In Chapter 3, we aimed to determine if high adiposity independently associates with longer survival and concurrently to determine the type of adiposity contributing to this association. We were also interested to investigate if the presence of low muscle mass affects survival in patients of any given adiposity. It was hypothesized that high adiposity, mainly subcutaneous adiposity associates with lower mortality risks in a model adjusted for known prognostic factors including age, sex, cancer type, stage, performance status as well as body composition variables. In this study, using a fully-adjusted multivariate model including all known prognostic variables, we were able to establish sex-specific adiposity values associated with lower mortality risk and reported that high adiposity, as an independent predictor of mortality risk associated with longer survival in cancer patients, with subcutaneous adiposity mainly driving this association. Lastly, as previous studies have indicated, we also observed that a critically low level of muscle mass decreases the median survival of high adiposity patients.

However, it should be noted that sarcopenia was not an independent predictor of mortality risk in this study. On the other hand, low muscle attenuation, which reflects elevated fat content of muscle, remained an independent prognostic factor which supports very recent emerging literature and work being conducted by others in our lab. It may be that low muscle attenuation is a manifestation of muscle loss in cancer.

In the majority of previous studies examining the independent prognostic significance of adipose tissue, the median of adiposity variables was applied as a point to discriminate between low and high mortality risk groups. However, in this study, adiposity levels (high vs. low), associated with mortality, were derived from fully-adjusted multivariate models, therefore controlling for confounding factors. It was observed that both low adiposity and low muscle attenuation (fat infiltration into muscle) significantly associated with increased mortality risk in cancer patients. This demonstrates the need for future studies to investigate which models of body composition variables provides the best discrimination in predicting mortality. At present, each variable has been studied as a single measure outcome. Also, interaction between adiposity levels (for both VAT and SAT) and muscle radiodensity should be examined using robust statistical analyses, beyond exploring median survival using Kaplan-Meier which has been done in previous studies. In summary, based on the results of this study, recommendations to lose weight cannot apply to cancer population and instead, preserving fat and gaining muscle maybe the best strategies to prolong survival of cancer patients after a cancer diagnosis.

6.3 Alterations in adipose tissue cross sectional area in cancer

In Chapter 4, we were interested to investigate the intensity and time course changes in TAT, VAT and SAT areas in the year preceding death in a cohort of advanced gastrointestinal

cancer patients. Chapter 4 hypothesized and also demonstrated that in the year preceding death, adipose loss is exacerbated with exponential losses in the last months of life. Stability or even gain of adipose tissue occurred further away from death whereas close to death, loss of both depots was observed in majority of patients. Given that VAT and SAT are metabolically different depots with VAT being more responsive to lipolytic factors [reviewed in (Ibrahim, 2010; Wajchenberg, 2000)], it was also hypothesized that VAT loss may precede SAT loss in the last year of life. In line with our hypothesis, loss of VAT occurred further away from death, and preceded SAT loss. This is an important finding since free fatty acids released by VAT lipolysis are delivered to the liver which may associate with TG accumulation within liver and consequently, lead to alterations in liver metabolism to evoke peripheral changes in energy utilization and availability.

This study is the first to outline the intensity of alterations and diverse behaviours of adipose tissues depots that exists in cancer populations. Loss of adipose tissue occurs in the majority of patients as death approaches. This is important because the majority of studies attempting interventions to ameliorate wasting in cancer have selected patients at advanced stages when it is unlikely that any intervention would be effective. Our study showed anabolic potential of adipose tissue exists further away from death as it does for muscle tissue, therefore, earlier interventions at a time when anabolic potential exists may be more effective.

The research in Chapters 3 and 4 assessed adipose tissue mass in cancer by applying diagnostic CT images as a precise and accurate method in an oncology setting. CT image analysis is also able to quantify VAT and SAT depots as components of TAT (Fabbro et al., 2010). Research presented in chapter 4 was the first study to assess the alterations in VAT and

SAT depots using longitudinal CT images in a year prior to death. Although Chapter 3 suggests that high adiposity, especially subcutaneous adiposity, decreases mortality risk in cancer, based on the results presented in chapter 4 showing different behavior of VAT and SAT, it is possible that VAT loss and subsequent release of fatty acids into liver could have important effects on cancer survival that have yet to be realized. Prospective longitudinal studies evaluating changes in total and adipose tissue depots over time (repeated evaluation) in relation to survival have yet to be conducted.

6. 4 Adipose tissue alterations in an animal model of colorectal cancer

Chapter 5 focuses on adipose tissue alterations in cancer and after chemotherapy with a view to develop nutritional interventions that have potential to improve adipose tissue metabolism in an experimental model of colorectal cancer. This study aimed to assess the effect of tumour and chemotherapy on periuterine adipose tissue fatty acid composition, morphology, lipogenesis and the expression of proteins involved in adipose lipid metabolism. It was hypothesized that tumour-bearing animals will exhibit adipose atrophy, depleted n-3 fatty acids and inhibited lipid synthetic and storage pathways. We also hypothesized that chemotherapy will have a greater effect than a tumour on adipose atrophy and inhibition of lipid accumulating pathways. Lastly, it would seem highly important to clarify if fish oil supplementation, concurrent with chemotherapy treatment, helps to maintain points of metabolism, altered by tumor and chemotherapy in adipose tissue. In this study, we also hypothesized that dietary fish oil intervention prevents fat loss by maintaining adipose tissue composition and metabolism in tumor-bearing animals undergoing chemotherapy.

Opposed to our hypothesis, we observed larger adipocytes in tumour-bearing animals,

which were associated with reduced expression of proteins involvd in lipolysis and mitochondrial fatty acid oxidation. It should be noted that depending on the time (stage) of tumour growth and type of adipose tissue, previous studies are reporting smaller or larger adipocytes in tumour-bearing animals (Batista et al., 2012; Bertevello & Seelaender, 2001). Smaller epididymal adipocytes but larger mesenteric adipocytes were observed in rats bearing the Walker 256 carcinoma (Batista et al., 2012). In our study, chemotherapy treatment was associated with smaller adipocytes, depleted n-3 fatty acids and reduced expression of proteins involved in lipid accumulation. Two weeks of fish oil intervention associated with minor incorporation of EPA and DHA into adipose tissue which was associated with higher mRNA expression of PGC-1α and CIDEA but was not effective in altering the expression of proteins that may function to reverse altered adipose tissue metabolism. Therefore, considering only minor incorporation of EPA and DHA into PL of adipose tissue, perhaps it is not surprising to see few functional differences between groups after chemotherapy.

In this study, reduced expression of proteins involved in mitochondrial function and associated metabolic adaptations, appears to be a major reason for diminished lipid storage capacity of adipose tissue and subsequent reduction in adipocyte size by chemotherapy treatment. Although food intake decreased for a few days following chemotherapy initiation, it was restored to baseline by the end of each cycle. Previous studies showed that despite providing energy requirements to cancer patients (Fouladiun et al., 2005) or using pair-fed animals (Bing et al., 2006), other mechanisms rather than reduced food intake contributes to adipose atrophy in cancer. During energy deficiency, increased mitochondrial oxidation compensates for decreased glucose availability, to produce energy (Verhoef et al., 2013). However, in this study reduction in protein expression of GLUT4, involved in glucose uptake by adipose tissue, occurred

concurrent with diminished mitochondrial fatty acid oxidation. Thus, it seems that reduction in pathways such as glycolysis and lipolysis that produce substrate (pyruvate, fatty acids) for mitochondria compensates for mitochondrial dysfunction. Mitochondrial damage in tumour cells by 5-FU (Sanchez-Arago et al., 2010) and mitochondrial membrane interruption by CPT-11 + 5-FU in colon cancer cell lines (Grivicich et al., 2005) have been reported in previous studies. Therefore, it would seem that this drug combination also has capacity to evoke these alterations in tissues other than the tumour.

Toxic side effects of chemotherapy limit the treatment cancer patients are able to tolerate and also reduce quality of life in patients who have a short life expectancy. Research in our lab has shown that depletion of fat mass and plasma essential fatty acids elevates the severity of toxicity side effects, contributing to deterioration of body composition (Murphy et al., 2010). Overall, adipose tissue is not only providing energy but is also a metabolically active tissue that produces various adipokines such as leptin and adiponectin. Moreover, preventing loss of adipose in an experimental model of cancer prevented muscle loss (Das et al., 2011). Reduced lipid storage capacity of adipose tissue would be expected to associate with ectopic fat accumulation in peripheral tissues such as liver and muscle and consequently, alterations in whole body metabolism. Therefore, given adipose tissue contribution to mediate whole body metabolism, identification of mechanisms underlying fat loss following chemotherapy treatment will enhance our understanding of aberrations of lipid metabolism in cancer and help define interventions to circumvent wasting.

6.5 Considerations for future experimental studies

Our study did not fast animals when multiple tissues were harvested. However, we

conducted various analyses to determine whether all groups were in the same feeding status. Plasma insulin levels [Ultrasensitive Rat Insulin ELISA kit (ALPCO, Salem, NH)] and mRNA expression of IRS-1 were measured. Overall, there was no significant difference between groups (Figures 6-1, 6-2) demonstrating that all groups were in the same fed state. However, we acknowledge that mRNA expression of IRS-1 may not be a good indicator of insulin signaling as post-translational modifications of IRS-1 play an important role in regulating insulin signaling (Klein et al., 2009). The primary focus of this study was on the enzymes involved in lipogenic pathways and a review by (Madsen et al., 2005) indicated that the effect of PUFAs on SREBP-target genes should be evaluated in fed state as the expression of lipogenic genes are extremely low in fasting state in both liver (Horton et al., 1998) and adipose tissue (Kim et al., 1998). Future experiments could be designed so animals are in fed state after overnight fasting as marked effects can be observed in fasting-refeeding state [reviewed in (Madsen et al., 2005)] which stimulate expression of genes involved in fatty acid synthesis [reviewed in (Strable & Ntambi, 2010)].

Besides changes in the expression of proteins, discussed in chapter 5, alterations in mitochondrial antioxidant proteins were also observed in tumour-bearing animals. Proteins such as glutathione peroxidase 1 (GPX1), glutathione peroxidase 3 (GPX3), peroxiredoxin 2 (PRDX2) were down regulated. Previous studies reported that adipocyte enlargement was associated with oxidative stress in the tissue [reviewed in (Cildir et al., 2013)]. Therefore, oxidative stress induced by the loss of mitochondrial antioxidant system may have occurred concurrent with adipocytes enlargement in tumour-bearing animals.

There was a 10-fold increase in the expression of lysosome-associated membrane protein, (Lamp1) in adipose tissue following tumour growth. Elevated Lamp1 expression might

be related to the digestion and clearance of dying organelles and cells such as autophagy of dying adipocytes by adipose macrophage lysosomal LAMP-1 due to its cell-cell adhesion activity (Haka et al., 2016; Kwon et al., 2016; Xu et al., 2013) or be a response to elevated mitochondrial oxidative stress through reactive oxygen species -mediated mitochondrial-lysosomal pathway (Zhao et al., 2003). Further studies are required to investigate the association between lysosomes and adipose tissue alterations in tumour-bearing state.

Adipocyte hypertrophy associates with oxidative stress and necrotic cell death initiation followed by macrophage activation (Alkhouri et al., 2010). Macrophage activation, however, is required to inhibit accumulation of dead cells to maintain inflammatory homeostasis (Feng et al., 2011). In this study, we speculated that due to the presence of larger adipocytes in tumour-bearing animals, macrophage accumulation would be observed. However, no sign of crown like structures (accumulated macrophages around dead adipocytes) were identified in H&E slides nor changes in the mRNA expression of macrophage markers (CD68 and EMR1- F4/80) detected (Figure 6-3). Although no changes in macrophage markers were observed, we acknowledge that a single measurement of macrophage markers could have masked the changes in M1/M2 phenotypes (Goh et al., 2016). However, elevated Lamp-1 expression in tumour group may also suggest subsequent digestion of molecules and organelles by lysosomes and therefore, inhibition of accumulation of dead cells, and macrophages in these animals. This all indicates a need for further investigation of lysosomal functions as well as macrophage phenotypes in these animal models.

Two weeks of dietary fish oil resulted in minor incorporation of EPA and DHA into adipose tissue by 10-20% elevation in EPA and DHA in TG. In PLs, there was a 50-70% and 30-50% increase in EPA and DHA proportions, respectively. Therefore, when designing future

trials, several key points such as optimal dose and duration, ratio of EPA/DHA and composition of background diet should be considered, particularly in the context of a neoplastic model. The amount of EPA and DHA specifically required to maintain adipose tissue mass during chemotherapy has not been explored in previous cancer studies. If incorporation of EPA and DHA into adipose tissue is minor and elicited few changes, then supplemental EPA and DHA should be provided prior to chemotherapy initiation. Future trials aimed at attenuating adipose wasting should be implemented earlier in the disease trajectory (as early as tumour diagnosis and prior to delivering chemotherapy) or they might provide a higher dose (3- 4 times greater than the does applied in this study) to observe improvements in adipose tissue function in such a short period of time.

This research confirmed an alteration in the expesssion of proteins involved in mitochondrial function following chemotherapy in adipose tissue and this could be the focus of future studies investigating underlying mechanisms of fat loss in cancer. Another consideration for future trials is to assess body composition, in order to determine the effect of tumour and chemotherapy on various fat depots mass but not just the periuterine adipose tissue investigated in this study. Previous studies have reported different mechanisms contributing to fat accumulation and mobilization in various adipose tissue depots (Palou et al., 2010). Given that variable effects of tumour have been observed on adipose tissue depots (Batista et al., 2012; Bertevello & Seelaender, 2001), the effects of the presence of a tumour and chemotherapy on the other adipose depots should also be investigated as they all contribute to whole body lipid metabolism.

6.6 Conclusions

Adipose wasting is prevalent in advanced cancer patients with VAT loss proceeding SAT loss, however, there is capacity for an increase in adipose tissue mass further away from death. Understanding the mechanisms of adipose tissue loss in neoplastic state and following chemotherapy treatment will enhance our understanding of aberrations of lipid metabolism in cancer and help define interventions to circumvent wasting. Taken together, this work suggests alterations in the expression of mitochondrial proteins contribute to the loss of adipose tissue in anti-cancer therapy. Reduced expression of proteins regulating mitochondrial function influences the adipose tissue metabolism mainly in relation to fat oxidation and synthesis. Overall, it associates with decreased expression of proteins involved in ATP generation, β-oxidation, and lipogenesis. Therefore, interventions to maintain mitochondrial functions may be effective in preventing adipose atrophy during chemotherapy treatment.

Figures

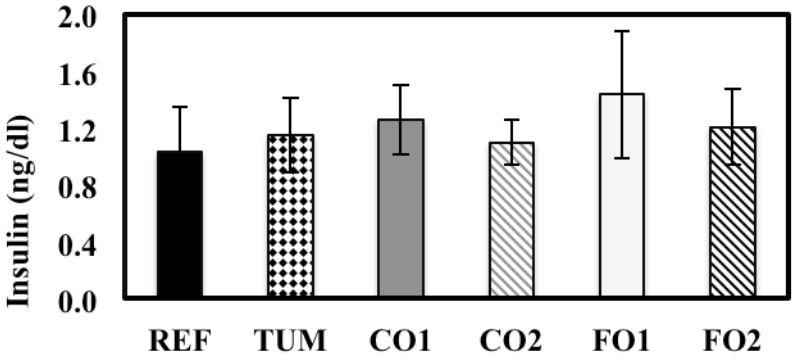

Figure 6-1. Plasma insulin concentrations.

No significant differences between groups ($p<0.05$) determined by Kruskal–Wallis Test. Data are means ± SEM. Abbreviations: REF, Healthy; TUM, Tumour-bearing; CO1, Control diet +1-cycle; CO2, Control diet + 2-cycles; FO1, Fish oil diet + 1-cycle; FO2, Fish oil diet + 2-cycles

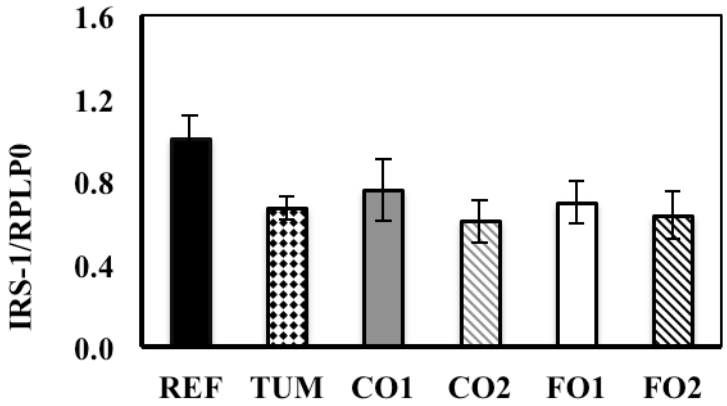

Figure 6-2. Relative mRNA levels of IRS-1 assessed using Real-time PCR.

The mRNA levels of IRS-1 was normalized to the expression of RPLP0 and are shown as mean ± SEM. Results are fold change of gene expression relative to the reference group; No significant differences between groups ($p<0.05$) determined by Kruskal–Wallis Test. Abbreviations: REF, Healthy; TUM, Tumour-bearing; CO1, Control diet +1-cycle; CO2, Control diet + 2-cycles; FO1, Fish oil diet + 1-cycle; FO2, Fish oil diet + 2-cycles

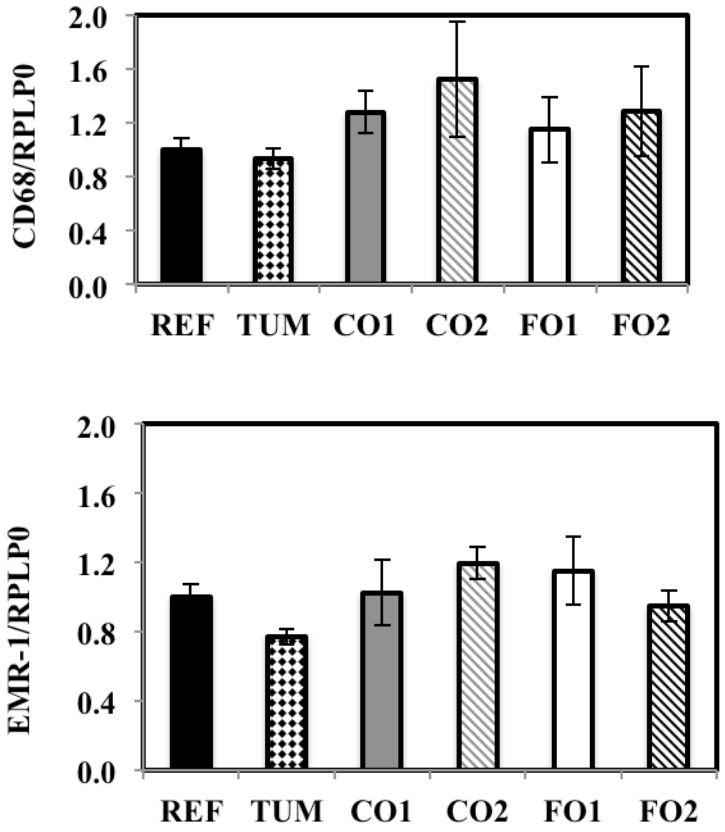

Figure 6-3. Relative mRNA levels of macrophage markers assessed using Real-time PCR.

The mRNA levels of CD68 (macrophage marker) and Emr-1 (F4/80; marker of activated macrophages) were normalized to the expression of RPLP0 and are shown as mean ± SEM. Results are fold change of gene expression relative to the reference group; No significant differences between groups ($p<0.05$) determined by Kruskal–Wallis Test. Abbreviations: REF, Healthy; TUM, Tumour-bearing; CO1, Control diet + 1-cycle; CO2, Control diet + 2-cycles; FO1, Fish oil diet + 1-cycle; FO2, Fish oil diet + 2-cycles

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Appendix A:

Method development for adipocytes isolation from muscle and/or adipose tissue biopsies

Excess fat accumulation in the muscle (myosteatosis) is a pathophysiological condition associated with shorter survival in cancer patients (Antoun et al., 2013; Martin et al., 2013; Sabel et al., 2011). However, it has not been determined whether this condition associates with elevated intramyocellular triglyceride or increased number of adipocytes. The objective was isolating mononuclear cells and adipocytes from skeletal muscle to study their function.

The Alberta Cancer Research Ethics Board approved this study. All patients provided written informed consent to participate. Intraoperative muscle samples were obtained from rectus abdominis (n=19) muscles of gastrointestinal cancer patients (stage II-IV) undergoing surgery. Biopsies were placed in a sterile transfer media containing DMEM /F-12 with (L)-glutamine and HEPES (25mM) included [Gibco™ Dulbecco's Modified Eagle Medium: Nutrient Mixture F-12 (DMEM/F-12)]. One percent antibiotics (penicillin + streptomycin), and 20% fetal bovine serum (FBS) were added to DMEM/F-12 media. Samples were placed in the pre-prepared media and transported on ice to the laboratory within 1 hour of excision. Approximately 150 mg of tissue was used to isolate mononuclear cells, adipocytes, and other cell populations. Any remaining tissue was frozen directly in liquid nitrogen for future analyses.

Adipocyte isolation from skeletal muscle

The goal was to have ability isolate both mononuclear and adipocytes from a muscle biopsy. Therefore, previously published methods were reviewed and a protocol was developed and optimized to enable isolation of both, mononuclear cells and adipocytes, to yield both cell

types. No published study was found that had evaluated simultaneous extraction of these two cell types as each study focused solely on extraction of one or the other. Considering previous available methods for mononuclear cell isolation (McKay et al., 2010) and adipocyte isolation from adipose tissue (Carswell et al., 2012; Laforenza et al., 2013; RODBELL, 1964), an optimized method is summarized in Figure 1. A summary of various tested conditions is presented in Table 1.

Under a sterile flow hood, a 150 mg piece of the muscle biopsy was weighed and minced in 3mL of a collagenase-dispase digestion solution (10 mg/mL collagenase I, Gibco/Invitrogen + 2.4 U/mL Dispase II, Gibco/Invitrogen + 0.5 M calcium chloride; PH adjusted to 7.4) made in sterile culture medium, until tissue is minced into tiny pieces, followed by 10 min incubation at 37℃ (5% CO2). After 10 min, collagenase-dispase solution (1.5 mL) was added to the mixture, agitated by trituration and incubated for another 10 min at 37℃ (5% CO2). Digestion reaction was stopped by adding 15 mL of pre-warmed (room temperature) sterile wash medium containing 20% FBS and 1% antibiotics, transferred to a centrifuge tube, vortexed for 10 sec, followed by centrifugation at 200 x g for 10 min at RT. The two top 500 µL layers of the supernatant (the layers containing adipocytes) were transferred to a separate tube for adipocyte count under a haemocytometer. The remaining layers underwent further steps for mononuclear cell isolation. For adipocyte counting, 20 µL of each 500 µL layers were removed, mixed in equal volume with trypan blue (1:1), triturated and adipocytes in a 20µL solution was counted using haemocytometer under light microscopy.

The yield range varied between (3-74)* 2* 10^4 /ml, however, yield was dependent on tissue appearance with higher yields from fatty muscle samples that had visible fat. A major

limitation was distinguishing between lipid droplets and adipocytes. We approached Oil Red O and Hematoxylin staining on adipose tissue isolated adipocyte, attached to matrigel-cotaed coverslip (explained in the next section). Quantification was not possible with this method and therefore, more robust approaches such as immunohistochemistry for adipocyte markers should be taken instead to verify presence of adipocytes in the skeletal muscle of cancer patients.

Adipocyte isolation from adipose tissue (Carswell et al., 2012; Laforenza et al., 2013; RODBELL, 1964)

Reagents (Digestion buffer), PH=7.4

4% BSA (fatty acid free)

1% Antibiotics

DMEM/F12 containing 15mM HEPES

25 mM HEPES (Media contains 15 mM HEPES, so 10mM extra is required)

Collagenase type I (2mg/ml)

100 μM Adenosine Stock. MW: 267.2

Reagents (Wash Buffer), PH=7.4

4% BSA (fatty acid free)

1% Antibiotics

DMEM/F12 containing 15mM HEPES

25 mM HEPES (Media contains 15 mM HEPES, so 10mM extra is required)

100 μM Adenosine Stock. MW: 267.2

Isolation Procedure:

Adipose tissue samples (1.3-1.5 g) were minced into 5-10mg pieces, and subsequently, 4ml of digestion buffer (2-3ml buffer/1g adipose tissue) containing DMEM F-12 HAM (Sigma), 25 mM HEPES, 40 mg/ml BSA, 2 mg/ml collagenase type I, pH 7.4 were added and incubated in shaking water bath at 37°C for 60 min (80-100rpm). Solution was then filtered through 250 μm mesh filters and washed three times (5ml/each) by wash buffer, pH 7.4. Adipocytes were centrifuged at 400 g for 1 min at room temperature. The upper floating adipocyte layer were taken and stored in ice until counting and culturing.

In order to distinguish adipocytes from lipid droplets, isolated cells were stained with Oil Red O and Hematoxylin. First step was adipocyte attachment to Matrigel-coated coverslips. To do this, isolated adipocytes were maintained in conical tubes containing media at 37°C. Matrigel was thawed at 4°C overnight and coverslips and pipettes were chilled on ice. Using cooled pipetes, 50μl/cm^2 of matrigel were added to the surface of coverslips and smeared across the coverslip to obtain a thin coating of matrigel. Isolated adipocytes were added to the surface of coverslip using plastic pasteur, incubated in 10% formalin for 30-60 min. Coverslips were then rinsed carefully in distilled water, incubated for 5min in 60% isopropanol, followed by 5 min incubation in Oil Red O (300 mg Oil Red O in 100 ml of 99% isopropanol) at RT. Coverslips were rinsed with tap water and immersed in Hematoxylin, incubated 1 min at RT. Following, slides were rinsed with water tap, and observed under phase-contrast microscope. Unfortunately, cells were just attached to the edges of coverslips but most of the cells were washed and could not attach to the coverslip using this technique.

Table A1. Applied changes to the skeletal muscle adipocyte isolation procedure for patients 1-19.

Patient	Digestion buffer	Was buffer	Centrifugation
1-6	710µl of cold solution	710µl of cold solution	200 x g at 4°C for 5 min
7-13	**4.5 ml** of cold solution, **calcium chloride added**	**15ml** of cold solution	200 x g at 4°C for **10** min
14-19	4.5 ml of **pre-warmed (37°C)** solution, calcium chloride added	15ml of **pre-warmed (room temperature)** solution	200 x g at **21°C (room temperature)** for 10 min

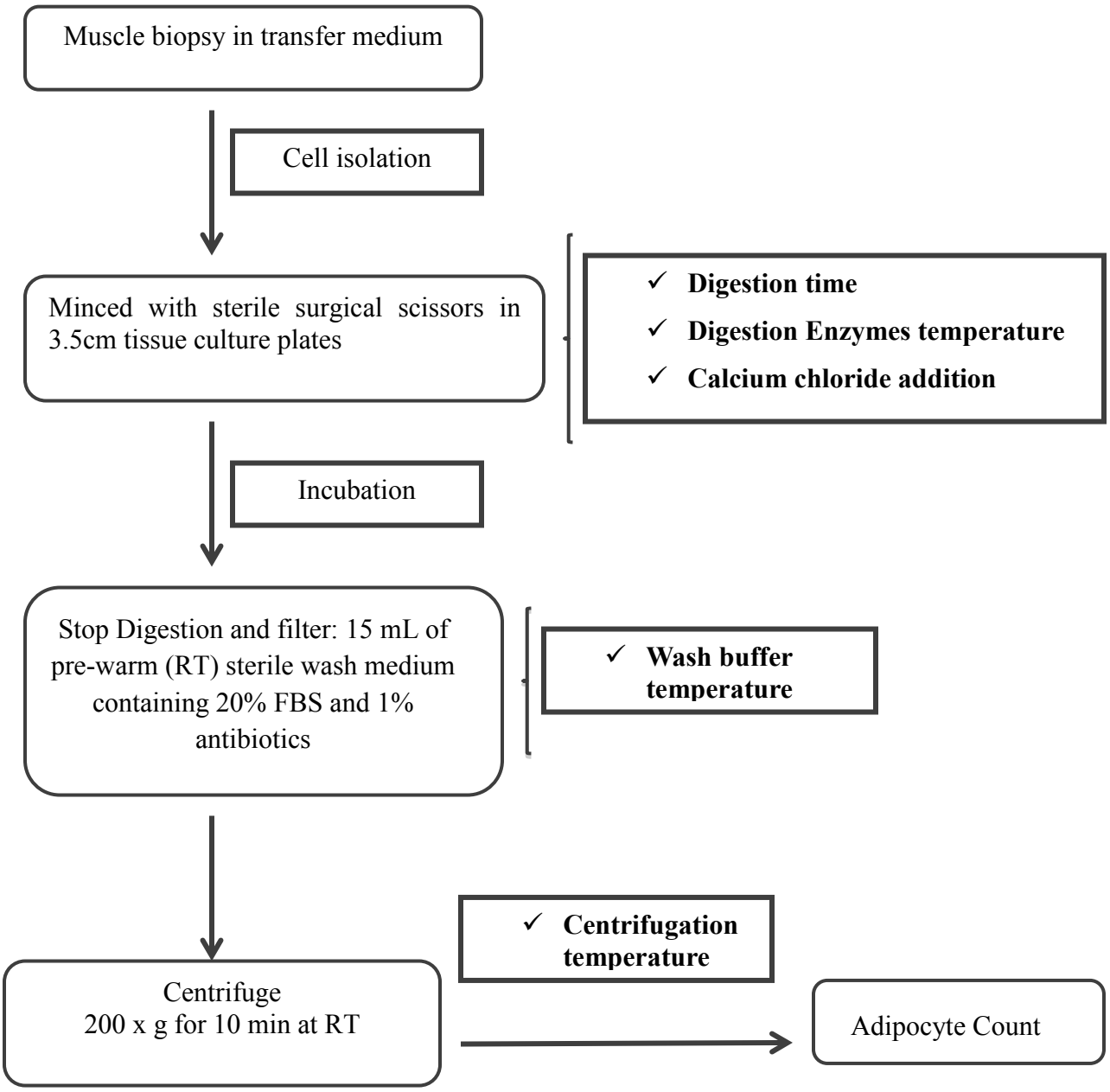

Figure A1. Optimized procedure to isolate adipocytes from skeletal muscle

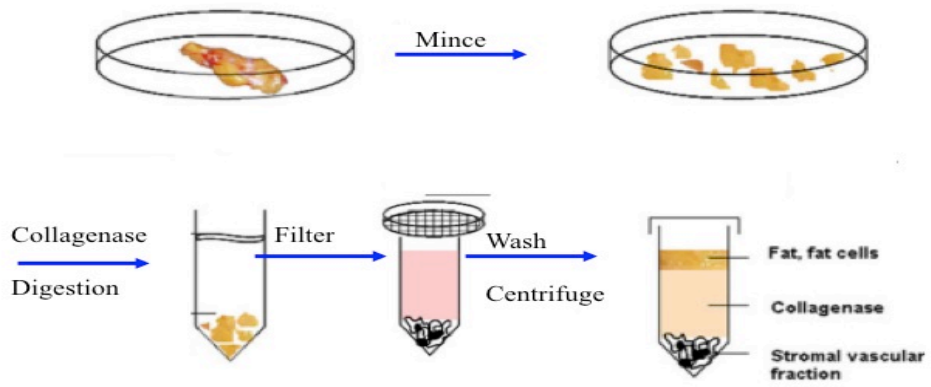

Figure A2. Summary of the procedure to isolate adipocytes from adipose tissue

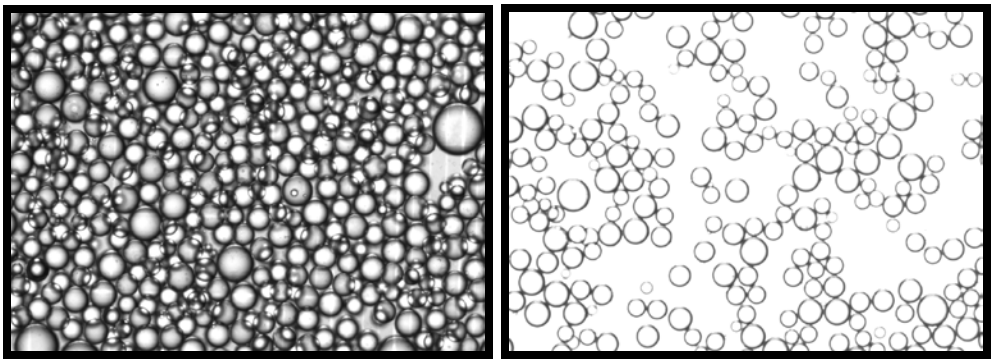

Figure A3. Example of adipocytes isolated from visceral adipose tissue

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Appendix B: Mediators of Inflammation manuscript

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Review Article

Potential Biomarkers of Fat Loss as a Feature of Cancer Cachexia

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Fat loss is associated with shorter survival and reduced quality of life in cancer patients. Effective intervention for fat loss in cachexia requires identification of the condition using prognostic biomarkers for early detection and prevention of further depletion. !No biomarkers of fat mass alterations have been defined for application to the neoplastic state. Several inflammatory cytokines have been implicated in mediating fat loss associated with cachexia; however, plasma levels may not relate to adipose atrophy. Zinc- 2-glycoprotein may be a local catabolic mediator within adipose tissue rather than serving as a plasma biomarker of fat loss. Plasma glycerol and leptin associate with adipose tissue atrophy and mass, respectively; however, no study has evaluated their potential as a prognostic biomarker of cachexia-associated fat loss.This review confirms the need for further studies to identify valid prognostic biomarkers to identify loss of fat based on changes in plasma levels of biomarkers.

1. Introduction

Cancer cachexia is associated with increased mortality and morbidity in cancer patients [1]. By international consensus, cancer cachexia is proposed to be "a multifactorial syndrome defined by an ongoing loss of skeletal muscle mass with or without loss of fat mass that cannot be fully reversed by conventional nutritional support and leads to progressive functional impairment" [2]. A recent review [3] reported elevated lipolysis to be the major reason for fat loss in cancer cachexia [4, 5] although the underlying mechanisms are undefined. As cancer progresses, the majority of patients experience loss of fat. Fat loss precedes muscle loss, associates with shorter survival [6, 7], and is variable with respect to timing and intensity in various cancer populations [3]. Therefore, identification and validation of markers of fat loss are crucial not only for a better understanding of mechanisms, but also to identify fat losing cancer patients who will subsequently develop cachexia. Effective management of cancer cachexia is restricted to early identification of the syndrome; therefore, biomarkers are vital for development of appropriate therapeutic interventions to achieve better outcomes for individual cancer patients.

Adipose tissue (AT) is an active secretory organ, composed mainly of adipocytes and nonadipocyte cells such as inflammatory cells, immune cells, preadipocytes, and fibroblasts [8]. Adipokines are proteins synthesized and secreted from adipocytes which act both locally and distally, contributing to whole body lipid metabolism [9, 10]. In pathophysiological conditions like cancer, macrophage infiltration into AT increases [11, 12], leading to alterations in adipokine production affecting adipose tissue mass and function. Local adipokines produced by AT, circulating cytokines, and lipid mobilizing factors are collectively involved in adipose atrophy in cancer cachexia [13, 14]. Considering adipose tissue as a metabolically active organ as well as the relationship between fat loss and shorter survival in cancer, early identification of fat losing patients may increase the opportunity for therapeutic management of cachexia.

Biomarkers can be applied to represent tissue alterations under both physiological and pathological conditions [15]. A biomarker is "a biological molecule found in blood, other body fluids, or tissues that is a sign of a normal or abnormal process or of a condition or disease." [16]. Biomarkers indicate normal biologic processes, pathogenic processes, or pharmacological responses to a treatment [15]. Biomarkers in the oncology setting, identified using high-throughput sequencing, gene expression arrays, and mass spectroscopy [17], are classified into prognostic, predictive, and pharmacodynamic categories [18–20]. Prognostic biomarkers provide information about likely outcome of a disease, regardless of treatment, whilst predictive biomarkers assess the effect of a particular treatment. Pharmacodynamic biomarkers assess drug treatment effects on a tumour [18–20]. Ideal biomarkers are easily accessible, available, specific and sensitive, noninvasive, inexpensive, consistent, safe, and easy quantifiable in a biological fluid or clinical sample. Biomarkers are consistent across genders and ethnic groups. Levels of the biomarker should not overlap between controls and patients while significantly relating to the outcome of interest using appropriate statistical analysis [18].

While it seems important to identify a prognostic biomarker of cancer cachexia-associated fat loss, no ideal clinical biomarker has been defined yet, which demonstrates a need to identify and subsequently validate potential biomarkers in independent studies. Studies focusing on adipose tissue have identified leptin, free fatty acids (FFAs), and glycerol in plasma as indicators of fat alterations in health and diseases. On the other hand, adipokines including inflammatory cytokines such as interleukin-6 (IL-6) and tumour necrosis factor-α (TNF-α) [21] as well as Zinc-α2-glycoprotein (ZAG) [22] have also been associated with weight and fat loss in cancer. Therefore, circulating levels of these factors may represent new noninvasive prognostic biomarker of adipose atrophy and targets in the detection and management of fat loss in cancer.

One of the major obstacles to identify reliable biomarkers of fat loss in cancer cachexia is variation between studies in how fat loss is assessed. Body mass index (BMI) is frequently used as a clinically accessible measure of human body composition. However, as BMI does not distinguish between fat and fat-free mass, its utility in the settings of fat loss in cancer cachexia is limited [23]. Various methods including bioelectrical impedance analysis (BIA), dual-energy X-ray absorptiometry (DEXA), magnetic resonance imaging (MRI), and computed tomography (CT) scan analysis [24] have been applied to assess body composition in cancer population. CT image analysis, as the gold standard for body composition assessment in cancer patients, has an ability to discriminate and precisely quantify different adipose tissue depots. Many patients have repeated scans over the cancer trajectory enabling assessments in the same individual over time. Application of body composition assessment in the cancer setting has focussed primarily on lean body mass. The studies that do exist reveal loss of adipose tissue as cancer progress [25, 26]. However, further studies are required to establish the timeline and pattern of fat mass alterations in different adipose tissue depots during cancer progression [3]. Moreover, the majority of studies assessing fat mass focus on gastrointestinal cancer patients; there remains a gap in knowledge related to other malignant tumours. Finally, timing of CT scans differs between patients and scans may not be available over a specific time points demonstrating the need for other important prognostic biomarkers of fat loss. Overall, gaps remain related to the association between fat mass alterations assessed by CT scans and circulating markers of fat loss. This article reviews current knowledge around potential prognostic biomarkers of fat loss in cancer which may identify fat-losing cancer patients who would benefit from early therapeutic interventions to improve outcome of cancer patients. Possibilities and potential to apply these markers as prognostic biomarkers of fat loss will be discussed.

2. Inflammatory Cytokines

Serum levels of cytokines associate with clinical features of cancer cachexia such as weight loss; however, no study has specifically assessed the association between serum cytokines and the extent of fat loss in cancer patients. Inflammatory cytokines, such as IL-6 and TNF-α, are produced by tumours and by nonfat cells residing in AT [21] in addition to adipocytes. Plasma levels of inflammatory cytokines are elevated in cachexia [27] and are thought to promote adipose atrophy in animal and human models of cachexia [13]. Pathways of adipose tissue metabolism evoked by IL-6 and TNF-α include inhibition of lipoprotein lipase mRNA expression and activity which prevents fat cells from taking up fatty acids from lipoproteins [28, 29]. These cytokines stimulate hormone sensitive lipase (HSL) and adipose triglyceride lipase (ATGL) activity [30, 31], leading to elevated lipolysis. TNF-α has been reported to prevent preadipocyte differentiation [32] and inhibit expression of lipogenic transcription factors [33]. Collectively, these alterations would result in fat loss.

Serum TNF-α levels negatively correlate with body weight and BMI in pancreatic cancer patients [34]. Tumour presence has been associated with elevated serum IL-6 and TNF-α in mice bearing the Lewis lung carcinoma or B16 melanoma cells compared to controls [35]. In humans, data regarding the role of TNF-α in cancer-associated wasting are controversial. Measuring TNF-α in plasma is challenging due to short half-life and transient nature. Further, the sensitivity of assays used to measure plasma TNF-α is variable, making comparisons between studies limited [36]. On the other hand, TNF-R1 and TNF-R2 (soluble TNF-α membrane receptors) have been applied as serum markers of TNF-α activity due to their longer half-life and greater stability [37].

A comprehensive review of clinical factors associated with cachexia [38] showed little evidence for the association between serum TNF-α and weight loss in cancer, while several studies report

an association of plasma IL-6 but not TNF-α with cachexia-associated wasting rather than cancer per se. Serum IL-6 levels were higher in fat losing gastrointestinal cachectic cancer patients compared to weight stable and noncancer controls. However, no changes in mRNA expression or secretion of IL-6 and TNF-α from SAT were observed [4]. This finding was confirmed in another study showing that circulating IL-6 levels were higher in weight losing non-small-cell lung carcinoma patients compared to weight stable cancer patients [39].

Adipose atrophy has been associated with elevated IL-6 signalling in a preclinical model of cancer cachexia [40]. In patients with gastrointestinal cancer, plasma IL-6 levels significantly correlated with the presence of tumour and increased with each progressive stage of cancer [41]. IL-6 has been reported to be involved in early stages of cachexia [42, 43] and a study conducted in patients with mixed tumor types showed IL-6 levels gradually increased during early stages of cachexia followed by rapid increase prior to death [44]. In contrast, a study in 61 patients with advanced cancer showed no correlation between IL-6, TNF-α, and weight loss [45]. Although circulating IL-6 levels were higher in cachectic mice compared to controls [46], IL-6 receptors deficient (IL-6-R-KO) mice were partially protected so other cytokines may involve in cachexia-associated wasting. Moreover, a study published in 2012 reported that other cytokines, such as IL-1β but not IL-6, may be better indicator of cachexia features such as weight loss and body composition alterations [43].

Collectively, evidence would suggest that inflammatory cytokines are involved in AT depletion in cancer [13, 36, 42]; however, plasma concentrations may represent the presence of a tumour rather than cachexia-associated adipose atrophy per se [41]. Future studies are required to assess changes in adipose tissue depots, both visceral adipose tissue (VAT) and subcutaneous adipose tissue (SAT) over the disease trajectory using validated body composition assessment tools and

correlating those to changes in circulating cytokines. Given that there could be various sources of cytokines contributing to plasma levels, the transient nature of cytokines, as well as the cost associated with cytokine measures, the application of plasma measures of cytokines as biomarkers of adipose tissue atrophy in the clinical study is likely limited. Moreover, the ability of cytokines to evoke cancer cachexia depends on tumour type and the complex response within a network of mediators, rather than a single cytokine [47, 48]. Major gaps remain regarding the association between plasma cytokine levels and fat loss, clinical ranges of abnormal measures, and method sensitivity.

3. Leptin

Leptin is an adipokine, produced mainly by adipocytes [49]. Leptin regulates body weight by activating the anorexigenic neuropeptides and inhibiting the orexigenic neurons such neuropeptide Y (NPY) [50, 51]. Besides body weight and fat mass regulation, leptin is involved in immune function and inflammation [52]. Normally, a lower plasma concentration of leptin is associated with higher NPY secretion; however, NPY pathways have been reported to be dysfunctional in anorectic tumour-bearing rats [53]. Many factors influence leptin synthesis and secretion in adipocytes such as insulin, TNF-α, glucocorticoids, reproductive hormones, and prostaglandins [54, 55]. In humans, the main factor influencing plasma leptin concentration is adipose tissue mass.

A higher concentration of serum leptin in obese individuals is associated with increased fat mass and cell size [10]. Serum leptin is considered to be an accurate, reliable, and highly correlated measure of total body fat [56]. In healthy subjects [57], elderly adults [58], and obesity [52], plasma leptin levels have been shown to be a precise measure of adiposity. A relationship between low fat mass and low plasma leptin levels has also been reported in cancer patients [59–

67]. Advanced gastrointestinal and lung cancer patients experiencing cachexia-associated adipose atrophy exhibited hypoleptinemia [67–69]. On the other hand, breast and gynaecological cancer patients exhibited elevated plasma leptin levels that related to the elevated levels of sex hormones and receptors, rather than cachexia per se [70].

Circulating leptin concentrations have been used as an indicator of fat mass; however further studies are required to examine changes in leptin concentrations that occur throughout the disease trajectory and relative to body fat mass alterations. Longitudinal studies that employ a precise measure of body fat would enable determination of whether changes in plasma levels of leptin change proportional to fat mass alterations. An added level of complexity is that leptin is secreted by both VAT and SAT, with SAT contributing the majority of leptin to plasma due to its larger contribution to overall body mass [65]. Therefore, measures of changes in leptin concentrations over time do not currently represent the type of fat being lost or gained.

Comparison between studies is limited by different assay sensitivities and how leptin values are reported as total, free, or bound leptin. Further, factors such as the type of cancer, BMI, and sex and age influence serum leptin concentration, as reported in adolescents [71], also need to be considered in study interpretation. Low leptin concentrations could be considered a result, not a cause of cachexia, which significantly relates to adipose atrophy and low fat mass in cachexia.

4. Plasma Glycerol

Studies indicate elevated lipolysis to be the main cause of fat loss in cancer [4, 5, 72–75]. During AT lipolysis, FFAs and glycerol molecules are produced by the action of lipolytic enzymes such as ATGL and HSL, which hydrolyze stored triglyceride [30]. Adipose atrophy has been associated with elevated activity of ATGL and HSL in human and animal models of cancer [35,

40, 46]. Elevated lipolysis produces higher plasma glycerol in cachectic cancer patients compared to healthy subjects [74] or weight-stable controls [5]. Lipolytic activity was assessed in 13 cachectic and 14 weight-stable cancer patients by assessing circulating glycerol levels (μmol/L/Kg body fat) as an indicator of *in vivo* lipolysis. Cachexia was defined as >5% weight loss over 3 months or >10% within the previous 6 months. Body fat mass, assessed using BIA, showed lower body fat (% and kg) in the cachectic group compared to weight stable patients. Elevated levels of plasma glycerol, FFAs, and higher expression of genes involved in energy turnover pathways and oxidative phosphorylation revealed increased lipid mobilization from subcutaneous adipose tissue in the cachectic group [72]. These results support those of Agustsson et al. [76] who showed plasma glycerol and FFAs to be higher in newly diagnosed gastrointestinal cancer patients with cachexia who had low body fat mass (kg), assessed using CT images, compared to the weight-stable group. Higher plasma glycerol and FFAs in the cachectic group positively correlated with percent weight loss and negatively correlated with visceral adipose tissue area [76].

Plasma glycerol values in cancer cachectic patients have been reported as μmol/L [77] or μmol/L/Kg body fat [4, 5, 72, 76]. Interestingly, studies focusing on lipolytic activity in cancer cachexia report a narrow range of plasma glycerol for cachectic patients between studies [4, 5, 72, 76], strengthening its use a potential biomarker. Plasma glycerol has been reported as 6.2 ± 2.7 [5], 6.9 ± 1.3 [76], 7.0 ± 4.3 [72], and 9.8 ± 2 [4] (μmol/L/Kg body fat) in cachectic patients compared to weight stable cancer patients reported at 3.1 ± 0.7 [5], 3.9 ± 0.6 [76], 3.4 ± 1.6 [72], and 3.3 ± 0.3 [4] (μmol/L/Kg body fat). Postabsorptive whole body lipolytic rate, assessed by glycerol infusion technique, revealed basal levels of plasma glycerol to be higher in a cancer group compared to controls. While lipolytic rates were similar, glycerol clearance rate varied

between the two groups and contributed to higher glycerol levels. Although preillness weight loss ranged from 0 to 20% in cancer patients, the same results were obtained when data was corrected for body weight [78].

Despite the use of plasma glycerol as an index of whole-body lipolysis, caution should be exercised when considering the results of these studies. Lipolysis results in the release of fatty acids and glycerol from adipose tissue, with glycerol being a better index of lipolysis as FFAs liberated by lipolysis may be reesterified within adipose tissue [79]. AT has very low glycerol kinase activity [80], and glycerol released by lipolysis enters into the bloodstream. However, lipolytic activity is not specific to adipose tissue and occurs also from intermuscular triglyceride stores and plasma lipoproteins [79]. Glycerol concentration may indicate that lipolysis occurs in SAT as glycerol released from visceral adipose tissue lipolysis enters the liver via the portal vein [81]. Therefore, plasma concentrations of glycerol reflect the balance between glycerol release by lipolysis (predominantly adipose tissue) and clearance of glycerol by liver [79] and should be interpreted with caution.

5. Zinc-*α*2-glycoprotein

ZAG is a protein discovered in human plasma [82] that has been associated with presence of several types of carcinomas such as breast, prostate, and lung [83–85]. Elevated serum ZAG, as a routine and reliable measurement, may apply to early diagnosis of cachectic cancer patients with adipose atrophy [86]. ZAG has been considered as an adipokine involved in lipid metabolism in adipose tissue [87, 88]. Both *in vivo* and *in vitro* studies have shown that increased ZAG expression in adipose tissue is associated with increased lipolysis and subsequent fat and weight loss [89, 90]. The exact mechanism by which ZAG participates in fat loss in cancer is not known. ZAG may induce lipolysis through activation of *β*-adrenoreceptors [89, 91] and elevated HSL

activity [92, 93]. Although the mechanism behind ZAG regulation in AT is still unknown, glucocorticoids have been suggested to stimulate ZAG expression in AT [94]. Increased plasma cortisol levels in cachectic tumor bearing mice [93] and in cancer patients [95] have been associated with higher AT ZAG expression and elevated lipolysis. This implies that, in cachexia, glucocorticoids may induce lipolytic activity through an increase in ZAG expression [94, 96].

There is discrepancy in the association between circulating ZAG levels and weight or fat loss in various conditions. Data on serum ZAG levels in obesity are inconsistent, being reported as either increased [97] or decreased [98] which positively and negatively correlated, respectively, with BMI. Elevated serum ZAG levels have been observed in chronic heart failure and haemodialysis patients suggesting ZAG to be a marker of fat catabolism [22]. In contrast, two studies in cancer patients [77, 92] demonstrated that plasma ZAG levels may not be a good biomarker of cachexia-associated features such as weight and fat loss. Twenty-five GI cancer patients underwent curative abdominal surgery and were categorized as cachectic or weight stable. Cachexia was defined as unintentional weight loss of more than 5% during the previous 6 months. mRNA and protein levels of ZAG in subcutaneous adipose tissue were higher in cachectic cancer patients compared to weight-stable cancer patients which significantly correlated with fasting serum glycerol levels and weight loss. In this study, however, there was no significant difference in circulating ZAG levels between cachectic and weight stable cancer patients. Production of ZAG by tumours and nonadipose tissue, such as the liver, may also affect ZAG plasma levels [92]. This result is consistent with Rydén et al. [77] who report that ZAG is a locally produced factor, promoting AT lipolysis, but not secreted predominately to circulation [77]. Therefore, circulating levels of ZAG are not likely to relate to fat loss in cancer cachectic patients but instead may mediate local lipid mobilising action in adipose tissue.

6. Conclusion

Patients with advanced cancer frequently suffer weight and fat loss. Accelerated loss of adipose tissue is associated with shorter survival, reduced quality of life, and decreased muscle mass during cancer progression [6]. Due to the role of adipose tissue in mediating human metabolism, identification of prognostic biomarkers of fat loss in cancer may help to identify fat losing cancer patients for early therapeutic interventions, improved survival, and prevention of muscle atrophy in cancer patients.

No studies in cancer have identified a prognostic biomarker of fat mass alterations nor have the sensitivity, specificity, and reproducibility of potential indicators been assessed in the neoplastic state. Inconsistency in the literature may be due to varying sensitivity of assays used to measure plasma levels of mediators, heterogeneity of patient populations and treatment, and various body composition assessment methods. Inflammatory cytokines appear to be mediators of cachexia-associated features such as fat loss [13, 36, 42]; however, they do not fulfill several components of biomarker criteria. Relationship between circulating cytokines and degree of fat loss in cancer has not been assessed. ZAG in plasma has been suggested to indicate the presence of some type of tumours, and in AT, ZAG can act locally to modulate lipolysis. Literature regarding the potential of plasma ZAG to be a biomarker of fat loss during the development of cancer cachexia is inconsistent. Enhanced adipose tissue ZAG expression in cancer cachexia suggests that ZAG could be a local catabolic mediator within the tissue rather than being a biomarker of fat loss [77]. Therefore, the ability of ZAG to be applied as a marker of lipid utilization in cachexia syndrome and to indirectly represent fat loss is limited.

Plasma glycerol and leptin may have potential to be considered as biomarkers of lipolysis and fat mass, respectively; however, no study has defined a confirmed range and optimal cut-off points

for these markers. It is not clear whether a single biomarker or combination may have the most prognostic value, as no study has assessed various combinations in a cancer population. Measuring changes in fat mass over time concurrent with circulating levels of biomarkers of fat mass would provide valuable information about application of proposed fat loss biomarkers throughout the disease trajectory. These studies would help establish valid criteria to identify loss of whole body fat mass based on changes in plasma levels of these specific biomarkers.

Alterations in fat mass and composition between visceral and subcutaneous depots are divergent and vary over the cancer trajectory. The proportional reduction of each fat depot may be a consideration when establishing biomarkers. For example, it remains to be determined whether decreased leptin levels indicate the loss of visceral or subcutaneous adipose tissue in cancer. Future studies should consider the metabolic differences between these depots in determining specific biomarkers.

Although many of the proposed biomarkers are economical, easy, and quick to quantify in plasma, further steps such as comparison of plasma levels in healthy, weight stable, and weight losing cancer patients as well as their correlation with various degrees of fat loss assessed by CT images should be considered in determining capacity for application of a prognostic biomarker of fat loss in cancer. Proper study design, combined with extensive testing, and quantitative measurement of large numbers of proteins in body fluids using advanced techniques [99] as well as statistical validation of prognostic biomarkers [100] are important factors in identification of fat loss biomarkers. This review confirms the need for further studies to (1) assess how alterations in fat mass is reflected in measurable biomarkers, (2) minimize variations that may confound establishment of a biomarker, and (3) increase specificity and sensitivity of methods to detect biomarkers in samples at minimum levels or in repeated measures.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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Apendix C: Clinical Nutrition manuscript

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Original article

Loss of visceral adipose tissue precedes subcutaneous adipose tissue and associates with n-6 fatty acid content

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Summary:

Background & aim: During cancer development, fat loss occurs in most cancer patients. Characterization of the behavior of fat loss from visceral (VAT) and subcutaneous adipose tissue (SAT) depots has not been established. The first objective of this study was to assess the intensity and time course of changes in VAT and SAT depots of advanced cancer patients in the year preceding death. Secondly, this study explored the differences in adipokine content and fatty acid composition between VAT and SAT depots and in relation to changes in fat mass.

Methods: Longitudinal quantitative analyses of computed tomography images was conducted to define changes in adipose tissue cross sectional areas in fat depots in advanced colorectal and chol- angiocarcinoma cancer patients (n=46) at mean time points corresponding to 9, 6, 3 and 1 month before death. Proportions of adipose tissue fatty acid and adipokine content were characterized in a second cohort of advanced colorectal cancer patients (n =16).

Results: On average, loss of total adipose tissue (TAT) happens at all time intervals but there is an elevation in the intensity of loss close to death. Nine months from death, 42% of patients were losing fat (Mean TAT cross sectional area change = -0.2 ± 13 cm^2) whereas within one month from death, fat wasting was observed in 78% of patients (-60.1 ± 9.2 cm^2, P =0.001). However, loss of TAT did not reflect changes in VAT and SAT in the same direction or intensity. Intensity of VAT loss remains constant throughout the disease progression whereas SAT is more likely to be gained further way from death. Nine month prior to death, mean change in cross sectional area of VAT was _7.9 ± 6.8 cm^2 whereas, mean change in CSA of SAT was 7.4 ± 7.7 cm^2 (p = 0.03). One month before death, mean VAT and SAT absolute changes were -24.5 ± 4.9 cm^2 and

-34.5 ± 5.2 cm^2, respectively (p=0.05). Moreover, fat losing patients had higher proportions of polyunsaturated fatty acids, especially n-6 fatty acids, in VAT compared to patients who were gaining fat (mean = 15.4% in losing group vs. 13.4% in gaining group; p=0.03). VAT contained more monocyte chemoattractant protein-1 than SAT, whereas leptin levels were higher in SAT. Conclusions: Further from death, VAT and SAT behave differently whereas close to death, accelerated loss occurs in both depots. These differences are further characterized by differences in fatty acid composition and adipokine levels.

1. Introduction

Body composition assessment using computed tomography (CT) images in advanced cancer patients reveals rapid loss of adipose tissue as cancer progresses [1e3]. Fat loss has been reported to be an important predictor of the length of survival [4,5]. Loss of fat occurs from both visceral (VAT) and subcutaneous adipose tissue (SAT) depots; however, the severity of loss and the type of fat being lost (VAT vs. SAT) have not been consistently demonstrated. VAT and SAT vary in anatomic location, endocrine function and adipo- kine secretion, lipolytic activity, response to insulin and cytokine production. Lipolysis of VAT enables direct delivery of free fatty acids to liver, which may exacerbate an already dysregulated metabolic state [6,7]. This divergent behavior demonstrates the need to understand the pattern of loss in both visceral and sub- cutaneous adipose depots using validated body composition assessment tools.

Alterations in adipose metabolism can be induced by inflam- matory adipokines [8] and may also be associated with altered fatty acid composition of the tissue. Although adipose tissue composi- tion is a major indicator of fatty acid dietary intake, especially for n- 3 and n-6 polyunsaturated fatty acids [9], alterations in adipose tissue fatty acid composition may alter the production of carcino- genic mediators [10], lead to adipose atrophy and affect cancer progression.

Retrospective analysis of serial CT images analysis in colorectal cancer (CRC) patients [2] as well as quantitative analysis of CT images in a cohort of patients with advanced solid tumors [1] showed fat loss increases exponentially in the year preceding death with the greatest loss of adipose tissue occurring within 3 month prior to death [4]. While there was a general trajectory involving loss of adipose tissue, tissue stability and even gain of adipose tissue can occur during some periods at >3 months prior to death [1]. However, these previous studies have focused on

total adipose tissue (TAT). A major gap remains regarding the specific behavior of VAT and SAT in cancer patients which led us to explore the severity and time course of changes in VAT and SAT cross sectional areas (CSA) in a retrospective cohort of advanced cancer patients during the year approaching death. In a second cross- sectional study, we aimed to identify adipose tissue characteris- tics such as adipokine levels, and fatty acid composition of VAT and SAT depots and to determine the relationship between adipokine content, fatty acid composition and change in fat mass assessed using CT images. It was hypothesized that VAT would be lost at a greater intensity than SAT and would be associated with higher concentrations of adipokines and a greater proportion of PUFAs. Characterizing this association will enhance our understanding of aberrations of adipose tissue metabolism in cancer patients.

2. Materials and methods

2.1. Cohort1: retrospectivelongitudinalstudytoidentifyalterations in visceral and subcutaneous adipose tissue areas in the year preceding death

Alberta Cancer Board Research Ethics Board (Edmonton, Alberta, Canada) reviewed and approved this study. Our site encompasses patients in northern Alberta, Canada. Data regarding cancer site, morphology, clinical and demographic characteristics for each of the subjects were collected from the Alberta Cancer Registry. De- tails regarding the patients' characteristics and sampling have been previously described in Lieffers et al. [2] and Prado et al. [1]. Loss of adipose tissue is noticeable approaching the end of life and to take advantages of repeated measures, we focused on colorectal and cholangiocarcinoma cancer patients with !4 CT images in the year preceding death. Colorectal and cholangiocarcinoma patients were not different in sex distribution, age at death, survival time, and tumor morphology and body composition features

(ie, muscle and adipose tissues) at the same time to death [1].

Date of death rather than the date of diagnosis, was selected as the point of departure for this analysis to capture patients at the

same time in cancer trajectory. Changes in total, visceral and sub- cutaneous adipose tissue cross-sectional areas were calculated as the absolute change between two consecutive CT images (i.e., CT_2-CT_1). Date of CT_1 (CT closer to death) was subtracted from the date of death to define the time to death. Longitudinal quantitative analysis of CT images for changes in VAT, SAT and TAT CSAs were evaluated for mean time points categorized into 9 (220-365d), 6 (140-219d), 3 (60-139d) and 1(0-59d) month before death.

Using absolute values of changes in cross sectional areas in this cohort, total adipose tissue categories for loss, gain and stable changes were defined based on a previous report by Prado et al. [1]. As 14.7 cm^2 total adipose cross sectional area at L3 is equal to 1 kg of whole body fat mass [11], TAT changes were categorized as stable if the values were _14.7 < stable < 14.7 cm^2 in the period of assess- ment. For VAT and SAT, changes between _3 and þ3 cm^2 were considered stable as the minimum detectable change of CT mea- surements is 3 cm^2 [12].

2.2. Cohort 2: biological analysis of adipose tissue to assess fatty acid composition and adipokines

Alberta Cancer Board Research Ethics Board (Edmonton, Alberta, Canada) reviewed and approved this study. Data regarding cancer site, morphology, clinical and demographic characteristics for each of the subjects were collected from the Alberta Cancer Registry. Patients

were recruited from the Tom Baker Cancer Centre, Uni- versity of Calgary Medical Clinic, Foothills Medical Center and Peter Lougheed Hospital (Calgary, Alberta, Canada) between January 2008 and December 2010. Colorectal cancer patients with liver metastases undergoing abdominal surgery as part of clinical care, who provided signed informed consent were eligible to participate in this study. At the start of the surgical procedure, biopsies of adipose tissue (1e2 g) were taken using sharp dissection without using electrocautery. Subcutaneous fat was harvested from the periumbilical area; VAT was collected from subomental fat at the surgical site. Biopsies were directly snap frozen using liquid nitro- gen and stored at _80 –C until assayed. Collected samples were kept at the Alberta Cancer Research Biorepository/Canadian Breast Cancer Foundation Tumor Bank and the University of Calgary HPB/ GI Tumor Tissue Bank. Analysis was performed on patients who had provided both subcutaneous and visceral fat (n =16).

CT images for this study were taken prior to surgery (within 79 ± 80 days) and after the procedure (at 149 ± 89 days) surgery. In this study, the timing and the interval between the two scans differed between patients, therefore, the rate of change between the two CTs was calculated, expressed as a percentage, and divided by the number of days in each interval to calculate the daily rate of change for each patient. Then, the daily rate of change was multi- plied by 100, and expressed %change/100d to enable comparison between patients. The precision error for adipose is ~1.5% [12], therefore, a change between -2% and + 2% was considered tissue maintenance.

2.3. CT image analysis

In an oncologic population, CT images as a routine part of treatment are available from patient

records. All participants in both cohorts had body composition measured using secondary analysis of images that were retrieved from the patient clinical record. Total adipose tissue area measurement was conducted by analyzing CT scans at the 3rd lumbar vertebra (L3). The third lumbar was selected as a standardized landmark, as adipose tissue areas in a single CT image at L3 correlate well with whole body fat mass [11,12]. Regression equations for VAT have not been estab- lished for cancer populations; however, VAT cross sectional area at L3 strongly correlate with whole-body VAT volume in healthy populations [13]. Two consecutive transverse CT images extending from L3 to the iliac crest were assessed using Slice-O-Matic (V4.2; Tomovision, Montreal, QC, Canada). Adipose tissue cross-sectional areas were calculated by using standard Hounsfield unit thresh- olds of -150 to -50 for visceral adipose tissue [14] and -190 to -30 for subcutaneous adipose tissue [15]. Tissue cross-sectional areas (cm^2) were calculated by summing the given tissue pixels and multiplying by the pixel surface area. Average of tissue areas was calculated for 2 consecutive images; the average CV of paired im- ages was 2.7% for adipose tissue areas. Cross sectional areas of visceral and subcutaneous adipose tissues were summed to calculate total adipose tissue (TAT) areas.

2.4. Adipose tissue fatty acid analysis

Frozen adipose tissue was ground in liquid nitrogen using mortar and pestle until crushed into a fine powder. Lipids were extracted using modification of the Folch procedure [16], by adding chloroform/methanol (2:1, vol/vol). Thin layer chromatography was used to isolate triglyceride and phospholipids, followed by sapon- ification and methylation for TG and direct methylation for PL containing tubes. Gas-liquid chromatograph was used to separate Fatty acid methyl esters (Vista 8400 autosampler, Varian CP-3400). The system used a bonded phase fused silica

capillary column, BP20: 25 mm 0.25 OD SGE product. Splitless injector was used to flow Helium, as the carrier gas, at a flow rate of 2.6 ml/min. These conditions separate saturated, monounsaturated and poly- unsaturated fatty acids from 12 to 24 carbon chain lengths by comparison with known standards. Proportions of saturated (SFA), monounsaturated (MUFA), polyunsaturated (PUFA), n-6 and n-3 fatty acids were calculated.

2.5. Adipokine protein analysis

Visceral and subcutaneous adipose tissue samples were mixed with NP40 Cell lysis buffer (Invitrogen Corporation, Frederick, MD, USA) in a 1:2 ratio for homogenization. A glass on glass homoge- nizer was used to homogenize the tissue. The samples were then centrifuged at 20000 g for 10 min at 4 –C. Lipid fractions were discarded and the supernatant fraction separated from the pellet. Supernatant fractions were stored at -80º C prior to analysis. Supernatant fractions were diluted in phosphate buffered saline and protein was quantified using Pierce BCA Protein Assay (Thermo Scientific, Rockford, IL, USA). Absorbance was read by spectropho- tometry at 562 nm. Tissue homogenate was standardized for pro- tein content based on the sample with the lowest protein content and analyzed for presence of interleukin 6 (IL-6), leptin, monocyte chemotactic protein 1(MCP-1), and tumor necrosis factor alpha (TNF-a) (Human Adipocyte Milliplex kit, Millipore, Billerica, MA, USA) using Luminex xMAP technology (Bioplex-200, Bio-Rad Lab- oratories, Mississauga, ON, Canada). Adiponectin was quantified by enzyme-linked immunosorbent assay (Human Adiponectin ELISA, Millipore, Billerica, MA, USA).

2.6. Statistical analysis

In the longitudinal cohort study, data are reported as mean ± SEM and generalized estimating

equations (GEE) was used to analyze the longitudinal changes of visceral, subcutaneous and total adipose tissue cross sectional area. A bonferroni test was used for post-hoc analysis of the data. In this study, GEE was preferred to repeated-measures ANOVA for analyze of longitudinal data due to the presence of missing CTs for some data points. GEE provides unbiased results where the number of measurements for each individual may differ. Differences in proportions between gaining, losing and stable groups were compared using Chi-square test. Data were expressed as mean ± SD in the second study and statistical analysis was completed using the paired two-sample t-tests in the second study. Spearman's rank correlation tests were used to determine relationships between fatty acid composition and fat mass change. Statistical analyses were conducted using SPSS (SPSS for Windows, version 22.0, SPSS, Chicago, IL) and the p value less than 0.05 was considered as a statistically significant difference.

3. Results

3.1. Cohort1: retrospective longitudinal study to identify alterations in visceral and subcutaneous adipose tissue areas in the year preceding death

All patients had stage IV colorectal cancer or chol- angiocarcinoma with a mean age of 57 years and median 13 months to death (Table 1). There were no differences in demographics between patients ($P > 0.05$). Variation in total adipose tissue cross sectional area at L3 ranged from 5.1 cm^2 to 858.9 cm^2. On average, loss of TAT occurred at all time- points but the intensity of loss increased as patients approach death (Fig. 1). Nine months prior to death, fat loss was happenning in 42% of patients (Mean TAT cross sectional area change = -0.2 ± 13 cm^2) whereas one month prior to death, 78% of patients were experiencing fat loss (-60.1 ± 9.2 cm^2, P =0.001) (Fig. 1).

Stratification of patients into fat stable, losing and gaining groups showed that some patients experienced tissue stability or gain at some time-points, primarily further from death. Nearly half the patients were gaining fat at 9 months (46%) whereas only 10% were gaining fat at 1 month (Table 2). Assessment of TAT cross sectional area changes during cancer trajectory can mask what is occurring specifically in each depot. Data reveals divergent behavior between visceral and subcutaneous depots. No significant differences in TAT, VAT or SAT cross sectional area were observed between 3 and 6 months. Intensity of VAT loss was not significantly different at times close to death compared to 9 and 6 months (Fig. 1). Loss of SAT was at its lowest intensity 9 months from death, with 59% of patients experiencing gains in SAT during this time period. Loss of SAT was more prevalent as death approaches (Fig. 1). Nine months before death, mean change in CSA of VAT was -7.9 ± 6.8 cm^2 whereas, mean change in CSA of SAT was 7.4 ± 7.7 cm^2 ($p = 0.03$), (Fig. 1), suggesting different behavior of VAT and SAT further away from death in this group. Variability in VAT and SAT behavior is exemplified by two cancer patients of the same age, sex, and BMI who are losing approximately the same amount of TAT. Patient 1 was losing TAT at the intensity of -55.5 cm^2 nine months prior to death; patient 2 was losing TAT at -49.9 cm^2. However, patient 1 lost -80.4 cm^2 of VAT and gained 24.9 cm^2 of SAT whereas patient 2 lost -33.8 cm^2 of VAT and -16.1 cm^2 of SAT. Mean time to death was 11 months and 18 months, respectively for patient 1 and patient 2. This example illustrates the variability expected among cancer populations for adipose tissue changes during the last year of life.

To further elucidate depot specific behaviors, patients were classified into groups according to whether they were experiencing loss or gain of VAT and SAT. As illustrated in Fig. 2, nine months before death, 42% of patients were gaining both VAT and SAT while 23% were

experiencing VAT loss concurrent with SAT gain. Within one month from death, however, the majority of patients (86%) were experiencing loss of both VAT and SAT. There was a clear downward trend in the percentage of patients who were gaining SAT, which decreased from 62% to 9% over the study period.

3.2. Cohort 2: biological analysis of adipose tissue to assess fatty acid composition and adipokines

3.2.1. Patient population

Cohort 2 was similar to cohort 1 in diagnosis, advanced stage, age, BMI and the proportions of male patients. These similarities between cohort 1 and 2 patient populations enable an informative picture of adipose tissue alterations in advanced cancer patients. Cohort 2 consisted of stage IV colorectal cancer patients who pro- vided both visceral and subcutaneous adipose tissue samples (n=16) and all had liver metastases (Table 1). Despite generally advanced disease, the majority of patients were overweight or obese (mean BMI =27.9 ± 5.2 kg/m2). Not all subjects had a weight loss history available.

3.2.2. Adipose tissue triglyceride fatty acid composition

The most abundant TG fatty acids in both VAT and SAT depots were 18:1 n-9 > 16:0 > 18:2 n-6. The types of fatty acids found in TG of VAT and SAT were similar, with the exception of 16:1n-9 which was more abundant in VAT. Proportion of total saturated fatty acids (30.8 ± 4.3% vs. 30.1 ± 4.2%; p =0.64), monounsaturated fatty acids (54.5 ± 3.0% vs. 54.2 ± 6.7%; p =0.86), or n-3 (1.2 ± 0.4% vs. 1.2 ± 0.4%; p =0.99) and n-6 (13.5 ± 2.5% vs. 14.4 ± 6.9%; p =0.57) polyunsaturated fatty acids were not significantly different be- tween visceral and subcutaneous

depots, respectively.

3.2.3. Adipose tissue phospholipid fatty acid composition

The fatty acid composition of PLs of visceral and subcutaneous adipose tissue is shown in Table 3. The fatty acid composition of PLs in VAT differs significantly from that of SAT, with respect to SFA and PUFA content (Table 3). There was a significantly higher proportion of SFAs in SAT contributed by higher proportions of 14:0, 16:0 and 18:0. The higher proportions of n-6 FA in visceral adipose tissue PLs were attributable to 20:3 n-6, 20:4 n-6, and 22:2 n-6.

3.2.4. Adipose tissue adipokine composition

The protein levels of 5 adipokines including IL-6, TNF-a, leptin, adiponectin and MCP-1 were compared between visceral and subcutaneous adipose tissue (Table 4). Adipokine amounts were variable between depots but overall, there was no significant dif- ference in adiponectin, IL-6, TNF-a between these depots. SAT contained higher protein levels of leptin compared to VAT (Table 4). MCP-1 levels were significantly higher in VAT compared to SAT. For TNF-a, values were below the level of quantification in 11 subjects of 16; therefore these values are not shown.

3.2.5. Fat mass alterations over time and association with adipose tissue fatty acid composition and adipokine content

Among patients with both VAT and SAT samples available (n =16), 7 had CT images available before and after surgery. From the first to the second CT image, the majority of patients (n =5) were losing fat and just 2 patients were gaining fat. In the group losing fat, mean total AT rate of change was -21.3 ± 18.3%/100d whereas for those gaining fat, the mean increase was 5.3 ± 1.5%/ 100d. In the fat losing group, mean rate of loss from VAT (-60.7 ± 57%/100d) was greater

than for SAT (-10 ± 10.6%/100d) between CT scans (p =0.05).

None of the adipokines measured in both VAT and SAT at the time of operation correlated with fat mass alterations after surgery (r = 0.9, p > 0.05). No correlation between changes in fat mass and proportion of FAs in subcutaneous adipose tissue PLs and TGs were observed. A statistically significant inverse correlation was found between the changes in fat mass and proportions of TG-PUFAs within the VAT depot (r =-0.8, P=0.03). Patients who were losing fat had higher proportions of PUFAs in their VAT compared to patients gaining fat (16.8% vs 14.5%; p=0.02). Proportions of SFA and MUFA in VAT did not differ between fat losing and gaining group (P =0.42, P= 0.64, respectively), however, proportions of n- 6 fatty acids in VAT were negatively correlated with fat mass al- terations (r =-0.8, p= 0.03) (Fig. 3).

Mean concentrations of VAT n-6 PUFAs were significantly higher in the fat losing group compared to gaining group (mean= 15.4% in losing group vs. 13.4% in gaining group; p =0.03). N-6 PUFAs decreased linearly from a maximum of 16.3 (% total fatty acid content) in patients with loss of fat to 13.1% in patients gaining fat.

4. Discussion

Adipose tissue can be gained or lost in the year preceding death. As death approaches, the majority of patients lose fat with many experiencing what would be considered high intensity of loss. Gain or stability of adipose tissue was observed at 9 and 6 months prior to death. We observed that changes in different fat depots did not necessarily coincide. Therefore, assessment of depot behavior rather than total adipose tissue per se, may be a better indicator of alter- ations in adipose tissue, especially further away from death as changes in TAT masks what occurs specifically in each depot. Moreover, the underlying physiologic changes leading to alterations in

each depot may vary, and this will require further interrogation.

Previous studies have reported greater fat loss from the intra- abdominal depot than abdominal subcutaneous regions in cancer patients [17,18]. This is the first study assessing changes in VAT and SAT cross sectional areas in a year preceding death using longitu- dinal CT images. Focusing on gain or loss of each depot specifically, intensity of VAT loss remains constant throughout the disease progression whereas SAT is more likely to be gained further way from death. Therefore, further away from death, behavior of VAT and SAT are divergent whereas close to death, marked loss occurs from both depots. Identifying the time course of changes and the intensity of VAT and SAT change over the disease trajectory may help to define the onset of wasting.

There are few data on adipose tissue fatty acid composition in cancer [19,20], and the adipose tissue fatty acid profile of cancer patients is not well established. Our data demonstrate differences in visceral and subcutaneous adipose tissue of patients with advanced CRC. While there was no significant difference in TG composition between VAT and SAT, a higher proportion of SFAs was observed in phospholipids of SAT and more PUFAs in visceral adi- pose phospholipids which may be related to membrane associated functions [21,22]. The variability is likely driven by diet of in- dividuals as the major determinant of adipose tissue composition is dietary intake [21,22]. The retrospective study design did not allow for determination of dietary intake and this information is not routinely collected. Dietary intake of an individual can change

through the cancer trajectory to influence adipose tissue mass and composition. Moreover, we had only one time assessment of adi- pose tissue fatty acid composition at the time of surgery,

which limits our ability to interpret if there was any alteration due to cancer presence and progression.

Studies in non-cancer states reported higher amounts of satu- rated fatty acids in visceral adipose tissue compared to subcutaneous [6,23]. However, site associated differences in AT fatty acid compo- sition [23] should be considered when comparing the results of these studies. Higher amounts of SFAs in abdominal SAT compared to gluteal-femoral subcutaneous fat has been reported [24] which may contribute to the higher SFAs in SAT observed in this study compared to the previous studies. Also, in the current study we focused on TG and PL fatty acid composition separately whereas the majority of studies report FA composition of whole tissue [6].

Assessing the relation between adipose tissue composition and mass changes in the second study, we found that, in general, patients were losing visceral adipose tissue at an accelerated rate compared to subcutaneous, consistent with our first study, and the patients with higher amounts of PUFAs, especially n-6 fatty acids in their VAT TGs were losing fat. On the other hand, patients who gained fat had the least amount of n-6 fatty acids in their visceral adipose tissue. This relationship may alternatively be explained by observations of enhanced expression and activity of hormone- sensitive lipase (HSL) in adipocytes of weight losing cancer cachectic patients [25,26]. HSL shows selective hydrolysis of TGs which preferentially releases fatty acids from sn-1 and sn-3 positions of TGs [25] and PUFA is typically found at the sn-2 in a TG molecule [27].

The protein level of 5 adipokines were compared between depots to reveal that MCP-1 levels were higher in VAT whereas SAT had higher leptin levels. There was no significant difference

in the amounts of adiponectin and IL-6 between depots. TNF-a levels were below detectable limits. A previous study reported MCP-1 and TNF-a mRNA levels in both intra-abdominal and subcutaneous depots to be similar between pancreatic cancer patients and non-cancer controls [18]. However, there was a negative association between mRNA expression of MCP-1 and TNF-a in intra-abdominal adipose tissue and post-operative change in intra-abdominal mass assessed by CT scans [18]. We observed in the first cohort that VAT loss occurred with greater intensity than SAT, further away from death so it is possible that increased MCP-1 production by VAT, observed in our second study, might contribute to greater fat loss from VAT in cancer. However, due to small number of patients with two CT scans avail- able in this study, the difference did not reach statistical significance.

Longitudinal CT imaging to describe changes in adipose tissue in advanced cancer patients is a major strength of this study. CT im- aging, as a gold standard method, has the ability to precisely

quantify adipose depots. Understanding the fatty acid composition of depots as a first step may be important in determining different metabolic behaviors of VAT and SAT. No studies to date have assessed the relationship between adipose tissue fatty acid composition and mass alterations in cancer. To relate fat mass changes to adipose tissue fatty acid composition, it was necessary to provide a defined time period between the collection of adipose tissue and CT image. However, due to small number of subjects, patients with a CT image within 2e7 months of a surgery were selected from the population. Therefore, CT images that were available in study 2 depict changes mostly due to surgery not CRC per se. Previous studies have reported that six months following surgery, weight was reduced from baseline due to the catabolic response to the operation [28e30] and stabilizes after 12 months [30]. Therefore, fat loss observed in these patients may also be due to the surgery associated-catabolic and inflammatory response in addition to cancer presence.

We acknowledge that our cross- sectional study has limitations of having small number of patients and no non-cancer controls were assessed. What was consistent, however, is that those losing fat, lost VAT at an accel- erated rate compared to SAT. This may reflect fat loss would happen regardless of where a patient is in the disease trajectory. Therefore, for both cohorts we can conclude that VAT loss occurs at greater intensity and precedes SAT loss in the disease trajectory. We acknowledge that our results need to be confirmed in larger pop- ulation of cancer patients; however, the association between n-6 PUFAs amount and fat mass alterations was remarkable even with a small number of patients.

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Authors' contributions

M.E. conducted research, analyzed data and wrote the paper; V.C.M assisted with data analysis and writing of manuscript; V.E.B, O.F. B and L.E. R contributed to writing and revising the manuscript. All authors have commented on the manuscript and approved the final version.

Conflicts of interest The authors have no conflict of interest to declare.

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Table 1: Patient characteristics in cohort 1 and cohort 2

Cohort 1		
Patients Characteristics	**Colorectal**	**Cholangiocarcinoma**
Patients (n)	29	17
Male (%)	67	63
Median time to death at diagnosis (months)	11.5 (6, 24)	16.0 (6, 91)
*Age (y)	55.5±11.2	58.0±7.3
*[a] BMI (kg/m^2)	25.0±6.5	25.9±5.0
Cohort 2		
	Colorectal	
Patients (n)	16	
Male (%)	69	
*Age (y)	58.2 ±10.3	
*BMI (kg/m^2)	27.9 ± 5.2	

*Mean± SD, [a] BMI information was available for 23 colorectal and 15 Cholangiocarcinoma patients

Table 2. Proportions of patients of losing, gaining or stable in total adipose tissue at 9, 6, 3 and 1 month prior to death

Group	Mean Time to Death (months)				
	9	**6**	**3**	**1**	**P-value***
TAT Loss (%)	42	50	55	78	0.048
TAT Gain (%)	46	22	12	10	0.016
TAT Stable (%)	12	28	33	12	0.040
P-value**	0.026	0.049	0.004	0.000	

Changes between CTs were categorized as loss or gain if the values were $x \geq 14.7$ cm^2 and stable if the values were -14.6 $cm^2 > x < 14.6$ cm^2. TAT, total adipose tissue

*Chi square test was used to compare proportions of patients between 9 (n=42), 6 (n=40), 3(n=46) and 1 (n=34) month prior to death

** Chi square test was used to compare proportions of losing, gaining and stable patients within each time point

Table 3: Fatty acid composition of phospholipids in visceral and subcutaneous adipose tissue of colorectal patients

Fatty acid	VAT (% of total)			SAT (% of total)			P-value
C16:0	23.4	±	2.9	25.6	±	2.9	0.04
C16:1	1.1	±	1.4	0.5	±	1.1	0.14
C18:0	15.4	±	1.5	17.4	±	2.8	0.02
C18:1(9)	11.7	±	3.8	12.3	±	3.1	0.64
C18:2(6)	7.2	±	2.0	6.2	±	3.0	0.27
C20:0	5.2	±	1.8	3.1	±	2.4	0.01
C20:3(6)	5.0	±	1.9	3.1	±	2.1	0.01
C20:4(6)	4.8	±	1.2	3.3	±	1.8	0.01
C20:5(3)	4.5	±	1.5	2.4	±	1.9	0.001
C22:2(6)	3.7	±	1.8	1.3	±	1.6	0.001
ΣSFA	57.6	±	4.5	62.5	±	4.7	0.01
ΣMUFA	15.2	±	6	17.4	±	3.5	0.41
Σn-6	20.9	±	3.8	14.6	±	4.7	0.0007
Σn-3	5.4	±	1.9	4.7	±	4.1	0.28

SFA, saturated fatty acids; MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids; VAT, visceral adipose tissue; SAT, subcutaneous adipose tissue; DHA (C22:6 (3) was not detected.
Mean ± SD, paired student's t-test, n=16, $P<0.05$

Table 4: Adipokine protein levels in visceral and subcutaneous adipose tissue of colorectal cancer patients

Adipokine	VAT	SAT	P-value
MCP-1 (ng/ml)	119.7 ± 42.0	79.5 ± 36.4	0.003
Leptin (ng/ml)	1284.6 ± 964.0	2329.0 ± 1490.8	0.04
IL-6 (ng/ml)	3.3 ± 2.0	3.4 ± 1.4	0.39
Adiponectin (pg/ml)	520.8 ± 181.7	507.8 ± 170.4	0.68

MCP- 1, Monocyte chemotactic protein-1; IL-6, Interleukin-6; VAT, visceral adipose tissue; SAT, subcutaneous adipose tissue
Mean ± SD, paired student's t-test, n=16, $P<0.05$.

Fig 1. Pattern of change for each depot at 9 (n=42), 6 (n=40), 3(n=46) and 1 (n=34) months prior to death. Data are presented as Mean ± SEM, Generalized Estimating Equations (GEE), different superscripts for each depot are significantly different ($p < 0.05$).
VAT, visceral adipose tissue; SAT, subcutaneous adipose tissue; TAT, total adipose tissue; CSA, cross sectional area

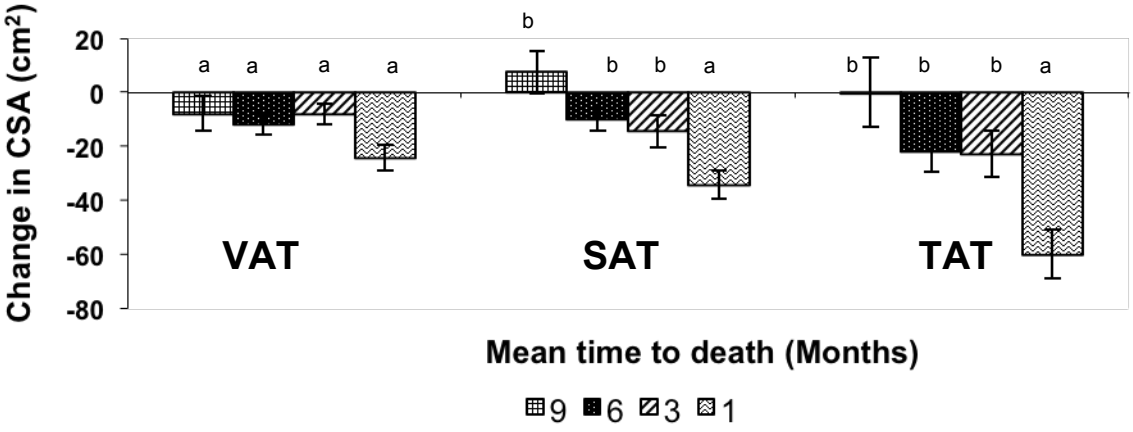
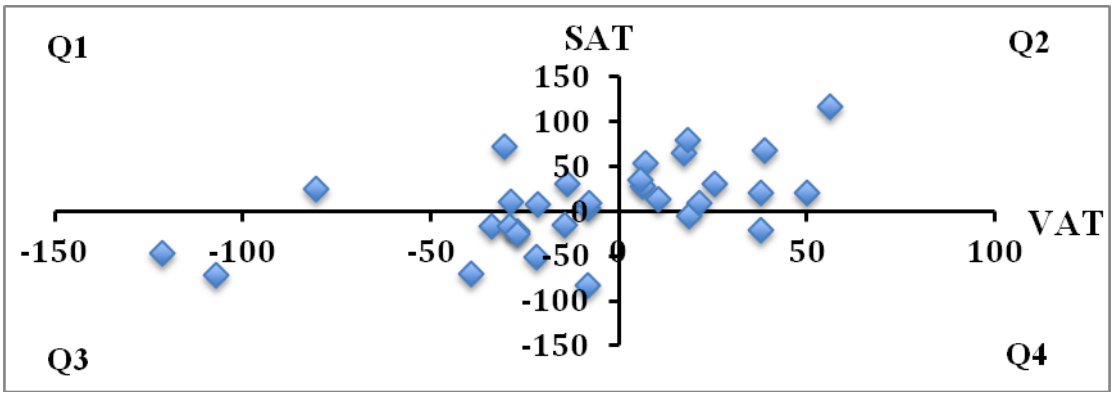


Figure2: Scatter plot displays the distribution of VAT and SAT losing and gaining patients at 1 and 9 months prior to death.
In both graphs, the y-axis represents the changes in SAT cross sectional area and the X-axis represent the changes in VAT cross sectional area which were divided into quadrants (Q1, Q2, Q3, and Q4) to reveal the loss or gain of the depot as follows: Q1, VAT Loss, SAT gain; Q2, VAT gain, SAT gain; Q3, VAT Loss, SAT Loss; Q4, VAT gain, SAT Loss.
A: 9 month to death; Q1(28% of patients), Q2 (42% of patients), Q3 (29% of patients), Q4 (7% of patients). The Chi-square P-value when comparing the four quartiles was significant (0.02).
B: 1 month to death; Q1(3% of patients), Q2 (6% of patients), Q3 (86% of patients), Q4 (6% of patients). The Chi-square P-value when comparing the four quartiles was significant (0.002).
VAT, visceral adipose tissue; SAT, subcutaneous adipose tissue; CSA, cross sectional area
A: 9 month to death



B:1 month to death

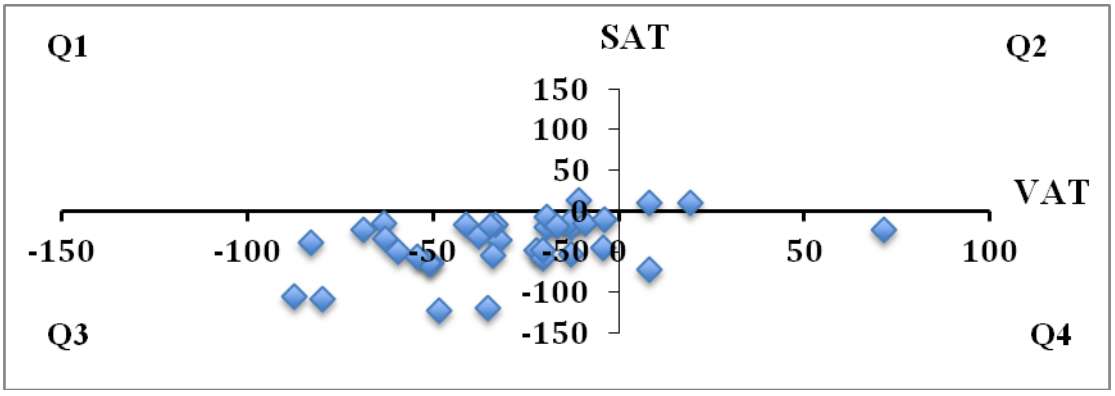
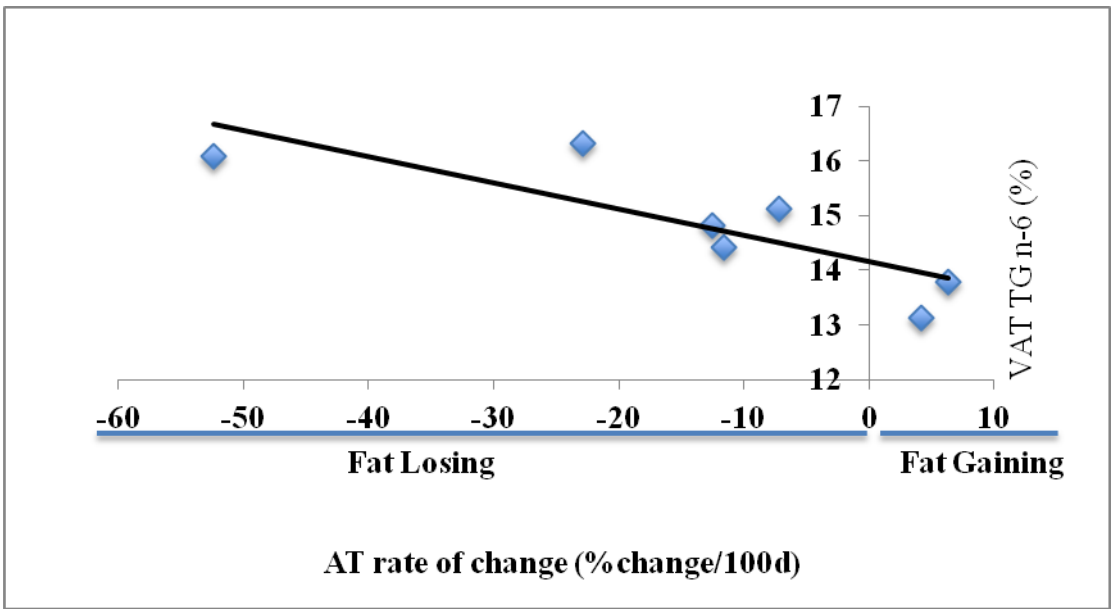


Figure 3: Relationship between adipose tissue rate of change (%change/100d) and visceral adipose tissue triglyceride n-6 levels (%)
Using Spearman's rank correlation, proportions of n-6 fatty acids in VAT correlated negatively with fat mass alterations; r =-0.8, p=0.03.
Abbreviations: VAT, visceral adipose tissue; TG, triglyceride; AT, adipose tissue



Appendix D: Proteomics profile of reference, tumor beaing and chemotherapy reciving animals

Tumor versus reference

Accession	Description	Σ Coverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	P-value
Q920J4	Thioredoxin-like protein 1 OS=Rattus norvegicus GN=Txnl1 PE=1 SV=3 - [TXNL1_RAT]	13.15	1	2	2	2	0.0007
Q8CFN2	Cell division control protein 42 homolog OS=Rattus norvegicus GN=Cdc42 PE=1 SV=2 - [CDC42_RAT]	26.7	1	3	4	85	0.0009
P04916	Retinol-binding protein 4 OS=Rattus norvegicus GN=Rbp4 PE=1 SV=1 - [RET4_RAT]	23.88	1	4	4	44	0.0023
Q5I0E7	Transmembrane emp24 domain-containing protein 9 OS=Rattus norvegicus GN=Tmed9 PE=1 SV=1 - [TMED9_RAT]	15.74	1	3	3	11	0.0023
P14141	Carbonic anhydrase 3 OS=Rattus norvegicus GN=Ca3 PE=1 SV=3 - [CAH3_RAT]	87.31	1	22	22	13415	0.0023
Q6AXX6	Redox-regulatory protein FAM213A OS=Rattus norvegicus GN=Fam213a PE=1 SV=1 - [F213A_RAT]	17.9	1	4	4	27	0.0026
P24368	Peptidyl-prolyl cis-trans isomerase B OS=Rattus norvegicus GN=Ppib PE=1 SV=3 - [PPIB_RAT]	54.63	1	13	13	183	0.0027
P23764	Glutathione peroxidase 3 OS=Rattus norvegicus GN=Gpx3 PE=2 SV=2 - [GPX3_RAT]	29.2	1	5	5	92	0.0030
P14841	Cystatin-C OS=Rattus norvegicus GN=Cst3 PE=1 SV=2 - [CYTC_RAT]	20	1	2	2	17	0.0038
P63159	High mobility group protein B1 OS=Rattus norvegicus GN=Hmgb1 PE=1 SV=2 - [HMGB1_RAT]	33.49	1	6	6	14	0.0045
P20762	Ig gamma-2C chain C region OS=Rattus norvegicus PE=2 SV=1 - [IGG2C_RAT]	20.06	1	4	4	11	0.0047
P63102	14-3-3 protein zeta/delta OS=Rattus norvegicus GN=Ywhaz PE=1 SV=1 - [1433Z_RAT]	74.29	1	14	19	530	0.0052
Q5XIU9	Membrane-associated progesterone receptor component 2 OS=Rattus norvegicus GN=Pgrmc2 PE=1 SV=1 - [PGRC2_RAT]	34.1	1	6	6	38	0.0059
P56571	ES1 protein homolog, mitochondrial OS=Rattus norvegicus PE=1 SV=2 - [ES1_RAT]	35.71	1	7	7	38	0.0061
P14562	Lysosome-associated membrane glycoprotein 1 OS=Rattus norvegicus GN=Lamp1 PE=1 SV=1 - [LAMP1_RAT]	14.74	1	5	5	17	0.0062
Q6IFW6	Keratin, type I cytoskeletal 10 OS=Rattus norvegicus GN=Krt10 PE=3 SV=1 - [K1C10_RAT]	15.4	1	7	8	33	0.0064
Q00438	Polypyrimidine tract-binding protein 1 OS=Rattus norvegicus GN=Ptbp1 PE=1 SV=1 - [PTBP1_RAT]	14.95	1	3	3	19	0.0064
Q6RUV5	Ras-related C3 botulinum toxin substrate 1 OS=Rattus norvegicus GN=Rac1 PE=1 SV=1 - [RAC1_RAT]	36.46	1	5	6	22	0.0070
Q9Z2G8	Nucleosome assembly protein 1-like 1 OS=Rattus norvegicus GN=Nap1l1 PE=1 SV=1 - [NP1L1_RAT]	7.18	1	2	2	14	0.0071
P42930	Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1 - [HSPB1_RAT]	59.22	1	11	11	250	0.0093
P0CG51	Polyubiquitin-B OS=Rattus norvegicus GN=Ubb PE=1 SV=1 - [UBB_RAT]	61.64	4	5	5	397	0.0101
Q63507	60S ribosomal protein L14 OS=Rattus norvegicus GN=Rpl14 PE=1 SV=3 - [RL14_RAT]	10.28	1	2	2	8	0.0102
Q5XI73	Rho GDP-dissociation inhibitor 1 OS=Rattus norvegicus GN=Arhgdia PE=1 SV=1 - [GDIR1_RAT]	59.31	1	11	11	213	0.0106
P04041	Glutathione peroxidase 1 OS=Rattus norvegicus GN=Gpx1 PE=1 SV=4 - [GPX1_RAT]	72.64	1	11	11	220	0.0117
P61023	Calcineurin B homologous protein 1 OS=Rattus norvegicus GN=Chp1 PE=1 SV=2 - [CHP1_RAT]	65.64	1	10	10	61	0.0119
Q6MG61	Chloride intracellular channel protein 1 OS=Rattus norvegicus GN=Clic1 PE=1 SV=1 - [CLIC1_RAT]	37.76	1	6	6	35	0.0120
P27791	cAMP-dependent protein kinase catalytic subunit alpha OS=Rattus norvegicus GN=Prkaca PE=1 SV=2 - [KAPCA_RAT]	7.12	1	3	3	14	0.0124

Q63544	Gamma-synuclein OS=Rattus norvegicus GN=Sncg PE=1 SV=2 - [SYUG_RAT]	74.8	1	10	10	477	0.0131
P36972	Adenine phosphoribosyltransferase OS=Rattus norvegicus GN=Aprt PE=1 SV=1 - [APT_RAT]	80.56	1	12	12	204	0.0133
Q63584	Transmembrane emp24 domain-containing protein 10 OS=Rattus norvegicus GN=Tmed10 PE=1 SV=2 - [TMEDA_RAT]	18.26	1	4	4	39	0.0133
P05942	Protein S100-A4 OS=Rattus norvegicus GN=S100a4 PE=2 SV=1 - [S10A4_RAT]	17.82	1	2	2	20	0.0136
Q62638	Golgi apparatus protein 1 OS=Rattus norvegicus GN=Glg1 PE=1 SV=1 - [GSLG1_RAT]	5.47	1	4	4	6	0.0137
Q6P5P5	Mesoderm-specific transcript homolog protein OS=Rattus norvegicus GN=Mest PE=2 SV=1 - [MEST_RAT]	26.87	1	5	5	121	0.0137
P05545	Serine protease inhibitor A3K OS=Rattus norvegicus GN=Serpina3k PE=1 SV=3 - [SPA3K_RAT]	61.06	1	16	21	1190	0.0145
O35509	Ras-related protein Rab-11B OS=Rattus norvegicus GN=Rab11b PE=1 SV=4 - [RB11B_RAT]	41.28	1	8	8	64	0.0160
Q2MHH0	Tumor suppressor candidate 5 homolog OS=Rattus norvegicus GN=Tusc5 PE=1 SV=1 - [TUSC5_RAT]	24.86	1	3	3	118	0.0165
Q63556	Serine protease inhibitor A3M (Fragment) OS=Rattus norvegicus GN=Serpina3m PE=2 SV=1 - [SPA3M_RAT]	14.56	1	2	5	28	0.0166
O70351	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Rattus norvegicus GN=Hsd17b10 PE=1 SV=3 - [HCD2_RAT]	72.41	1	10	11	211	0.0170
Q6IMF3	Keratin, type II cytoskeletal 1 OS=Rattus norvegicus GN=Krt1 PE=2 SV=1 - [K2C1_RAT]	8.96	1	5	7	62	0.0173
O35303	Dynamin-1-like protein OS=Rattus norvegicus GN=Dnm1l PE=1 SV=1 - [DNM1L_RAT]	10.33	1	3	4	16	0.0174
Q9QY44	ATP-binding cassette sub-family D member 2 OS=Rattus norvegicus GN=Abcd2 PE=1 SV=1 - [ABCD2_RAT]	13.77	1	5	6	14	0.0175
P24942	Excitatory amino acid transporter 1 OS=Rattus norvegicus GN=Slc1a3 PE=1 SV=2 - [EAA1_RAT]	7.92	1	3	3	25	0.0181
P21670	Proteasome subunit alpha type-4 OS=Rattus norvegicus GN=Psma4 PE=1 SV=1 - [PSA4_RAT]	42.91	1	6	6	42	0.0184
P40112	Proteasome subunit beta type-3 OS=Rattus norvegicus GN=Psmb3 PE=1 SV=1 - [PSB3_RAT]	26.83	1	4	4	53	0.0186
P61589	Transforming protein RhoA OS=Rattus norvegicus GN=Rhoa PE=1 SV=1 - [RHOA_RAT]	66.84	1	8	8	102	0.0190
P43244	Matrin-3 OS=Rattus norvegicus GN=Matr3 PE=1 SV=2 - [MATR3_RAT]	5.44	1	2	2	5	0.0204
P35704	Peroxiredoxin-2 OS=Rattus norvegicus GN=Prdx2 PE=1 SV=3 - [PRDX2_RAT]	57.58	1	9	9	402	0.0204
P47875	Cysteine and glycine-rich protein 1 OS=Rattus norvegicus GN=Csrp1 PE=1 SV=2 - [CSRP1_RAT]	39.38	1	6	6	69	0.0207
P16975	SPARC OS=Rattus norvegicus GN=Sparc PE=1 SV=4 - [SPRC_RAT]	15.95	1	4	4	14	0.0210
P05544	Serine protease inhibitor A3L OS=Rattus norvegicus GN=Serpina3l PE=1 SV=3 - [SPA3L_RAT]	61.74	1	18	23	827	0.0237
B0BNN3	Carbonic anhydrase 1 OS=Rattus norvegicus GN=Ca1 PE=1 SV=1 - [CAH1_RAT]	85.82	1	13	13	646	0.0248
Q63081	Protein disulfide-isomerase A6 OS=Rattus norvegicus GN=Pdia6 PE=1 SV=2 - [PDIA6_RAT]	41.82	1	14	14	415	0.0249
Q6MG60	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Rattus norvegicus GN=Ddah2 PE=1 SV=1 - [DDAH2_RAT]	50.18	1	8	8	71	0.0269
P02091	Hemoglobin subunit beta-1 OS=Rattus norvegicus GN=Hbb PE=1 SV=3 - [HBB1_RAT]	89.8	1	5	19	15581	0.0273
Q5XFX0	Transgelin-2 OS=Rattus norvegicus GN=Tagln2 PE=1 SV=1 - [TAGL2_RAT]	81.91	1	16	16	513	0.0287
P48037	Annexin A6 OS=Rattus norvegicus GN=Anxa6 PE=1 SV=2 - [ANXA6_RAT]	67.31	1	45	45	1103	0.0295
P14604	Enoyl-CoA hydratase, mitochondrial OS=Rattus norvegicus GN=Echs1 PE=1 SV=1 - [ECHM_RAT]	50.69	1	10	10	296	0.0302
O35814	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1 - [STIP1_RAT]	6.81	1	2	2	14	0.0317
Q6P9T8	Tubulin beta-4B chain OS=Rattus norvegicus GN=Tubb4b PE=1 SV=1 - [TBB4B_RAT]	68.31	1	4	24	2051	0.0328
P69897	Tubulin beta-5 chain OS=Rattus norvegicus GN=Tubb5 PE=1 SV=1 - [TBB5_RAT]	71.4	1	3	24	2010	0.0328

Q497B0	Omega-amidase NIT2 OS=Rattus norvegicus GN=Nit2 PE=1 SV=1 - [NIT2_RAT]	39.13	1	6	6	21	0.0332
P62198	26S protease regulatory subunit 8 OS=Rattus norvegicus GN=Psmc5 PE=1 SV=1 - [PRS8_RAT]	5.42	1	2	2	2	0.0335
P24090	Alpha-2-HS-glycoprotein OS=Rattus norvegicus GN=Ahsg PE=1 SV=2 - [FETUA_RAT]	40.91	1	9	9	537	0.0338
P02767	Transthyretin OS=Rattus norvegicus GN=Ttr PE=1 SV=1 - [TTHY_RAT]	62.59	1	6	6	165	0.0338
P63029	Translationally-controlled tumor protein OS=Rattus norvegicus GN=Tpt1 PE=1 SV=1 - [TCTP_RAT]	36.05	1	5	5	67	0.0343
P85108	Tubulin beta-2A chain OS=Rattus norvegicus GN=Tubb2a PE=1 SV=1 - [TBB2A_RAT]	73.93	2	5	25	1863	0.0355
P58775	Tropomyosin beta chain OS=Rattus norvegicus GN=Tpm2 PE=1 SV=1 - [TPM2_RAT]	28.52	1	2	13	96	0.0358
O08619	Coagulation factor XIII A chain OS=Rattus norvegicus GN=F13a1 PE=2 SV=3 - [F13A_RAT]	19.4	1	10	10	135	0.0359
P04906	Glutathione S-transferase P OS=Rattus norvegicus GN=Gstp1 PE=1 SV=2 - [GSTP1_RAT]	59.52	1	8	8	254	0.0368
Q64550	UDP-glucuronosyltransferase 1-1 OS=Rattus norvegicus GN=Ugt1a1 PE=1 SV=1 - [UD11_RAT]	11.21	6	1	3	72	0.0377
P0CC09	Histone H2A type 2-A OS=Rattus norvegicus GN=Hist2h2aa3 PE=1 SV=1 - [H2A2A_RAT]	57.69	8	4	6	298	0.0378
P31044	Phosphatidylethanolamine-binding protein 1 OS=Rattus norvegicus GN=Pebp1 PE=1 SV=3 - [PEBP1_RAT]	65.24	1	7	7	95	0.0379
P08430	UDP-glucuronosyltransferase 1-6 OS=Rattus norvegicus GN=Ugt1a6 PE=1 SV=1 - [UD16_RAT]	10.78	6	2	4	75	0.0380
P53534	Glycogen phosphorylase, brain form (Fragment) OS=Rattus norvegicus GN=Pygb PE=1 SV=3 - [PYGB_RAT]	12.17	1	5	7	25	0.0381
P63025	Vesicle-associated membrane protein 3 OS=Rattus norvegicus GN=Vamp3 PE=1 SV=1 - [VAMP3_RAT]	38.83	2	3	3	24	0.0389
P04639	Apolipoprotein A-I OS=Rattus norvegicus GN=Apoa1 PE=1 SV=2 - [APOA1_RAT]	66.8	1	16	16	437	0.0396
P11915	Non-specific lipid-transfer protein OS=Rattus norvegicus GN=Scp2 PE=1 SV=3 - [NLTP_RAT]	16.64	1	11	11	116	0.0396
P11517	Hemoglobin subunit beta-2 OS=Rattus norvegicus PE=1 SV=2 - [HBB2_RAT]	88.44	1	4	18	10442	0.0401
P38718	Mitochondrial pyruvate carrier 2 OS=Rattus norvegicus GN=Mpc2 PE=2 SV=1 - [MPC2_RAT]	25.98	1	3	3	9	0.0408
P23965	Enoyl-CoA delta isomerase 1, mitochondrial OS=Rattus norvegicus GN=Eci1 PE=1 SV=1 - [ECI1_RAT]	42.91	1	9	9	159	0.0429
P48004	Proteasome subunit alpha type-7 OS=Rattus norvegicus GN=Psma7 PE=1 SV=1 - [PSA7_RAT]	30.31	1	4	5	25	0.0445
P62914	60S ribosomal protein L11 OS=Rattus norvegicus GN=Rpl11 PE=1 SV=2 - [RL11_RAT]	16.85	1	3	3	39	0.0455
P48199	C-reactive protein OS=Rattus norvegicus GN=Crp PE=1 SV=1 - [CRP_RAT]	32.61	1	5	5	185	0.0469
Q6P9V9	Tubulin alpha-1B chain OS=Rattus norvegicus GN=Tuba1b PE=1 SV=1 - [TBA1B_RAT]	66.52	1	3	23	1564	0.0474
P68370	Tubulin alpha-1A chain OS=Rattus norvegicus GN=Tuba1a PE=1 SV=1 - [TBA1A_RAT]	66.52	1	2	22	1439	0.0487
Q9QZA2	Programmed cell death 6-interacting protein OS=Rattus norvegicus GN=Pdcd6ip PE=1 SV=2 - [PDC6I_RAT]	18.79	1	7	8	96	0.0487
O08651	D-3-phosphoglycerate dehydrogenase OS=Rattus norvegicus GN=Phgdh PE=1 SV=3 - [SERA_RAT]	26.64	1	10	10	266	0.0492
Q63610	Tropomyosin alpha-3 chain OS=Rattus norvegicus GN=Tpm3 PE=1 SV=2 - [TPM3_RAT]	48.79	1	8	16	167	0.0495
P63324	40S ribosomal protein S12 OS=Rattus norvegicus GN=Rps12 PE=1 SV=2 - [RS12_RAT]	22.73	1	3	3	29	0.0509
P01946	Hemoglobin subunit alpha-1/2 OS=Rattus norvegicus GN=Hba1 PE=1 SV=3 - [HBA_RAT]	95.77	1	14	14	14370	0.0515
P85973	Purine nucleoside phosphorylase OS=Rattus norvegicus GN=Pnp PE=1 SV=1 - [PNPH_RAT]	69.55	1	13	13	337	0.0520
P62703	40S ribosomal protein S4, X isoform OS=Rattus norvegicus GN=Rps4x PE=2 SV=2 - [RS4X_RAT]	15.97	1	5	5	13	0.0528
P27605	Hypoxanthine-guanine phosphoribosyltransferase OS=Rattus norvegicus GN=Hprt1 PE=1 SV=1 - [HPRT_RAT]	44.95	1	8	8	50	0.0532

P0C5H9	Mesencephalic astrocyte-derived neurotrophic factor OS=Rattus norvegicus GN=Manf PE=1 SV=1 - [MANF_RAT]	21.79	1	4	4	17	0.0542
P85971	6-phosphogluconolactonase OS=Rattus norvegicus GN=Pgls PE=1 SV=1 - [6PGL_RAT]	51.75	1	6	6	132	0.0544
P19511	ATP synthase F(0) complex subunit B1, mitochondrial OS=Rattus norvegicus GN=Atp5f1 PE=1 SV=1 - [AT5F1_RAT]	27.34	1	7	8	157	0.0545
Q62745	CD81 antigen OS=Rattus norvegicus GN=Cd81 PE=1 SV=1 - [CD81_RAT]	15.25	1	2	2	2	0.0555
Q4KLF8	Actin-related protein 2/3 complex subunit 5 OS=Rattus norvegicus GN=Arpc5 PE=1 SV=3 - [ARPC5_RAT]	16.56	1	2	2	8	0.0555
P07153	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Rattus norvegicus GN=Rpn1 PE=2 SV=1 - [RPN1_RAT]	20.66	1	9	9	47	0.0562
Q02253	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Rattus norvegicus GN=Aldh6a1 PE=1 SV=1 - [MMSA_RAT]	42.8	1	14	14	147	0.0565
P04937	Fibronectin OS=Rattus norvegicus GN=Fn1 PE=1 SV=2 - [FINC_RAT]	4.97	1	7	7	18	0.0567
P11232	Thioredoxin OS=Rattus norvegicus GN=Txn PE=1 SV=2 - [THIO_RAT]	31.43	1	4	4	44	0.0572
Q6AYQ4	Transmembrane protein 109 OS=Rattus norvegicus GN=Tmem109 PE=2 SV=1 - [TM109_RAT]	8.64	1	2	2	2	0.0576
Q4KM74	Vesicle-trafficking protein SEC22b OS=Rattus norvegicus GN=Sec22b PE=1 SV=3 - [SC22B_RAT]	36.28	1	6	7	53	0.0579
O35952	Hydroxyacylglutathione hydrolase, mitochondrial OS=Rattus norvegicus GN=Hagh PE=1 SV=2 - [GLO2_RAT]	16.5	1	3	3	6	0.0591
P04785	Protein disulfide-isomerase OS=Rattus norvegicus GN=P4hb PE=1 SV=2 - [PDIA1_RAT]	56.78	1	21	22	532	0.0592
P30904	Macrophage migration inhibitory factor OS=Rattus norvegicus GN=Mif PE=1 SV=4 - [MIF_RAT]	13.91	1	2	2	3	0.0593
Q01066	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1B OS=Rattus norvegicus GN=Pde1b PE=1 SV=1 - [PDE1B_RAT]	6.73	1	2	3	5	0.0602
P10719	ATP synthase subunit beta, mitochondrial OS=Rattus norvegicus GN=Atp5b PE=1 SV=2 - [ATPB_RAT]	77.88	1	27	27	1785	0.0606
Q68A21	Transcriptional activator protein Pur-beta OS=Rattus norvegicus GN=Purb PE=1 SV=3 - [PURB_RAT]	15.24	1	2	2	2	0.0609
P62836	Ras-related protein Rap-1A OS=Rattus norvegicus GN=Rap1a PE=1 SV=1 - [RAP1A_RAT]	30.98	1	1	6	120	0.0612
P00762	Anionic trypsin-1 OS=Rattus norvegicus GN=Prss1 PE=1 SV=1 - [TRY1_RAT]	14.23	1	2	2	102	0.0625
Q4QQT4	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Rattus norvegicus GN=Ppp2r1b PE=2 SV=1 - [2AAB_RAT]	6.99	1	3	3	27	0.0634
Q63569	26S protease regulatory subunit 6A OS=Rattus norvegicus GN=Psmc3 PE=2 SV=1 - [PRS6A_RAT]	5.92	1	2	2	2	0.0649
Q920A6	Retinoid-inducible serine carboxypeptidase OS=Rattus norvegicus GN=Scpep1 PE=2 SV=1 - [RISC_RAT]	14.82	1	5	5	101	0.0654
Q0ZHH6	Atlastin-3 OS=Rattus norvegicus GN=Atl3 PE=2 SV=2 - [ATLA3_RAT]	21.44	1	6	6	87	0.0662
Q66H12	Alpha-N-acetylgalactosaminidase OS=Rattus norvegicus GN=Naga PE=2 SV=1 - [NAGAB_RAT]	9.4	1	3	3	3	0.0665
P25113	Phosphoglycerate mutase 1 OS=Rattus norvegicus GN=Pgam1 PE=1 SV=4 - [PGAM1_RAT]	72.05	1	17	17	377	0.0669
Q64611	Cysteine sulfinic acid decarboxylase OS=Rattus norvegicus GN=Csad PE=1 SV=1 - [CSAD_RAT]	42.19	1	14	14	317	0.0675
P23562	Band 3 anion transport protein OS=Rattus norvegicus GN=Slc4a1 PE=1 SV=3 - [B3AT_RAT]	28.69	1	17	17	335	0.0682
Q1JU68	Eukaryotic translation initiation factor 3 subunit A OS=Rattus norvegicus GN=Eif3a PE=2 SV=2 - [EIF3A_RAT]	3.69	1	3	3	18	0.0692
P04692	Tropomyosin alpha-1 chain OS=Rattus norvegicus GN=Tpm1 PE=1 SV=3 - [TPM1_RAT]	37.32	1	3	14	111	0.0701
Q8VI04	Isoaspartyl peptidase/L-asparaginase OS=Rattus norvegicus GN=Asrgl1 PE=1 SV=1 - [ASGL1_RAT]	19.52	1	4	4	7	0.0702

Q63862	Myosin-11 (Fragments) OS=Rattus norvegicus GN=Myh11 PE=1 SV=3 - [MYH11_RAT]	33.53	1	26	35	411	0.0703
P55260	Annexin A4 OS=Rattus norvegicus GN=Anxa4 PE=1 SV=3 - [ANXA4_RAT]	53.61	1	14	14	92	0.0723
P15800	Laminin subunit beta-2 OS=Rattus norvegicus GN=Lamb2 PE=2 SV=1 - [LAMB2_RAT]	19.99	1	26	27	132	0.0725
P11884	Aldehyde dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Aldh2 PE=1 SV=1 - [ALDH2_RAT]	56.26	1	20	20	691	0.0731
P16391	RT1 class I histocompatibility antigen, AA alpha chain OS=Rattus norvegicus PE=1 SV=2 - [HA12_RAT]	8.63	1	3	3	8	0.0732
Q63041	Alpha-1-macroglobulin OS=Rattus norvegicus GN=A1m PE=1 SV=1 - [A1M_RAT]	54.27	1	57	58	1554	0.0752
P08009	Glutathione S-transferase Yb-3 OS=Rattus norvegicus GN=Gstm3 PE=1 SV=2 - [GSTM4_RAT]	33.49	1	2	7	135	0.0756
P48721	Stress-70 protein, mitochondrial OS=Rattus norvegicus GN=Hspa9 PE=1 SV=3 - [GRP75_RAT]	43.74	1	24	24	335	0.0760
Q6B345	Protein S100-A11 OS=Rattus norvegicus GN=S100a11 PE=3 SV=1 - [S10AB_RAT]	82.65	1	5	5	94	0.0784
Q9ESS6	Basal cell adhesion molecule OS=Rattus norvegicus GN=Bcam PE=2 SV=1 - [BCAM_RAT]	4.49	1	2	2	5	0.0791
P19944	60S acidic ribosomal protein P1 OS=Rattus norvegicus GN=Rplp1 PE=3 SV=1 - [RLA1_RAT]	51.75	1	2	2	46	0.0793
P67779	Prohibitin OS=Rattus norvegicus GN=Phb PE=1 SV=1 - [PHB_RAT]	76.1	1	14	14	135	0.0799
P62963	Profilin-1 OS=Rattus norvegicus GN=Pfn1 PE=1 SV=2 - [PROF1_RAT]	73.57	1	10	10	536	0.0801
P13832	Myosin regulatory light chain RLC-A OS=Rattus norvegicus GN=Rlc-a PE=2 SV=2 - [MRLCA_RAT]	34.3	2	5	5	31	0.0810
P97697	Inositol monophosphatase 1 OS=Rattus norvegicus GN=Impa1 PE=1 SV=2 - [IMPA1_RAT]	7.58	1	2	2	2	0.0815
Q5U1Z2	Trafficking protein particle complex subunit 3 OS=Rattus norvegicus GN=Trappc3 PE=2 SV=1 - [TPPC3_RAT]	18.33	1	3	3	4	0.0816
P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	72.29	1	11	11	283	0.0817
P18886	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Rattus norvegicus GN=Cpt2 PE=1 SV=1 - [CPT2_RAT]	21.28	1	8	8	21	0.0824
P26644	Beta-2-glycoprotein 1 OS=Rattus norvegicus GN=Apoh PE=2 SV=2 - [APOH_RAT]	15.15	1	5	5	16	0.0830
Q6P7Q4	Lactoylglutathione lyase OS=Rattus norvegicus GN=Glo1 PE=1 SV=3 - [LGUL_RAT]	28.26	1	5	5	79	0.0830
Q9QX79	Fetuin-B OS=Rattus norvegicus GN=Fetub PE=2 SV=2 - [FETUB_RAT]	58.47	1	16	16	378	0.0834
P04797	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus GN=Gapdh PE=1 SV=3 - [G3P_RAT]	75.98	1	18	18	1638	0.0847
B0BNM1	NAD(P)H-hydrate epimerase OS=Rattus norvegicus GN=Apoa1bp PE=2 SV=1 - [NNRE_RAT]	21.28	1	3	3	13	0.0854
Q6P6V0	Glucose-6-phosphate isomerase OS=Rattus norvegicus GN=Gpi PE=1 SV=1 - [G6PI_RAT]	55.2	1	23	23	541	0.0855
P61206	ADP-ribosylation factor 3 OS=Rattus norvegicus GN=Arf3 PE=2 SV=2 - [ARF3_RAT]	54.7	2	5	8	211	0.0863
Q7TP48	Adipocyte plasma membrane-associated protein OS=Rattus norvegicus GN=Apmap PE=2 SV=2 - [APMAP_RAT]	67.29	1	16	16	516	0.0866
O35244	Peroxiredoxin-6 OS=Rattus norvegicus GN=Prdx6 PE=1 SV=3 - [PRDX6_RAT]	67.86	1	13	13	212	0.0874
P09495	Tropomyosin alpha-4 chain OS=Rattus norvegicus GN=Tpm4 PE=1 SV=3 - [TPM4_RAT]	49.19	1	6	15	164	0.0878
P60901	Proteasome subunit alpha type-6 OS=Rattus norvegicus GN=Psma6 PE=1 SV=1 - [PSA6_RAT]	30.08	1	6	6	57	0.0878
P07871	3-ketoacyl-CoA thiolase B, peroxisomal OS=Rattus norvegicus GN=Acaa1b PE=1 SV=2 - [THIKB_RAT]	13.68	2	5	5	36	0.0886
P38659	Protein disulfide-isomerase A4 OS=Rattus norvegicus GN=Pdia4 PE=1 SV=2 - [PDIA4_RAT]	23.33	1	12	12	41	0.0888
P62909	40S ribosomal protein S3 OS=Rattus norvegicus GN=Rps3 PE=1 SV=1 - [RS3_RAT]	44.44	1	8	8	58	0.0888
P12346	Serotransferrin OS=Rattus norvegicus GN=Tf PE=1 SV=3 - [TRFE_RAT]	70.34	1	40	40	4273	0.0888

Q66HG6	Carbonic anhydrase 5B, mitochondrial OS=Rattus norvegicus GN=Ca5b PE=2 SV=1 - [CAH5B_RAT]	19.24	1	4	4	26	0.0891
P09527	Ras-related protein Rab-7a OS=Rattus norvegicus GN=Rab7a PE=1 SV=2 - [RAB7A_RAT]	57.49	1	9	9	114	0.0904
P57113	Maleylacetoacetate isomerase OS=Rattus norvegicus GN=Gstz1 PE=1 SV=2 - [MAAI_RAT]	63.89	1	9	9	174	0.0909
P62260	14-3-3 protein epsilon OS=Rattus norvegicus GN=Ywhae PE=1 SV=1 - [1433E_RAT]	76.08	1	19	22	433	0.0924
P19357	Solute carrier family 2, facilitated glucose transporter member 4 OS=Rattus norvegicus GN=Slc2a4 PE=1 SV=1 - [GTR4_RAT]	8.06	1	3	3	15	0.0926
P50398	Rab GDP dissociation inhibitor alpha OS=Rattus norvegicus GN=Gdi1 PE=1 SV=1 - [GDIA_RAT]	42.28	1	8	13	184	0.0931
P11348	Dihydropteridine reductase OS=Rattus norvegicus GN=Qdpr PE=1 SV=1 - [DHPR_RAT]	50.21	1	8	8	61	0.0943
Q63691	Monocyte differentiation antigen CD14 OS=Rattus norvegicus GN=Cd14 PE=2 SV=2 - [CD14_RAT]	31.18	1	7	7	88	0.0952
P01026	Complement C3 OS=Rattus norvegicus GN=C3 PE=1 SV=3 - [CO3_RAT]	59.17	1	73	76	1701	0.0960
Q7M0E3	Destrin OS=Rattus norvegicus GN=Dstn PE=1 SV=3 - [DEST_RAT]	55.15	1	8	8	173	0.0968
Q63170	Dynein heavy chain 7, axonemal OS=Rattus norvegicus GN=Dnah7 PE=2 SV=2 - [DYH7_RAT]	1.65	1	3	4	5	0.0968
P10686	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 OS=Rattus norvegicus GN=Plcg1 PE=1 SV=1 - [PLCG1_RAT]	2.33	1	2	2	6	0.0970
P01015	Angiotensinogen OS=Rattus norvegicus GN=Agt PE=1 SV=1 - [ANGT_RAT]	23.69	1	5	6	41	0.0983
P27139	Carbonic anhydrase 2 OS=Rattus norvegicus GN=Ca2 PE=1 SV=2 - [CAH2_RAT]	64.62	1	13	13	406	0.0986
P61983	14-3-3 protein gamma OS=Rattus norvegicus GN=Ywhag PE=1 SV=2 - [1433G_RAT]	80.97	1	12	19	613	0.0993
P16303	Carboxylesterase 1D OS=Rattus norvegicus GN=Ces1d PE=1 SV=2 - [CES1D_RAT]	52.92	1	27	27	3133	0.0998
P56574	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus GN=Idh2 PE=1 SV=2 - [IDHP_RAT]	37.61	1	13	15	109	0.1002
P14480	Fibrinogen beta chain OS=Rattus norvegicus GN=Fgb PE=1 SV=4 - [FIBB_RAT]	44.26	1	14	14	172	0.1008
P06866	Haptoglobin OS=Rattus norvegicus GN=Hp PE=1 SV=3 - [HPT_RAT]	32.85	1	10	11	131	0.1012
P23514	Coatomer subunit beta OS=Rattus norvegicus GN=Copb1 PE=1 SV=1 - [COPB_RAT]	11.44	1	5	6	68	0.1034
Q9JLJ3	4-trimethylaminobutyraldehyde dehydrogenase OS=Rattus norvegicus GN=Aldh9a1 PE=1 SV=1 - [AL9A1_RAT]	55.26	1	14	16	189	0.1053
P19132	Ferritin heavy chain OS=Rattus norvegicus GN=Fth1 PE=1 SV=3 - [FRIH_RAT]	57.14	1	10	10	69	0.1058
Q9R1T3	Cathepsin Z OS=Rattus norvegicus GN=Ctsz PE=1 SV=2 - [CATZ_RAT]	18.95	1	4	4	21	0.1062
O88767	Protein deglycase DJ-1 OS=Rattus norvegicus GN=Park7 PE=1 SV=1 - [PARK7_RAT]	75.13	1	10	11	197	0.1073
Q794F9	4F2 cell-surface antigen heavy chain OS=Rattus norvegicus GN=Slc3a2 PE=1 SV=1 - [4F2_RAT]	18.03	1	6	6	11	0.1081
P17475	Alpha-1-antiproteinase OS=Rattus norvegicus GN=Serpina1 PE=1 SV=2 - [A1AT_RAT]	51.82	1	18	18	871	0.1082
P82995	Heat shock protein HSP 90-alpha OS=Rattus norvegicus GN=Hsp90aa1 PE=1 SV=3 - [HS90A_RAT]	57.98	1	22	34	752	0.1085
P14668	Annexin A5 OS=Rattus norvegicus GN=Anxa5 PE=1 SV=3 - [ANXA5_RAT]	75.55	1	24	24	1074	0.1102
P04276	Vitamin D-binding protein OS=Rattus norvegicus GN=Gc PE=1 SV=3 - [VTDB_RAT]	50	1	16	16	314	0.1108
Q6AYG5	Ethylmalonyl-CoA decarboxylase OS=Rattus norvegicus GN=Echdc1 PE=1 SV=1 - [ECHD1_RAT]	49.83	1	10	10	98	0.1111
P05943	Protein S100-A10 OS=Rattus norvegicus GN=S100a10 PE=1 SV=2 - [S10AA_RAT]	31.58	1	4	4	13	0.1112
P42123	L-lactate dehydrogenase B chain OS=Rattus norvegicus GN=Ldhb PE=1 SV=2 - [LDHB_RAT]	69.46	1	19	22	722	0.1116

P80254	D-dopachrome decarboxylase OS=Rattus norvegicus GN=Ddt PE=1 SV=3 - [DOPD_RAT]	77.97	1	7	7	132	0.1119
P34058	Heat shock protein HSP 90-beta OS=Rattus norvegicus GN=Hsp90ab1 PE=1 SV=4 - [HS90B_RAT]	62.85	1	23	37	951	0.1127
Q62636	Ras-related protein Rap-1b OS=Rattus norvegicus GN=Rap1b PE=1 SV=2 - [RAP1B_RAT]	52.17	1	3	8	138	0.1129
P04904	Glutathione S-transferase alpha-3 OS=Rattus norvegicus GN=Gsta3 PE=1 SV=3 - [GSTA3_RAT]	63.8	1	10	10	166	0.1132
P31977	Ezrin OS=Rattus norvegicus GN=Ezr PE=1 SV=3 - [EZRI_RAT]	15.7	1	3	8	116	0.1134
Q6VBQ5	Myeloid-associated differentiation marker OS=Rattus norvegicus GN=Myadm PE=1 SV=1 - [MYADM_RAT]	21.7	1	4	4	42	0.1134
P15999	ATP synthase subunit alpha, mitochondrial OS=Rattus norvegicus GN=Atp5a1 PE=1 SV=2 - [ATPA_RAT]	50.63	1	23	23	1190	0.1135
Q66HA6	ADP-ribosylation factor-like protein 8B OS=Rattus norvegicus GN=Arl8b PE=2 SV=1 - [ARL8B_RAT]	21.51	1	2	2	2	0.1139
P62890	60S ribosomal protein L30 OS=Rattus norvegicus GN=Rpl30 PE=3 SV=2 - [RL30_RAT]	24.35	1	2	2	11	0.1142
P26453	Basigin OS=Rattus norvegicus GN=Bsg PE=1 SV=2 - [BASI_RAT]	21.39	1	8	8	57	0.1146
Q6NYB7	Ras-related protein Rab-1A OS=Rattus norvegicus GN=Rab1A PE=1 SV=3 - [RAB1A_RAT]	56.1	1	4	8	164	0.1178
Q68FS4	Cytosol aminopeptidase OS=Rattus norvegicus GN=Lap3 PE=1 SV=1 - [AMPL_RAT]	39.31	1	12	12	98	0.1179
Q01129	Decorin OS=Rattus norvegicus GN=Dcn PE=1 SV=1 - [PGS2_RAT]	32.77	1	11	12	403	0.1185
P61107	Ras-related protein Rab-14 OS=Rattus norvegicus GN=Rab14 PE=1 SV=3 - [RAB14_RAT]	20	1	3	4	39	0.1188
P63245	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Rattus norvegicus GN=Gnb2l1 PE=1 SV=3 - [GBLP_RAT]	32.18	1	7	7	31	0.1203
P04644	40S ribosomal protein S17 OS=Rattus norvegicus GN=Rps17 PE=1 SV=3 - [RS17_RAT]	57.78	1	6	6	35	0.1210
B2GV06	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Rattus norvegicus GN=Oxct1 PE=1 SV=1 - [SCOT1_RAT]	43.46	1	13	13	116	0.1217
P19804	Nucleoside diphosphate kinase B OS=Rattus norvegicus GN=Nme2 PE=1 SV=1 - [NDKB_RAT]	75	1	5	11	554	0.1219
P62630	Elongation factor 1-alpha 1 OS=Rattus norvegicus GN=Eef1a1 PE=2 SV=1 - [EF1A1_RAT]	54.76	1	19	19	1772	0.1228
Q66H98	Serum deprivation-response protein OS=Rattus norvegicus GN=Sdpr PE=1 SV=3 - [SDPR_RAT]	45.08	1	13	13	344	0.1237
P10860	Glutamate dehydrogenase 1, mitochondrial OS=Rattus norvegicus GN=Glud1 PE=1 SV=2 - [DHE3_RAT]	50.72	1	19	19	145	0.1252
P70619	Glutathione reductase (Fragment) OS=Rattus norvegicus GN=Gsr PE=2 SV=2 - [GSHR_RAT]	8.02	1	2	2	2	0.1258
B0LPN4	Ryanodine receptor 2 OS=Rattus norvegicus GN=Ryr2 PE=1 SV=2 - [RYR2_RAT]	1.03	1	3	3	5	0.1272
P62271	40S ribosomal protein S18 OS=Rattus norvegicus GN=Rps18 PE=1 SV=3 - [RS18_RAT]	48.68	1	10	10	65	0.1273
P08460	Nidogen-1 (Fragment) OS=Rattus norvegicus GN=Nid1 PE=1 SV=2 - [NID1_RAT]	29.94	1	5	5	33	0.1274
P25235	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Rattus norvegicus GN=Rpn2 PE=2 SV=2 - [RPN2_RAT]	39.14	1	12	12	187	0.1277
Q08290	Calponin-1 OS=Rattus norvegicus GN=Cnn1 PE=1 SV=1 - [CNN1_RAT]	30.3	1	5	5	12	0.1281
P48500	Triosephosphate isomerase OS=Rattus norvegicus GN=Tpi1 PE=1 SV=2 - [TPIS_RAT]	85.54	1	16	16	637	0.1282
Q6P7S1	Acid ceramidase OS=Rattus norvegicus GN=Asah1 PE=2 SV=1 - [ASAH1_RAT]	24.62	1	6	6	35	0.1282
Q99NA5	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Rattus norvegicus GN=Idh3a PE=1 SV=1 - [IDH3A_RAT]	29.23	1	8	8	198	0.1287
Q63279	Keratin, type I cytoskeletal 19 OS=Rattus norvegicus GN=Krt19 PE=1 SV=2 - [K1C19_RAT]	42.68	1	12	14	35	0.1311
P85834	Elongation factor Tu, mitochondrial OS=Rattus norvegicus GN=Tufm PE=1 SV=1 - [EFTU_RAT]	4.87	1	2	2	4	0.1329

P11980	Pyruvate kinase PKM OS=Rattus norvegicus GN=Pkm PE=1 SV=3 - [KPYM_RAT]	47.46	1	22	22	587	0.1334
Q99ML5	Prenylcysteine oxidase OS=Rattus norvegicus GN=Pcyox1 PE=1 SV=1 - [PCYOX_RAT]	7.74	1	2	2	4	0.1378
P31000	Vimentin OS=Rattus norvegicus GN=Vim PE=1 SV=2 - [VIME_RAT]	78.54	1	36	40	1727	0.1380
P20070	NADH-cytochrome b5 reductase 3 OS=Rattus norvegicus GN=Cyb5r3 PE=1 SV=2 - [NB5R3_RAT]	80.07	1	16	16	395	0.1382
O88989	Malate dehydrogenase, cytoplasmic OS=Rattus norvegicus GN=Mdh1 PE=1 SV=3 - [MDHC_RAT]	61.38	1	16	16	1211	0.1382
P06761	78 kDa glucose-regulated protein OS=Rattus norvegicus GN=Hspa5 PE=1 SV=1 - [GRP78_RAT]	51.22	1	28	30	818	0.1392
Q6AY20	Cation-dependent mannose-6-phosphate receptor OS=Rattus norvegicus GN=M6pr PE=1 SV=1 - [MPRD_RAT]	8.27	1	2	2	2	0.1392
P63322	Ras-related protein Ral-A OS=Rattus norvegicus GN=Rala PE=1 SV=1 - [RALA_RAT]	27.18	1	4	4	14	0.1395
P15178	Aspartate--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Dars PE=2 SV=1 - [SYDC_RAT]	15.77	1	5	5	8	0.1405
P07756	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Rattus norvegicus GN=Cps1 PE=1 SV=1 - [CPSM_RAT]	22.47	1	23	23	125	0.1436
Q6PCT3	Tumor protein D54 OS=Rattus norvegicus GN=Tpd52l2 PE=1 SV=1 - [TPD54_RAT]	14.55	1	2	2	4	0.1456
Q07969	Platelet glycoprotein 4 OS=Rattus norvegicus GN=Cd36 PE=1 SV=3 - [CD36_RAT]	36.86	1	11	11	638	0.1456
P62859	40S ribosomal protein S28 OS=Rattus norvegicus GN=Rps28 PE=1 SV=1 - [RS28_RAT]	30.43	1	2	2	8	0.1459
P07824	Arginase-1 OS=Rattus norvegicus GN=Arg1 PE=1 SV=2 - [ARGI1_RAT]	11.76	1	2	2	3	0.1462
O08678	Serine/threonine-protein kinase MARK1 OS=Rattus norvegicus GN=Mark1 PE=1 SV=1 - [MARK1_RAT]	3.28	2	2	2	3	0.1486
B2RZ37	Receptor expression-enhancing protein 5 OS=Rattus norvegicus GN=Reep5 PE=1 SV=1 - [REEP5_RAT]	22.22	1	8	8	277	0.1490
P85970	Actin-related protein 2/3 complex subunit 2 OS=Rattus norvegicus GN=Arpc2 PE=1 SV=1 - [ARPC2_RAT]	18.33	1	3	3	19	0.1491
Q4V8F7	Coiled-coil domain-containing protein 63 OS=Rattus norvegicus GN=Ccdc63 PE=2 SV=1 - [CCD63_RAT]	5.55	1	2	2	2	0.1497
P08699	Galectin-3 OS=Rattus norvegicus GN=Lgals3 PE=1 SV=4 - [LEG3_RAT]	18.32	1	3	3	4	0.1506
O88761	26S proteasome non-ATPase regulatory subunit 1 OS=Rattus norvegicus GN=Psmd1 PE=1 SV=1 - [PSMD1_RAT]	6.09	1	3	3	8	0.1510
P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	64.48	1	123	125	1844	0.1513
P11507	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Rattus norvegicus GN=Atp2a2 PE=1 SV=1 - [AT2A2_RAT]	14.67	1	11	11	76	0.1521
Q00715	Histone H2B type 1 OS=Rattus norvegicus PE=1 SV=2 - [H2B1_RAT]	39.2	1	5	5	271	0.1522
Q9EQP5	Prolargin OS=Rattus norvegicus GN=Prelp PE=2 SV=1 - [PRELP_RAT]	42.44	1	12	12	65	0.1527
P36953	Afamin OS=Rattus norvegicus GN=Afm PE=3 SV=1 - [AFAM_RAT]	24.84	1	11	11	51	0.1532
P52303	AP-1 complex subunit beta-1 OS=Rattus norvegicus GN=Ap1b1 PE=1 SV=1 - [AP1B1_RAT]	19.81	1	3	8	103	0.1534
Q64428	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus GN=Hadha PE=1 SV=2 - [ECHA_RAT]	53.47	1	28	28	857	0.1539
Q6PDU7	ATP synthase subunit g, mitochondrial OS=Rattus norvegicus GN=Atp5l PE=1 SV=2 - [ATP5L_RAT]	53.4	1	4	4	30	0.1546
Q63525	Nuclear migration protein nudC OS=Rattus norvegicus GN=Nudc PE=1 SV=1 - [NUDC_RAT]	6.02	1	2	2	2	0.1546
P0C0S7	Histone H2A.Z OS=Rattus norvegicus GN=H2afz PE=1 SV=2 - [H2AZ_RAT]	31.25	1	2	4	70	0.1550
G3V7P1	Syntaxin-12 OS=Rattus norvegicus GN=Stx12 PE=1 SV=1 - [STX12_RAT]	20.8	1	4	4	6	0.1555
Q6IFU8	Keratin, type I cytoskeletal 17 OS=Rattus norvegicus	16.86	1	4	7	13	0.1568

	GN=Krt17 PE=1 SV=1 - [K1C17_RAT]						
P08010	Glutathione S-transferase Mu 2 OS=Rattus norvegicus GN=Gstm2 PE=1 SV=2 - [GSTM2_RAT]	67.89	1	11	16	284	0.1593
P14669	Annexin A3 OS=Rattus norvegicus GN=Anxa3 PE=1 SV=4 - [ANXA3_RAT]	64.81	1	17	19	232	0.1594
P62804	Histone H4 OS=Rattus norvegicus GN=Hist1h4b PE=1 SV=2 - [H4_RAT]	53.4	1	9	9	261	0.1601
Q9WUW3	Complement factor I OS=Rattus norvegicus GN=Cfi PE=2 SV=1 - [CFAI_RAT]	5.79	1	2	2	2	0.1603
Q66X93	Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus GN=Snd1 PE=1 SV=1 - [SND1_RAT]	18.37	1	8	9	21	0.1617
P02770	Serum albumin OS=Rattus norvegicus GN=Alb PE=1 SV=2 - [ALBU_RAT]	80.26	1	54	54	28722	0.1619
A7VJC2	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1 - [ROA2_RAT]	33.14	1	8	10	101	0.1620
Q62812	Myosin-9 OS=Rattus norvegicus GN=Myh9 PE=1 SV=3 - [MYH9_RAT]	34.42	1	43	51	731	0.1621
D3ZHA0	Filamin-C OS=Rattus norvegicus GN=Flnc PE=1 SV=1 - [FLNC_RAT]	4.29	1	8	9	62	0.1622
Q66HF1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus GN=Ndufs1 PE=1 SV=1 - [NDUS1_RAT]	37.28	1	17	17	147	0.1632
Q9EPF2	Cell surface glycoprotein MUC18 OS=Rattus norvegicus GN=Mcam PE=1 SV=2 - [MUC18_RAT]	44.91	1	22	22	333	0.1639
P62161	Calmodulin OS=Rattus norvegicus GN=Calm1 PE=1 SV=2 - [CALM_RAT]	48.99	1	6	6	59	0.1641
Q66H80	Coatomer subunit delta OS=Rattus norvegicus GN=Arcn1 PE=2 SV=1 - [COPD_RAT]	12.33	1	4	4	19	0.1651
Q99PF5	Far upstream element-binding protein 2 OS=Rattus norvegicus GN=Khsrp PE=1 SV=1 - [FUBP2_RAT]	4.99	1	3	3	3	0.1655
P70623	Fatty acid-binding protein, adipocyte OS=Rattus norvegicus GN=Fabp4 PE=1 SV=3 - [FABP4_RAT]	77.27	1	15	15	6451	0.1662
Q5I0D7	Xaa-Pro dipeptidase OS=Rattus norvegicus GN=Pepd PE=2 SV=1 - [PEPD_RAT]	10.57	1	4	4	69	0.1664
A1L1J9	Lipase maturation factor 2 OS=Rattus norvegicus GN=Lmf2 PE=2 SV=1 - [LMF2_RAT]	7.12	1	4	4	5	0.1668
Q8VBU2	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1 - [NDRG2_RAT]	24.8	1	4	5	68	0.1712
P12001	60S ribosomal protein L18 OS=Rattus norvegicus GN=Rpl18 PE=1 SV=2 - [RL18_RAT]	25	1	4	4	32	0.1724
P61751	ADP-ribosylation factor 4 OS=Rattus norvegicus GN=Arf4 PE=2 SV=2 - [ARF4_RAT]	52.78	1	3	6	153	0.1735
P62083	40S ribosomal protein S7 OS=Rattus norvegicus GN=Rps7 PE=1 SV=1 - [RS7_RAT]	47.42	1	4	5	59	0.1743
P00787	Cathepsin B OS=Rattus norvegicus GN=Ctsb PE=1 SV=2 - [CATB_RAT]	27.73	1	8	8	127	0.1765
P06685	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Rattus norvegicus GN=Atp1a1 PE=1 SV=1 - [AT1A1_RAT]	13.59	1	9	9	141	0.1769
Q07066	Peroxisomal membrane protein 2 OS=Rattus norvegicus GN=Pxmp2 PE=1 SV=2 - [PXMP2_RAT]	21.13	1	2	3	8	0.1783
P21396	Amine oxidase [flavin-containing] A OS=Rattus norvegicus GN=Maoa PE=1 SV=1 - [AOFA_RAT]	4.37	1	2	2	2	0.1783
P97629	Leucyl-cystinyl aminopeptidase OS=Rattus norvegicus GN=Lnpep PE=1 SV=1 - [LCAP_RAT]	6.73	1	6	6	21	0.1787
P21588	5'-nucleotidase OS=Rattus norvegicus GN=Nt5e PE=1 SV=1 - [5NTD_RAT]	11.11	1	4	4	8	0.1808
P41350	Caveolin-1 OS=Rattus norvegicus GN=Cav1 PE=1 SV=3 - [CAV1_RAT]	52.81	1	8	8	377	0.1815
Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	6.79	1	3	3	8	0.1815
P62775	Myotrophin OS=Rattus norvegicus GN=Mtpn PE=1 SV=2 - [MTPN_RAT]	25.42	1	2	2	16	0.1833
Q63570	26S protease regulatory subunit 6B OS=Rattus norvegicus GN=Psmc4 PE=1 SV=1 - [PRS6B_RAT]	12.2	1	2	2	84	0.1843
P35434	ATP synthase subunit delta, mitochondrial OS=Rattus	13.69	1	2	2	14	0.1860

	norvegicus GN=Atp5d PE=1 SV=2 - [ATPD_RAT]						
P38652	Phosphoglucomutase-1 OS=Rattus norvegicus GN=Pgm1 PE=1 SV=2 - [PGM1_RAT]	30.96	1	10	10	168	0.1866
P04638	Apolipoprotein A-II OS=Rattus norvegicus GN=Apoa2 PE=2 SV=1 - [APOA2_RAT]	19.61	1	2	2	4	0.1879
P13437	3-ketoacyl-CoA thiolase, mitochondrial OS=Rattus norvegicus GN=Acaa2 PE=2 SV=1 - [THIM_RAT]	61.46	1	17	17	361	0.1882
P63088	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Rattus norvegicus GN=Ppp1cc PE=1 SV=1 - [PP1G_RAT]	20.43	3	3	4	17	0.1884
P04166	Cytochrome b5 type B OS=Rattus norvegicus GN=Cyb5b PE=1 SV=2 - [CYB5B_RAT]	51.37	1	4	4	60	0.1892
P07335	Creatine kinase B-type OS=Rattus norvegicus GN=Ckb PE=1 SV=2 - [KCRB_RAT]	59.32	1	16	16	281	0.1893
P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	18.54	1	13	14	180	0.1894
P31211	Corticosteroid-binding globulin OS=Rattus norvegicus GN=Serpina6 PE=1 SV=2 - [CBG_RAT]	26.01	1	7	7	24	0.1915
D3Z8L7	Ras-related protein R-Ras OS=Rattus norvegicus GN=Rras PE=1 SV=1 - [RRAS_RAT]	29.36	1	5	5	37	0.1918
Q91Y80	SH3 domain-binding protein 5 OS=Rattus norvegicus GN=Sh3bp5 PE=1 SV=2 - [3BP5_RAT]	2.63	1	2	2	2	0.1918
Q8VIF7	Selenium-binding protein 1 OS=Rattus norvegicus GN=Selenbp1 PE=1 SV=1 - [SBP1_RAT]	66.53	1	23	23	162	0.1927
Q07984	Translocon-associated protein subunit delta OS=Rattus norvegicus GN=Ssr4 PE=2 SV=1 - [SSRD_RAT]	30.64	1	4	4	7	0.1935
P08503	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acadm PE=1 SV=1 - [ACADM_RAT]	19.48	1	5	5	59	0.1944
Q09073	ADP/ATP translocase 2 OS=Rattus norvegicus GN=Slc25a5 PE=1 SV=3 - [ADT2_RAT]	44.3	1	5	12	278	0.1949
Q07009	Calpain-2 catalytic subunit OS=Rattus norvegicus GN=Capn2 PE=1 SV=3 - [CAN2_RAT]	24.86	1	12	12	109	0.1956
P30009	Myristoylated alanine-rich C-kinase substrate OS=Rattus norvegicus GN=Marcks PE=1 SV=2 - [MARCS_RAT]	28.48	1	5	5	37	0.1977
P52555	Endoplasmic reticulum resident protein 29 OS=Rattus norvegicus GN=Erp29 PE=1 SV=2 - [ERP29_RAT]	50.38	1	8	8	77	0.1988
P0C2X9	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Aldh4a1 PE=1 SV=1 - [AL4A1_RAT]	6.57	1	2	2	3	0.2006
P18297	Sepiapterin reductase OS=Rattus norvegicus GN=Spr PE=1 SV=1 - [SPRE_RAT]	21.76	1	2	2	3	0.2007
P34064	Proteasome subunit alpha type-5 OS=Rattus norvegicus GN=Psma5 PE=1 SV=1 - [PSA5_RAT]	18.26	1	4	4	8	0.2035
P32038	Complement factor D OS=Rattus norvegicus GN=Cfd PE=1 SV=2 - [CFAD_RAT]	51.71	1	7	7	64	0.2044
P29457	Serpin H1 OS=Rattus norvegicus GN=Serpinh1 PE=1 SV=1 - [SERPH_RAT]	53.24	1	16	16	607	0.2047
Q68FU3	Electron transfer flavoprotein subunit beta OS=Rattus norvegicus GN=Etfb PE=2 SV=3 - [ETFB_RAT]	46.67	1	10	10	169	0.2057
P58365	Cadherin-23 OS=Rattus norvegicus GN=Cdh23 PE=2 SV=1 - [CAD23_RAT]	1.12	1	2	2	4	0.2059
Q00657	Chondroitin sulfate proteoglycan 4 OS=Rattus norvegicus GN=Cspg4 PE=1 SV=2 - [CSPG4_RAT]	1.33	1	2	2	2	0.2061
O35763	Moesin OS=Rattus norvegicus GN=Msn PE=1 SV=3 - [MOES_RAT]	27.56	1	11	15	186	0.2074
P62870	Transcription elongation factor B polypeptide 2 OS=Rattus norvegicus GN=Tceb2 PE=1 SV=1 - [ELOB_RAT]	34.75	1	2	2	2	0.2082
Q05962	ADP/ATP translocase 1 OS=Rattus norvegicus GN=Slc25a4 PE=1 SV=3 - [ADT1_RAT]	40.94	1	4	11	257	0.2084
P00388	NADPH--cytochrome P450 reductase OS=Rattus norvegicus GN=Por PE=1 SV=3 - [NCPR_RAT]	30.83	1	13	13	124	0.2086
Q9JJ31	Cullin-5 OS=Rattus norvegicus GN=Cul5 PE=1 SV=3 - [CUL5_RAT]	4.49	1	2	2	3	0.2102
Q6IFV1	Keratin, type I cytoskeletal 14 OS=Rattus norvegicus GN=Krt14 PE=2 SV=1 - [K1C14_RAT]	15.88	1	2	6	25	0.2110

P18418	Calreticulin OS=Rattus norvegicus GN=Calr PE=1 SV=1 - [CALR_RAT]	66.11	1	19	19	293	0.2117
P61959	Small ubiquitin-related modifier 2 OS=Rattus norvegicus GN=Sumo2 PE=1 SV=1 - [SUMO2_RAT]	23.16	1	2	2	4	0.2125
A0JPJ7	Obg-like ATPase 1 OS=Rattus norvegicus GN=Ola1 PE=2 SV=1 - [OLA1_RAT]	14.14	1	4	4	23	0.2127
Q9EST6	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Rattus norvegicus GN=Anp32b PE=1 SV=1 - [AN32B_RAT]	11.76	1	2	3	10	0.2146
O35796	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Rattus norvegicus GN=C1qbp PE=1 SV=2 - [C1QBP_RAT]	22.58	1	3	3	8	0.2161
Q9QWN8	Spectrin beta chain, non-erythrocytic 2 OS=Rattus norvegicus GN=Sptbn2 PE=1 SV=2 - [SPTN2_RAT]	3.02	1	6	6	23	0.2173
Q6UPE1	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Rattus norvegicus GN=Etfdh PE=1 SV=1 - [ETFD_RAT]	3.73	1	2	2	2	0.2173
Q63010	Liver carboxylesterase B-1 OS=Rattus norvegicus PE=1 SV=1 - [EST5_RAT]	13.37	1	1	4	89	0.2186
Q64119	Myosin light polypeptide 6 OS=Rattus norvegicus GN=Myl6 PE=1 SV=3 - [MYL6_RAT]	58.28	1	7	7	145	0.2188
O08590	Membrane primary amine oxidase OS=Rattus norvegicus GN=Aoc3 PE=1 SV=4 - [AOC3_RAT]	45.87	1	23	23	1340	0.2189
P47245	Nardilysin OS=Rattus norvegicus GN=Nrd1 PE=1 SV=1 - [NRDC_RAT]	6.46	1	4	4	14	0.2189
Q62940	E3 ubiquitin-protein ligase NEDD4 OS=Rattus norvegicus GN=Nedd4 PE=1 SV=1 - [NEDD4_RAT]	11.5	1	8	8	78	0.2210
P01836	Ig kappa chain C region, A allele OS=Rattus norvegicus PE=1 SV=1 - [KACA_RAT]	76.42	1	6	6	566	0.2211
P28480	T-complex protein 1 subunit alpha OS=Rattus norvegicus GN=Tcp1 PE=1 SV=1 - [TCPA_RAT]	15.47	1	3	3	26	0.2229
P18484	AP-2 complex subunit alpha-2 OS=Rattus norvegicus GN=Ap2a2 PE=1 SV=3 - [AP2A2_RAT]	18.55	1	9	9	74	0.2235
P24268	Cathepsin D OS=Rattus norvegicus GN=Ctsd PE=1 SV=1 - [CATD_RAT]	29.73	1	7	8	29	0.2250
Q9Z2Q1	Protein transport protein Sec31A OS=Rattus norvegicus GN=Sec31a PE=1 SV=2 - [SC31A_RAT]	12.97	1	9	9	68	0.2265
Q6AY30	Saccharopine dehydrogenase-like oxidoreductase OS=Rattus norvegicus GN=Sccpdh PE=1 SV=1 - [SCPDL_RAT]	12.12	1	2	2	16	0.2265
Q5M7W5	Microtubule-associated protein 4 OS=Rattus norvegicus GN=Map4 PE=1 SV=1 - [MAP4_RAT]	16.65	1	10	10	44	0.2267
P04256	Heterogeneous nuclear ribonucleoprotein A1 OS=Rattus norvegicus GN=Hnrnpa1 PE=1 SV=3 - [ROA1_RAT]	17.19	1	3	5	28	0.2278
P11442	Clathrin heavy chain 1 OS=Rattus norvegicus GN=Cltc PE=1 SV=3 - [CLH1_RAT]	52.6	1	63	63	918	0.2288
Q9Z339	Glutathione S-transferase omega-1 OS=Rattus norvegicus GN=Gsto1 PE=1 SV=2 - [GSTO1_RAT]	39	1	6	6	39	0.2327
P61980	Heterogeneous nuclear ribonucleoprotein K OS=Rattus norvegicus GN=Hnrnpk PE=1 SV=1 - [HNRPK_RAT]	27	1	8	9	47	0.2338
B2GUZ5	F-actin-capping protein subunit alpha-1 OS=Rattus norvegicus GN=Capza1 PE=1 SV=1 - [CAZA1_RAT]	20.28	1	3	4	23	0.2347
P16446	Phosphatidylinositol transfer protein alpha isoform OS=Rattus norvegicus GN=Pitpna PE=1 SV=2 - [PIPNA_RAT]	12.18	1	2	2	3	0.2353
P54921	Alpha-soluble NSF attachment protein OS=Rattus norvegicus GN=Napa PE=1 SV=2 - [SNAA_RAT]	7.46	1	2	2	2	0.2354
P10111	Peptidyl-prolyl cis-trans isomerase A OS=Rattus norvegicus GN=Ppia PE=1 SV=2 - [PPIA_RAT]	59.76	1	11	11	793	0.2360
B0K020	CDGSH iron-sulfur domain-containing protein 1 OS=Rattus norvegicus GN=Cisd1 PE=3 SV=1 - [CISD1_RAT]	34.26	1	3	3	8	0.2367
Q62658	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Rattus norvegicus GN=Fkbp1a PE=1 SV=3 - [FKB1A_RAT]	29.63	1	2	2	7	0.2367
P09006	Serine protease inhibitor A3N OS=Rattus norvegicus GN=Serpina3n PE=1 SV=3 - [SPA3N_RAT]	40.91	1	10	10	96	0.2373
Q64537	Calpain small subunit 1 OS=Rattus norvegicus GN=Capns1 PE=1 SV=3 - [CPNS1_RAT]	62.59	1	8	8	52	0.2394

Q62868	Rho-associated protein kinase 2 OS=Rattus norvegicus GN=Rock2 PE=1 SV=2 - [ROCK2_RAT]	3.6	1	1	2	5	0.2403
Q6QA69	1-acylglycerol-3-phosphate O-acyltransferase ABHD5 OS=Rattus norvegicus GN=Abhd5 PE=1 SV=1 - [ABHD5_RAT]	35.04	1	7	7	131	0.2452
P21913	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Rattus norvegicus GN=Sdhb PE=2 SV=2 - [SDHB_RAT]	23.05	1	6	6	15	0.2489
Q63210	Guanine nucleotide-binding protein subunit alpha-12 OS=Rattus norvegicus GN=Gna12 PE=1 SV=3 - [GNA12_RAT]	7.92	1	1	2	5	0.2493
P13635	Ceruloplasmin OS=Rattus norvegicus GN=Cp PE=1 SV=3 - [CERU_RAT]	49.2	1	37	38	607	0.2495
P50503	Hsc70-interacting protein OS=Rattus norvegicus GN=St13 PE=1 SV=1 - [F10A1_RAT]	10.33	1	3	3	19	0.2496
Q9Z0V6	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Rattus norvegicus GN=Prdx3 PE=1 SV=2 - [PRDX3_RAT]	36.96	1	6	6	120	0.2500
Q9Z0W7	Chloride intracellular channel protein 4 OS=Rattus norvegicus GN=Clic4 PE=1 SV=3 - [CLIC4_RAT]	20.95	1	3	4	28	0.2503
Q5I0P2	Glycine cleavage system H protein, mitochondrial OS=Rattus norvegicus GN=Gcsh PE=2 SV=1 - [GCSH_RAT]	33.53	1	3	3	29	0.2506
P62832	60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1 - [RL23_RAT]	32.14	1	3	3	15	0.2525
Q66H89	Centrosomal protein of 83 kDa OS=Rattus norvegicus GN=Cep83 PE=2 SV=1 - [CEP83_RAT]	2.46	1	2	2	2	0.2528
P25093	Fumarylacetoacetase OS=Rattus norvegicus GN=Fah PE=1 SV=1 - [FAAA_RAT]	43.44	1	11	11	227	0.2536
Q63258	Integrin alpha-7 OS=Rattus norvegicus GN=Itga7 PE=1 SV=2 - [ITA7_RAT]	2.03	1	2	2	2	0.2544
Q6PEC4	S-phase kinase-associated protein 1 OS=Rattus norvegicus GN=Skp1 PE=1 SV=3 - [SKP1_RAT]	12.88	1	2	2	2	0.2547
P12075	Cytochrome c oxidase subunit 5B, mitochondrial OS=Rattus norvegicus GN=Cox5b PE=1 SV=2 - [COX5B_RAT]	36.43	1	5	5	12	0.2548
P00406	Cytochrome c oxidase subunit 2 OS=Rattus norvegicus GN=Mtco2 PE=1 SV=3 - [COX2_RAT]	18.94	1	4	4	164	0.2557
Q5XI32	F-actin-capping protein subunit beta OS=Rattus norvegicus GN=Capzb PE=1 SV=1 - [CAPZB_RAT]	29.04	1	5	6	19	0.2573
Q5U318	Astrocytic phosphoprotein PEA-15 OS=Rattus norvegicus GN=Pea15 PE=1 SV=1 - [PEA15_RAT]	16.15	1	2	2	3	0.2573
Q5XIE6	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Rattus norvegicus GN=Hibch PE=1 SV=2 - [HIBCH_RAT]	18.18	1	4	4	7	0.2585
P13803	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Rattus norvegicus GN=Etfa PE=1 SV=4 - [ETFA_RAT]	56.76	1	12	12	342	0.2603
P35171	Cytochrome c oxidase subunit 7A2, mitochondrial OS=Rattus norvegicus GN=Cox7a2 PE=1 SV=1 - [CX7A2_RAT]	27.71	1	2	2	4	0.2635
Q9WUH4	Four and a half LIM domains protein 1 OS=Rattus norvegicus GN=Fhl1 PE=2 SV=1 - [FHL1_RAT]	12.5	1	3	3	20	0.2640
P07895	Superoxide dismutase [Mn], mitochondrial OS=Rattus norvegicus GN=Sod2 PE=1 SV=2 - [SODM_RAT]	27.03	1	5	5	57	0.2654
P19234	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Rattus norvegicus GN=Ndufv2 PE=1 SV=2 - [NDUV2_RAT]	21.77	1	4	4	53	0.2675
O88600	Heat shock 70 kDa protein 4 OS=Rattus norvegicus GN=Hspa4 PE=1 SV=1 - [HSP74_RAT]	16.55	1	8	9	70	0.2679
P04764	Alpha-enolase OS=Rattus norvegicus GN=Eno1 PE=1 SV=4 - [ENOA_RAT]	70.05	1	19	23	1278	0.2681
Q6IG02	Keratin, type II cytoskeletal 2 epidermal OS=Rattus norvegicus GN=Krt2 PE=3 SV=1 - [K22E_RAT]	4.53	1	2	3	5	0.2691
P10959	Carboxylesterase 1C OS=Rattus norvegicus GN=Ces1c PE=1 SV=3 - [EST1C_RAT]	10.75	1	3	4	5	0.2711
P97675	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3 OS=Rattus norvegicus GN=Enpp3 PE=1 SV=2	7.43	1	4	4	38	0.2715

	- [ENPP3_RAT]						
P43884	Perilipin-1 OS=Rattus norvegicus GN=Plin1 PE=1 SV=1 - [PLIN1_RAT]	65.38	1	22	22	1123	0.2720
P05508	NADH-ubiquinone oxidoreductase chain 4 OS=Rattus norvegicus GN=Mtnd4 PE=3 SV=3 - [NU4M_RAT]	12.42	1	3	3	50	0.2727
Q5PPN5	Tubulin polymerization-promoting protein family member 3 OS=Rattus norvegicus GN=Tppp3 PE=2 SV=1 - [TPPP3_RAT]	31.82	1	5	5	12	0.2759
P20059	Hemopexin OS=Rattus norvegicus GN=Hpx PE=1 SV=3 - [HEMO_RAT]	63.04	1	25	25	915	0.2766
P17988	Sulfotransferase 1A1 OS=Rattus norvegicus GN=Sult1a1 PE=1 SV=1 - [ST1A1_RAT]	26.46	1	5	5	11	0.2771
P21263	Nestin OS=Rattus norvegicus GN=Nes PE=1 SV=2 - [NEST_RAT]	1.27	1	2	2	2	0.2784
Q5I0D1	Glyoxalase domain-containing protein 4 OS=Rattus norvegicus GN=Glod4 PE=1 SV=1 - [GLOD4_RAT]	27.18	1	6	6	26	0.2823
Q99PS8	Histidine-rich glycoprotein OS=Rattus norvegicus GN=Hrg PE=1 SV=1 - [HRG_RAT]	8.38	1	4	4	18	0.2832
P49303	Genome polyprotein OS=Foot-and-mouth disease virus (isolate -/Azerbaijan/A22-550/1965 serotype A) PE=1 SV=1 - [POLG_FMDVZ]	1.76	1	2	2	3	0.2833
P40307	Proteasome subunit beta type-2 OS=Rattus norvegicus GN=Psmb2 PE=1 SV=1 - [PSB2_RAT]	26.37	1	4	4	45	0.2851
Q2TL32	E3 ubiquitin-protein ligase UBR4 OS=Rattus norvegicus GN=Ubr4 PE=1 SV=2 - [UBR4_RAT]	1.62	1	5	5	6	0.2867
P07150	Annexin A1 OS=Rattus norvegicus GN=Anxa1 PE=1 SV=2 - [ANXA1_RAT]	72.54	1	27	27	2282	0.2872
P55053	Fatty acid-binding protein, epidermal OS=Rattus norvegicus GN=Fabp5 PE=1 SV=3 - [FABP5_RAT]	69.63	1	9	9	182	0.2873
P70615	Lamin-B1 OS=Rattus norvegicus GN=Lmnb1 PE=1 SV=3 - [LMNB1_RAT]	14.99	1	4	6	28	0.2888
P08011	Microsomal glutathione S-transferase 1 OS=Rattus norvegicus GN=Mgst1 PE=1 SV=3 - [MGST1_RAT]	69.68	1	8	8	1445	0.2900
Q6AXM8	Serum paraoxonase/arylesterase 2 OS=Rattus norvegicus GN=Pon2 PE=2 SV=1 - [PON2_RAT]	11.58	1	2	2	7	0.2985
P15865	Histone H1.4 OS=Rattus norvegicus GN=Hist1h1e PE=1 SV=3 - [H14_RAT]	15.53	1	6	6	194	0.2986
P85125	Polymerase I and transcript release factor OS=Rattus norvegicus GN=Ptrf PE=1 SV=1 - [PTRF_RAT]	39.29	1	16	16	1673	0.3041
P05964	Protein S100-A6 OS=Rattus norvegicus GN=S100a6 PE=1 SV=3 - [S10A6_RAT]	19.1	1	3	3	10	0.3045
Q64057	Alpha-aminoadipic semialdehyde dehydrogenase OS=Rattus norvegicus GN=Aldh7a1 PE=1 SV=2 - [AL7A1_RAT]	34.14	1	11	11	30	0.3046
P97576	GrpE protein homolog 1, mitochondrial OS=Rattus norvegicus GN=Grpel1 PE=1 SV=2 - [GRPE1_RAT]	11.52	1	2	2	4	0.3050
P31232	Transgelin OS=Rattus norvegicus GN=Tagln PE=1 SV=2 - [TAGL_RAT]	73.13	1	15	15	683	0.3067
Q5BK81	Prostaglandin reductase 2 OS=Rattus norvegicus GN=Ptgr2 PE=2 SV=2 - [PTGR2_RAT]	25.36	1	6	6	17	0.3073
Q9Z270	Vesicle-associated membrane protein-associated protein A OS=Rattus norvegicus GN=Vapa PE=1 SV=3 - [VAPA_RAT]	28.92	1	7	7	37	0.3073
P07632	Superoxide dismutase [Cu-Zn] OS=Rattus norvegicus GN=Sod1 PE=1 SV=2 - [SODC_RAT]	53.25	1	8	8	216	0.3084
Q8VHF5	Citrate synthase, mitochondrial OS=Rattus norvegicus GN=Cs PE=1 SV=1 - [CISY_RAT]	41.63	1	14	14	200	0.3085
P00884	Fructose-bisphosphate aldolase B OS=Rattus norvegicus GN=Aldob PE=1 SV=2 - [ALDOB_RAT]	22.8	1	6	6	9	0.3092
P52631	Signal transducer and activator of transcription 3 OS=Rattus norvegicus GN=Stat3 PE=1 SV=1 - [STAT3_RAT]	4.16	1	2	2	3	0.3098
Q5EB77	Ras-related protein Rab-18 OS=Rattus norvegicus GN=Rab18 PE=2 SV=1 - [RAB18_RAT]	46.12	1	7	7	25	0.3101
P17074	40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3 - [RS19_RAT]	45.52	1	7	7	52	0.3111
P84817	Mitochondrial fission 1 protein OS=Rattus norvegicus GN=Fis1 PE=1 SV=1 - [FIS1_RAT]	24.34	1	4	4	88	0.3123

Q08163	Adenylyl cyclase-associated protein 1 OS=Rattus norvegicus GN=Cap1 PE=1 SV=3 - [CAP1_RAT]	23.42	1	4	6	300	0.3141
P85968	6-phosphogluconate dehydrogenase, decarboxylating OS=Rattus norvegicus GN=Pgd PE=1 SV=1 - [6PGD_RAT]	61.9	1	20	20	562	0.3147
P04550	Parathymosin OS=Rattus norvegicus GN=Ptms PE=1 SV=2 - [PTMS_RAT]	22.55	1	2	2	2	0.3152
P97852	Peroxisomal multifunctional enzyme type 2 OS=Rattus norvegicus GN=Hsd17b4 PE=1 SV=3 - [DHB4_RAT]	18.78	1	9	11	110	0.3155
Q5XI78	2-oxoglutarate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ogdh PE=1 SV=1 - [ODO1_RAT]	41.84	1	29	29	429	0.3178
Q9QXQ0	Alpha-actinin-4 OS=Rattus norvegicus GN=Actn4 PE=1 SV=2 - [ACTN4_RAT]	48.3	1	21	32	255	0.3186
Q9R063	Peroxiredoxin-5, mitochondrial OS=Rattus norvegicus GN=Prdx5 PE=1 SV=1 - [PRDX5_RAT]	51.17	1	9	9	253	0.3192
P50137	Transketolase OS=Rattus norvegicus GN=Tkt PE=1 SV=1 - [TKT_RAT]	61.64	1	27	27	985	0.3203
P50475	Alanine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Aars PE=1 SV=3 - [SYAC_RAT]	6.71	1	4	4	10	0.3217
Q920L2	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Rattus norvegicus GN=Sdha PE=1 SV=1 - [SDHA_RAT]	24.24	1	10	11	107	0.3224
Q9EQS0	Transaldolase OS=Rattus norvegicus GN=Taldo1 PE=1 SV=2 - [TALDO_RAT]	39.17	1	13	13	107	0.3232
Q99J82	Integrin-linked protein kinase OS=Rattus norvegicus GN=Ilk PE=2 SV=1 - [ILK_RAT]	10.18	1	4	4	10	0.3240
Q68FT1	Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Rattus norvegicus GN=Coq9 PE=1 SV=2 - [COQ9_RAT]	6.09	1	2	2	4	0.3243
Q62736	Non-muscle caldesmon OS=Rattus norvegicus GN=Cald1 PE=1 SV=1 - [CALD1_RAT]	18.46	1	8	8	37	0.3267
P27274	CD59 glycoprotein OS=Rattus norvegicus GN=Cd59 PE=1 SV=2 - [CD59_RAT]	23.81	1	3	3	34	0.3270
Q9WVB1	Ras-related protein Rab-6A OS=Rattus norvegicus GN=Rab6a PE=1 SV=2 - [RAB6A_RAT]	9.62	1	1	2	5	0.3297
P10536	Ras-related protein Rab-1B OS=Rattus norvegicus GN=Rab1b PE=1 SV=1 - [RAB1B_RAT]	48.26	1	3	7	186	0.3299
P62944	AP-2 complex subunit beta OS=Rattus norvegicus GN=Ap2b1 PE=1 SV=1 - [AP2B1_RAT]	13.66	1	3	6	194	0.3301
P12785	Fatty acid synthase OS=Rattus norvegicus GN=Fasn PE=1 SV=3 - [FAS_RAT]	75.05	1	129	131	8547	0.3303
P07338	Chymotrypsinogen B OS=Rattus norvegicus GN=Ctrb1 PE=1 SV=1 - [CTRB1_RAT]	14.45	1	2	2	2	0.3328
P30277	G2/mitotic-specific cyclin-B1 OS=Rattus norvegicus GN=Ccnb1 PE=2 SV=1 - [CCNB1_RAT]	7.09	1	2	2	2	0.3341
Q9Z1P2	Alpha-actinin-1 OS=Rattus norvegicus GN=Actn1 PE=1 SV=1 - [ACTN1_RAT]	38.45	1	12	23	203	0.3347
Q9Z2L0	Voltage-dependent anion-selective channel protein 1 OS=Rattus norvegicus GN=Vdac1 PE=1 SV=4 - [VDAC1_RAT]	44.88	1	9	9	85	0.3354
Q4KM73	UMP-CMP kinase OS=Rattus norvegicus GN=Cmpk1 PE=1 SV=2 - [KCY_RAT]	58.67	1	9	9	25	0.3377
P62246	40S ribosomal protein S15a OS=Rattus norvegicus GN=Rps15a PE=1 SV=2 - [RS15A_RAT]	17.69	1	2	2	2	0.3401
P09330	Ribose-phosphate pyrophosphokinase 2 OS=Rattus norvegicus GN=Prps2 PE=1 SV=3 - [PRPS2_RAT]	10.06	2	2	2	2	0.3407
P36370	Antigen peptide transporter 1 OS=Rattus norvegicus GN=Tap1 PE=1 SV=2 - [TAP1_RAT]	3.17	1	2	2	2	0.3409
Q8R4C1	Calcium-transporting ATPase type 2C member 2 OS=Rattus norvegicus GN=Atp2c2 PE=2 SV=1 - [AT2C2_RAT]	5.08	1	2	2	2	0.3409
Q6AXZ4	Centrosomal protein CEP57L1 OS=Rattus norvegicus GN=Cep57l1 PE=2 SV=1 - [CE57L_RAT]	7.91	1	2	2	2	0.3409
P02454	Collagen alpha-1(I) chain OS=Rattus norvegicus GN=Col1a1 PE=1 SV=5 - [CO1A1_RAT]	2.34	1	2	2	2	0.3409
Q5U3Z3	Isochorismatase domain-containing protein 2 OS=Rattus norvegicus GN=Isoc2 PE=2 SV=1 - [ISOC2_RAT]	22.86	1	2	2	2	0.3409
Q4V7F3	Probable tRNA N6-adenosine	12.56	1	2	2	2	0.3409

	threonylcarbamoyltransferase, mitochondrial OS=Rattus norvegicus GN=Osgepl1 PE=2 SV=1 - [OSGP2_RAT]						
O35412	Signal-induced proliferation-associated 1-like protein 1 OS=Rattus norvegicus GN=Sipa1l1 PE=1 SV=1 - [SI1L1_RAT]	3.46	1	2	2	2	0.3409
Q99N27	Sorting nexin-1 OS=Rattus norvegicus GN=Snx1 PE=1 SV=1 - [SNX1_RAT]	7.09	1	2	2	3	0.3409
Q68FQ0	T-complex protein 1 subunit epsilon OS=Rattus norvegicus GN=Cct5 PE=1 SV=1 - [TCPE_RAT]	7.21	1	2	2	4	0.3409
Q9JJ22	Endoplasmic reticulum aminopeptidase 1 OS=Rattus norvegicus GN=Erap1 PE=2 SV=2 - [ERAP1_RAT]	5.91	1	4	4	7	0.3413
Q4V7C7	Actin-related protein 3 OS=Rattus norvegicus GN=Actr3 PE=1 SV=1 - [ARP3_RAT]	48.56	1	10	12	79	0.3479
P20767	Ig lambda-2 chain C region OS=Rattus norvegicus PE=4 SV=1 - [LAC2_RAT]	76.92	1	5	5	24	0.3487
P18292	Prothrombin OS=Rattus norvegicus GN=F2 PE=1 SV=1 - [THRB_RAT]	16.21	1	6	6	20	0.3489
P15684	Aminopeptidase N OS=Rattus norvegicus GN=Anpep PE=1 SV=2 - [AMPN_RAT]	14.92	1	8	8	26	0.3501
B3DMA2	Acyl-CoA dehydrogenase family member 11 OS=Rattus norvegicus GN=Acad11 PE=1 SV=1 - [ACD11_RAT]	10.27	1	6	6	18	0.3507
Q6Q0N1	Cytosolic non-specific dipeptidase OS=Rattus norvegicus GN=Cndp2 PE=1 SV=1 - [CNDP2_RAT]	37.68	1	14	14	84	0.3508
P68035	Actin, alpha cardiac muscle 1 OS=Rattus norvegicus GN=Actc1 PE=2 SV=1 - [ACTC_RAT]	83.82	2	10	24	3410	0.3553
Q6IE52	Murinoglobulin-2 OS=Rattus norvegicus GN=Mug2 PE=1 SV=1 - [MUG2_RAT]	32.8	1	5	35	1766	0.3561
Q5XIC0	Enoyl-CoA delta isomerase 2, mitochondrial OS=Rattus norvegicus GN=Eci2 PE=1 SV=1 - [ECI2_RAT]	6.14	1	2	2	4	0.3567
P02793	Ferritin light chain 1 OS=Rattus norvegicus GN=Ftl1 PE=1 SV=3 - [FRIL1_RAT]	69.4	1	10	10	280	0.3583
P63039	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspd1 PE=1 SV=1 - [CH60_RAT]	65.45	1	30	30	1409	0.3586
P17220	Proteasome subunit alpha type-2 OS=Rattus norvegicus GN=Psma2 PE=1 SV=3 - [PSA2_RAT]	50.85	1	8	8	82	0.3587
P52759	Ribonuclease UK114 OS=Rattus norvegicus GN=Hrsp12 PE=1 SV=3 - [UK114_RAT]	52.55	1	5	5	25	0.3627
P47942	Dihydropyrimidinase-related protein 2 OS=Rattus norvegicus GN=Dpysl2 PE=1 SV=1 - [DPYL2_RAT]	36.36	1	10	12	205	0.3629
P41123	60S ribosomal protein L13 OS=Rattus norvegicus GN=Rpl13 PE=1 SV=2 - [RL13_RAT]	15.64	1	3	3	21	0.3630
P04631	Protein S100-B OS=Rattus norvegicus GN=S100b PE=1 SV=2 - [S100B_RAT]	40.22	1	2	2	45	0.3651
Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	23.56	1	7	8	52	0.3654
P27867	Sorbitol dehydrogenase OS=Rattus norvegicus GN=Sord PE=1 SV=4 - [DHSO_RAT]	9.8	1	2	2	2	0.3660
P97532	3-mercaptopyruvate sulfurtransferase OS=Rattus norvegicus GN=Mpst PE=1 SV=3 - [THTM_RAT]	40.4	1	9	9	94	0.3666
Q68FR6	Elongation factor 1-gamma OS=Rattus norvegicus GN=Eef1g PE=2 SV=3 - [EF1G_RAT]	36.38	1	8	9	62	0.3696
P13383	Nucleolin OS=Rattus norvegicus GN=Ncl PE=1 SV=3 - [NUCL_RAT]	16.69	1	8	8	66	0.3698
P41542	General vesicular transport factor p115 OS=Rattus norvegicus GN=Uso1 PE=1 SV=1 - [USO1_RAT]	7.51	1	5	6	26	0.3701
P32089	Tricarboxylate transport protein, mitochondrial OS=Rattus norvegicus GN=Slc25a1 PE=1 SV=1 - [TXTP_RAT]	34.41	1	7	8	229	0.3711
Q9Z1H9	Protein kinase C delta-binding protein OS=Rattus norvegicus GN=Prkcdbp PE=1 SV=1 - [PRDBP_RAT]	37.64	1	10	10	71	0.3712
Q64542	Plasma membrane calcium-transporting ATPase 4 OS=Rattus norvegicus GN=Atp2b4 PE=1 SV=1 - [AT2B4_RAT]	5.4	1	3	4	6	0.3728
P38656	Lupus La protein homolog OS=Rattus norvegicus GN=Ssb PE=1 SV=1 - [LA_RAT]	11.57	1	2	3	3	0.3742
Q9ES21	Phosphatidylinositide phosphatase SAC1 OS=Rattus norvegicus GN=Sacm1l PE=1 SV=1 - [SAC1_RAT]	11.41	1	5	6	19	0.3747
P32551	Cytochrome b-c1 complex subunit 2, mitochondrial	67.48	1	16	16	303	0.3747

	OS=Rattus norvegicus GN=Uqcrc2 PE=1 SV=2 - [QCR2_RAT]						
P43278	Histone H1.0 OS=Rattus norvegicus GN=H1f0 PE=2 SV=2 - [H10_RAT]	22.16	1	4	4	11	0.3780
P15429	Beta-enolase OS=Rattus norvegicus GN=Eno3 PE=1 SV=3 - [ENOB_RAT]	26.96	1	3	7	259	0.3780
P22734	Catechol O-methyltransferase OS=Rattus norvegicus GN=Comt PE=1 SV=2 - [COMT_RAT]	18.18	1	2	2	3	0.3790
Q6P734	Plasma protease C1 inhibitor OS=Rattus norvegicus GN=Serping1 PE=2 SV=1 - [IC1_RAT]	16.27	1	6	6	18	0.3807
P21531	60S ribosomal protein L3 OS=Rattus norvegicus GN=Rpl3 PE=1 SV=3 - [RL3_RAT]	17.12	1	4	4	13	0.3811
P04143	Thyroid hormone-inducible hepatic protein OS=Rattus norvegicus GN=Thrsp PE=1 SV=1 - [THRSP_RAT]	24	1	2	2	31	0.3835
P42346	Serine/threonine-protein kinase mTOR OS=Rattus norvegicus GN=Mtor PE=1 SV=1 - [MTOR_RAT]	1.88	1	2	2	2	0.3836
Q6IRK9	Carboxypeptidase Q OS=Rattus norvegicus GN=Cpq PE=1 SV=1 - [CBPQ_RAT]	34.96	1	10	10	41	0.3859
P07872	Peroxisomal acyl-coenzyme A oxidase 1 OS=Rattus norvegicus GN=Acox1 PE=1 SV=1 - [ACOX1_RAT]	19.36	1	6	7	15	0.3867
P35213	14-3-3 protein beta/alpha OS=Rattus norvegicus GN=Ywhab PE=1 SV=3 - [1433B_RAT]	71.54	1	9	16	458	0.3876
P81128	Rho GTPase-activating protein 35 OS=Rattus norvegicus GN=Arhgap35 PE=1 SV=2 - [RHG35_RAT]	2.38	1	2	2	2	0.3902
P08934	Kininogen-1 OS=Rattus norvegicus GN=Kng1 PE=2 SV=1 - [KNG1_RAT]	10.02	1	4	5	15	0.3940
Q64640	Adenosine kinase OS=Rattus norvegicus GN=Adk PE=1 SV=3 - [ADK_RAT]	20.5	1	3	3	21	0.3942
P35565	Calnexin OS=Rattus norvegicus GN=Canx PE=1 SV=1 - [CALX_RAT]	37.56	1	17	17	187	0.3951
Q9HB97	Alpha-parvin OS=Rattus norvegicus GN=Parva PE=1 SV=2 - [PARVA_RAT]	21.24	1	5	5	20	0.3953
Q9EPH1	Alpha-1B-glycoprotein OS=Rattus norvegicus GN=A1bg PE=2 SV=2 - [A1BG_RAT]	31.38	1	13	13	192	0.3967
Q5RJP0	Aldose reductase-related protein 1 OS=Rattus norvegicus GN=Akr1b7 PE=1 SV=1 - [ALD1_RAT]	12.66	1	1	3	8	0.3970
Q9WU49	Calcium-regulated heat stable protein 1 OS=Rattus norvegicus GN=Carhsp1 PE=1 SV=1 - [CHSP1_RAT]	18.37	1	2	2	3	0.4006
P29315	Ribonuclease inhibitor OS=Rattus norvegicus GN=Rnh1 PE=1 SV=2 - [RINI_RAT]	26.1	1	6	6	30	0.4016
Q80U96	Exportin-1 OS=Rattus norvegicus GN=Xpo1 PE=1 SV=1 - [XPO1_RAT]	7	1	3	4	6	0.4022
P05065	Fructose-bisphosphate aldolase A OS=Rattus norvegicus GN=Aldoa PE=1 SV=2 - [ALDOA_RAT]	81.32	1	24	25	1405	0.4036
Q9Z0V5	Peroxiredoxin-4 OS=Rattus norvegicus GN=Prdx4 PE=2 SV=1 - [PRDX4_RAT]	29.3	1	4	6	124	0.4062
Q91Y81	Septin-2 OS=Rattus norvegicus GN=Sept2 PE=1 SV=1 - [SEPT2_RAT]	36.01	1	8	8	26	0.4089
P11240	Cytochrome c oxidase subunit 5A, mitochondrial OS=Rattus norvegicus GN=Cox5a PE=1 SV=1 - [COX5A_RAT]	54.79	1	7	7	93	0.4120
Q62930	Complement component C9 OS=Rattus norvegicus GN=C9 PE=2 SV=1 - [CO9_RAT]	16.79	1	5	5	25	0.4157
F1LMZ8	26S proteasome non-ATPase regulatory subunit 11 OS=Rattus norvegicus GN=Psmd11 PE=1 SV=2 - [PSD11_RAT]	10.66	1	3	4	5	0.4192
Q8CG45	Aflatoxin B1 aldehyde reductase member 2 OS=Rattus norvegicus GN=Akr7a2 PE=1 SV=2 - [ARK72_RAT]	20.44	1	6	6	25	0.4194
B1H268	Mini-chromosome maintenance complex-binding protein OS=Rattus norvegicus GN=Mcmbp PE=2 SV=1 - [MCMBP_RAT]	6.7	1	2	2	2	0.4220
Q4FZT9	26S proteasome non-ATPase regulatory subunit 2 OS=Rattus norvegicus GN=Psmd2 PE=1 SV=1 - [PSMD2_RAT]	16.3	1	9	9	59	0.4226
Q9WVK7	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Hadh PE=2 SV=1 - [HCDH_RAT]	67.52	1	12	12	567	0.4244
Q6RJR6	Reticulon-3 OS=Rattus norvegicus GN=Rtn3 PE=1 SV=1	2.02	1	2	2	17	0.4246

	- [RTN3_RAT]						
O88644	Grifin OS=Rattus norvegicus GN=Grifin PE=1 SV=1 - [GRIFN_RAT]	22.22	1	3	3	28	0.4257
O55012	Phosphatidylinositol-binding clathrin assembly protein OS=Rattus norvegicus GN=Picalm PE=1 SV=1 - [PICAL_RAT]	9.53	1	3	4	7	0.4259
P16617	Phosphoglycerate kinase 1 OS=Rattus norvegicus GN=Pgk1 PE=1 SV=2 - [PGK1_RAT]	74.1	1	25	25	388	0.4262
Q62969	Prostacyclin synthase OS=Rattus norvegicus GN=Ptgis PE=2 SV=1 - [PTGIS_RAT]	9.78	1	3	3	17	0.4285
O35795	Ectonucleoside triphosphate diphosphohydrolase 2 OS=Rattus norvegicus GN=Entpd2 PE=1 SV=1 - [ENTP2_RAT]	6.87	1	2	2	7	0.4292
P02680	Fibrinogen gamma chain OS=Rattus norvegicus GN=Fgg PE=1 SV=3 - [FIBG_RAT]	50.56	1	15	16	92	0.4300
P08461	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Rattus norvegicus GN=Dlat PE=1 SV=3 - [ODP2_RAT]	34.02	1	13	13	84	0.4318
Q6AYD3	Proliferation-associated protein 2G4 OS=Rattus norvegicus GN=Pa2g4 PE=1 SV=1 - [PA2G4_RAT]	10.91	1	3	4	13	0.4336
Q6URK4	Heterogeneous nuclear ribonucleoprotein A3 OS=Rattus norvegicus GN=Hnrnpa3 PE=1 SV=1 - [ROA3_RAT]	10.29	1	3	3	23	0.4340
P14408	Fumarate hydratase, mitochondrial OS=Rattus norvegicus GN=Fh PE=1 SV=1 - [FUMH_RAT]	28.01	1	7	7	44	0.4344
Q07936	Annexin A2 OS=Rattus norvegicus GN=Anxa2 PE=1 SV=2 - [ANXA2_RAT]	71.98	1	27	27	1818	0.4369
P51886	Lumican OS=Rattus norvegicus GN=Lum PE=1 SV=1 - [LUM_RAT]	36.09	1	11	11	344	0.4387
Q68FY0	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Rattus norvegicus GN=Uqcrc1 PE=1 SV=1 - [QCR1_RAT]	33.75	1	10	10	238	0.4422
P18421	Proteasome subunit beta type-1 OS=Rattus norvegicus GN=Psmb1 PE=1 SV=3 - [PSB1_RAT]	39.17	1	7	7	55	0.4432
Q63416	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Rattus norvegicus GN=Itih3 PE=2 SV=1 - [ITIH3_RAT]	30.21	1	15	16	280	0.4459
P15304	Hormone-sensitive lipase OS=Rattus norvegicus GN=Lipe PE=1 SV=3 - [LIPS_RAT]	50.66	1	33	33	969	0.4468
Q5U316	Ras-related protein Rab-35 OS=Rattus norvegicus GN=Rab35 PE=1 SV=1 - [RAB35_RAT]	37.81	1	2	5	34	0.4508
Q3MIE4	Synaptic vesicle membrane protein VAT-1 homolog OS=Rattus norvegicus GN=Vat1 PE=1 SV=1 - [VAT1_RAT]	46.78	1	12	12	74	0.4512
P30835	ATP-dependent 6-phosphofructokinase, liver type OS=Rattus norvegicus GN=Pfkl PE=1 SV=3 - [PFKAL_RAT]	7.82	1	4	4	11	0.4534
P17764	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus GN=Acat1 PE=1 SV=1 - [THIL_RAT]	49.06	1	13	13	169	0.4539
P63018	Heat shock cognate 71 kDa protein OS=Rattus norvegicus GN=Hspa8 PE=1 SV=1 - [HSP7C_RAT]	73.84	1	33	38	1143	0.4554
P14046	Alpha-1-inhibitor 3 OS=Rattus norvegicus GN=A1i3 PE=1 SV=1 - [A1I3_RAT]	52.61	1	21	56	2854	0.4563
Q03626	Murinoglobulin-1 OS=Rattus norvegicus GN=Mug1 PE=2 SV=1 - [MUG1_RAT]	50.98	1	15	54	2642	0.4563
P24050	40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=1 SV=3 - [RS5_RAT]	24.02	1	4	4	5	0.4591
Q66HD0	Endoplasmin OS=Rattus norvegicus GN=Hsp90b1 PE=1 SV=2 - [ENPL_RAT]	52.36	1	35	37	604	0.4616
P62278	40S ribosomal protein S13 OS=Rattus norvegicus GN=Rps13 PE=1 SV=2 - [RS13_RAT]	45.03	1	5	6	9	0.4623
Q68FR9	Elongation factor 1-delta OS=Rattus norvegicus GN=Eef1d PE=1 SV=2 - [EF1D_RAT]	21.71	1	4	4	19	0.4634
Q63617	Hypoxia up-regulated protein 1 OS=Rattus norvegicus GN=Hyou1 PE=1 SV=1 - [HYOU1_RAT]	20.22	1	13	13	122	0.4649
P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	57.57	1	31	31	560	0.4662
P85972	Vinculin OS=Rattus norvegicus GN=Vcl PE=1 SV=1 - [VINC_RAT]	66.79	1	55	58	1129	0.4677

P27321	Calpastatin OS=Rattus norvegicus GN=Cast PE=1 SV=3 - [ICAL_RAT]	9.12	1	2	2	4	0.4697
P10252	CD48 antigen OS=Rattus norvegicus GN=Cd48 PE=1 SV=1 - [CD48_RAT]	12.5	1	2	2	2	0.4738
P05712	Ras-related protein Rab-2A OS=Rattus norvegicus GN=Rab2a PE=2 SV=1 - [RAB2A_RAT]	32.55	1	3	4	14	0.4743
P04762	Catalase OS=Rattus norvegicus GN=Cat PE=1 SV=3 - [CATA_RAT]	62.05	1	23	23	421	0.4800
P81155	Voltage-dependent anion-selective channel protein 2 OS=Rattus norvegicus GN=Vdac2 PE=1 SV=2 - [VDAC2_RAT]	27.8	1	6	6	45	0.4807
Q64232	Very-long-chain enoyl-CoA reductase OS=Rattus norvegicus GN=Tecr PE=1 SV=1 - [TECR_RAT]	18.18	1	6	6	28	0.4818
O88664	Serine/threonine-protein kinase TAO1 OS=Rattus norvegicus GN=Taok1 PE=1 SV=1 - [TAOK1_RAT]	2	1	2	2	2	0.4823
P09811	Glycogen phosphorylase, liver form OS=Rattus norvegicus GN=Pygl PE=1 SV=5 - [PYGL_RAT]	35.41	1	18	20	191	0.4848
P00564	Creatine kinase M-type OS=Rattus norvegicus GN=Ckm PE=1 SV=2 - [KCRM_RAT]	24.93	1	7	7	17	0.4892
P10760	Adenosylhomocysteinase OS=Rattus norvegicus GN=Ahcy PE=1 SV=3 - [SAHH_RAT]	31.48	1	10	10	114	0.4894
Q9Z311	Trans-2-enoyl-CoA reductase, mitochondrial OS=Rattus norvegicus GN=Mecr PE=1 SV=1 - [MECR_RAT]	20.64	1	2	2	31	0.4896
Q9EQX9	Ubiquitin-conjugating enzyme E2 N OS=Rattus norvegicus GN=Ube2n PE=1 SV=1 - [UBE2N_RAT]	42.11	1	5	5	79	0.4916
Q5BK63	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Rattus norvegicus GN=Ndufa9 PE=1 SV=2 - [NDUA9_RAT]	22.55	1	5	5	49	0.4923
P48679	Prelamin-A/C OS=Rattus norvegicus GN=Lmna PE=1 SV=1 - [LMNA_RAT]	35.79	1	19	20	76	0.4931
P07861	Neprilysin OS=Rattus norvegicus GN=Mme PE=1 SV=2 - [NEP_RAT]	3.87	1	2	2	3	0.4953
O54728	Phospholipase B1, membrane-associated OS=Rattus norvegicus GN=Plb1 PE=1 SV=1 - [PLB1_RAT]	3.93	1	2	2	8	0.4968
Q64240	Protein AMBP OS=Rattus norvegicus GN=Ambp PE=1 SV=1 - [AMBP_RAT]	12.61	1	3	3	17	0.4973
Q06647	ATP synthase subunit O, mitochondrial OS=Rattus norvegicus GN=Atp5o PE=1 SV=1 - [ATPO_RAT]	62.91	1	10	11	196	0.4976
P62907	60S ribosomal protein L10a OS=Rattus norvegicus GN=Rpl10a PE=1 SV=2 - [RL10A_RAT]	18.89	1	3	4	17	0.4980
P04905	Glutathione S-transferase Mu 1 OS=Rattus norvegicus GN=Gstm1 PE=1 SV=2 - [GSTM1_RAT]	51.38	1	6	9	72	0.4981
Q63028	Alpha-adducin OS=Rattus norvegicus GN=Add1 PE=1 SV=2 - [ADDA_RAT]	12.24	1	3	4	5	0.4985
P27881	Hexokinase-2 OS=Rattus norvegicus GN=Hk2 PE=1 SV=1 - [HXK2_RAT]	5.67	1	3	4	6	0.5012
B0BNE5	S-formylglutathione hydrolase OS=Rattus norvegicus GN=Esd PE=2 SV=1 - [ESTD_RAT]	33.69	1	4	4	19	0.5026
P11960	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial (Fragment) OS=Rattus norvegicus GN=Bckdha PE=1 SV=1 - [ODBA_RAT]	8.62	1	2	2	11	0.5036
P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	50.47	1	32	32	851	0.5058
Q6DGG0	Peptidyl-prolyl cis-trans isomerase D OS=Rattus norvegicus GN=Ppid PE=1 SV=3 - [PPID_RAT]	14.05	1	3	3	9	0.5083
P23358	60S ribosomal protein L12 OS=Rattus norvegicus GN=Rpl12 PE=2 SV=1 - [RL12_RAT]	54.55	1	6	6	75	0.5086
P18420	Proteasome subunit alpha type-1 OS=Rattus norvegicus GN=Psma1 PE=1 SV=2 - [PSA1_RAT]	23.95	1	6	6	10	0.5111
Q9Z1X1	Extended synaptotagmin-1 OS=Rattus norvegicus GN=Esyt1 PE=1 SV=1 - [ESYT1_RAT]	47.7	1	35	35	517	0.5138
P13084	Nucleophosmin OS=Rattus norvegicus GN=Npm1 PE=1 SV=1 - [NPM_RAT]	13.36	1	2	2	6	0.5149
P26772	10 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspe1 PE=1 SV=3 - [CH10_RAT]	66.67	1	8	8	61	0.5215
Q5RKI0	WD repeat-containing protein 1 OS=Rattus norvegicus GN=Wdr1 PE=1 SV=3 - [WDR1_RAT]	4.79	1	2	2	2	0.5227
Q5RJR8	Leucine-rich repeat-containing protein 59 OS=Rattus	6.84	1	2	2	5	0.5250

	norvegicus GN=Lrrc59 PE=1 SV=1 - [LRC59_RAT]						
Q9ERM3	Diacylglycerol O-acyltransferase 1 OS=Rattus norvegicus GN=Dgat1 PE=2 SV=1 - [DGAT1_RAT]	7.03	1	2	2	2	0.5256
Q4AEF8	Coatomer subunit gamma-1 OS=Rattus norvegicus GN=Copg1 PE=2 SV=1 - [COPG1_RAT]	10.3	1	5	6	22	0.5262
P27952	40S ribosomal protein S2 OS=Rattus norvegicus GN=Rps2 PE=1 SV=1 - [RS2_RAT]	12.29	1	3	3	12	0.5273
P09606	Glutamine synthetase OS=Rattus norvegicus GN=Glul PE=1 SV=3 - [GLNA_RAT]	34.85	1	11	11	144	0.5277
P05369	Farnesyl pyrophosphate synthase OS=Rattus norvegicus GN=Fdps PE=2 SV=2 - [FPPS_RAT]	17	1	5	5	15	0.5297
Q9JJ79	Cytoplasmic dynein 2 heavy chain 1 OS=Rattus norvegicus GN=Dync2h1 PE=1 SV=1 - [DYHC2_RAT]	2.48	1	4	6	7	0.5302
Q60587	Trifunctional enzyme subunit beta, mitochondrial OS=Rattus norvegicus GN=Hadhb PE=1 SV=1 - [ECHB_RAT]	49.47	1	19	19	176	0.5310
P17046	Lysosome-associated membrane glycoprotein 2 OS=Rattus norvegicus GN=Lamp2 PE=1 SV=2 - [LAMP2_RAT]	7.3	1	2	2	8	0.5336
Q6PCU2	V-type proton ATPase subunit E 1 OS=Rattus norvegicus GN=Atp6v1e1 PE=1 SV=1 - [VATE1_RAT]	15.93	1	1	2	13	0.5353
Q63377	Sodium/potassium-transporting ATPase subunit beta-3 OS=Rattus norvegicus GN=Atp1b3 PE=2 SV=1 - [AT1B3_RAT]	11.83	1	2	2	5	0.5395
P21533	60S ribosomal protein L6 OS=Rattus norvegicus GN=Rpl6 PE=1 SV=5 - [RL6_RAT]	10.74	1	2	2	6	0.5426
B2GV38	Ubiquitin-like protein 4A OS=Rattus norvegicus GN=Ubl4a PE=2 SV=1 - [UBL4A_RAT]	19.75	1	2	2	2	0.5440
P10688	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1 OS=Rattus norvegicus GN=Plcd1 PE=1 SV=1 - [PLCD1_RAT]	7.41	1	2	3	4	0.5445
B0BN93	26S proteasome non-ATPase regulatory subunit 13 OS=Rattus norvegicus GN=Psmd13 PE=1 SV=1 - [PSD13_RAT]	7.71	1	2	2	2	0.5446
P45953	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acadvl PE=1 SV=1 - [ACADV_RAT]	25.5	1	10	10	85	0.5447
P11030	Acyl-CoA-binding protein OS=Rattus norvegicus GN=Dbi PE=1 SV=3 - [ACBP_RAT]	54.02	1	5	5	103	0.5450
P00507	Aspartate aminotransferase, mitochondrial OS=Rattus norvegicus GN=Got2 PE=1 SV=2 - [AATM_RAT]	26.98	1	9	9	74	0.5474
Q9WTT6	Guanine deaminase OS=Rattus norvegicus GN=Gda PE=1 SV=1 - [GUAD_RAT]	74.45	1	23	23	941	0.5474
Q66HG4	Aldose 1-epimerase OS=Rattus norvegicus GN=Galm PE=1 SV=1 - [GALM_RAT]	28.07	1	6	6	26	0.5479
P20760	Ig gamma-2A chain C region OS=Rattus norvegicus GN=Igg-2a PE=1 SV=1 - [IGG2A_RAT]	63.04	1	15	15	660	0.5492
P20650	Protein phosphatase 1A OS=Rattus norvegicus GN=Ppm1a PE=1 SV=1 - [PPM1A_RAT]	5.5	2	2	2	2	0.5497
P20171	GTPase HRas OS=Rattus norvegicus GN=Hras PE=1 SV=2 - [RASH_RAT]	33.33	2	4	4	9	0.5545
O09171	Betaine--homocysteine S-methyltransferase 1 OS=Rattus norvegicus GN=Bhmt PE=1 SV=1 - [BHMT1_RAT]	11.06	1	4	4	9	0.5583
Q5XIM9	T-complex protein 1 subunit beta OS=Rattus norvegicus GN=Cct2 PE=1 SV=3 - [TCPB_RAT]	14.39	1	4	4	15	0.5584
Q4FZU2	Keratin, type II cytoskeletal 6A OS=Rattus norvegicus GN=Krt6a PE=1 SV=1 - [K2C6A_RAT]	10.87	1	4	7	57	0.5587
P06399	Fibrinogen alpha chain OS=Rattus norvegicus GN=Fga PE=1 SV=3 - [FIBA_RAT]	17.52	1	11	11	106	0.5588
P12007	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ivd PE=1 SV=2 - [IVD_RAT]	39.39	1	11	11	88	0.5588
O35077	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Rattus norvegicus GN=Gpd1 PE=1 SV=4 - [GPDA_RAT]	91.4	1	27	27	3199	0.5637
O89049	Thioredoxin reductase 1, cytoplasmic OS=Rattus norvegicus GN=Txnrd1 PE=1 SV=5 - [TRXR1_RAT]	16.63	1	4	4	6	0.5642
P26284	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Rattus norvegicus	53.59	1	18	19	177	0.5649

	GN=Pdha1 PE=1 SV=2 - [ODPA_RAT]						
P10824	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Rattus norvegicus GN=Gnai1 PE=1 SV=3 - [GNAI1_RAT]	21.75	1	2	6	76	0.5683
Q9JLZ1	Glutaredoxin-3 OS=Rattus norvegicus GN=Glrx3 PE=1 SV=2 - [GLRX3_RAT]	6.53	1	2	2	2	0.5685
Q6DGG1	Alpha/beta hydrolase domain-containing protein 14B OS=Rattus norvegicus GN=Abhd14b PE=2 SV=1 - [ABHEB_RAT]	15.71	1	2	2	2	0.5704
P02651	Apolipoprotein A-IV OS=Rattus norvegicus GN=Apoa4 PE=1 SV=2 - [APOA4_RAT]	62.4	1	19	19	125	0.5706
P68255	14-3-3 protein theta OS=Rattus norvegicus GN=Ywhaq PE=1 SV=1 - [1433T_RAT]	72.24	1	14	20	448	0.5732
P68511	14-3-3 protein eta OS=Rattus norvegicus GN=Ywhah PE=1 SV=2 - [1433F_RAT]	52.85	1	7	14	248	0.5776
Q5QD51	A-kinase anchor protein 12 OS=Rattus norvegicus GN=Akap12 PE=1 SV=1 - [AKA12_RAT]	5.63	1	6	7	34	0.5777
P29314	40S ribosomal protein S9 OS=Rattus norvegicus GN=Rps9 PE=1 SV=4 - [RS9_RAT]	12.89	1	3	4	15	0.5778
P19945	60S acidic ribosomal protein P0 OS=Rattus norvegicus GN=Rplp0 PE=1 SV=2 - [RLA0_RAT]	42.59	1	8	9	131	0.5780
Q8VHE9	All-trans-retinol 13,14-reductase OS=Rattus norvegicus GN=Retsat PE=2 SV=1 - [RETST_RAT]	30.54	1	11	11	249	0.5789
P83868	Prostaglandin E synthase 3 OS=Rattus norvegicus GN=Ptges3 PE=1 SV=2 - [TEBP_RAT]	32.5	1	4	4	10	0.5789
P08649	Complement C4 OS=Rattus norvegicus GN=C4 PE=1 SV=3 - [CO4_RAT]	48.47	1	55	56	1299	0.5821
P41498	Low molecular weight phosphotyrosine protein phosphatase OS=Rattus norvegicus GN=Acp1 PE=1 SV=3 - [PPAC_RAT]	24.05	1	3	3	10	0.5936
Q9WVC0	Septin-7 OS=Rattus norvegicus GN=Sept7 PE=1 SV=1 - [SEPT7_RAT]	17.43	1	6	6	31	0.5941
Q9JHW0	Proteasome subunit beta type-7 OS=Rattus norvegicus GN=Psmb7 PE=1 SV=1 - [PSB7_RAT]	13.72	1	3	3	6	0.5946
P17077	60S ribosomal protein L9 OS=Rattus norvegicus GN=Rpl9 PE=1 SV=1 - [RL9_RAT]	23.96	1	2	2	2	0.5950
P32755	4-hydroxyphenylpyruvate dioxygenase OS=Rattus norvegicus GN=Hpd PE=1 SV=3 - [HPPD_RAT]	8.65	1	2	2	3	0.5959
P02401	60S acidic ribosomal protein P2 OS=Rattus norvegicus GN=Rplp2 PE=1 SV=2 - [RLA2_RAT]	74.78	1	5	6	52	0.6039
Q4V8F9	Hydroxysteroid dehydrogenase-like protein 2 OS=Rattus norvegicus GN=Hsdl2 PE=2 SV=1 - [HSDL2_RAT]	5.53	1	2	2	7	0.6070
P28077	Proteasome subunit beta type-9 OS=Rattus norvegicus GN=Psmb9 PE=1 SV=2 - [PSB9_RAT]	14.16	1	3	3	6	0.6071
P49911	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Rattus norvegicus GN=Anp32a PE=2 SV=1 - [AN32A_RAT]	29.15	1	4	5	23	0.6105
P41562	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Rattus norvegicus GN=Idh1 PE=1 SV=1 - [IDHC_RAT]	59.66	1	19	20	324	0.6107
P62902	60S ribosomal protein L31 OS=Rattus norvegicus GN=Rpl31 PE=2 SV=1 - [RL31_RAT]	18.4	1	2	2	9	0.6114
P11951	Cytochrome c oxidase subunit 6C-2 OS=Rattus norvegicus GN=Cox6c2 PE=1 SV=3 - [CX6C2_RAT]	25	1	2	2	21	0.6151
Q62952	Dihydropyrimidinase-related protein 3 OS=Rattus norvegicus GN=Dpysl3 PE=1 SV=2 - [DPYL3_RAT]	30	1	10	12	50	0.6172
P46844	Biliverdin reductase A OS=Rattus norvegicus GN=Blvra PE=1 SV=1 - [BIEA_RAT]	41.02	1	9	9	36	0.6175
Q63965	Sideroflexin-1 OS=Rattus norvegicus GN=Sfxn1 PE=2 SV=4 - [SFXN1_RAT]	25.78	1	5	5	18	0.6180
P70587	Leucine-rich repeat-containing protein 7 OS=Rattus norvegicus GN=Lrrc7 PE=1 SV=2 - [LRRC7_RAT]	2.62	1	3	3	3	0.6183
Q8VHV7	Heterogeneous nuclear ribonucleoprotein H OS=Rattus norvegicus GN=Hnrnph1 PE=1 SV=2 - [HNRH1_RAT]	11.14	1	1	3	7	0.6196
O35828	Coronin-7 OS=Rattus norvegicus GN=Coro7 PE=1 SV=2 - [CORO7_RAT]	3.8	1	2	2	2	0.6280
Q5RKI1	Eukaryotic initiation factor 4A-II OS=Rattus norvegicus GN=Eif4a2 PE=1 SV=1 - [IF4A2_RAT]	29.98	1	10	10	117	0.6290
P52873	Pyruvate carboxylase, mitochondrial OS=Rattus	68.59	1	54	54	2594	0.6290

	norvegicus GN=Pc PE=1 SV=2 - [PYC_RAT]						
Q63524	Transmembrane emp24 domain-containing protein 2 OS=Rattus norvegicus GN=Tmed2 PE=1 SV=1 - [TMED2_RAT]	20.4	1	2	2	11	0.6292
P10888	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Rattus norvegicus GN=Cox4i1 PE=1 SV=1 - [COX41_RAT]	31.36	1	5	5	133	0.6327
Q641Y0	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Rattus norvegicus GN=Ddost PE=2 SV=1 - [OST48_RAT]	16.1	1	5	5	16	0.6327
Q9ES40	PRA1 family protein 3 OS=Rattus norvegicus GN=Arl6ip5 PE=1 SV=1 - [PRAF3_RAT]	15.96	1	2	2	2	0.6359
Q6IG12	Keratin, type II cytoskeletal 7 OS=Rattus norvegicus GN=Krt7 PE=3 SV=1 - [K2C7_RAT]	12.69	1	3	7	33	0.6361
Q05982	Nucleoside diphosphate kinase A OS=Rattus norvegicus GN=Nme1 PE=1 SV=1 - [NDKA_RAT]	63.16	1	3	9	279	0.6367
P13086	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Rattus norvegicus GN=Suclg1 PE=2 SV=2 - [SUCA_RAT]	32.08	1	7	8	69	0.6391
P28023	Dynactin subunit 1 OS=Rattus norvegicus GN=Dctn1 PE=1 SV=2 - [DCTN1_RAT]	4.22	1	3	3	7	0.6395
P49242	40S ribosomal protein S3a OS=Rattus norvegicus GN=Rps3a PE=1 SV=2 - [RS3A_RAT]	19.7	1	4	4	12	0.6423
Q9JK11	Reticulon-4 OS=Rattus norvegicus GN=Rtn4 PE=1 SV=1 - [RTN4_RAT]	4.21	1	4	4	25	0.6431
P62898	Cytochrome c, somatic OS=Rattus norvegicus GN=Cycs PE=1 SV=2 - [CYC_RAT]	50.48	1	7	7	156	0.6437
P11497	Acetyl-CoA carboxylase 1 OS=Rattus norvegicus GN=Acaca PE=1 SV=1 - [ACACA_RAT]	54.2	1	87	87	1248	0.6441
P13697	NADP-dependent malic enzyme OS=Rattus norvegicus GN=Me1 PE=1 SV=2 - [MAOX_RAT]	78.67	1	30	31	1482	0.6442
P29994	Inositol 1,4,5-trisphosphate receptor type 1 OS=Rattus norvegicus GN=Itpr1 PE=1 SV=2 - [ITPR1_RAT]	1.02	1	2	2	4	0.6443
P16638	ATP-citrate synthase OS=Rattus norvegicus GN=Acly PE=1 SV=1 - [ACLY_RAT]	60.45	1	52	53	2466	0.6444
Q8R431	Monoglyceride lipase OS=Rattus norvegicus GN=Mgll PE=1 SV=1 - [MGLL_RAT]	67.66	1	17	17	625	0.6446
Q4V8H8	EH domain-containing protein 2 OS=Rattus norvegicus GN=Ehd2 PE=1 SV=1 - [EHD2_RAT]	73.3	1	31	32	2143	0.6478
P07943	Aldose reductase OS=Rattus norvegicus GN=Akr1b1 PE=1 SV=3 - [ALDR_RAT]	59.49	1	14	16	259	0.6517
Q5M7U6	Actin-related protein 2 OS=Rattus norvegicus GN=Actr2 PE=2 SV=1 - [ARP2_RAT]	28.17	1	7	7	25	0.6543
P02692	Fatty acid-binding protein, liver OS=Rattus norvegicus GN=Fabp1 PE=1 SV=1 - [FABPL_RAT]	62.2	1	6	6	72	0.6568
P50399	Rab GDP dissociation inhibitor beta OS=Rattus norvegicus GN=Gdi2 PE=1 SV=2 - [GDIB_RAT]	58.43	1	16	21	452	0.6569
P61805	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Rattus norvegicus GN=Dad1 PE=3 SV=3 - [DAD1_RAT]	17.7	1	2	2	5	0.6583
P15651	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acads PE=1 SV=2 - [ACADS_RAT]	25	1	6	7	27	0.6596
Q3T1K5	F-actin-capping protein subunit alpha-2 OS=Rattus norvegicus GN=Capza2 PE=1 SV=1 - [CAZA2_RAT]	27.97	1	4	5	29	0.6626
P28037	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Rattus norvegicus GN=Aldh1l1 PE=1 SV=3 - [AL1L1_RAT]	33.15	1	20	20	92	0.6657
P14740	Dipeptidyl peptidase 4 OS=Rattus norvegicus GN=Dpp4 PE=1 SV=2 - [DPP4_RAT]	17.47	1	9	10	59	0.6697
P98158	Low-density lipoprotein receptor-related protein 2 OS=Rattus norvegicus GN=Lrp2 PE=1 SV=1 - [LRP2_RAT]	0.6	1	2	2	2	0.6707
P29975	Aquaporin-1 OS=Rattus norvegicus GN=Aqp1 PE=1 SV=4 - [AQP1_RAT]	26.77	1	4	4	7	0.6732
Q6P6Q2	Keratin, type II cytoskeletal 5 OS=Rattus norvegicus GN=Krt5 PE=1 SV=1 - [K2C5_RAT]	19.97	1	4	11	76	0.6759
P55051	Fatty acid-binding protein, brain OS=Rattus norvegicus	24.24	1	1	2	18	0.6806

	GN=Fabp7 PE=1 SV=2 - [FABP7_RAT]						
P06214	Delta-aminolevulinic acid dehydratase OS=Rattus norvegicus GN=Alad PE=1 SV=1 - [HEM2_RAT]	35.45	1	6	6	59	0.6822
Q3KR86	MICOS complex subunit Mic60 (Fragment) OS=Rattus norvegicus GN=Immt PE=1 SV=1 - [MIC60_RAT]	17.9	1	8	8	24	0.6822
P06302	Prothymosin alpha OS=Rattus norvegicus GN=Ptma PE=1 SV=2 - [PTMA_RAT]	22.32	1	3	3	3	0.6834
P51635	Alcohol dehydrogenase [NADP(+)] OS=Rattus norvegicus GN=Akr1a1 PE=1 SV=2 - [AK1A1_RAT]	43.08	1	12	12	100	0.6878
Q7M767	Ubiquitin-conjugating enzyme E2 variant 2 OS=Rattus norvegicus GN=Ube2v2 PE=1 SV=3 - [UB2V2_RAT]	34.48	1	4	4	10	0.6896
Q6P6R2	Dihydrolipoyl dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Dld PE=1 SV=1 - [DLDH_RAT]	42.04	1	14	14	349	0.6899
P33124	Long-chain-fatty-acid--CoA ligase 6 OS=Rattus norvegicus GN=Acsl6 PE=1 SV=1 - [ACSL6_RAT]	2.73	1	1	2	221	0.6930
Q63797	Proteasome activator complex subunit 1 OS=Rattus norvegicus GN=Psme1 PE=2 SV=1 - [PSME1_RAT]	44.18	1	10	10	66	0.6933
P47853	Biglycan OS=Rattus norvegicus GN=Bgn PE=2 SV=1 - [PGS1_RAT]	52.57	1	12	14	142	0.6938
B5DFC9	Nidogen-2 OS=Rattus norvegicus GN=Nid2 PE=2 SV=1 - [NID2_RAT]	15.04	1	13	13	74	0.6954
P85515	Alpha-centractin OS=Rattus norvegicus GN=Actr1a PE=1 SV=1 - [ACTZ_RAT]	22.07	1	5	5	16	0.6985
P29410	Adenylate kinase 2, mitochondrial OS=Rattus norvegicus GN=Ak2 PE=2 SV=2 - [KAD2_RAT]	54.39	1	11	11	201	0.7016
Q62651	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Rattus norvegicus GN=Ech1 PE=1 SV=2 - [ECH1_RAT]	39.14	1	10	10	47	0.7027
P35435	ATP synthase subunit gamma, mitochondrial OS=Rattus norvegicus GN=Atp5c1 PE=1 SV=2 - [ATPG_RAT]	35.9	1	7	7	59	0.7037
Q5XIH7	Prohibitin-2 OS=Rattus norvegicus GN=Phb2 PE=1 SV=1 - [PHB2_RAT]	44.48	1	9	10	129	0.7037
P54313	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Rattus norvegicus GN=Gnb2 PE=1 SV=4 - [GBB2_RAT]	43.24	1	5	10	116	0.7051
Q01177	Plasminogen OS=Rattus norvegicus GN=Plg PE=2 SV=2 - [PLMN_RAT]	28.33	1	17	17	77	0.7064
Q5EB81	NADH-cytochrome b5 reductase 1 OS=Rattus norvegicus GN=Cyb5r1 PE=2 SV=1 - [NB5R1_RAT]	6.56	1	2	2	2	0.7076
Q68FP1	Gelsolin OS=Rattus norvegicus GN=Gsn PE=1 SV=1 - [GELS_RAT]	48.97	1	22	22	419	0.7093
P20788	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Rattus norvegicus GN=Uqcrfs1 PE=1 SV=2 - [UCRI_RAT]	22.63	1	3	4	17	0.7098
Q6P0K8	Junction plakoglobin OS=Rattus norvegicus GN=Jup PE=1 SV=1 - [PLAK_RAT]	6.17	1	3	3	3	0.7108
P07687	Epoxide hydrolase 1 OS=Rattus norvegicus GN=Ephx1 PE=1 SV=1 - [HYEP_RAT]	12.09	1	3	3	5	0.7142
Q3T1J1	Eukaryotic translation initiation factor 5A-1 OS=Rattus norvegicus GN=Eif5a PE=1 SV=3 - [IF5A1_RAT]	46.1	1	8	8	101	0.7163
P11762	Galectin-1 OS=Rattus norvegicus GN=Lgals1 PE=1 SV=2 - [LEG1_RAT]	61.48	1	10	10	566	0.7170
P54311	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Rattus norvegicus GN=Gnb1 PE=1 SV=4 - [GBB1_RAT]	40.88	1	5	11	132	0.7184
P28073	Proteasome subunit beta type-6 OS=Rattus norvegicus GN=Psmb6 PE=1 SV=3 - [PSB6_RAT]	29.41	1	4	4	44	0.7185
P62250	40S ribosomal protein S16 OS=Rattus norvegicus GN=Rps16 PE=1 SV=2 - [RS16_RAT]	32.88	1	4	4	18	0.7208
P16257	Translocator protein OS=Rattus norvegicus GN=Tspo PE=1 SV=1 - [TSPO_RAT]	27.22	1	2	2	7	0.7299
Q9JIL8	DNA repair protein RAD50 OS=Rattus norvegicus GN=Rad50 PE=1 SV=1 - [RAD50_RAT]	2.06	1	2	2	2	0.7311
P22985	Xanthine dehydrogenase/oxidase OS=Rattus norvegicus GN=Xdh PE=1 SV=3 - [XDH_RAT]	31.25	1	24	24	842	0.7335
P23457	3-alpha-hydroxysteroid dehydrogenase OS=Rattus norvegicus GN=Akr1c9 PE=1 SV=1 - [DIDH_RAT]	47.52	1	9	11	151	0.7336
P07633	Propionyl-CoA carboxylase beta chain, mitochondrial	18.11	1	5	6	12	0.7370

	OS=Rattus norvegicus GN=Pccb PE=2 SV=1 - [PCCB_RAT]						
Q63798	Proteasome activator complex subunit 2 OS=Rattus norvegicus GN=Psme2 PE=2 SV=3 - [PSME2_RAT]	26.89	1	5	5	47	0.7400
P82471	Guanine nucleotide-binding protein G(q) subunit alpha OS=Rattus norvegicus GN=Gnaq PE=2 SV=2 - [GNAQ_RAT]	19.78	1	5	5	29	0.7422
P05708	Hexokinase-1 OS=Rattus norvegicus GN=Hk1 PE=1 SV=4 - [HXK1_RAT]	8.17	1	5	6	40	0.7453
Q5U300	Ubiquitin-like modifier-activating enzyme 1 OS=Rattus norvegicus GN=Uba1 PE=1 SV=1 - [UBA1_RAT]	47.83	1	31	31	440	0.7481
Q63598	Plastin-3 OS=Rattus norvegicus GN=Pls3 PE=1 SV=2 - [PLST_RAT]	28.57	1	9	10	52	0.7485
P62425	60S ribosomal protein L7a OS=Rattus norvegicus GN=Rpl7a PE=1 SV=2 - [RL7A_RAT]	15.04	1	2	3	15	0.7552
P84245	Histone H3.3 OS=Rattus norvegicus GN=H3f3b PE=1 SV=2 - [H33_RAT]	40.44	2	4	4	20	0.7558
P08932	T-kininogen 2 OS=Rattus norvegicus PE=1 SV=2 - [KNT2_RAT]	56.74	1	6	17	226	0.7606
Q9ER34	Aconitate hydratase, mitochondrial OS=Rattus norvegicus GN=Aco2 PE=1 SV=2 - [ACON_RAT]	54.74	1	33	33	864	0.7608
P30839	Fatty aldehyde dehydrogenase OS=Rattus norvegicus GN=Aldh3a2 PE=1 SV=1 - [AL3A2_RAT]	16.94	1	6	6	33	0.7632
Q6AYR8	Secernin-2 OS=Rattus norvegicus GN=Scrn2 PE=2 SV=1 - [SCRN2_RAT]	15.13	1	2	3	4	0.7643
P49432	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Rattus norvegicus GN=Pdhb PE=1 SV=2 - [ODPB_RAT]	42.62	1	11	11	380	0.7663
Q64591	2,4-dienoyl-CoA reductase, mitochondrial OS=Rattus norvegicus GN=Decr1 PE=1 SV=2 - [DECR_RAT]	44.18	1	10	10	116	0.7703
P97849	Long-chain fatty acid transport protein 1 OS=Rattus norvegicus GN=Slc27a1 PE=2 SV=1 - [S27A1_RAT]	14.86	1	5	5	81	0.7708
Q01205	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Rattus norvegicus GN=Dlst PE=1 SV=2 - [ODO2_RAT]	14.32	1	4	4	18	0.7725
P62959	Histidine triad nucleotide-binding protein 1 OS=Rattus norvegicus GN=Hint1 PE=1 SV=5 - [HINT1_RAT]	58.73	1	5	5	12	0.7768
Q6AYS7	Aminoacylase-1A OS=Rattus norvegicus GN=Acy1a PE=1 SV=1 - [ACY1A_RAT]	42.16	1	10	11	49	0.7784
Q921A4	Cytoglobin OS=Rattus norvegicus GN=Cygb PE=1 SV=1 - [CYGB_RAT]	10.53	1	3	3	4	0.7787
P16036	Phosphate carrier protein, mitochondrial OS=Rattus norvegicus GN=Slc25a3 PE=1 SV=1 - [MPCP_RAT]	40.45	1	9	9	145	0.7810
Q63270	Cytoplasmic aconitate hydratase OS=Rattus norvegicus GN=Aco1 PE=1 SV=1 - [ACOC_RAT]	43.31	1	26	26	534	0.7816
P49134	Integrin beta-1 OS=Rattus norvegicus GN=Itgb1 PE=2 SV=1 - [ITB1_RAT]	22.78	1	14	14	175	0.7867
P20761	Ig gamma-2B chain C region OS=Rattus norvegicus GN=Igh-1a PE=1 SV=1 - [IGG2B_RAT]	34.83	1	6	6	303	0.7900
P05426	60S ribosomal protein L7 OS=Rattus norvegicus GN=Rpl7 PE=1 SV=2 - [RL7_RAT]	9.62	1	2	2	5	0.7914
P07379	Phosphoenolpyruvate carboxykinase, cytosolic [GTP] OS=Rattus norvegicus GN=Pck1 PE=1 SV=1 - [PCKGC_RAT]	15.59	1	5	6	22	0.7931
P06757	Alcohol dehydrogenase 1 OS=Rattus norvegicus GN=Adh1 PE=1 SV=3 - [ADH1_RAT]	9.04	1	3	3	6	0.7967
Q10758	Keratin, type II cytoskeletal 8 OS=Rattus norvegicus GN=Krt8 PE=1 SV=3 - [K2C8_RAT]	16.36	1	3	9	46	0.7988
P05370	Glucose-6-phosphate 1-dehydrogenase OS=Rattus norvegicus GN=G6pdx PE=1 SV=3 - [G6PD_RAT]	21.75	1	8	8	39	0.7993
P60868	40S ribosomal protein S20 OS=Rattus norvegicus GN=Rps20 PE=3 SV=1 - [RS20_RAT]	25.21	1	3	3	23	0.7993
Q5XI22	Acetyl-CoA acetyltransferase, cytosolic OS=Rattus norvegicus GN=Acat2 PE=1 SV=1 - [THIC_RAT]	20.91	1	4	4	8	0.8016
O35142	Coatomer subunit beta' OS=Rattus norvegicus GN=Copb2 PE=1 SV=3 - [COPB2_RAT]	9.5	1	5	5	39	0.8095
Q99MZ8	LIM and SH3 domain protein 1 OS=Rattus norvegicus	8.37	1	2	2	2	0.8128

	GN=Lasp1 PE=1 SV=1 - [LASP1_RAT]						
P38983	40S ribosomal protein SA OS=Rattus norvegicus GN=Rpsa PE=1 SV=3 - [RSSA_RAT]	42.37	1	8	8	116	0.8201
Q7TP52	Carboxymethylenebutenolidase homolog OS=Rattus norvegicus GN=Cmbl PE=2 SV=1 - [CMBL_RAT]	22.45	1	5	5	9	0.8205
Q04462	Valine--tRNA ligase OS=Rattus norvegicus GN=Vars PE=2 SV=2 - [SYVC_RAT]	8.86	1	6	6	8	0.8207
P29266	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Hibadh PE=1 SV=3 - [3HIDH_RAT]	30.75	1	7	7	48	0.8213
P53987	Monocarboxylate transporter 1 OS=Rattus norvegicus GN=Slc16a1 PE=1 SV=1 - [MOT1_RAT]	12.15	1	4	4	79	0.8217
P86252	Transcriptional activator protein Pur-alpha (Fragments) OS=Rattus norvegicus GN=Pura PE=1 SV=1 - [PURA_RAT]	63.77	1	4	4	22	0.8298
P38650	Cytoplasmic dynein 1 heavy chain 1 OS=Rattus norvegicus GN=Dync1h1 PE=1 SV=1 - [DYHC1_RAT]	26.14	1	84	87	430	0.8398
P18163	Long-chain-fatty-acid--CoA ligase 1 OS=Rattus norvegicus GN=Acsl1 PE=1 SV=1 - [ACSL1_RAT]	71.67	1	39	41	3377	0.8426
Q641Z6	EH domain-containing protein 1 OS=Rattus norvegicus GN=Ehd1 PE=1 SV=1 - [EHD1_RAT]	70.79	1	25	26	499	0.8433
Q5U211	Sorting nexin-3 OS=Rattus norvegicus GN=Snx3 PE=1 SV=1 - [SNX3_RAT]	31.48	1	5	5	9	0.8438
Q9WUJ3	Myomegalin OS=Rattus norvegicus GN=Pde4dip PE=1 SV=1 - [MYOME_RAT]	1.76	1	2	2	7	0.8442
P29411	GTP:AMP phosphotransferase AK3, mitochondrial OS=Rattus norvegicus GN=Ak3 PE=2 SV=2 - [KAD3_RAT]	58.59	1	12	12	86	0.8448
A2RRU1	Glycogen [starch] synthase, muscle OS=Rattus norvegicus GN=Gys1 PE=1 SV=1 - [GYS1_RAT]	5.96	1	2	2	2	0.8469
Q6GQP4	Ras-related protein Rab-31 OS=Rattus norvegicus GN=Rab31 PE=1 SV=2 - [RAB31_RAT]	9.28	1	2	2	2	0.8488
P63326	40S ribosomal protein S10 OS=Rattus norvegicus GN=Rps10 PE=2 SV=1 - [RS10_RAT]	14.55	1	2	2	3	0.8518
P23680	Serum amyloid P-component OS=Rattus norvegicus GN=Apcs PE=2 SV=2 - [SAMP_RAT]	26.32	1	3	3	4	0.8524
Q811M5	Complement component C6 OS=Rattus norvegicus GN=C6 PE=2 SV=1 - [CO6_RAT]	14.67	1	10	10	59	0.8525
Q5XHZ0	Heat shock protein 75 kDa, mitochondrial OS=Rattus norvegicus GN=Trap1 PE=1 SV=1 - [TRAP1_RAT]	6.09	1	1	2	21	0.8558
Q13409	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3 - [DC1I2_HUMAN]	3.45	1	2	2	9	0.8562
P31399	ATP synthase subunit d, mitochondrial OS=Rattus norvegicus GN=Atp5h PE=1 SV=3 - [ATP5H_RAT]	34.16	1	5	5	41	0.8599
Q5FVQ4	Malectin OS=Rattus norvegicus GN=Mlec PE=2 SV=1 - [MLEC_RAT]	10.65	1	2	2	2	0.8605
P15650	Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acadl PE=1 SV=1 - [ACADL_RAT]	26.28	1	9	9	58	0.8620
Q8R4Z9	Mitofusin-1 OS=Rattus norvegicus GN=Mfn1 PE=1 SV=1 - [MFN1_RAT]	3.78	1	2	2	2	0.8621
P01041	Cystatin-B OS=Rattus norvegicus GN=Cstb PE=1 SV=1 - [CYTB_RAT]	34.69	1	3	3	10	0.8623
Q6AY09	Heterogeneous nuclear ribonucleoprotein H2 OS=Rattus norvegicus GN=Hnrnph2 PE=1 SV=1 - [HNRH2_RAT]	9.58	1	1	3	4	0.8624
Q711G3	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Rattus norvegicus GN=Iah1 PE=2 SV=2 - [IAH1_RAT]	15.26	1	2	2	2	0.8646
F1LNJ2	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Rattus norvegicus GN=Snrnp200 PE=1 SV=1 - [U520_RAT]	1.36	1	2	2	5	0.8667
P13471	40S ribosomal protein S14 OS=Rattus norvegicus GN=Rps14 PE=2 SV=3 - [RS14_RAT]	29.8	1	3	3	54	0.8674
P52296	Importin subunit beta-1 OS=Rattus norvegicus GN=Kpnb1 PE=1 SV=1 - [IMB1_RAT]	38.86	1	18	20	172	0.8684
P04642	L-lactate dehydrogenase A chain OS=Rattus norvegicus GN=Ldha PE=1 SV=1 - [LDHA_RAT]	85.54	1	23	26	848	0.8693
O35331	Pyridoxal kinase OS=Rattus norvegicus GN=Pdxk PE=1	5.13	1	2	2	2	0.8700

	SV=1 - [PDXK_RAT]						
Q64573	Liver carboxylesterase 4 OS=Rattus norvegicus PE=2 SV=2 - [EST4_RAT]	16.22	1	2	5	95	0.8721
O35854	Branched-chain-amino-acid aminotransferase, mitochondrial OS=Rattus norvegicus GN=Bcat2 PE=1 SV=1 - [BCAT2_RAT]	16.54	1	5	5	11	0.8820
P00173	Cytochrome b5 OS=Rattus norvegicus GN=Cyb5a PE=1 SV=2 - [CYB5_RAT]	41.04	1	4	4	65	0.8820
Q80Z29	Nicotinamide phosphoribosyltransferase OS=Rattus norvegicus GN=Nampt PE=1 SV=1 - [NAMPT_RAT]	14.26	1	3	3	4	0.8830
P02650	Apolipoprotein E OS=Rattus norvegicus GN=Apoe PE=1 SV=2 - [APOE_RAT]	52.56	1	14	14	254	0.8851
B0BNA5	Coactosin-like protein OS=Rattus norvegicus GN=Cotl1 PE=1 SV=1 - [COTL1_RAT]	49.3	1	8	8	12	0.8865
Q63716	Peroxiredoxin-1 OS=Rattus norvegicus GN=Prdx1 PE=1 SV=1 - [PRDX1_RAT]	70.85	1	12	14	509	0.8890
Q9JLA3	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Rattus norvegicus GN=Uggt1 PE=1 SV=2 - [UGGG1_RAT]	22.95	1	20	22	120	0.8930
P11598	Protein disulfide-isomerase A3 OS=Rattus norvegicus GN=Pdia3 PE=1 SV=2 - [PDIA3_RAT]	58.42	1	28	29	472	0.9043
P04182	Ornithine aminotransferase, mitochondrial OS=Rattus norvegicus GN=Oat PE=1 SV=1 - [OAT_RAT]	20.27	1	5	5	5	0.9071
P62828	GTP-binding nuclear protein Ran OS=Rattus norvegicus GN=Ran PE=1 SV=3 - [RAN_RAT]	25.93	2	5	5	22	0.9118
P70580	Membrane-associated progesterone receptor component 1 OS=Rattus norvegicus GN=Pgrmc1 PE=1 SV=3 - [PGRC1_RAT]	33.85	1	4	4	11	0.9122
P0DMW0	Heat shock 70 kDa protein 1A OS=Rattus norvegicus GN=Hspa1a PE=2 SV=1 - [HS71A_RAT]	17.63	1	4	8	293	0.9158
P29419	ATP synthase subunit e, mitochondrial OS=Rattus norvegicus GN=Atp5i PE=1 SV=3 - [ATP5I_RAT]	45.07	1	3	3	29	0.9169
O08662	Phosphatidylinositol 4-kinase alpha OS=Rattus norvegicus GN=Pi4ka PE=1 SV=1 - [PI4KA_RAT]	4.41	1	3	5	9	0.9174
B2RZ78	Vacuolar protein sorting-associated protein 29 OS=Rattus norvegicus GN=Vps29 PE=1 SV=2 - [VPS29_RAT]	12.64	1	2	2	4	0.9187
P12369	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus GN=Prkar2b PE=1 SV=3 - [KAP3_RAT]	55.53	1	14	14	146	0.9306
Q6P7R8	Very-long-chain 3-oxoacyl-CoA reductase OS=Rattus norvegicus GN=Hsd17b12 PE=2 SV=1 - [DHB12_RAT]	19.55	1	4	4	58	0.9369
P07151	Beta-2-microglobulin OS=Rattus norvegicus GN=B2m PE=1 SV=1 - [B2MG_RAT]	34.45	1	5	5	21	0.9371
O35264	Platelet-activating factor acetylhydrolase IB subunit beta OS=Rattus norvegicus GN=Pafah1b2 PE=1 SV=1 - [PA1B2_RAT]	12.23	1	2	2	16	0.9376
Q5XIP9	Transmembrane protein 43 OS=Rattus norvegicus GN=Tmem43 PE=2 SV=1 - [TMM43_RAT]	42	1	9	9	78	0.9377
Q6AYC4	Macrophage-capping protein OS=Rattus norvegicus GN=Capg PE=1 SV=1 - [CAPG_RAT]	30.37	1	6	6	48	0.9381
O55096	Dipeptidyl peptidase 3 OS=Rattus norvegicus GN=Dpp3 PE=1 SV=2 - [DPP3_RAT]	20.46	1	7	7	23	0.9440
P18422	Proteasome subunit alpha type-3 OS=Rattus norvegicus GN=Psma3 PE=1 SV=3 - [PSA3_RAT]	18.43	1	4	4	20	0.9471
Q2PQA9	Kinesin-1 heavy chain OS=Rattus norvegicus GN=Kif5b PE=1 SV=1 - [KINH_RAT]	6.65	1	3	3	5	0.9548
P01048	T-kininogen 1 OS=Rattus norvegicus GN=Map1 PE=1 SV=2 - [KNT1_RAT]	48.84	1	7	17	435	0.9616
Q9Z1A6	Vigilin OS=Rattus norvegicus GN=Hdlbp PE=1 SV=1 - [VIGLN_RAT]	6.15	1	6	6	9	0.9635
P61621	Protein transport protein Sec61 subunit alpha isoform 1 OS=Rattus norvegicus GN=Sec61a1 PE=2 SV=2 - [S61A1_RAT]	21.85	1	5	5	34	0.9650
O54921	Exocyst complex component 2 OS=Rattus norvegicus GN=Exoc2 PE=1 SV=1 - [EXOC2_RAT]	6.17	1	3	3	3	0.9664
Q62667	Major vault protein OS=Rattus norvegicus GN=Mvp PE=1 SV=4 - [MVP_RAT]	21.6	1	8	9	26	0.9691
P34067	Proteasome subunit beta type-4 OS=Rattus norvegicus	25.86	1	4	4	13	0.9694

	GN=Psmb4 PE=1 SV=2 - [PSB4_RAT]						
Q63644	Rho-associated protein kinase 1 OS=Rattus norvegicus GN=Rock1 PE=1 SV=1 - [ROCK1_RAT]	3.29	1	2	3	9	0.9706
P30427	Plectin OS=Rattus norvegicus GN=Plec PE=1 SV=2 - [PLEC_RAT]	7.81	1	21	22	60	0.9713
Q5SGE0	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=1 SV=1 - [LPPRC_RAT]	16.31	1	13	14	71	0.9718
P24329	Thiosulfate sulfurtransferase OS=Rattus norvegicus GN=Tst PE=1 SV=3 - [THTR_RAT]	29.63	1	5	6	50	0.9719
P09117	Fructose-bisphosphate aldolase C OS=Rattus norvegicus GN=Aldoc PE=1 SV=3 - [ALDOC_RAT]	11.85	1	3	5	183	0.9720
P25409	Alanine aminotransferase 1 OS=Rattus norvegicus GN=Gpt PE=1 SV=2 - [ALAT1_RAT]	51.81	1	14	14	140	0.9756
Q5U2Q3	Ester hydrolase C11orf54 homolog OS=Rattus norvegicus PE=1 SV=1 - [CK054_RAT]	24.13	1	6	6	118	0.9761
P63095	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Rattus norvegicus GN=Gnas PE=1 SV=1 - [GNAS2_RAT]	27.16	2	6	7	108	0.9764
P47727	Carbonyl reductase [NADPH] 1 OS=Rattus norvegicus GN=Cbr1 PE=1 SV=2 - [CBR1_RAT]	76.17	1	19	19	1136	0.9765
O88656	Actin-related protein 2/3 complex subunit 1B OS=Rattus norvegicus GN=Arpc1b PE=1 SV=3 - [ARC1B_RAT]	8.33	1	2	2	4	0.9795
Q641Y8	ATP-dependent RNA helicase DDX1 OS=Rattus norvegicus GN=Ddx1 PE=1 SV=1 - [DDX1_RAT]	7.7	1	4	4	9	0.9805
P04636	Malate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Mdh2 PE=1 SV=2 - [MDHM_RAT]	63.61	1	17	17	691	0.9807
F1MA98	Nucleoprotein TPR OS=Rattus norvegicus GN=Tpr PE=1 SV=1 - [TPR_RAT]	4.07	1	4	5	13	0.9843
Q7TQ94	Nitrilase homolog 1 OS=Rattus norvegicus GN=Nit1 PE=2 SV=1 - [NIT1_RAT]	38.7	1	5	6	47	0.9844
Q924S5	Lon protease homolog, mitochondrial OS=Rattus norvegicus GN=Lonp1 PE=2 SV=1 - [LONM_RAT]	8.32	1	3	3	10	0.9853
P26376	Interferon-induced transmembrane protein 3 OS=Rattus norvegicus GN=ifitm3 PE=2 SV=1 - [IFM3_RAT]	20.44	1	2	2	8	0.9853
P31430	Dipeptidase 1 OS=Rattus norvegicus GN=Dpep1 PE=2 SV=2 - [DPEP1_RAT]	36.83	1	8	8	88	0.9858
Q63355	Unconventional myosin-Ic OS=Rattus norvegicus GN=Myo1c PE=1 SV=2 - [MYO1C_RAT]	54.12	1	50	51	1336	0.9859
P04897	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Rattus norvegicus GN=Gnai2 PE=1 SV=3 - [GNAI2_RAT]	49.01	1	9	13	128	0.9899
O35567	Bifunctional purine biosynthesis protein PURH OS=Rattus norvegicus GN=Atic PE=1 SV=2 - [PUR9_RAT]	25.84	1	9	9	35	0.9932
D3ZAF6	ATP synthase subunit f, mitochondrial OS=Rattus norvegicus GN=Atp5j2 PE=1 SV=1 - [ATPK_RAT]	23.86	1	2	2	21	0.9932
P63255	Cysteine-rich protein 1 OS=Rattus norvegicus GN=Crip1 PE=1 SV=2 - [CRIP1_RAT]	61.04	1	3	3	6	0.9997
P60711	Actin, cytoplasmic 1 OS=Rattus norvegicus GN=Actb PE=1 SV=1 - [ACTB_RAT]	82.67	2	12	26	5348	

2-cycles chemotherapy (control-diet) versus tumor

Accession	Description	Σ Coverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	P-value
P31232	Transgelin OS=Rattus norvegicus GN=Tagln PE=1 SV=2 - [TAGL_RAT]	73.13	1	15	15	594	0.0000
P05065	Fructose-bisphosphate aldolase A OS=Rattus norvegicus GN=Aldoa PE=1 SV=2 - [ALDOA_RAT]	81.04	1	23	24	1246	0.0001
P07871	3-ketoacyl-CoA thiolase B, peroxisomal OS=Rattus norvegicus GN=Acaa1b PE=1 SV=2 - [THIKB_RAT]	13.68	2	5	5	21	0.0005
P20788	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Rattus norvegicus GN=Uqcrfs1	22.63	1	3	4	12	0.0006

	PE=1 SV=2 - [UCRI_RAT]						
Q920J4	Thioredoxin-like protein 1 OS=Rattus norvegicus GN=Txnl1 PE=1 SV=3 - [TXNL1_RAT]	19.38	1	4	4	4	0.0007
P04797	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus GN=Gapdh PE=1 SV=3 - [G3P_RAT]	75.98	1	18	18	1640	0.0010
P29410	Adenylate kinase 2, mitochondrial OS=Rattus norvegicus GN=Ak2 PE=2 SV=2 - [KAD2_RAT]	54.39	1	11	11	161	0.0012
P52759	Ribonuclease UK114 OS=Rattus norvegicus GN=Hrsp12 PE=1 SV=3 - [UK114_RAT]	52.55	1	5	5	17	0.0015
Q5XI22	Acetyl-CoA acetyltransferase, cytosolic OS=Rattus norvegicus GN=Acat2 PE=1 SV=1 - [THIC_RAT]	16.88	1	3	3	4	0.0018
P11497	Acetyl-CoA carboxylase 1 OS=Rattus norvegicus GN=Acaca PE=1 SV=1 - [ACACA_RAT]	54.58	1	87	87	901	0.0020
P07379	Phosphoenolpyruvate carboxykinase, cytosolic [GTP] OS=Rattus norvegicus GN=Pck1 PE=1 SV=1 - [PCKGC_RAT]	15.59	1	5	6	32	0.0022
P12785	Fatty acid synthase OS=Rattus norvegicus GN=Fasn PE=1 SV=3 - [FAS_RAT]	74.93	1	129	130	6207	0.0031
P08461	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Rattus norvegicus GN=Dlat PE=1 SV=3 - [ODP2_RAT]	34.02	1	13	13	65	0.0033
Q06647	ATP synthase subunit O, mitochondrial OS=Rattus norvegicus GN=Atp5o PE=1 SV=1 - [ATPO_RAT]	66.20	1	11	12	205	0.0033
P32089	Tricarboxylate transport protein, mitochondrial OS=Rattus norvegicus GN=Slc25a1 PE=1 SV=1 - [TXTP_RAT]	34.41	1	7	8	152	0.0035
P19234	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Rattus norvegicus GN=Ndufv2 PE=1 SV=2 - [NDUV2_RAT]	21.77	1	4	4	46	0.0036
P07335	Creatine kinase B-type OS=Rattus norvegicus GN=Ckb PE=1 SV=2 - [KCRB_RAT]	59.32	1	16	16	263	0.0041
Q8R431	Monoglyceride lipase OS=Rattus norvegicus GN=Mgll PE=1 SV=1 - [MGLL_RAT]	67.66	1	17	17	656	0.0048
P29411	GTP:AMP phosphotransferase AK3, mitochondrial OS=Rattus norvegicus GN=Ak3 PE=2 SV=2 - [KAD3_RAT]	58.15	1	11	11	88	0.0049
P31430	Dipeptidase 1 OS=Rattus norvegicus GN=Dpep1 PE=2 SV=2 - [DPEP1_RAT]	36.83	1	8	8	70	0.0055
P11240	Cytochrome c oxidase subunit 5A, mitochondrial OS=Rattus norvegicus GN=Cox5a PE=1 SV=1 - [COX5A_RAT]	54.79	1	7	7	89	0.0061
P26284	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Rattus norvegicus GN=Pdha1 PE=1 SV=2 - [ODPA_RAT]	49.49	1	16	17	153	0.0062
P11030	Acyl-CoA-binding protein OS=Rattus norvegicus GN=Dbi PE=1 SV=3 - [ACBP_RAT]	54.02	1	5	5	82	0.0065
P07150	Annexin A1 OS=Rattus norvegicus GN=Anxa1 PE=1 SV=2 - [ANXA1_RAT]	72.54	1	27	27	2433	0.0066
P18886	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Rattus norvegicus GN=Cpt2 PE=1 SV=1 - [CPT2_RAT]	21.28	1	8	8	19	0.0068
P00406	Cytochrome c oxidase subunit 2 OS=Rattus norvegicus GN=Mtco2 PE=1 SV=3 - [COX2_RAT]	18.94	1	4	4	141	0.0069
P19357	Solute carrier family 2, facilitated glucose transporter member 4 OS=Rattus norvegicus GN=Slc2a4 PE=1 SV=1 - [GTR4_RAT]	8.06	1	3	3	15	0.0069
P45953	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acadvl PE=1 SV=1 - [ACADV_RAT]	25.50	1	10	10	81	0.0077
P05369	Farnesyl pyrophosphate synthase OS=Rattus norvegicus GN=Fdps PE=2 SV=2 - [FPPS_RAT]	13.03	1	4	4	13	0.0077
P09117	Fructose-bisphosphate aldolase C OS=Rattus norvegicus GN=Aldoc PE=1 SV=3 - [ALDOC_RAT]	11.85	1	3	5	163	0.0079
B5DFC9	Nidogen-2 OS=Rattus norvegicus GN=Nid2 PE=2 SV=1 - [NID2_RAT]	15.76	1	14	14	66	0.0079
Q6AYS7	Aminoacylase-1A OS=Rattus norvegicus GN=Acy1a PE=1 SV=1 - [ACY1A_RAT]	37.50	2	9	10	35	0.0083

P04762	Catalase OS=Rattus norvegicus GN=Cat PE=1 SV=3 - [CATA_RAT]	55.22	1	21	21	379	0.0087
P67779	Prohibitin OS=Rattus norvegicus GN=Phb PE=1 SV=1 - [PHB_RAT]	67.28	1	13	13	120	0.0090
Q66HG6	Carbonic anhydrase 5B, mitochondrial OS=Rattus norvegicus GN=Ca5b PE=2 SV=1 - [CAH5B_RAT]	19.24	1	4	4	18	0.0099
Q5BK63	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Rattus norvegicus GN=Ndufa9 PE=1 SV=2 - [NDUA9_RAT]	27.59	1	5	6	41	0.0100
P97532	3-mercaptopyruvate sulfurtransferase OS=Rattus norvegicus GN=Mpst PE=1 SV=3 - [THTM_RAT]	40.40	1	9	9	90	0.0100
Q5U2Q3	Ester hydrolase C11orf54 homolog OS=Rattus norvegicus PE=1 SV=1 - [CK054_RAT]	24.13	1	6	6	95	0.0107
O35077	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Rattus norvegicus GN=Gpd1 PE=1 SV=4 - [GPDA_RAT]	91.40	1	27	27	2394	0.0110
P32551	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Rattus norvegicus GN=Uqcrc2 PE=1 SV=2 - [QCR2_RAT]	67.48	1	17	17	239	0.0113
P09811	Glycogen phosphorylase, liver form OS=Rattus norvegicus GN=Pygl PE=1 SV=5 - [PYGL_RAT]	33.29	1	17	19	123	0.0120
Q5BJY9	Keratin, type I cytoskeletal 18 OS=Rattus norvegicus GN=Krt18 PE=1 SV=3 - [K1C18_RAT]	20.80	1	5	7	16	0.0127
P50137	Transketolase OS=Rattus norvegicus GN=Tkt PE=1 SV=1 - [TKT_RAT]	61.64	1	26	26	785	0.0131
P08460	Nidogen-1 (Fragment) OS=Rattus norvegicus GN=Nid1 PE=1 SV=2 - [NID1_RAT]	29.94	1	5	5	37	0.0132
P51886	Lumican OS=Rattus norvegicus GN=Lum PE=1 SV=1 - [LUM_RAT]	36.09	1	11	11	383	0.0134
P14408	Fumarate hydratase, mitochondrial OS=Rattus norvegicus GN=Fh PE=1 SV=1 - [FUMH_RAT]	31.76	1	9	9	47	0.0137
Q6AYG5	Ethylmalonyl-CoA decarboxylase OS=Rattus norvegicus GN=Echdc1 PE=1 SV=1 - [ECHD1_RAT]	45.15	1	9	9	72	0.0140
P23764	Glutathione peroxidase 3 OS=Rattus norvegicus GN=Gpx3 PE=2 SV=2 - [GPX3_RAT]	29.20	1	5	5	111	0.0140
Q91ZN1	Coronin-1A OS=Rattus norvegicus GN=Coro1a PE=1 SV=3 - [COR1A_RAT]	13.67	1	2	2	3	0.0141
Q68FY0	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Rattus norvegicus GN=Uqcrc1 PE=1 SV=1 - [QCR1_RAT]	35.83	1	11	11	185	0.0142
Q6P7R8	Very-long-chain 3-oxoacyl-CoA reductase OS=Rattus norvegicus GN=Hsd17b12 PE=2 SV=1 - [DHB12_RAT]	19.55	1	4	4	72	0.0142
O88644	Grifin OS=Rattus norvegicus GN=Grifin PE=1 SV=1 - [GRIFN_RAT]	15.28	1	2	2	30	0.0145
P31044	Phosphatidylethanolamine-binding protein 1 OS=Rattus norvegicus GN=Pebp1 PE=1 SV=3 - [PEBP1_RAT]	57.22	1	7	7	102	0.0146
Q05962	ADP/ATP translocase 1 OS=Rattus norvegicus GN=Slc25a4 PE=1 SV=3 - [ADT1_RAT]	40.94	1	4	11	339	0.0149
P48004	Proteasome subunit alpha type-7 OS=Rattus norvegicus GN=Psma7 PE=1 SV=1 - [PSA7_RAT]	38.19	1	8	8	26	0.0156
P85968	6-phosphogluconate dehydrogenase, decarboxylating OS=Rattus norvegicus GN=Pgd PE=1 SV=1 - [6PGD_RAT]	54.66	1	18	18	497	0.0161
P25093	Fumarylacetoacetase OS=Rattus norvegicus GN=Fah PE=1 SV=1 - [FAAA_RAT]	45.82	1	12	12	198	0.0163
P49432	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Rattus norvegicus GN=Pdhb PE=1 SV=2 - [ODPB_RAT]	42.62	1	11	11	241	0.0166
P52873	Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus GN=Pc PE=1 SV=2 - [PYC_RAT]	68.42	1	52	52	1914	0.0169
P07633	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Rattus norvegicus GN=Pccb PE=2 SV=1 - [PCCB_RAT]	20.15	1	6	7	15	0.0170
Q8VHF5	Citrate synthase, mitochondrial OS=Rattus norvegicus GN=Cs PE=1 SV=1 - [CISY_RAT]	41.63	1	14	14	182	0.0173
P25409	Alanine aminotransferase 1 OS=Rattus norvegicus GN=Gpt PE=1 SV=2 - [ALAT1_RAT]	51.81	1	14	14	98	0.0176

P25113	Phosphoglycerate mutase 1 OS=Rattus norvegicus GN=Pgam1 PE=1 SV=4 - [PGAM1_RAT]	74.41	1	18	18	323	0.0176
Q99NA5	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Rattus norvegicus GN=Idh3a PE=1 SV=1 - [IDH3A_RAT]	29.23	1	8	8	183	0.0178
P20070	NADH-cytochrome b5 reductase 3 OS=Rattus norvegicus GN=Cyb5r3 PE=1 SV=2 - [NB5R3_RAT]	77.08	1	15	15	308	0.0182
P27605	Hypoxanthine-guanine phosphoribosyltransferase OS=Rattus norvegicus GN=Hprt1 PE=1 SV=1 - [HPRT_RAT]	49.54	1	9	9	67	0.0184
Q8CG45	Aflatoxin B1 aldehyde reductase member 2 OS=Rattus norvegicus GN=Akr7a2 PE=1 SV=2 - [ARK72_RAT]	20.44	1	6	6	22	0.0185
Q9Z2L0	Voltage-dependent anion-selective channel protein 1 OS=Rattus norvegicus GN=Vdac1 PE=1 SV=4 - [VDAC1_RAT]	44.88	1	9	9	83	0.0188
P02692	Fatty acid-binding protein, liver OS=Rattus norvegicus GN=Fabp1 PE=1 SV=1 - [FABPL_RAT]	62.20	1	6	6	51	0.0190
P08932	T-kininogen 2 OS=Rattus norvegicus PE=1 SV=2 - [KNT2_RAT]	63.49	1	8	22	551	0.0195
Q09073	ADP/ATP translocase 2 OS=Rattus norvegicus GN=Slc25a5 PE=1 SV=3 - [ADT2_RAT]	44.30	1	5	12	334	0.0196
P21913	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Rattus norvegicus GN=Sdhb PE=2 SV=2 - [SDHB_RAT]	23.05	1	6	6	25	0.0199
Q7TP48	Adipocyte plasma membrane-associated protein OS=Rattus norvegicus GN=Apmap PE=2 SV=2 - [APMAP_RAT]	63.30	1	14	14	349	0.0200
P56574	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus GN=Idh2 PE=1 SV=2 - [IDHP_RAT]	38.50	1	13	15	115	0.0203
Q64537	Calpain small subunit 1 OS=Rattus norvegicus GN=Capns1 PE=1 SV=3 - [CPNS1_RAT]	62.59	1	7	7	60	0.0205
P62243	40S ribosomal protein S8 OS=Rattus norvegicus GN=Rps8 PE=1 SV=2 - [RS8_RAT]	9.62	1	2	2	3	0.0206
P04764	Alpha-enolase OS=Rattus norvegicus GN=Eno1 PE=1 SV=4 - [ENOA_RAT]	70.05	1	17	23	1183	0.0212
P13697	NADP-dependent malic enzyme OS=Rattus norvegicus GN=Me1 PE=1 SV=2 - [MAOX_RAT]	78.67	1	30	31	995	0.0216
P14604	Enoyl-CoA hydratase, mitochondrial OS=Rattus norvegicus GN=Echs1 PE=1 SV=1 - [ECHM_RAT]	48.97	1	9	9	212	0.0223
P15429	Beta-enolase OS=Rattus norvegicus GN=Eno3 PE=1 SV=3 - [ENOB_RAT]	33.87	1	2	8	243	0.0229
Q6P686	Osteoclast-stimulating factor 1 OS=Rattus norvegicus GN=Ostf1 PE=1 SV=1 - [OSTF1_RAT]	11.21	1	2	2	2	0.0230
P04636	Malate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Mdh2 PE=1 SV=2 - [MDHM_RAT]	63.61	1	17	17	626	0.0239
Q6AYC4	Macrophage-capping protein OS=Rattus norvegicus GN=Capg PE=1 SV=1 - [CAPG_RAT]	41.26	1	8	8	82	0.0242
Q5XIH7	Prohibitin-2 OS=Rattus norvegicus GN=Phb2 PE=1 SV=1 - [PHB2_RAT]	47.16	1	10	11	127	0.0242
P24329	Thiosulfate sulfurtransferase OS=Rattus norvegicus GN=Tst PE=1 SV=3 - [THTR_RAT]	29.63	1	6	6	46	0.0248
Q68FS2	COP9 signalosome complex subunit 4 OS=Rattus norvegicus GN=Cops4 PE=1 SV=1 - [CSN4_RAT]	11.08	1	2	2	2	0.0261
P13803	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Rattus norvegicus GN=Etfa PE=1 SV=4 - [ETFA_RAT]	56.76	1	12	12	288	0.0266
Q5BK81	Prostaglandin reductase 2 OS=Rattus norvegicus GN=Ptgr2 PE=2 SV=2 - [PTGR2_RAT]	22.79	1	5	5	18	0.0268
Q9Z1A6	Vigilin OS=Rattus norvegicus GN=Hdlbp PE=1 SV=1 - [VIGLN_RAT]	14.59	1	14	14	62	0.0276
P04905	Glutathione S-transferase Mu 1 OS=Rattus norvegicus GN=Gstm1 PE=1 SV=2 - [GSTM1_RAT]	51.38	1	6	9	58	0.0278
P29266	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Hibadh PE=1 SV=3 - [3HIDH_RAT]	35.82	1	8	8	52	0.0280
Q5XFX0	Transgelin-2 OS=Rattus norvegicus GN=Tagln2 PE=1 SV=1 - [TAGL2_RAT]	81.91	1	16	16	525	0.0283

Q5XIP9	Transmembrane protein 43 OS=Rattus norvegicus GN=Tmem43 PE=2 SV=1 - [TMM43_RAT]	35.00	1	8	8	64	0.0287
O35244	Peroxiredoxin-6 OS=Rattus norvegicus GN=Prdx6 PE=1 SV=3 - [PRDX6_RAT]	67.86	1	13	13	203	0.0290
P04143	Thyroid hormone-inducible hepatic protein OS=Rattus norvegicus GN=Thrsp PE=1 SV=1 - [THRSP_RAT]	24.00	1	2	2	27	0.0291
Q641Z6	EH domain-containing protein 1 OS=Rattus norvegicus GN=Ehd1 PE=1 SV=1 - [EHD1_RAT]	70.79	1	25	26	507	0.0299
O88767	Protein deglycase DJ-1 OS=Rattus norvegicus GN=Park7 PE=1 SV=1 - [PARK7_RAT]	83.07	1	11	11	184	0.0300
P06214	Delta-aminolevulinic acid dehydratase OS=Rattus norvegicus GN=Alad PE=1 SV=1 - [HEM2_RAT]	35.45	1	6	6	41	0.0302
P35565	Calnexin OS=Rattus norvegicus GN=Canx PE=1 SV=1 - [CALX_RAT]	37.56	1	17	17	199	0.0304
Q9Z0V6	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Rattus norvegicus GN=Prdx3 PE=1 SV=2 - [PRDX3_RAT]	36.96	1	6	6	137	0.0305
P61621	Protein transport protein Sec61 subunit alpha isoform 1 OS=Rattus norvegicus GN=Sec61a1 PE=2 SV=2 - [S61A1_RAT]	15.76	1	4	4	17	0.0308
P01048	T-kininogen 1 OS=Rattus norvegicus GN=Map1 PE=1 SV=2 - [KNT1_RAT]	49.53	1	7	19	748	0.0310
F1LNJ2	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Rattus norvegicus GN=Snrnp200 PE=1 SV=1 - [U520_RAT]	2.66	1	3	4	6	0.0312
P12007	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ivd PE=1 SV=2 - [IVD_RAT]	36.32	1	10	10	69	0.0323
P85971	6-phosphogluconolactonase OS=Rattus norvegicus GN=Pgls PE=1 SV=1 - [6PGL_RAT]	36.96	1	5	5	96	0.0334
Q68FT1	Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Rattus norvegicus GN=Coq9 PE=1 SV=2 - [COQ9_RAT]	6.09	1	2	2	6	0.0337
P41562	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Rattus norvegicus GN=Idh1 PE=1 SV=1 - [IDHC_RAT]	66.91	1	22	23	362	0.0347
Q8VBU2	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1 - [NDRG2_RAT]	24.80	1	4	5	48	0.0349
P38983	40S ribosomal protein SA OS=Rattus norvegicus GN=Rpsa PE=1 SV=3 - [RSSA_RAT]	52.20	1	9	9	133	0.0362
P20760	Ig gamma-2A chain C region OS=Rattus norvegicus GN=Igg-2a PE=1 SV=1 - [IGG2A_RAT]	63.66	1	13	16	1574	0.0384
P11915	Non-specific lipid-transfer protein OS=Rattus norvegicus GN=Scp2 PE=1 SV=3 - [NLTP_RAT]	16.64	1	10	11	139	0.0384
Q5I0P2	Glycine cleavage system H protein, mitochondrial OS=Rattus norvegicus GN=Gcsh PE=2 SV=1 - [GCSH_RAT]	33.53	1	3	3	12	0.0402
P26772	10 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspe1 PE=1 SV=3 - [CH10_RAT]	66.67	1	8	8	66	0.0403
P16617	Phosphoglycerate kinase 1 OS=Rattus norvegicus GN=Pgk1 PE=1 SV=2 - [PGK1_RAT]	74.10	1	24	24	445	0.0403
P21396	Amine oxidase [flavin-containing] A OS=Rattus norvegicus GN=Maoa PE=1 SV=1 - [AOFA_RAT]	6.84	1	3	3	4	0.0408
P38718	Mitochondrial pyruvate carrier 2 OS=Rattus norvegicus GN=Mpc2 PE=2 SV=1 - [MPC2_RAT]	25.98	1	3	3	9	0.0408
P16638	ATP-citrate synthase OS=Rattus norvegicus GN=Acly PE=1 SV=1 - [ACLY_RAT]	59.09	1	50	51	1770	0.0430
P13832	Myosin regulatory light chain RLC-A OS=Rattus norvegicus GN=Rlc-a PE=2 SV=2 - [MRLCA_RAT]	34.30	2	5	5	44	0.0431
Q63507	60S ribosomal protein L14 OS=Rattus norvegicus GN=Rpl14 PE=1 SV=3 - [RL14_RAT]	10.28	1	2	2	15	0.0434
P20759	Ig gamma-1 chain C region OS=Rattus norvegicus PE=1 SV=1 - [IGHG1_RAT]	20.55	1	2	5	350	0.0454
P14669	Annexin A3 OS=Rattus norvegicus GN=Anxa3 PE=1 SV=4 - [ANXA3_RAT]	64.81	1	18	20	227	0.0458
P17764	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus GN=Acat1 PE=1 SV=1 - [THIL_RAT]	54.01	1	15	15	145	0.0458

Q9EQP5	Prolargin OS=Rattus norvegicus GN=Prelp PE=2 SV=1 - [PRELP_RAT]	42.44	1	12	12	81	0.0462
P15304	Hormone-sensitive lipase OS=Rattus norvegicus GN=Lipe PE=1 SV=3 - [LIPS_RAT]	46.25	1	33	33	884	0.0474
P86252	Transcriptional activator protein Pur-alpha (Fragments) OS=Rattus norvegicus GN=Pura PE=1 SV=1 - [PURA_RAT]	63.77	1	4	4	22	0.0485
Q3T1K5	F-actin-capping protein subunit alpha-2 OS=Rattus norvegicus GN=Capza2 PE=1 SV=1 - [CAZA2_RAT]	27.97	1	4	5	45	0.0485
P52555	Endoplasmic reticulum resident protein 29 OS=Rattus norvegicus GN=Erp29 PE=1 SV=2 - [ERP29_RAT]	55.38	1	10	10	97	0.0499
P85972	Vinculin OS=Rattus norvegicus GN=Vcl PE=1 SV=1 - [VINC_RAT]	65.76	1	56	59	1286	0.0501
P48721	Stress-70 protein, mitochondrial OS=Rattus norvegicus GN=Hspa9 PE=1 SV=3 - [GRP75_RAT]	40.65	1	23	23	313	0.0507
P18420	Proteasome subunit alpha type-1 OS=Rattus norvegicus GN=Psma1 PE=1 SV=2 - [PSA1_RAT]	17.87	1	4	4	8	0.0517
P13635	Ceruloplasmin OS=Rattus norvegicus GN=Cp PE=1 SV=3 - [CERU_RAT]	47.97	1	41	42	1029	0.0520
P17988	Sulfotransferase 1A1 OS=Rattus norvegicus GN=Sult1a1 PE=1 SV=1 - [ST1A1_RAT]	26.46	1	5	5	8	0.0521
P05508	NADH-ubiquinone oxidoreductase chain 4 OS=Rattus norvegicus GN=Mtnd4 PE=3 SV=3 - [NU4M_RAT]	12.42	1	3	3	22	0.0528
P57113	Maleylacetoacetate isomerase OS=Rattus norvegicus GN=Gstz1 PE=1 SV=2 - [MAAI_RAT]	63.89	1	9	9	126	0.0531
P19945	60S acidic ribosomal protein P0 OS=Rattus norvegicus GN=Rplp0 PE=1 SV=2 - [RLA0_RAT]	43.22	1	9	9	151	0.0534
O35796	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Rattus norvegicus GN=C1qbp PE=1 SV=2 - [C1QBP_RAT]	22.58	1	3	3	10	0.0535
P48037	Annexin A6 OS=Rattus norvegicus GN=Anxa6 PE=1 SV=2 - [ANXA6_RAT]	68.65	1	45	45	1108	0.0536
P08934	Kininogen-1 OS=Rattus norvegicus GN=Kng1 PE=2 SV=1 - [KNG1_RAT]	19.72	1	7	9	47	0.0542
Q63413	Spliceosome RNA helicase Ddx39b OS=Rattus norvegicus GN=Ddx39b PE=2 SV=3 - [DX39B_RAT]	9.35	1	3	3	4	0.0543
P04644	40S ribosomal protein S17 OS=Rattus norvegicus GN=Rps17 PE=1 SV=3 - [RS17_RAT]	57.78	1	6	6	53	0.0547
Q9JHW0	Proteasome subunit beta type-7 OS=Rattus norvegicus GN=Psmb7 PE=1 SV=1 - [PSB7_RAT]	13.72	1	3	3	8	0.0556
P20767	Ig lambda-2 chain C region OS=Rattus norvegicus PE=4 SV=1 - [LAC2_RAT]	76.92	1	5	5	90	0.0564
G3V7P1	Syntaxin-12 OS=Rattus norvegicus GN=Stx12 PE=1 SV=1 - [STX12_RAT]	20.80	1	4	4	6	0.0565
Q75WE7	von Willebrand factor A domain-containing protein 5A OS=Rattus norvegicus GN=Vwa5a PE=2 SV=1 - [VWA5A_RAT]	9.49	1	5	5	8	0.0566
P70619	Glutathione reductase (Fragment) OS=Rattus norvegicus GN=Gsr PE=2 SV=2 - [GSHR_RAT]	8.02	1	2	2	2	0.0589
Q63355	Unconventional myosin-Ic OS=Rattus norvegicus GN=Myo1c PE=1 SV=2 - [MYO1C_RAT]	52.11	1	46	47	1417	0.0591
Q66HF1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus GN=Ndufs1 PE=1 SV=1 - [NDUS1_RAT]	39.89	1	18	18	116	0.0594
P62898	Cytochrome c, somatic OS=Rattus norvegicus GN=Cycs PE=1 SV=2 - [CYC_RAT]	50.48	1	7	7	145	0.0595
Q9EQS0	Transaldolase OS=Rattus norvegicus GN=Taldo1 PE=1 SV=2 - [TALDO_RAT]	34.72	1	12	12	97	0.0603
P50878	60S ribosomal protein L4 OS=Rattus norvegicus GN=Rpl4 PE=1 SV=3 - [RL4_RAT]	11.88	1	3	4	10	0.0604
P10719	ATP synthase subunit beta, mitochondrial OS=Rattus norvegicus GN=Atp5b PE=1 SV=2 - [ATPB_RAT]	77.88	1	26	26	1546	0.0608
P06685	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Rattus norvegicus GN=Atp1a1 PE=1 SV=1 - [AT1A1_RAT]	15.64	1	11	11	149	0.0612
Q64611	Cysteine sulfinic acid decarboxylase OS=Rattus norvegicus GN=Csad PE=1 SV=1 - [CSAD_RAT]	40.16	1	13	13	200	0.0612
Q6PDU7	ATP synthase subunit g, mitochondrial OS=Rattus	53.40	1	4	4	19	0.0614

	norvegicus GN=Atp5l PE=1 SV=2 - [ATP5L_RAT]						
P06866	Haptoglobin OS=Rattus norvegicus GN=Hp PE=1 SV=3 - [HPT_RAT]	47.26	1	16	17	320	0.0614
Q63170	Dynein heavy chain 7, axonemal OS=Rattus norvegicus GN=Dnah7 PE=2 SV=2 - [DYH7_RAT]	1.65	1	4	4	5	0.0622
Q63584	Transmembrane emp24 domain-containing protein 10 OS=Rattus norvegicus GN=Tmed10 PE=1 SV=2 - [TMEDA_RAT]	18.26	1	4	4	41	0.0624
Q9ER34	Aconitate hydratase, mitochondrial OS=Rattus norvegicus GN=Aco2 PE=1 SV=2 - [ACON_RAT]	54.74	1	33	33	806	0.0626
P80254	D-dopachrome decarboxylase OS=Rattus norvegicus GN=Ddt PE=1 SV=3 - [DOPD_RAT]	77.97	1	7	7	118	0.0628
P04904	Glutathione S-transferase alpha-3 OS=Rattus norvegicus GN=Gsta3 PE=1 SV=3 - [GSTA3_RAT]	63.80	1	10	10	119	0.0636
P23358	60S ribosomal protein L12 OS=Rattus norvegicus GN=Rpl12 PE=2 SV=1 - [RL12_RAT]	54.55	1	6	6	86	0.0653
P07323	Gamma-enolase OS=Rattus norvegicus GN=Eno2 PE=1 SV=2 - [ENOG_RAT]	20.97	1	2	5	218	0.0654
P05370	Glucose-6-phosphate 1-dehydrogenase OS=Rattus norvegicus GN=G6pdx PE=1 SV=3 - [G6PD_RAT]	18.45	1	7	7	40	0.0664
P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	64.64	1	36	36	662	0.0666
Q63798	Proteasome activator complex subunit 2 OS=Rattus norvegicus GN=Psme2 PE=2 SV=3 - [PSME2_RAT]	32.77	1	6	6	29	0.0674
P02401	60S acidic ribosomal protein P2 OS=Rattus norvegicus GN=Rplp2 PE=1 SV=2 - [RLA2_RAT]	66.96	1	4	4	68	0.0681
Q4KM74	Vesicle-trafficking protein SEC22b OS=Rattus norvegicus GN=Sec22b PE=1 SV=3 - [SC22B_RAT]	36.74	1	6	7	69	0.0687
Q66H98	Serum deprivation-response protein OS=Rattus norvegicus GN=Sdpr PE=1 SV=3 - [SDPR_RAT]	45.08	1	13	13	320	0.0687
Q63010	Liver carboxylesterase B-1 OS=Rattus norvegicus PE=1 SV=1 - [EST5_RAT]	12.83	1	1	4	61	0.0706
Q63797	Proteasome activator complex subunit 1 OS=Rattus norvegicus GN=Psme1 PE=2 SV=1 - [PSME1_RAT]	49.80	1	12	12	83	0.0711
Q8CFN2	Cell division control protein 42 homolog OS=Rattus norvegicus GN=Cdc42 PE=1 SV=2 - [CDC42_RAT]	32.46	1	4	5	88	0.0718
Q6AXX6	Redox-regulatory protein FAM213A OS=Rattus norvegicus GN=Fam213a PE=1 SV=1 - [F213A_RAT]	15.72	1	3	3	23	0.0722
P14668	Annexin A5 OS=Rattus norvegicus GN=Anxa5 PE=1 SV=3 - [ANXA5_RAT]	75.55	1	24	24	1084	0.0722
P62859	40S ribosomal protein S28 OS=Rattus norvegicus GN=Rps28 PE=1 SV=1 - [RS28_RAT]	30.43	1	2	2	15	0.0725
P04642	L-lactate dehydrogenase A chain OS=Rattus norvegicus GN=Ldha PE=1 SV=1 - [LDHA_RAT]	84.94	1	23	26	795	0.0727
P62271	40S ribosomal protein S18 OS=Rattus norvegicus GN=Rps18 PE=1 SV=3 - [RS18_RAT]	48.68	1	10	10	114	0.0727
P08009	Glutathione S-transferase Yb-3 OS=Rattus norvegicus GN=Gstm3 PE=1 SV=2 - [GSTM4_RAT]	33.49	1	1	7	149	0.0731
Q6P7Q4	Lactoylglutathione lyase OS=Rattus norvegicus GN=Glo1 PE=1 SV=3 - [LGUL_RAT]	37.50	1	6	6	71	0.0733
P38652	Phosphoglucomutase-1 OS=Rattus norvegicus GN=Pgm1 PE=1 SV=2 - [PGM1_RAT]	30.96	1	10	10	106	0.0734
Q64633	UDP-glucuronosyltransferase 1-7 OS=Rattus norvegicus GN=Ugt1a7c PE=2 SV=1 - [UD17_RAT]	15.07	5	1	4	54	0.0738
P12369	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus GN=Prkar2b PE=1 SV=3 - [KAP3_RAT]	55.53	1	14	14	154	0.0743
P63326	40S ribosomal protein S10 OS=Rattus norvegicus GN=Rps10 PE=2 SV=1 - [RS10_RAT]	14.55	1	2	2	3	0.0744
P60892	Ribose-phosphate pyrophosphokinase 1 OS=Rattus norvegicus GN=Prps1 PE=1 SV=2 - [PRPS1_RAT]	18.24	2	4	4	7	0.0745
P09006	Serine protease inhibitor A3N OS=Rattus norvegicus GN=Serpina3n PE=1 SV=3 - [SPA3N_RAT]	65.55	1	22	22	281	0.0749
P58365	Cadherin-23 OS=Rattus norvegicus GN=Cdh23 PE=2 SV=1 - [CAD23_RAT]	0.69	1	2	2	5	0.0769
P31721	Complement C1q subcomponent subunit B OS=Rattus norvegicus GN=C1qb PE=1 SV=2 - [C1QB_RAT]	9.88	1	2	2	3	0.0781
Q64640	Adenosine kinase OS=Rattus norvegicus GN=Adk	20.50	1	3	3	5	0.0790

	PE=1 SV=3 - [ADK_RAT]						
P04639	Apolipoprotein A-I OS=Rattus norvegicus GN=Apoa1 PE=1 SV=2 - [APOA1_RAT]	64.48	1	16	16	508	0.0801
P62083	40S ribosomal protein S7 OS=Rattus norvegicus GN=Rps7 PE=1 SV=1 - [RS7_RAT]	52.06	1	6	7	54	0.0815
Q63279	Keratin, type I cytoskeletal 19 OS=Rattus norvegicus GN=Krt19 PE=1 SV=2 - [K1C19_RAT]	45.91	1	11	14	57	0.0820
P0C2X9	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Aldh4a1 PE=1 SV=1 - [AL4A1_RAT]	6.57	1	2	2	3	0.0842
P10111	Peptidyl-prolyl cis-trans isomerase A OS=Rattus norvegicus GN=Ppia PE=1 SV=2 - [PPIA_RAT]	59.76	1	11	11	725	0.0842
P63039	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspd1 PE=1 SV=1 - [CH60_RAT]	65.45	1	30	30	1087	0.0850
P53534	Glycogen phosphorylase, brain form (Fragment) OS=Rattus norvegicus GN=Pygb PE=1 SV=3 - [PYGB_RAT]	18.26	1	8	10	32	0.0855
P04631	Protein S100-B OS=Rattus norvegicus GN=S100b PE=1 SV=2 - [S100B_RAT]	40.22	1	2	2	17	0.0862
P02680	Fibrinogen gamma chain OS=Rattus norvegicus GN=Fgg PE=1 SV=3 - [FIBG_RAT]	59.33	1	21	21	403	0.0869
P12075	Cytochrome c oxidase subunit 5B, mitochondrial OS=Rattus norvegicus GN=Cox5b PE=1 SV=2 - [COX5B_RAT]	36.43	1	5	5	9	0.0870
B0K020	CDGSH iron-sulfur domain-containing protein 1 OS=Rattus norvegicus GN=Cisd1 PE=3 SV=1 - [CISD1_RAT]	34.26	1	3	3	10	0.0871
O35567	Bifunctional purine biosynthesis protein PURH OS=Rattus norvegicus GN=Atic PE=1 SV=2 - [PUR9_RAT]	34.12	1	11	11	25	0.0873
O88989	Malate dehydrogenase, cytoplasmic OS=Rattus norvegicus GN=Mdh1 PE=1 SV=3 - [MDHC_RAT]	48.80	1	14	14	965	0.0885
P48500	Triosephosphate isomerase OS=Rattus norvegicus GN=Tpi1 PE=1 SV=2 - [TPIS_RAT]	85.54	1	16	16	667	0.0898
P08430	UDP-glucuronosyltransferase 1-6 OS=Rattus norvegicus GN=Ugt1a6 PE=1 SV=1 - [UD16_RAT]	12.85	5	2	5	55	0.0899
Q64057	Alpha-aminoadipic semialdehyde dehydrogenase OS=Rattus norvegicus GN=Aldh7a1 PE=1 SV=2 - [AL7A1_RAT]	34.14	1	11	11	34	0.0904
P51635	Alcohol dehydrogenase [NADP(+)] OS=Rattus norvegicus GN=Akr1a1 PE=1 SV=2 - [AK1A1_RAT]	52.00	1	14	14	130	0.0906
P04937	Fibronectin OS=Rattus norvegicus GN=Fn1 PE=1 SV=2 - [FINC_RAT]	18.57	1	29	29	167	0.0920
Q4QQT4	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Rattus norvegicus GN=Ppp2r1b PE=2 SV=1 - [2AAB_RAT]	8.82	1	4	4	37	0.0926
P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	52.91	1	34	34	855	0.0933
Q812D1	PC4 and SFRS1-interacting protein OS=Rattus norvegicus GN=Psip1 PE=1 SV=1 - [PSIP1_RAT]	5.68	1	2	2	2	0.0936
Q6P5P5	Mesoderm-specific transcript homolog protein OS=Rattus norvegicus GN=Mest PE=2 SV=1 - [MEST_RAT]	26.87	1	5	5	94	0.0937
Q62689	Tyrosine-protein kinase JAK2 OS=Rattus norvegicus GN=Jak2 PE=1 SV=1 - [JAK2_RAT]	4.24	1	2	3	9	0.0944
Q8VI04	Isoaspartyl peptidase/L-asparaginase OS=Rattus norvegicus GN=Asrgl1 PE=1 SV=1 - [ASGL1_RAT]	23.72	1	5	5	9	0.0945
P10888	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Rattus norvegicus GN=Cox4i1 PE=1 SV=1 - [COX41_RAT]	36.09	1	6	6	133	0.0956
Q9WVK7	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Hadh PE=2 SV=1 - [HCDH_RAT]	67.52	1	12	12	381	0.0963
P00564	Creatine kinase M-type OS=Rattus norvegicus GN=Ckm PE=1 SV=2 - [KCRM_RAT]	24.93	1	7	7	18	0.0968
Q6P6V0	Glucose-6-phosphate isomerase OS=Rattus norvegicus GN=Gpi PE=1 SV=1 - [G6PI_RAT]	53.94	1	24	24	472	0.0976
P05943	Protein S100-A10 OS=Rattus norvegicus GN=S100a10	28.42	1	3	3	10	0.0978

	PE=1 SV=2 - [S10AA_RAT]						
P50398	Rab GDP dissociation inhibitor alpha OS=Rattus norvegicus GN=Gdi1 PE=1 SV=1 - [GDIA_RAT]	42.28	1	8	13	156	0.0982
P38656	Lupus La protein homolog OS=Rattus norvegicus GN=Ssb PE=1 SV=1 - [LA_RAT]	11.57	1	2	3	3	0.0995
P07861	Neprilysin OS=Rattus norvegicus GN=Mme PE=1 SV=2 - [NEP_RAT]	3.87	1	2	2	3	0.1004
Q0ZHH6	Atlastin-3 OS=Rattus norvegicus GN=Atl3 PE=2 SV=2 - [ATLA3_RAT]	24.21	1	7	7	76	0.1005
Q9JJ31	Cullin-5 OS=Rattus norvegicus GN=Cul5 PE=1 SV=3 - [CUL5_RAT]	4.49	1	2	2	3	0.1005
P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	72.29	1	11	11	215	0.1017
P08010	Glutathione S-transferase Mu 2 OS=Rattus norvegicus GN=Gstm2 PE=1 SV=2 - [GSTM2_RAT]	67.89	1	10	16	290	0.1019
Q64591	2,4-dienoyl-CoA reductase, mitochondrial OS=Rattus norvegicus GN=Decr1 PE=1 SV=2 - [DECR_RAT]	49.55	1	11	11	126	0.1022
Q6MG60	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Rattus norvegicus GN=Ddah2 PE=1 SV=1 - [DDAH2_RAT]	50.18	1	8	8	73	0.1029
Q5XIE6	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Rattus norvegicus GN=Hibch PE=1 SV=2 - [HIBCH_RAT]	18.18	1	4	4	9	0.1035
P15651	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acads PE=1 SV=2 - [ACADS_RAT]	25.00	1	6	7	27	0.1036
P62914	60S ribosomal protein L11 OS=Rattus norvegicus GN=Rpl11 PE=1 SV=2 - [RL11_RAT]	16.85	1	3	3	55	0.1042
Q80Z29	Nicotinamide phosphoribosyltransferase OS=Rattus norvegicus GN=Nampt PE=1 SV=1 - [NAMPT_RAT]	8.35	1	2	2	4	0.1044
Q64573	Liver carboxylesterase 4 OS=Rattus norvegicus PE=2 SV=2 - [EST4_RAT]	12.83	1	1	4	57	0.1044
Q64232	Very-long-chain enoyl-CoA reductase OS=Rattus norvegicus GN=Tecr PE=1 SV=1 - [TECR_RAT]	18.18	1	6	6	24	0.1047
Q4V8H8	EH domain-containing protein 2 OS=Rattus norvegicus GN=Ehd2 PE=1 SV=1 - [EHD2_RAT]	74.59	1	32	33	2197	0.1071
P25235	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Rattus norvegicus GN=Rpn2 PE=2 SV=2 - [RPN2_RAT]	39.14	1	12	12	135	0.1092
Q5XI73	Rho GDP-dissociation inhibitor 1 OS=Rattus norvegicus GN=Arhgdia PE=1 SV=1 - [GDIR1_RAT]	50.00	1	10	10	214	0.1092
P01836	Ig kappa chain C region, A allele OS=Rattus norvegicus PE=1 SV=1 - [KACA_RAT]	76.42	1	6	6	827	0.1106
P97943	Scavenger receptor class B member 1 OS=Rattus norvegicus GN=Scarb1 PE=1 SV=1 - [SCRB1_RAT]	10.02	1	2	2	2	0.1125
Q5I0E7	Transmembrane emp24 domain-containing protein 9 OS=Rattus norvegicus GN=Tmed9 PE=1 SV=1 - [TMED9_RAT]	15.74	1	3	3	20	0.1127
P63088	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Rattus norvegicus GN=Ppp1cc PE=1 SV=1 - [PP1G_RAT]	20.43	3	3	4	36	0.1148
O35142	Coatomer subunit beta' OS=Rattus norvegicus GN=Copb2 PE=1 SV=3 - [COPB2_RAT]	14.03	1	8	9	57	0.1151
Q9WUW3	Complement factor I OS=Rattus norvegicus GN=Cfi PE=2 SV=1 - [CFAI_RAT]	5.79	1	2	2	2	0.1159
Q01129	Decorin OS=Rattus norvegicus GN=Dcn PE=1 SV=1 - [PGS2_RAT]	36.72	1	12	13	485	0.1165
P04166	Cytochrome b5 type B OS=Rattus norvegicus GN=Cyb5b PE=1 SV=2 - [CYB5B_RAT]	51.37	1	4	4	53	0.1168
P20761	Ig gamma-2B chain C region OS=Rattus norvegicus GN=Igh-1a PE=1 SV=1 - [IGG2B_RAT]	37.54	1	7	7	492	0.1193
Q63644	Rho-associated protein kinase 1 OS=Rattus norvegicus GN=Rock1 PE=1 SV=1 - [ROCK1_RAT]	2.26	1	2	2	3	0.1207
P85125	Polymerase I and transcript release factor OS=Rattus norvegicus GN=Ptrf PE=1 SV=1 - [PTRF_RAT]	43.88	1	18	18	1832	0.1209
Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	27.46	1	9	10	37	0.1210
Q9QZA2	Programmed cell death 6-interacting protein OS=Rattus	17.87	1	8	8	58	0.1237

	norvegicus GN=Pdcd6ip PE=1 SV=2 - [PDC6I_RAT]						
P00787	Cathepsin B OS=Rattus norvegicus GN=Ctsb PE=1 SV=2 - [CATB_RAT]	27.73	1	8	8	126	0.1238
P18297	Sepiapterin reductase OS=Rattus norvegicus GN=Spr PE=1 SV=1 - [SPRE_RAT]	21.76	1	2	2	3	0.1240
P61983	14-3-3 protein gamma OS=Rattus norvegicus GN=Ywhag PE=1 SV=2 - [1433G_RAT]	80.97	1	12	19	592	0.1241
P11348	Dihydropteridine reductase OS=Rattus norvegicus GN=Qdpr PE=1 SV=1 - [DHPR_RAT]	50.21	1	8	8	53	0.1242
P10860	Glutamate dehydrogenase 1, mitochondrial OS=Rattus norvegicus GN=Glud1 PE=1 SV=2 - [DHE3_RAT]	48.03	1	18	19	145	0.1247
Q63965	Sideroflexin-1 OS=Rattus norvegicus GN=Sfxn1 PE=2 SV=4 - [SFXN1_RAT]	20.19	1	3	3	5	0.1264
Q5XIU9	Membrane-associated progesterone receptor component 2 OS=Rattus norvegicus GN=Pgrmc2 PE=1 SV=1 - [PGRC2_RAT]	34.10	1	6	6	38	0.1285
P47942	Dihydropyrimidinase-related protein 2 OS=Rattus norvegicus GN=Dpysl2 PE=1 SV=1 - [DPYL2_RAT]	36.36	1	10	12	221	0.1294
Q68FU3	Electron transfer flavoprotein subunit beta OS=Rattus norvegicus GN=Etfb PE=2 SV=3 - [ETFB_RAT]	46.67	1	10	10	173	0.1309
Q4G075	Leukocyte elastase inhibitor A OS=Rattus norvegicus GN=Serpinb1a PE=1 SV=1 - [ILEUA_RAT]	10.55	1	3	3	3	0.1322
P11960	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial (Fragment) OS=Rattus norvegicus GN=Bckdha PE=1 SV=1 - [ODBA_RAT]	8.62	1	2	2	6	0.1325
Q62658	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Rattus norvegicus GN=Fkbp1a PE=1 SV=3 - [FKB1A_RAT]	29.63	1	2	2	22	0.1329
P10686	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 OS=Rattus norvegicus GN=Plcg1 PE=1 SV=1 - [PLCG1_RAT]	2.33	1	2	2	6	0.1330
P23457	3-alpha-hydroxysteroid dehydrogenase OS=Rattus norvegicus GN=Akr1c9 PE=1 SV=1 - [DIDH_RAT]	55.59	1	11	13	158	0.1331
Q64550	UDP-glucuronosyltransferase 1-1 OS=Rattus norvegicus GN=Ugt1a1 PE=1 SV=1 - [UD11_RAT]	13.27	5	1	4	53	0.1340
P02770	Serum albumin OS=Rattus norvegicus GN=Alb PE=1 SV=2 - [ALBU_RAT]	80.26	1	54	54	35577	0.1345
P10760	Adenosylhomocysteinase OS=Rattus norvegicus GN=Ahcy PE=1 SV=3 - [SAHH_RAT]	33.56	1	11	11	153	0.1354
P11884	Aldehyde dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Aldh2 PE=1 SV=1 - [ALDH2_RAT]	56.26	1	20	20	571	0.1366
Q63377	Sodium/potassium-transporting ATPase subunit beta-3 OS=Rattus norvegicus GN=Atp1b3 PE=2 SV=1 - [AT1B3_RAT]	11.83	1	2	2	5	0.1372
P05712	Ras-related protein Rab-2A OS=Rattus norvegicus GN=Rab2a PE=2 SV=1 - [RAB2A_RAT]	50.47	1	6	7	45	0.1374
P14480	Fibrinogen beta chain OS=Rattus norvegicus GN=Fgb PE=1 SV=4 - [FIBB_RAT]	65.34	1	24	24	391	0.1386
P26644	Beta-2-glycoprotein 1 OS=Rattus norvegicus GN=Apoh PE=2 SV=2 - [APOH_RAT]	26.26	1	7	7	33	0.1391
P31399	ATP synthase subunit d, mitochondrial OS=Rattus norvegicus GN=Atp5h PE=1 SV=3 - [ATP5H_RAT]	34.16	1	5	5	37	0.1394
P23514	Coatomer subunit beta OS=Rattus norvegicus GN=Copb1 PE=1 SV=1 - [COPB_RAT]	17.52	1	8	9	74	0.1399
P21263	Nestin OS=Rattus norvegicus GN=Nes PE=1 SV=2 - [NEST_RAT]	1.27	1	2	2	2	0.1414
P00507	Aspartate aminotransferase, mitochondrial OS=Rattus norvegicus GN=Got2 PE=1 SV=2 - [AATM_RAT]	30.93	1	11	12	97	0.1416
Q62651	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Rattus norvegicus GN=Ech1 PE=1 SV=2 - [ECH1_RAT]	38.84	1	9	9	46	0.1420
P40307	Proteasome subunit beta type-2 OS=Rattus norvegicus GN=Psmb2 PE=1 SV=1 - [PSB2_RAT]	26.37	1	4	4	55	0.1428
Q63691	Monocyte differentiation antigen CD14 OS=Rattus norvegicus GN=Cd14 PE=2 SV=2 - [CD14_RAT]	26.34	1	6	6	81	0.1429
Q9Z311	Trans-2-enoyl-CoA reductase, mitochondrial OS=Rattus norvegicus GN=Mecr PE=1 SV=1 - [MECR_RAT]	20.64	1	2	2	12	0.1441
Q7M767	Ubiquitin-conjugating enzyme E2 variant 2 OS=Rattus	44.83	1	5	5	17	0.1444

	norvegicus GN=Ube2v2 PE=1 SV=3 - [UB2V2_RAT]						
P07338	Chymotrypsinogen B OS=Rattus norvegicus GN=Ctrb1 PE=1 SV=1 - [CTRB1_RAT]	14.45	1	2	2	2	0.1446
P11507	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Rattus norvegicus GN=Atp2a2 PE=1 SV=1 - [AT2A2_RAT]	14.09	1	11	11	96	0.1446
P55260	Annexin A4 OS=Rattus norvegicus GN=Anxa4 PE=1 SV=3 - [ANXA4_RAT]	55.80	1	15	15	108	0.1448
P23928	Alpha-crystallin B chain OS=Rattus norvegicus GN=Cryab PE=1 SV=1 - [CRYAB_RAT]	18.29	1	3	3	7	0.1452
P17475	Alpha-1-antiproteinase OS=Rattus norvegicus GN=Serpina1 PE=1 SV=2 - [A1AT_RAT]	51.82	1	18	18	1099	0.1453
Q62975	Protein Z-dependent protease inhibitor OS=Rattus norvegicus GN=Serpina10 PE=2 SV=2 - [ZPI_RAT]	11.01	1	4	4	10	0.1454
P08011	Microsomal glutathione S-transferase 1 OS=Rattus norvegicus GN=Mgst1 PE=1 SV=3 - [MGST1_RAT]	69.68	1	8	8	1151	0.1460
Q63716	Peroxiredoxin-1 OS=Rattus norvegicus GN=Prdx1 PE=1 SV=1 - [PRDX1_RAT]	70.85	1	12	14	584	0.1462
P07943	Aldose reductase OS=Rattus norvegicus GN=Akr1b1 PE=1 SV=3 - [ALDR_RAT]	59.49	1	14	16	288	0.1465
P85845	Fascin OS=Rattus norvegicus GN=Fscn1 PE=1 SV=2 - [FSCN1_RAT]	6.90	1	2	2	2	0.1469
P85515	Alpha-centractin OS=Rattus norvegicus GN=Actr1a PE=1 SV=1 - [ACTZ_RAT]	17.29	1	4	4	23	0.1470
O89049	Thioredoxin reductase 1, cytoplasmic OS=Rattus norvegicus GN=Txnrd1 PE=1 SV=5 - [TRXR1_RAT]	16.63	1	4	4	12	0.1478
Q5U1Z2	Trafficking protein particle complex subunit 3 OS=Rattus norvegicus GN=Trappc3 PE=2 SV=1 - [TPPC3_RAT]	18.33	1	3	3	4	0.1488
P06762	Heme oxygenase 1 OS=Rattus norvegicus GN=Hmox1 PE=1 SV=1 - [HMOX1_RAT]	16.61	1	3	4	4	0.1492
P42123	L-lactate dehydrogenase B chain OS=Rattus norvegicus GN=Ldhb PE=1 SV=2 - [LDHB_RAT]	69.46	1	20	23	701	0.1493
Q5U300	Ubiquitin-like modifier-activating enzyme 1 OS=Rattus norvegicus GN=Uba1 PE=1 SV=1 - [UBA1_RAT]	46.22	1	31	31	467	0.1495
Q62636	Ras-related protein Rap-1b OS=Rattus norvegicus GN=Rap1b PE=1 SV=2 - [RAP1B_RAT]	46.20	1	2	8	145	0.1506
Q63598	Plastin-3 OS=Rattus norvegicus GN=Pls3 PE=1 SV=2 - [PLST_RAT]	26.83	1	9	10	44	0.1507
Q9EPF2	Cell surface glycoprotein MUC18 OS=Rattus norvegicus GN=Mcam PE=1 SV=2 - [MUC18_RAT]	43.06	1	22	22	325	0.1515
Q4V8F9	Hydroxysteroid dehydrogenase-like protein 2 OS=Rattus norvegicus GN=Hsdl2 PE=2 SV=1 - [HSDL2_RAT]	5.53	1	2	2	7	0.1530
P47875	Cysteine and glycine-rich protein 1 OS=Rattus norvegicus GN=Csrp1 PE=1 SV=2 - [CSRP1_RAT]	30.57	1	5	5	77	0.1537
O09171	Betaine--homocysteine S-methyltransferase 1 OS=Rattus norvegicus GN=Bhmt PE=1 SV=1 - [BHMT1_RAT]	11.06	1	4	4	7	0.1543
Q6QA69	1-acylglycerol-3-phosphate O-acyltransferase ABHD5 OS=Rattus norvegicus GN=Abhd5 PE=1 SV=1 - [ABHD5_RAT]	36.18	1	6	7	151	0.1543
Q63081	Protein disulfide-isomerase A6 OS=Rattus norvegicus GN=Pdia6 PE=1 SV=2 - [PDIA6_RAT]	41.82	1	13	13	413	0.1548
P62246	40S ribosomal protein S15a OS=Rattus norvegicus GN=Rps15a PE=1 SV=2 - [RS15A_RAT]	23.85	1	3	3	5	0.1550
P50399	Rab GDP dissociation inhibitor beta OS=Rattus norvegicus GN=Gdi2 PE=1 SV=2 - [GDIB_RAT]	58.43	1	16	21	461	0.1557
P62278	40S ribosomal protein S13 OS=Rattus norvegicus GN=Rps13 PE=1 SV=2 - [RS13_RAT]	45.03	1	5	6	16	0.1558
P62161	Calmodulin OS=Rattus norvegicus GN=Calm1 PE=1 SV=2 - [CALM_RAT]	36.91	1	6	6	76	0.1559
P28480	T-complex protein 1 subunit alpha OS=Rattus norvegicus GN=Tcp1 PE=1 SV=1 - [TCPA_RAT]	18.35	1	4	5	30	0.1562
P00884	Fructose-bisphosphate aldolase B OS=Rattus norvegicus GN=Aldob PE=1 SV=2 - [ALDOB_RAT]	22.80	1	6	6	9	0.1584
Q9Z2G8	Nucleosome assembly protein 1-like 1 OS=Rattus norvegicus GN=Nap1l1 PE=1 SV=1 - [NP1L1_RAT]	7.18	1	2	2	16	0.1587

P27139	Carbonic anhydrase 2 OS=Rattus norvegicus GN=Ca2 PE=1 SV=2 - [CAH2_RAT]	64.62	1	12	12	323	0.1588
Q4FZU2	Keratin, type II cytoskeletal 6A OS=Rattus norvegicus GN=Krt6a PE=1 SV=1 - [K2C6A_RAT]	11.05	1	5	7	48	0.1597
P18418	Calreticulin OS=Rattus norvegicus GN=Calr PE=1 SV=1 - [CALR_RAT]	66.11	1	20	20	293	0.1605
Q62969	Prostacyclin synthase OS=Rattus norvegicus GN=Ptgis PE=2 SV=1 - [PTGIS_RAT]	17.76	1	5	5	23	0.1606
Q9EPH1	Alpha-1B-glycoprotein OS=Rattus norvegicus GN=A1bg PE=2 SV=2 - [A1BG_RAT]	30.02	1	12	12	129	0.1607
P0CG51	Polyubiquitin-B OS=Rattus norvegicus GN=Ubb PE=1 SV=1 - [UBB_RAT]	70.82	4	7	7	418	0.1607
Q02253	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Rattus norvegicus GN=Aldh6a1 PE=1 SV=1 - [MMSA_RAT]	44.67	1	15	15	118	0.1618
Q9JJ79	Cytoplasmic dynein 2 heavy chain 1 OS=Rattus norvegicus GN=Dync2h1 PE=1 SV=1 - [DYHC2_RAT]	1.74	1	2	4	4	0.1625
Q6PCU2	V-type proton ATPase subunit E 1 OS=Rattus norvegicus GN=Atp6v1e1 PE=1 SV=1 - [VATE1_RAT]	17.26	1	3	3	16	0.1640
P84817	Mitochondrial fission 1 protein OS=Rattus norvegicus GN=Fis1 PE=1 SV=1 - [FIS1_RAT]	24.34	1	4	4	101	0.1642
Q9JJ22	Endoplasmic reticulum aminopeptidase 1 OS=Rattus norvegicus GN=Erap1 PE=2 SV=2 - [ERAP1_RAT]	6.99	1	5	5	22	0.1648
A1L1J9	Lipase maturation factor 2 OS=Rattus norvegicus GN=Lmf2 PE=2 SV=1 - [LMF2_RAT]	7.12	1	4	4	5	0.1668
P42930	Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1 - [HSPB1_RAT]	63.11	1	13	13	293	0.1677
P61980	Heterogeneous nuclear ribonucleoprotein K OS=Rattus norvegicus GN=Hnrnpk PE=1 SV=1 - [HNRPK_RAT]	15.98	1	6	6	88	0.1706
Q924S5	Lon protease homolog, mitochondrial OS=Rattus norvegicus GN=Lonp1 PE=2 SV=1 - [LONM_RAT]	6.53	1	3	3	4	0.1707
P63018	Heat shock cognate 71 kDa protein OS=Rattus norvegicus GN=Hspa8 PE=1 SV=1 - [HSP7C_RAT]	74.61	1	34	39	1225	0.1712
Q63514	C4b-binding protein alpha chain OS=Rattus norvegicus GN=C4bpa PE=2 SV=1 - [C4BPA_RAT]	7.35	1	3	3	13	0.1712
P20059	Hemopexin OS=Rattus norvegicus GN=Hpx PE=1 SV=3 - [HEMO_RAT]	63.04	1	28	28	1512	0.1713
Q9JJ54	Heterogeneous nuclear ribonucleoprotein D0 OS=Rattus norvegicus GN=Hnrnpd PE=1 SV=2 - [HNRPD_RAT]	6.23	1	2	2	6	0.1714
Q64428	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus GN=Hadha PE=1 SV=2 - [ECHA_RAT]	53.08	1	28	29	766	0.1737
P62832	60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1 - [RL23_RAT]	32.14	1	3	3	31	0.1765
P56571	ES1 protein homolog, mitochondrial OS=Rattus norvegicus PE=1 SV=2 - [ES1_RAT]	35.71	1	7	7	45	0.1767
Q6P6R2	Dihydrolipoyl dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Dld PE=1 SV=1 - [DLDH_RAT]	44.40	1	16	16	293	0.1768
P14141	Carbonic anhydrase 3 OS=Rattus norvegicus GN=Ca3 PE=1 SV=3 - [CAH3_RAT]	87.31	1	22	22	16071	0.1781
Q62740	Secreted phosphoprotein 24 OS=Rattus norvegicus GN=Spp2 PE=1 SV=2 - [SPP24_RAT]	11.82	1	2	2	5	0.1782
Q9QY44	ATP-binding cassette sub-family D member 2 OS=Rattus norvegicus GN=Abcd2 PE=1 SV=1 - [ABCD2_RAT]	13.77	1	5	6	14	0.1796
P07756	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Rattus norvegicus GN=Cps1 PE=1 SV=1 - [CPSM_RAT]	19.60	1	19	19	98	0.1818
Q7TQ94	Nitrilase homolog 1 OS=Rattus norvegicus GN=Nit1 PE=2 SV=1 - [NIT1_RAT]	38.70	1	5	6	30	0.1831
P30835	ATP-dependent 6-phosphofructokinase, liver type OS=Rattus norvegicus GN=Pfkl PE=1 SV=3 - [PFKAL_RAT]	2.69	1	2	2	3	0.1838
Q07936	Annexin A2 OS=Rattus norvegicus GN=Anxa2 PE=1	75.81	1	28	28	2015	0.1845

	SV=2 - [ANXA2_RAT]						
Q4TU93	C-type mannose receptor 2 OS=Rattus norvegicus GN=Mrc2 PE=1 SV=1 - [MRC2_RAT]	2.03	1	2	2	3	0.1847
P82471	Guanine nucleotide-binding protein G(q) subunit alpha OS=Rattus norvegicus GN=Gnaq PE=2 SV=2 - [GNAQ_RAT]	19.78	1	5	5	36	0.1873
P21533	60S ribosomal protein L6 OS=Rattus norvegicus GN=Rpl6 PE=1 SV=5 - [RL6_RAT]	17.11	1	4	4	33	0.1889
P62836	Ras-related protein Rap-1A OS=Rattus norvegicus GN=Rap1a PE=1 SV=1 - [RAP1A_RAT]	39.13	1	1	7	123	0.1894
Q9Z0V5	Peroxiredoxin-4 OS=Rattus norvegicus GN=Prdx4 PE=2 SV=1 - [PRDX4_RAT]	29.30	1	4	6	200	0.1902
Q6P6Q2	Keratin, type II cytoskeletal 5 OS=Rattus norvegicus GN=Krt5 PE=1 SV=1 - [K2C5_RAT]	15.10	1	2	9	52	0.1914
Q91Y80	SH3 domain-binding protein 5 OS=Rattus norvegicus GN=Sh3bp5 PE=1 SV=2 - [3BP5_RAT]	2.63	1	2	2	2	0.1918
P11598	Protein disulfide-isomerase A3 OS=Rattus norvegicus GN=Pdia3 PE=1 SV=2 - [PDIA3_RAT]	59.80	1	30	31	602	0.1934
D3ZAF6	ATP synthase subunit f, mitochondrial OS=Rattus norvegicus GN=Atp5j2 PE=1 SV=1 - [ATPK_RAT]	23.86	1	2	2	25	0.1936
Q63544	Gamma-synuclein OS=Rattus norvegicus GN=Sncg PE=1 SV=2 - [SYUG_RAT]	74.80	1	11	11	497	0.1955
P17220	Proteasome subunit alpha type-2 OS=Rattus norvegicus GN=Psma2 PE=1 SV=3 - [PSA2_RAT]	50.85	1	8	8	68	0.1955
Q66HG4	Aldose 1-epimerase OS=Rattus norvegicus GN=Galm PE=1 SV=1 - [GALM_RAT]	21.05	1	5	5	26	0.1959
P26453	Basigin OS=Rattus norvegicus GN=Bsg PE=1 SV=2 - [BASI_RAT]	21.39	1	8	8	72	0.1969
Q5XI78	2-oxoglutarate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ogdh PE=1 SV=1 - [ODO1_RAT]	41.84	1	30	30	418	0.1970
Q5XI32	F-actin-capping protein subunit beta OS=Rattus norvegicus GN=Capzb PE=1 SV=1 - [CAPZB_RAT]	30.51	1	6	7	28	0.2009
Q62940	E3 ubiquitin-protein ligase NEDD4 OS=Rattus norvegicus GN=Nedd4 PE=1 SV=1 - [NEDD4_RAT]	11.16	1	8	8	87	0.2016
P28037	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Rattus norvegicus GN=Aldh1l1 PE=1 SV=3 - [AL1L1_RAT]	34.15	1	21	22	85	0.2030
Q920L2	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Rattus norvegicus GN=Sdha PE=1 SV=1 - [SDHA_RAT]	32.47	1	13	14	111	0.2030
Q9QXQ0	Alpha-actinin-4 OS=Rattus norvegicus GN=Actn4 PE=1 SV=2 - [ACTN4_RAT]	59.28	1	27	43	360	0.2031
P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	17.80	1	14	14	164	0.2036
P16303	Carboxylesterase 1D OS=Rattus norvegicus GN=Ces1d PE=1 SV=2 - [CES1D_RAT]	52.92	1	26	26	2924	0.2038
Q5M7W5	Microtubule-associated protein 4 OS=Rattus norvegicus GN=Map4 PE=1 SV=1 - [MAP4_RAT]	23.75	1	15	15	72	0.2041
Q07009	Calpain-2 catalytic subunit OS=Rattus norvegicus GN=Capn2 PE=1 SV=3 - [CAN2_RAT]	30.57	1	14	14	92	0.2064
Q9HB97	Alpha-parvin OS=Rattus norvegicus GN=Parva PE=1 SV=2 - [PARVA_RAT]	20.43	1	5	5	28	0.2093
P06238	Alpha-2-macroglobulin OS=Rattus norvegicus GN=A2m PE=2 SV=2 - [A2MG_RAT]	5.23	1	5	6	73	0.2099
Q9Z1P2	Alpha-actinin-1 OS=Rattus norvegicus GN=Actn1 PE=1 SV=1 - [ACTN1_RAT]	51.01	1	17	33	259	0.2104
P15800	Laminin subunit beta-2 OS=Rattus norvegicus GN=Lamb2 PE=2 SV=1 - [LAMB2_RAT]	22.32	1	30	31	149	0.2111
Q6Q760	Sodium leak channel non-selective protein OS=Rattus norvegicus GN=Nalcn PE=1 SV=1 - [NALCN_RAT]	1.55	1	2	3	5	0.2117
P00388	NADPH--cytochrome P450 reductase OS=Rattus norvegicus GN=Por PE=1 SV=3 - [NCPR_RAT]	30.83	1	13	13	108	0.2121
B0BNF1	Septin-8 OS=Rattus norvegicus GN=Sept8 PE=1 SV=1 - [SEPT8_RAT]	4.07	1	1	2	2	0.2136
P06757	Alcohol dehydrogenase 1 OS=Rattus norvegicus GN=Adh1 PE=1 SV=3 - [ADH1_RAT]	9.04	1	3	3	6	0.2139

P08649	Complement C4 OS=Rattus norvegicus GN=C4 PE=1 SV=3 - [CO4_RAT]	53.31	1	64	64	1280	0.2157
O70351	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Rattus norvegicus GN=Hsd17b10 PE=1 SV=3 - [HCD2_RAT]	72.41	1	10	11	153	0.2164
P35435	ATP synthase subunit gamma, mitochondrial OS=Rattus norvegicus GN=Atp5c1 PE=1 SV=2 - [ATPG_RAT]	35.90	1	7	7	62	0.2171
P05964	Protein S100-A6 OS=Rattus norvegicus GN=S100a6 PE=1 SV=3 - [S10A6_RAT]	19.10	1	3	3	22	0.2177
B0BNN3	Carbonic anhydrase 1 OS=Rattus norvegicus GN=Ca1 PE=1 SV=1 - [CAH1_RAT]	85.82	1	13	13	562	0.2197
P97675	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3 OS=Rattus norvegicus GN=Enpp3 PE=1 SV=2 - [ENPP3_RAT]	20.69	1	12	12	119	0.2222
Q63617	Hypoxia up-regulated protein 1 OS=Rattus norvegicus GN=Hyou1 PE=1 SV=1 - [HYOU1_RAT]	26.03	1	17	18	166	0.2227
Q5RK27	Solute carrier family 12 member 7 OS=Rattus norvegicus GN=Slc12a7 PE=2 SV=2 - [S12A7_RAT]	1.29	1	2	2	2	0.2245
P62909	40S ribosomal protein S3 OS=Rattus norvegicus GN=Rps3 PE=1 SV=1 - [RS3_RAT]	53.09	1	11	11	96	0.2249
P17077	60S ribosomal protein L9 OS=Rattus norvegicus GN=Rpl9 PE=1 SV=1 - [RL9_RAT]	20.31	1	2	2	7	0.2265
P63025	Vesicle-associated membrane protein 3 OS=Rattus norvegicus GN=Vamp3 PE=1 SV=1 - [VAMP3_RAT]	38.83	2	3	3	27	0.2269
B2GV38	Ubiquitin-like protein 4A OS=Rattus norvegicus GN=Ubl4a PE=2 SV=1 - [UBL4A_RAT]	19.75	1	2	2	2	0.2276
P05942	Protein S100-A4 OS=Rattus norvegicus GN=S100a4 PE=2 SV=1 - [S10A4_RAT]	27.72	1	3	3	28	0.2299
P35171	Cytochrome c oxidase subunit 7A2, mitochondrial OS=Rattus norvegicus GN=Cox7a2 PE=1 SV=1 - [CX7A2_RAT]	27.71	1	2	2	8	0.2302
P28075	Proteasome subunit beta type-5 OS=Rattus norvegicus GN=Psmb5 PE=1 SV=3 - [PSB5_RAT]	14.83	1	3	3	4	0.2316
O70199	UDP-glucose 6-dehydrogenase OS=Rattus norvegicus GN=Ugdh PE=1 SV=1 - [UGDH_RAT]	10.14	1	3	3	3	0.2316
B2GV06	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Rattus norvegicus GN=Oxct1 PE=1 SV=1 - [SCOT1_RAT]	43.46	1	13	13	113	0.2331
P61589	Transforming protein RhoA OS=Rattus norvegicus GN=Rhoa PE=1 SV=1 - [RHOA_RAT]	67.36	1	10	10	127	0.2350
P02767	Transthyretin OS=Rattus norvegicus GN=Ttr PE=1 SV=1 - [TTHY_RAT]	62.59	1	6	6	116	0.2360
P16446	Phosphatidylinositol transfer protein alpha isoform OS=Rattus norvegicus GN=Pitpna PE=1 SV=2 - [PIPNA_RAT]	12.18	1	2	2	5	0.2383
Q07969	Platelet glycoprotein 4 OS=Rattus norvegicus GN=Cd36 PE=1 SV=3 - [CD36_RAT]	36.86	1	11	11	646	0.2401
P36972	Adenine phosphoribosyltransferase OS=Rattus norvegicus GN=Aprt PE=1 SV=1 - [APT_RAT]	80.56	1	12	12	182	0.2409
Q99PS8	Histidine-rich glycoprotein OS=Rattus norvegicus GN=Hrg PE=1 SV=1 - [HRG_RAT]	21.90	1	9	9	41	0.2426
P15865	Histone H1.4 OS=Rattus norvegicus GN=Hist1h1e PE=1 SV=3 - [H14_RAT]	17.35	1	7	7	289	0.2436
P31977	Ezrin OS=Rattus norvegicus GN=Ezr PE=1 SV=3 - [EZRI_RAT]	20.82	1	6	11	159	0.2452
Q08290	Calponin-1 OS=Rattus norvegicus GN=Cnn1 PE=1 SV=1 - [CNN1_RAT]	11.78	1	3	3	4	0.2457
P24268	Cathepsin D OS=Rattus norvegicus GN=Ctsd PE=1 SV=1 - [CATD_RAT]	29.73	1	7	8	55	0.2461
P06302	Prothymosin alpha OS=Rattus norvegicus GN=Ptma PE=1 SV=2 - [PTMA_RAT]	22.32	1	4	4	11	0.2477
Q62826	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=1 SV=4 - [HNRPM_RAT]	5.36	1	3	3	13	0.2480
Q4V886	RNA polymerase II-associated factor 1 homolog OS=Rattus norvegicus GN=Paf1 PE=2 SV=1 - [PAF1_RAT]	9.16	1	2	2	2	0.2485
O35814	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus	6.81	1	2	2	14	0.2508

	GN=Stip1 PE=1 SV=1 - [STIP1_RAT]						
Q00657	Chondroitin sulfate proteoglycan 4 OS=Rattus norvegicus GN=Cspg4 PE=1 SV=2 - [CSPG4_RAT]	1.33	1	2	2	2	0.2513
Q920A6	Retinoid-inducible serine carboxypeptidase OS=Rattus norvegicus GN=Scpep1 PE=2 SV=1 - [RISC_RAT]	17.48	1	5	6	98	0.2516
Q62952	Dihydropyrimidinase-related protein 3 OS=Rattus norvegicus GN=Dpysl3 PE=1 SV=2 - [DPYL3_RAT]	30.00	1	10	12	60	0.2523
P02764	Alpha-1-acid glycoprotein OS=Rattus norvegicus GN=Orm1 PE=2 SV=1 - [A1AG_RAT]	20.49	1	5	5	13	0.2524
Q3T1J1	Eukaryotic translation initiation factor 5A-1 OS=Rattus norvegicus GN=Eif5a PE=1 SV=3 - [IF5A1_RAT]	46.10	1	8	8	95	0.2529
P21708	Mitogen-activated protein kinase 3 OS=Rattus norvegicus GN=Mapk3 PE=1 SV=5 - [MK03_RAT]	7.11	1	2	2	2	0.2536
P07153	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Rattus norvegicus GN=Rpn1 PE=2 SV=1 - [RPN1_RAT]	26.45	1	11	11	78	0.2550
P28077	Proteasome subunit beta type-9 OS=Rattus norvegicus GN=Psmb9 PE=1 SV=2 - [PSB9_RAT]	14.16	1	3	3	16	0.2562
P27274	CD59 glycoprotein OS=Rattus norvegicus GN=Cd59 PE=1 SV=2 - [CD59_RAT]	30.16	1	4	4	57	0.2577
Q5QD51	A-kinase anchor protein 12 OS=Rattus norvegicus GN=Akap12 PE=1 SV=1 - [AKA12_RAT]	6.40	1	8	10	71	0.2586
Q5XIM9	T-complex protein 1 subunit beta OS=Rattus norvegicus GN=Cct2 PE=1 SV=3 - [TCPB_RAT]	14.39	1	4	4	19	0.2587
P46844	Biliverdin reductase A OS=Rattus norvegicus GN=Blvra PE=1 SV=1 - [BIEA_RAT]	41.02	1	9	9	48	0.2612
Q8VIF7	Selenium-binding protein 1 OS=Rattus norvegicus GN=Selenbp1 PE=1 SV=1 - [SBP1_RAT]	58.26	1	21	22	151	0.2616
O08662	Phosphatidylinositol 4-kinase alpha OS=Rattus norvegicus GN=Pi4ka PE=1 SV=1 - [PI4KA_RAT]	5.34	1	5	6	12	0.2643
D4AE41	RNA binding motif protein, X-linked-like-1 OS=Rattus norvegicus GN=Rbmxl1 PE=3 SV=1 - [RMXL1_RAT]	10.31	3	3	3	9	0.2688
P11232	Thioredoxin OS=Rattus norvegicus GN=Txn PE=1 SV=2 - [THIO_RAT]	31.43	1	5	5	82	0.2688
Q9JLT0	Myosin-10 OS=Rattus norvegicus GN=Myh10 PE=1 SV=1 - [MYH10_RAT]	8.70	1	4	13	112	0.2689
Q9QWE9	Gamma-glutamyltransferase 5 OS=Rattus norvegicus GN=Ggt5 PE=2 SV=1 - [GGT5_RAT]	8.74	1	3	3	4	0.2710
P02650	Apolipoprotein E OS=Rattus norvegicus GN=Apoe PE=1 SV=2 - [APOE_RAT]	55.77	1	16	16	472	0.2713
P55053	Fatty acid-binding protein, epidermal OS=Rattus norvegicus GN=Fabp5 PE=1 SV=3 - [FABP5_RAT]	69.63	1	9	9	226	0.2713
P16036	Phosphate carrier protein, mitochondrial OS=Rattus norvegicus GN=Slc25a3 PE=1 SV=1 - [MPCP_RAT]	41.01	1	10	10	186	0.2722
P04638	Apolipoprotein A-II OS=Rattus norvegicus GN=Apoa2 PE=2 SV=1 - [APOA2_RAT]	30.39	1	3	3	8	0.2744
Q62812	Myosin-9 OS=Rattus norvegicus GN=Myh9 PE=1 SV=3 - [MYH9_RAT]	40.39	1	53	65	937	0.2747
P97849	Long-chain fatty acid transport protein 1 OS=Rattus norvegicus GN=Slc27a1 PE=2 SV=1 - [S27A1_RAT]	23.22	1	9	9	95	0.2750
P21588	5'-nucleotidase OS=Rattus norvegicus GN=Nt5e PE=1 SV=1 - [5NTD_RAT]	11.11	1	4	4	15	0.2756
P47245	Nardilysin OS=Rattus norvegicus GN=Nrd1 PE=1 SV=1 - [NRDC_RAT]	6.46	1	4	4	14	0.2791
Q5PPN5	Tubulin polymerization-promoting protein family member 3 OS=Rattus norvegicus GN=Tppp3 PE=2 SV=1 - [TPPP3_RAT]	21.59	1	3	3	13	0.2807
Q68FS4	Cytosol aminopeptidase OS=Rattus norvegicus GN=Lap3 PE=1 SV=1 - [AMPL_RAT]	39.31	1	12	12	93	0.2813
Q62736	Non-muscle caldesmon OS=Rattus norvegicus GN=Cald1 PE=1 SV=1 - [CALD1_RAT]	19.40	1	8	8	31	0.2828
Q00438	Polypyrimidine tract-binding protein 1 OS=Rattus norvegicus GN=Ptbp1 PE=1 SV=1 - [PTBP1_RAT]	7.93	1	2	2	6	0.2835
Q4KLH6	Centrosomal protein of 162 kDa OS=Rattus norvegicus GN=Cep162 PE=1 SV=2 - [CE162_RAT]	1.14	1	2	2	3	0.2845
P0DMW0	Heat shock 70 kDa protein 1A OS=Rattus norvegicus GN=Hspa1a PE=2 SV=1 - [HS71A_RAT]	16.38	1	4	8	325	0.2853
Q497B0	Omega-amidase NIT2 OS=Rattus norvegicus GN=Nit2	39.13	1	6	6	17	0.2861

	PE=1 SV=1 - [NIT2_RAT]						
Q8VHE9	All-trans-retinol 13,14-reductase OS=Rattus norvegicus GN=Retsat PE=2 SV=1 - [RETST_RAT]	29.56	1	11	11	240	0.2868
P15684	Aminopeptidase N OS=Rattus norvegicus GN=Anpep PE=1 SV=2 - [AMPN_RAT]	26.22	1	15	16	86	0.2868
P60868	40S ribosomal protein S20 OS=Rattus norvegicus GN=Rps20 PE=3 SV=1 - [RS20_RAT]	28.57	1	4	4	40	0.2869
O08651	D-3-phosphoglycerate dehydrogenase OS=Rattus norvegicus GN=Phgdh PE=1 SV=3 - [SERA_RAT]	26.64	1	10	10	188	0.2870
P63331	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Rattus norvegicus GN=Ppp2ca PE=1 SV=1 - [PP2AA_RAT]	21.04	2	3	4	11	0.2896
Q6MG61	Chloride intracellular channel protein 1 OS=Rattus norvegicus GN=Clic1 PE=1 SV=1 - [CLIC1_RAT]	53.53	1	10	10	54	0.2897
P63159	High mobility group protein B1 OS=Rattus norvegicus GN=Hmgb1 PE=1 SV=2 - [HMGB1_RAT]	40.00	1	7	7	18	0.2917
P04041	Glutathione peroxidase 1 OS=Rattus norvegicus GN=Gpx1 PE=1 SV=4 - [GPX1_RAT]	76.62	1	11	11	192	0.2923
O35763	Moesin OS=Rattus norvegicus GN=Msn PE=1 SV=3 - [MOES_RAT]	41.07	1	15	20	265	0.2930
O08678	Serine/threonine-protein kinase MARK1 OS=Rattus norvegicus GN=Mark1 PE=1 SV=1 - [MARK1_RAT]	3.28	2	2	2	6	0.2938
P0C5H9	Mesencephalic astrocyte-derived neurotrophic factor OS=Rattus norvegicus GN=Manf PE=1 SV=1 - [MANF_RAT]	21.79	1	4	4	11	0.2950
Q60587	Trifunctional enzyme subunit beta, mitochondrial OS=Rattus norvegicus GN=Hadhb PE=1 SV=1 - [ECHB_RAT]	49.89	1	19	19	202	0.2964
Q99J82	Integrin-linked protein kinase OS=Rattus norvegicus GN=Ilk PE=2 SV=1 - [ILK_RAT]	10.18	1	4	4	12	0.2974
Q01205	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Rattus norvegicus GN=Dlst PE=1 SV=2 - [ODO2_RAT]	14.32	1	4	4	16	0.2983
P53565	Homeobox protein cut-like 1 OS=Rattus norvegicus GN=Cux1 PE=1 SV=2 - [CUX1_RAT]	1.80	1	2	2	2	0.2984
P23562	Band 3 anion transport protein OS=Rattus norvegicus GN=Slc4a1 PE=1 SV=3 - [B3AT_RAT]	31.93	1	18	18	321	0.2992
P04550	Parathymosin OS=Rattus norvegicus GN=Ptms PE=1 SV=2 - [PTMS_RAT]	22.55	1	2	2	2	0.3020
Q5XHZ0	Heat shock protein 75 kDa, mitochondrial OS=Rattus norvegicus GN=Trap1 PE=1 SV=1 - [TRAP1_RAT]	6.09	1	1	2	12	0.3048
P00786	Pro-cathepsin H OS=Rattus norvegicus GN=Ctsh PE=1 SV=1 - [CATH_RAT]	6.61	1	3	3	3	0.3065
P61023	Calcineurin B homologous protein 1 OS=Rattus norvegicus GN=Chp1 PE=1 SV=2 - [CHP1_RAT]	58.46	1	9	9	66	0.3097
Q3T1L0	Aldehyde dehydrogenase family 16 member A1 OS=Rattus norvegicus GN=Aldh16a1 PE=2 SV=1 - [A16A1_RAT]	5.74	1	2	2	2	0.3114
Q63258	Integrin alpha-7 OS=Rattus norvegicus GN=Itga7 PE=1 SV=2 - [ITA7_RAT]	2.03	1	2	2	4	0.3115
P29457	Serpin H1 OS=Rattus norvegicus GN=Serpinh1 PE=1 SV=1 - [SERPH_RAT]	61.15	1	19	19	542	0.3126
P35434	ATP synthase subunit delta, mitochondrial OS=Rattus norvegicus GN=Atp5d PE=1 SV=2 - [ATPD_RAT]	13.69	1	2	2	19	0.3151
P09895	60S ribosomal protein L5 OS=Rattus norvegicus GN=Rpl5 PE=1 SV=3 - [RL5_RAT]	10.77	1	2	2	4	0.3153
Q63945	Protein SET OS=Rattus norvegicus GN=Set PE=2 SV=2 - [SET_RAT]	20.42	1	5	5	6	0.3157
P18163	Long-chain-fatty-acid--CoA ligase 1 OS=Rattus norvegicus GN=Acsl1 PE=1 SV=1 - [ACSL1_RAT]	72.68	1	39	42	3273	0.3176
P04906	Glutathione S-transferase P OS=Rattus norvegicus GN=Gstp1 PE=1 SV=2 - [GSTP1_RAT]	59.52	1	9	9	263	0.3178
P13086	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Rattus norvegicus GN=Suclg1 PE=2 SV=2 - [SUCA_RAT]	32.37	1	8	9	74	0.3180
B2RZ37	Receptor expression-enhancing protein 5 OS=Rattus norvegicus GN=Reep5 PE=1 SV=1 - [REEP5_RAT]	20.63	1	7	7	290	0.3186

Q6AY30	Saccharopine dehydrogenase-like oxidoreductase OS=Rattus norvegicus GN=Sccpdh PE=1 SV=1 - [SCPDL_RAT]	12.12	1	2	2	5	0.3202
P18421	Proteasome subunit beta type-1 OS=Rattus norvegicus GN=Psmb1 PE=1 SV=3 - [PSB1_RAT]	39.17	1	7	7	74	0.3215
Q9Z2Q1	Protein transport protein Sec31A OS=Rattus norvegicus GN=Sec31a PE=1 SV=2 - [SC31A_RAT]	15.37	1	12	12	107	0.3221
Q9Z1X1	Extended synaptotagmin-1 OS=Rattus norvegicus GN=Esyt1 PE=1 SV=1 - [ESYT1_RAT]	45.31	1	34	34	570	0.3247
Q13409	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3 - [DC1I2_HUMAN]	13.17	1	5	5	22	0.3251
P33124	Long-chain-fatty-acid--CoA ligase 6 OS=Rattus norvegicus GN=Acsl6 PE=1 SV=1 - [ACSL6_RAT]	3.73	1	1	3	271	0.3253
P62907	60S ribosomal protein L10a OS=Rattus norvegicus GN=Rpl10a PE=1 SV=2 - [RL10A_RAT]	18.89	1	3	4	26	0.3256
P50115	Protein S100-A8 OS=Rattus norvegicus GN=S100a8 PE=1 SV=3 - [S10A8_RAT]	22.47	1	2	2	2	0.3265
P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	65.21	1	128	130	1774	0.3281
P15178	Aspartate--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Dars PE=2 SV=1 - [SYDC_RAT]	7.98	1	3	3	6	0.3330
Q5RJR8	Leucine-rich repeat-containing protein 59 OS=Rattus norvegicus GN=Lrrc59 PE=1 SV=1 - [LRC59_RAT]	10.10	1	3	3	22	0.3345
Q6PEC4	S-phase kinase-associated protein 1 OS=Rattus norvegicus GN=Skp1 PE=1 SV=3 - [SKP1_RAT]	12.88	1	2	2	2	0.3365
Q9WTT6	Guanine deaminase OS=Rattus norvegicus GN=Gda PE=1 SV=1 - [GUAD_RAT]	65.86	1	24	24	1093	0.3373
P05371	Clusterin OS=Rattus norvegicus GN=Clu PE=1 SV=2 - [CLUS_RAT]	12.30	1	4	4	13	0.3389
Q9EPH8	Polyadenylate-binding protein 1 OS=Rattus norvegicus GN=Pabpc1 PE=1 SV=1 - [PABP1_RAT]	8.49	1	3	4	13	0.3390
P16257	Translocator protein OS=Rattus norvegicus GN=Tspo PE=1 SV=1 - [TSPO_RAT]	27.22	1	2	2	4	0.3409
P24051	40S ribosomal protein S27-like OS=Rattus norvegicus GN=Rps27l PE=1 SV=3 - [RS27L_RAT]	25.00	2	2	2	3	0.3409
P55797	Apolipoprotein C-IV OS=Rattus norvegicus GN=Apoc4 PE=2 SV=2 - [APOC4_RAT]	25.00	1	2	2	3	0.3409
Q63690	Apoptosis regulator BAX OS=Rattus norvegicus GN=Bax PE=1 SV=2 - [BAX_RAT]	12.50	1	2	2	2	0.3409
P31720	Complement C1q subcomponent subunit A OS=Rattus norvegicus GN=C1qa PE=1 SV=2 - [C1QA_RAT]	12.24	1	2	2	7	0.3409
Q6AXZ4	Centrosomal protein CEP57L1 OS=Rattus norvegicus GN=Cep57l1 PE=2 SV=1 - [CE57L_RAT]	7.91	1	2	2	2	0.3409
P50617	Dendrin OS=Rattus norvegicus GN=Ddn PE=1 SV=3 - [DEND_RAT]	7.21	1	2	2	2	0.3409
P26051	CD44 antigen OS=Rattus norvegicus GN=Cd44 PE=1 SV=2 - [CD44_RAT]	4.97	1	2	2	3	0.3409
P13596	Neural cell adhesion molecule 1 OS=Rattus norvegicus GN=Ncam1 PE=1 SV=1 - [NCAM1_RAT]	4.08	1	2	3	3	0.3409
Q9R1J8	Prolyl 3-hydroxylase 1 OS=Rattus norvegicus GN=P3h1 PE=1 SV=1 - [P3H1_RAT]	3.02	1	2	2	2	0.3409
P13941	Collagen alpha-1(III) chain OS=Rattus norvegicus GN=Col3a1 PE=2 SV=3 - [CO3A1_RAT]	2.19	1	3	3	3	0.3409
P50475	Alanine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Aars PE=1 SV=3 - [SYAC_RAT]	8.57	1	5	5	20	0.3417
P16391	RT1 class I histocompatibility antigen, AA alpha chain OS=Rattus norvegicus PE=1 SV=2 - [HA12_RAT]	8.63	1	3	3	22	0.3430
P11442	Clathrin heavy chain 1 OS=Rattus norvegicus GN=Cltc PE=1 SV=3 - [CLH1_RAT]	55.82	1	70	70	1033	0.3451
P30427	Plectin OS=Rattus norvegicus GN=Plec PE=1 SV=2 - [PLEC_RAT]	25.28	1	87	90	281	0.3467
P20171	GTPase HRas OS=Rattus norvegicus GN=Hras PE=1 SV=2 - [RASH_RAT]	20.11	2	3	3	14	0.3514
Q62667	Major vault protein OS=Rattus norvegicus GN=Mvp PE=1 SV=4 - [MVP_RAT]	27.99	1	17	18	53	0.3524
O35264	Platelet-activating factor acetylhydrolase IB subunit beta OS=Rattus norvegicus GN=Pafah1b2 PE=1 SV=1	12.23	1	2	2	25	0.3532

	- [PA1B2_RAT]						
P17074	40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3 - [RS19_RAT]	44.14	1	7	7	85	0.3541
P47727	Carbonyl reductase [NADPH] 1 OS=Rattus norvegicus GN=Cbr1 PE=1 SV=2 - [CBR1_RAT]	76.17	1	19	19	1192	0.3543
P49134	Integrin beta-1 OS=Rattus norvegicus GN=Itgb1 PE=2 SV=1 - [ITB1_RAT]	26.66	1	15	16	219	0.3550
B0LPN4	Ryanodine receptor 2 OS=Rattus norvegicus GN=Ryr2 PE=1 SV=2 - [RYR2_RAT]	1.03	1	3	3	3	0.3562
Q9Z0U5	Aldehyde oxidase 1 OS=Rattus norvegicus GN=Aox1 PE=1 SV=1 - [AOXA_RAT]	2.40	1	2	2	3	0.3576
P04785	Protein disulfide-isomerase OS=Rattus norvegicus GN=P4hb PE=1 SV=2 - [PDIA1_RAT]	58.55	1	22	23	569	0.3588
P49242	40S ribosomal protein S3a OS=Rattus norvegicus GN=Rps3a PE=1 SV=2 - [RS3A_RAT]	22.73	1	5	5	10	0.3592
P29314	40S ribosomal protein S9 OS=Rattus norvegicus GN=Rps9 PE=1 SV=4 - [RS9_RAT]	22.16	1	5	6	24	0.3601
Q9Z1H9	Protein kinase C delta-binding protein OS=Rattus norvegicus GN=Prkcdbp PE=1 SV=1 - [PRDBP_RAT]	41.83	1	11	11	88	0.3604
P36370	Antigen peptide transporter 1 OS=Rattus norvegicus GN=Tap1 PE=1 SV=2 - [TAP1_RAT]	3.17	1	2	2	2	0.3610
P85970	Actin-related protein 2/3 complex subunit 2 OS=Rattus norvegicus GN=Arpc2 PE=1 SV=1 - [ARPC2_RAT]	46.00	1	11	11	21	0.3637
P13221	Aspartate aminotransferase, cytoplasmic OS=Rattus norvegicus GN=Got1 PE=1 SV=3 - [AATC_RAT]	8.72	1	3	3	5	0.3660
P14841	Cystatin-C OS=Rattus norvegicus GN=Cst3 PE=1 SV=2 - [CYTC_RAT]	20.00	1	2	2	29	0.3660
P84245	Histone H3.3 OS=Rattus norvegicus GN=H3f3b PE=1 SV=2 - [H33_RAT]	22.06	2	4	4	13	0.3670
P62902	60S ribosomal protein L31 OS=Rattus norvegicus GN=Rpl31 PE=2 SV=1 - [RL31_RAT]	18.40	1	2	2	19	0.3670
Q499R0	Zinc finger protein 518A OS=Rattus norvegicus GN=Znf518a PE=2 SV=1 - [Z518A_RAT]	2.91	1	3	3	4	0.3677
Q6IG02	Keratin, type II cytoskeletal 2 epidermal OS=Rattus norvegicus GN=Krt2 PE=3 SV=1 - [K22E_RAT]	4.67	1	2	4	4	0.3707
P41542	General vesicular transport factor p115 OS=Rattus norvegicus GN=Uso1 PE=1 SV=1 - [USO1_RAT]	9.07	1	6	7	31	0.3715
O55171	Acyl-coenzyme A thioesterase 2, mitochondrial OS=Rattus norvegicus GN=Acot2 PE=1 SV=1 - [ACOT2_RAT]	3.97	1	2	2	2	0.3716
P48199	C-reactive protein OS=Rattus norvegicus GN=Crp PE=1 SV=1 - [CRP_RAT]	32.61	1	5	5	185	0.3730
P24050	40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=1 SV=3 - [RS5_RAT]	24.02	1	4	4	5	0.3733
P81155	Voltage-dependent anion-selective channel protein 2 OS=Rattus norvegicus GN=Vdac2 PE=1 SV=2 - [VDAC2_RAT]	21.36	1	4	5	48	0.3760
Q66H12	Alpha-N-acetylgalactosaminidase OS=Rattus norvegicus GN=Naga PE=2 SV=1 - [NAGAB_RAT]	9.40	1	3	3	5	0.3764
P63029	Translationally-controlled tumor protein OS=Rattus norvegicus GN=Tpt1 PE=1 SV=1 - [TCTP_RAT]	36.05	1	5	5	80	0.3764
Q3KR86	MICOS complex subunit Mic60 (Fragment) OS=Rattus norvegicus GN=Immt PE=1 SV=1 - [MIC60_RAT]	21.84	1	9	10	28	0.3779
P18422	Proteasome subunit alpha type-3 OS=Rattus norvegicus GN=Psma3 PE=1 SV=3 - [PSA3_RAT]	14.12	1	3	3	26	0.3783
Q08163	Adenylyl cyclase-associated protein 1 OS=Rattus norvegicus GN=Cap1 PE=1 SV=3 - [CAP1_RAT]	28.06	1	7	8	213	0.3783
P26376	Interferon-induced transmembrane protein 3 OS=Rattus norvegicus GN=ifitm3 PE=2 SV=1 - [IFM3_RAT]	20.44	1	2	2	20	0.3800
P63322	Ras-related protein Ral-A OS=Rattus norvegicus GN=Rala PE=1 SV=1 - [RALA_RAT]	17.48	1	3	3	15	0.3801
P19944	60S acidic ribosomal protein P1 OS=Rattus norvegicus GN=Rplp1 PE=3 SV=1 - [RLA1_RAT]	51.75	1	2	2	48	0.3818
P02651	Apolipoprotein A-IV OS=Rattus norvegicus GN=Apoa4 PE=1 SV=2 - [APOA4_RAT]	67.26	1	20	20	175	0.3835
P30713	Glutathione S-transferase theta-2 OS=Rattus norvegicus GN=Gstt2 PE=1 SV=3 - [GSTT2_RAT]	18.85	1	3	4	6	0.3845
P01015	Angiotensinogen OS=Rattus norvegicus GN=Agt PE=1	22.85	1	5	6	33	0.3899

	SV=1 - [ANGT_RAT]						
P38659	Protein disulfide-isomerase A4 OS=Rattus norvegicus GN=Pdia4 PE=1 SV=2 - [PDIA4_RAT]	30.79	1	17	17	87	0.3902
P13471	40S ribosomal protein S14 OS=Rattus norvegicus GN=Rps14 PE=2 SV=3 - [RS14_RAT]	29.80	1	3	3	65	0.3906
Q62638	Golgi apparatus protein 1 OS=Rattus norvegicus GN=Glg1 PE=1 SV=1 - [GSLG1_RAT]	7.51	1	5	5	14	0.3915
P62890	60S ribosomal protein L30 OS=Rattus norvegicus GN=Rpl30 PE=3 SV=2 - [RL30_RAT]	40.87	1	4	4	28	0.3916
Q3MIE4	Synaptic vesicle membrane protein VAT-1 homolog OS=Rattus norvegicus GN=Vat1 PE=1 SV=1 - [VAT1_RAT]	46.78	1	12	12	126	0.3934
P09495	Tropomyosin alpha-4 chain OS=Rattus norvegicus GN=Tpm4 PE=1 SV=3 - [TPM4_RAT]	54.84	1	8	15	170	0.3942
P20762	Ig gamma-2C chain C region OS=Rattus norvegicus PE=2 SV=1 - [IGG2C_RAT]	23.10	1	5	5	29	0.3947
Q63862	Myosin-11 (Fragments) OS=Rattus norvegicus GN=Myh11 PE=1 SV=3 - [MYH11_RAT]	23.21	1	13	23	254	0.3968
Q9QX79	Fetuin-B OS=Rattus norvegicus GN=Fetub PE=2 SV=2 - [FETUB_RAT]	62.17	1	17	17	407	0.3991
P07872	Peroxisomal acyl-coenzyme A oxidase 1 OS=Rattus norvegicus GN=Acox1 PE=1 SV=1 - [ACOX1_RAT]	21.63	1	8	9	16	0.4004
Q811M5	Complement component C6 OS=Rattus norvegicus GN=C6 PE=2 SV=1 - [CO6_RAT]	29.55	1	20	20	99	0.4019
P54921	Alpha-soluble NSF attachment protein OS=Rattus norvegicus GN=Napa PE=1 SV=2 - [SNAA_RAT]	16.95	1	4	4	7	0.4088
Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	1.76	1	2	2	2	0.4092
Q66X93	Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus GN=Snd1 PE=1 SV=1 - [SND1_RAT]	28.49	1	17	18	57	0.4095
Q9Z270	Vesicle-associated membrane protein-associated protein A OS=Rattus norvegicus GN=Vapa PE=1 SV=3 - [VAPA_RAT]	28.92	1	7	7	47	0.4110
P16975	SPARC OS=Rattus norvegicus GN=Sparc PE=1 SV=4 - [SPRC_RAT]	11.63	1	3	3	5	0.4125
Q811A3	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Rattus norvegicus GN=Plod2 PE=2 SV=1 - [PLOD2_RAT]	22.66	1	12	13	48	0.4138
P28073	Proteasome subunit beta type-6 OS=Rattus norvegicus GN=Psmb6 PE=1 SV=3 - [PSB6_RAT]	29.41	1	4	4	40	0.4146
Q6AY20	Cation-dependent mannose-6-phosphate receptor OS=Rattus norvegicus GN=M6pr PE=1 SV=1 - [MPRD_RAT]	19.78	1	4	4	7	0.4154
P27881	Hexokinase-2 OS=Rattus norvegicus GN=Hk2 PE=1 SV=1 - [HXK2_RAT]	5.67	1	3	4	8	0.4175
Q9JLZ1	Glutaredoxin-3 OS=Rattus norvegicus GN=Glrx3 PE=1 SV=2 - [GLRX3_RAT]	14.54	1	4	4	6	0.4221
P19511	ATP synthase F(0) complex subunit B1, mitochondrial OS=Rattus norvegicus GN=Atp5f1 PE=1 SV=1 - [AT5F1_RAT]	27.34	1	7	8	127	0.4247
Q7TPJ0	Translocon-associated protein subunit alpha OS=Rattus norvegicus GN=Ssr1 PE=1 SV=1 - [SSRA_RAT]	8.15	1	2	2	2	0.4282
O35331	Pyridoxal kinase OS=Rattus norvegicus GN=Pdxk PE=1 SV=1 - [PDXK_RAT]	5.13	1	2	2	2	0.4285
Q5U211	Sorting nexin-3 OS=Rattus norvegicus GN=Snx3 PE=1 SV=1 - [SNX3_RAT]	36.42	1	6	6	22	0.4312
P63255	Cysteine-rich protein 1 OS=Rattus norvegicus GN=Crip1 PE=1 SV=2 - [CRIP1_RAT]	71.43	1	4	4	13	0.4313
Q9Z339	Glutathione S-transferase omega-1 OS=Rattus norvegicus GN=Gsto1 PE=1 SV=2 - [GSTO1_RAT]	39.00	1	5	5	41	0.4329
P06761	78 kDa glucose-regulated protein OS=Rattus norvegicus GN=Hspa5 PE=1 SV=1 - [GRP78_RAT]	48.93	1	27	29	858	0.4352
P62775	Myotrophin OS=Rattus norvegicus GN=Mtpn PE=1 SV=2 - [MTPN_RAT]	25.42	1	2	2	17	0.4362
P07483	Fatty acid-binding protein, heart OS=Rattus norvegicus GN=Fabp3 PE=1 SV=2 - [FABPH_RAT]	27.82	1	3	3	3	0.4367
P62260	14-3-3 protein epsilon OS=Rattus norvegicus	76.08	1	20	23	463	0.4371

	GN=Ywhae PE=1 SV=1 - [1433E_RAT]						
Q66H80	Coatomer subunit delta OS=Rattus norvegicus GN=Arcn1 PE=2 SV=1 - [COPD_RAT]	11.94	1	4	4	30	0.4374
Q9R1Z0	Voltage-dependent anion-selective channel protein 3 OS=Rattus norvegicus GN=Vdac3 PE=1 SV=2 - [VDAC3_RAT]	8.13	1	1	2	32	0.4380
Q6PCT3	Tumor protein D54 OS=Rattus norvegicus GN=Tpd52l2 PE=1 SV=1 - [TPD54_RAT]	20.91	1	3	3	6	0.4383
P05426	60S ribosomal protein L7 OS=Rattus norvegicus GN=Rpl7 PE=1 SV=2 - [RL7_RAT]	24.62	1	5	5	32	0.4384
B2GUZ5	F-actin-capping protein subunit alpha-1 OS=Rattus norvegicus GN=Capza1 PE=1 SV=1 - [CAZA1_RAT]	25.87	1	4	5	37	0.4400
P63102	14-3-3 protein zeta/delta OS=Rattus norvegicus GN=Ywhaz PE=1 SV=1 - [1433Z_RAT]	72.24	1	13	18	584	0.4404
P34064	Proteasome subunit alpha type-5 OS=Rattus norvegicus GN=Psma5 PE=1 SV=1 - [PSA5_RAT]	18.26	1	4	4	8	0.4408
Q9EST6	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Rattus norvegicus GN=Anp32b PE=1 SV=1 - [AN32B_RAT]	18.75	1	3	5	23	0.4409
Q6AYD3	Proliferation-associated protein 2G4 OS=Rattus norvegicus GN=Pa2g4 PE=1 SV=1 - [PA2G4_RAT]	10.91	1	3	4	18	0.4427
P21670	Proteasome subunit alpha type-4 OS=Rattus norvegicus GN=Psma4 PE=1 SV=1 - [PSA4_RAT]	36.78	1	5	5	44	0.4445
P22734	Catechol O-methyltransferase OS=Rattus norvegicus GN=Comt PE=1 SV=2 - [COMT_RAT]	37.50	1	5	5	8	0.4472
P32038	Complement factor D OS=Rattus norvegicus GN=Cfd PE=1 SV=2 - [CFAD_RAT]	51.33	1	7	7	58	0.4474
P12001	60S ribosomal protein L18 OS=Rattus norvegicus GN=Rpl18 PE=1 SV=2 - [RL18_RAT]	32.45	1	5	5	64	0.4484
Q6IRK9	Carboxypeptidase Q OS=Rattus norvegicus GN=Cpq PE=1 SV=1 - [CBPQ_RAT]	34.96	1	10	10	51	0.4497
A7VJC2	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1 - [ROA2_RAT]	37.11	1	10	11	150	0.4523
Q6NYB7	Ras-related protein Rab-1A OS=Rattus norvegicus GN=Rab1A PE=1 SV=3 - [RAB1A_RAT]	56.10	1	4	8	244	0.4534
Q63028	Alpha-adducin OS=Rattus norvegicus GN=Add1 PE=1 SV=2 - [ADDA_RAT]	16.05	1	6	7	11	0.4546
P61805	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Rattus norvegicus GN=Dad1 PE=3 SV=3 - [DAD1_RAT]	26.55	1	3	3	11	0.4557
P28023	Dynactin subunit 1 OS=Rattus norvegicus GN=Dctn1 PE=1 SV=2 - [DCTN1_RAT]	6.33	1	5	5	22	0.4586
Q6AY09	Heterogeneous nuclear ribonucleoprotein H2 OS=Rattus norvegicus GN=Hnrnph2 PE=1 SV=1 - [HNRH2_RAT]	9.58	1	2	3	12	0.4636
Q4KM35	Proteasome subunit beta type-10 OS=Rattus norvegicus GN=Psmb10 PE=2 SV=1 - [PSB10_RAT]	12.45	1	2	2	4	0.4651
Q68FP1	Gelsolin OS=Rattus norvegicus GN=Gsn PE=1 SV=1 - [GELS_RAT]	45.26	1	21	21	435	0.4667
P29315	Ribonuclease inhibitor OS=Rattus norvegicus GN=Rnh1 PE=1 SV=2 - [RINI_RAT]	26.75	1	8	8	37	0.4693
Q7TP52	Carboxymethylenebutenolidase homolog OS=Rattus norvegicus GN=Cmbl PE=2 SV=1 - [CMBL_RAT]	22.45	1	5	5	15	0.4712
Q63041	Alpha-1-macroglobulin OS=Rattus norvegicus GN=A1m PE=1 SV=1 - [A1M_RAT]	59.13	1	60	61	1936	0.4732
O35303	Dynamin-1-like protein OS=Rattus norvegicus GN=Dnm1l PE=1 SV=1 - [DNM1L_RAT]	8.61	1	3	3	7	0.4754
A0JPJ7	Obg-like ATPase 1 OS=Rattus norvegicus GN=Ola1 PE=2 SV=1 - [OLA1_RAT]	17.42	1	4	4	34	0.4792
P12346	Serotransferrin OS=Rattus norvegicus GN=Tf PE=1 SV=3 - [TRFE_RAT]	73.21	1	44	44	5571	0.4811
P00173	Cytochrome b5 OS=Rattus norvegicus GN=Cyb5a PE=1 SV=2 - [CYB5_RAT]	41.04	1	4	4	62	0.4829
D3ZW55	Inosine triphosphate pyrophosphatase OS=Rattus norvegicus GN=Itpa PE=3 SV=1 - [ITPA_RAT]	16.67	1	2	2	3	0.4848
P13437	3-ketoacyl-CoA thiolase, mitochondrial OS=Rattus norvegicus GN=Acaa2 PE=2 SV=1 - [THIM_RAT]	59.45	1	16	16	349	0.4852

P10252	CD48 antigen OS=Rattus norvegicus GN=Cd48 PE=1 SV=1 - [CD48_RAT]	12.50	1	2	2	2	0.4865
P61107	Ras-related protein Rab-14 OS=Rattus norvegicus GN=Rab14 PE=1 SV=3 - [RAB14_RAT]	59.07	1	7	9	64	0.4927
Q5I0D7	Xaa-Pro dipeptidase OS=Rattus norvegicus GN=Pepd PE=2 SV=1 - [PEPD_RAT]	12.20	1	5	5	79	0.4962
Q9JLA3	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Rattus norvegicus GN=Uggt1 PE=1 SV=2 - [UGGG1_RAT]	25.79	1	25	26	136	0.4998
P02454	Collagen alpha-1(I) chain OS=Rattus norvegicus GN=Col1a1 PE=1 SV=5 - [CO1A1_RAT]	5.02	1	5	5	29	0.5025
Q9QWN8	Spectrin beta chain, non-erythrocytic 2 OS=Rattus norvegicus GN=Sptbn2 PE=1 SV=2 - [SPTN2_RAT]	5.28	1	8	9	34	0.5046
P24942	Excitatory amino acid transporter 1 OS=Rattus norvegicus GN=Slc1a3 PE=1 SV=2 - [EAA1_RAT]	7.18	1	2	2	12	0.5058
P08699	Galectin-3 OS=Rattus norvegicus GN=Lgals3 PE=1 SV=4 - [LEG3_RAT]	18.70	1	4	4	13	0.5068
B3DMA2	Acyl-CoA dehydrogenase family member 11 OS=Rattus norvegicus GN=Acad11 PE=1 SV=1 - [ACD11_RAT]	10.27	1	6	6	18	0.5071
Q64240	Protein AMBP OS=Rattus norvegicus GN=Ambp PE=1 SV=1 - [AMBP_RAT]	12.61	1	3	3	42	0.5085
P20650	Protein phosphatase 1A OS=Rattus norvegicus GN=Ppm1a PE=1 SV=1 - [PPM1A_RAT]	5.50	2	2	2	2	0.5114
P24090	Alpha-2-HS-glycoprotein OS=Rattus norvegicus GN=Ahsg PE=1 SV=2 - [FETUA_RAT]	43.47	1	8	9	453	0.5131
Q68FR6	Elongation factor 1-gamma OS=Rattus norvegicus GN=Eef1g PE=2 SV=3 - [EF1G_RAT]	36.38	1	8	9	79	0.5196
P23680	Serum amyloid P-component OS=Rattus norvegicus GN=Apcs PE=2 SV=2 - [SAMP_RAT]	14.04	1	2	2	4	0.5208
O35952	Hydroxyacylglutathione hydrolase, mitochondrial OS=Rattus norvegicus GN=Hagh PE=1 SV=2 - [GLO2_RAT]	16.50	1	3	3	6	0.5214
P10536	Ras-related protein Rab-1B OS=Rattus norvegicus GN=Rab1b PE=1 SV=1 - [RAB1B_RAT]	48.26	1	3	7	232	0.5216
P00762	Anionic trypsin-1 OS=Rattus norvegicus GN=Prss1 PE=1 SV=1 - [TRY1_RAT]	14.23	1	2	2	102	0.5230
Q794F9	4F2 cell-surface antigen heavy chain OS=Rattus norvegicus GN=Slc3a2 PE=1 SV=1 - [4F2_RAT]	18.03	1	6	6	11	0.5239
O08619	Coagulation factor XIII A chain OS=Rattus norvegicus GN=F13a1 PE=2 SV=3 - [F13A_RAT]	20.77	1	11	11	161	0.5254
P02793	Ferritin light chain 1 OS=Rattus norvegicus GN=Ftl1 PE=1 SV=3 - [FRIL1_RAT]	69.95	1	11	11	379	0.5286
Q794E4	Heterogeneous nuclear ribonucleoprotein F OS=Rattus norvegicus GN=Hnrnpf PE=1 SV=3 - [HNRPF_RAT]	10.36	1	2	3	31	0.5291
P10959	Carboxylesterase 1C OS=Rattus norvegicus GN=Ces1c PE=1 SV=3 - [EST1C_RAT]	16.58	1	7	7	16	0.5338
Q4AEF8	Coatomer subunit gamma-1 OS=Rattus norvegicus GN=Copg1 PE=2 SV=1 - [COPG1_RAT]	24.60	1	12	13	66	0.5342
P29975	Aquaporin-1 OS=Rattus norvegicus GN=Aqp1 PE=1 SV=4 - [AQP1_RAT]	26.77	1	4	4	10	0.5371
O88656	Actin-related protein 2/3 complex subunit 1B OS=Rattus norvegicus GN=Arpc1b PE=1 SV=3 - [ARC1B_RAT]	11.02	1	3	3	18	0.5375
P09527	Ras-related protein Rab-7a OS=Rattus norvegicus GN=Rab7a PE=1 SV=2 - [RAB7A_RAT]	57.49	1	9	9	137	0.5380
Q63525	Nuclear migration protein nudC OS=Rattus norvegicus GN=Nudc PE=1 SV=1 - [NUDC_RAT]	6.02	1	2	2	4	0.5391
P36953	Afamin OS=Rattus norvegicus GN=Afm PE=3 SV=1 - [AFAM_RAT]	34.70	1	15	15	71	0.5407
P01041	Cystatin-B OS=Rattus norvegicus GN=Cstb PE=1 SV=1 - [CYTB_RAT]	34.69	1	3	3	20	0.5422
P24368	Peptidyl-prolyl cis-trans isomerase B OS=Rattus norvegicus GN=Ppib PE=1 SV=3 - [PPIB_RAT]	51.39	1	12	12	212	0.5429
B2RZ78	Vacuolar protein sorting-associated protein 29 OS=Rattus norvegicus GN=Vps29 PE=1 SV=2 - [VPS29_RAT]	17.58	1	3	3	9	0.5433
P31000	Vimentin OS=Rattus norvegicus GN=Vim PE=1 SV=2	78.97	1	37	41	2177	0.5509

	- [VIME_RAT]						
P53987	Monocarboxylate transporter 1 OS=Rattus norvegicus GN=Slc16a1 PE=1 SV=1 - [MOT1_RAT]	18.02	1	4	5	87	0.5513
Q66H89	Centrosomal protein of 83 kDa OS=Rattus norvegicus GN=Cep83 PE=2 SV=1 - [CEP83_RAT]	4.77	1	3	3	4	0.5535
P05708	Hexokinase-1 OS=Rattus norvegicus GN=Hk1 PE=1 SV=4 - [HXK1_RAT]	9.37	1	6	7	64	0.5563
P62944	AP-2 complex subunit beta OS=Rattus norvegicus GN=Ap2b1 PE=1 SV=1 - [AP2B1_RAT]	26.15	1	9	16	235	0.5565
P22985	Xanthine dehydrogenase/oxidase OS=Rattus norvegicus GN=Xdh PE=1 SV=3 - [XDH_RAT]	38.24	1	31	31	831	0.5615
P23965	Enoyl-CoA delta isomerase 1, mitochondrial OS=Rattus norvegicus GN=Eci1 PE=1 SV=1 - [ECI1_RAT]	42.91	1	9	9	158	0.5621
Q62930	Complement component C9 OS=Rattus norvegicus GN=C9 PE=2 SV=1 - [CO9_RAT]	55.78	1	23	23	142	0.5632
P29419	ATP synthase subunit e, mitochondrial OS=Rattus norvegicus GN=Atp5i PE=1 SV=3 - [ATP5I_RAT]	45.07	1	3	3	33	0.5665
Q6REY9	Rho GTPase-activating protein 20 OS=Rattus norvegicus GN=Arhgap20 PE=1 SV=2 - [RHG20_RAT]	3.30	1	2	2	3	0.5691
A2RRU1	Glycogen [starch] synthase, muscle OS=Rattus norvegicus GN=Gys1 PE=1 SV=1 - [GYS1_RAT]	5.96	1	2	2	2	0.5700
P40112	Proteasome subunit beta type-3 OS=Rattus norvegicus GN=Psmb3 PE=1 SV=1 - [PSB3_RAT]	26.83	1	4	4	58	0.5705
Q5EB77	Ras-related protein Rab-18 OS=Rattus norvegicus GN=Rab18 PE=2 SV=1 - [RAB18_RAT]	46.12	1	7	7	58	0.5715
P97697	Inositol monophosphatase 1 OS=Rattus norvegicus GN=Impa1 PE=1 SV=2 - [IMPA1_RAT]	7.58	1	2	2	2	0.5725
P52504	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Rattus norvegicus GN=Ndufs6 PE=3 SV=1 - [NDUS6_RAT]	21.55	1	2	2	2	0.5767
Q5FVI6	V-type proton ATPase subunit C 1 OS=Rattus norvegicus GN=Atp6v1c1 PE=2 SV=1 - [VATC1_RAT]	8.90	1	2	2	2	0.5794
Q63416	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Rattus norvegicus GN=Itih3 PE=2 SV=1 - [ITIH3_RAT]	31.34	1	17	18	337	0.5799
P81128	Rho GTPase-activating protein 35 OS=Rattus norvegicus GN=Arhgap35 PE=1 SV=2 - [RHG35_RAT]	2.38	1	2	2	2	0.5824
A1L1L2	Transmembrane protein 214 OS=Rattus norvegicus GN=Tmem214 PE=2 SV=1 - [TM214_RAT]	2.77	1	2	2	3	0.5825
P63095	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Rattus norvegicus GN=Gnas PE=1 SV=1 - [GNAS2_RAT]	29.44	2	7	8	117	0.5849
P29994	Inositol 1,4,5-trisphosphate receptor type 1 OS=Rattus norvegicus GN=Itpr1 PE=1 SV=2 - [ITPR1_RAT]	1.02	1	2	2	4	0.5916
Q9WVB1	Ras-related protein Rab-6A OS=Rattus norvegicus GN=Rab6a PE=1 SV=2 - [RAB6A_RAT]	27.40	1	4	5	30	0.5932
P70615	Lamin-B1 OS=Rattus norvegicus GN=Lmnb1 PE=1 SV=3 - [LMNB1_RAT]	16.52	1	5	8	24	0.5950
P61959	Small ubiquitin-related modifier 2 OS=Rattus norvegicus GN=Sumo2 PE=1 SV=1 - [SUMO2_RAT]	23.16	1	2	2	4	0.5995
O55012	Phosphatidylinositol-binding clathrin assembly protein OS=Rattus norvegicus GN=Picalm PE=1 SV=1 - [PICAL_RAT]	9.53	1	3	4	20	0.6035
P41123	60S ribosomal protein L13 OS=Rattus norvegicus GN=Rpl13 PE=1 SV=2 - [RL13_RAT]	15.64	1	3	3	33	0.6045
Q63270	Cytoplasmic aconitate hydratase OS=Rattus norvegicus GN=Aco1 PE=1 SV=1 - [ACOC_RAT]	40.94	1	25	25	515	0.6051
P68035	Actin, alpha cardiac muscle 1 OS=Rattus norvegicus GN=Actc1 PE=2 SV=1 - [ACTC_RAT]	83.82	2	10	23	3451	0.6058
P02696	Retinol-binding protein 1 OS=Rattus norvegicus GN=Rbp1 PE=1 SV=2 - [RET1_RAT]	17.78	1	2	2	2	0.6068
D3ZHA0	Filamin-C OS=Rattus norvegicus GN=Flnc PE=1 SV=1 - [FLNC_RAT]	6.49	1	10	13	87	0.6108
P11980	Pyruvate kinase PKM OS=Rattus norvegicus GN=Pkm PE=1 SV=3 - [KPYM_RAT]	54.24	1	25	25	695	0.6124
P15650	Long-chain specific acyl-CoA dehydrogenase,	29.77	1	11	11	73	0.6133

	mitochondrial OS=Rattus norvegicus GN=Acadl PE=1 SV=1 - [ACADL_RAT]						
P08503	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acadm PE=1 SV=1 - [ACADM_RAT]	19.48	1	5	5	43	0.6180
Q5RKI1	Eukaryotic initiation factor 4A-II OS=Rattus norvegicus GN=Eif4a2 PE=1 SV=1 - [IF4A2_RAT]	26.29	1	9	9	124	0.6183
P62853	40S ribosomal protein S25 OS=Rattus norvegicus GN=Rps25 PE=2 SV=1 - [RS25_RAT]	16.00	1	3	3	5	0.6191
P07151	Beta-2-microglobulin OS=Rattus norvegicus GN=B2m PE=1 SV=1 - [B2MG_RAT]	34.45	1	6	6	43	0.6297
P47853	Biglycan OS=Rattus norvegicus GN=Bgn PE=2 SV=1 - [PGS1_RAT]	52.57	1	13	15	284	0.6300
Q66HD0	Endoplasmin OS=Rattus norvegicus GN=Hsp90b1 PE=1 SV=2 - [ENPL_RAT]	53.86	1	35	37	747	0.6352
P62828	GTP-binding nuclear protein Ran OS=Rattus norvegicus GN=Ran PE=1 SV=3 - [RAN_RAT]	31.02	2	6	6	54	0.6360
P09606	Glutamine synthetase OS=Rattus norvegicus GN=Glul PE=1 SV=3 - [GLNA_RAT]	34.85	1	11	11	196	0.6403
O35509	Ras-related protein Rab-11B OS=Rattus norvegicus GN=Rab11b PE=1 SV=4 - [RB11B_RAT]	45.41	1	9	9	82	0.6407
F1LMZ8	26S proteasome non-ATPase regulatory subunit 11 OS=Rattus norvegicus GN=Psmd11 PE=1 SV=2 - [PSD11_RAT]	9.00	1	3	3	5	0.6420
P07895	Superoxide dismutase [Mn], mitochondrial OS=Rattus norvegicus GN=Sod2 PE=1 SV=2 - [SODM_RAT]	27.03	1	5	5	65	0.6446
P31211	Corticosteroid-binding globulin OS=Rattus norvegicus GN=Serpina6 PE=1 SV=2 - [CBG_RAT]	26.01	1	7	7	31	0.6455
P35704	Peroxiredoxin-2 OS=Rattus norvegicus GN=Prdx2 PE=1 SV=3 - [PRDX2_RAT]	57.07	1	8	8	387	0.6469
Q63210	Guanine nucleotide-binding protein subunit alpha-12 OS=Rattus norvegicus GN=Gna12 PE=1 SV=3 - [GNA12_RAT]	11.61	1	2	3	11	0.6485
Q6VBQ5	Myeloid-associated differentiation marker OS=Rattus norvegicus GN=Myadm PE=1 SV=1 - [MYADM_RAT]	21.70	1	4	4	52	0.6491
Q07984	Translocon-associated protein subunit delta OS=Rattus norvegicus GN=Ssr4 PE=2 SV=1 - [SSRD_RAT]	30.64	1	4	4	9	0.6493
Q4V7C7	Actin-related protein 3 OS=Rattus norvegicus GN=Actr3 PE=1 SV=1 - [ARP3_RAT]	56.94	1	14	14	97	0.6518
Q99MZ8	LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1 - [LASP1_RAT]	8.37	1	2	3	3	0.6526
Q7TMA5	Apolipoprotein B-100 OS=Rattus norvegicus GN=Apob PE=1 SV=1 - [APOB_RAT]	0.82	1	2	3	3	0.6529
Q63570	26S protease regulatory subunit 6B OS=Rattus norvegicus GN=Psmc4 PE=1 SV=1 - [PRS6B_RAT]	22.73	1	4	4	50	0.6530
Q5SGE0	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=1 SV=1 - [LPPRC_RAT]	16.74	1	13	14	66	0.6549
P0C0S7	Histone H2A.Z OS=Rattus norvegicus GN=H2afz PE=1 SV=2 - [H2AZ_RAT]	31.25	1	2	4	82	0.6586
Q5EB81	NADH-cytochrome b5 reductase 1 OS=Rattus norvegicus GN=Cyb5r1 PE=2 SV=1 - [NB5R1_RAT]	9.84	1	3	3	5	0.6596
Q6RJR6	Reticulon-3 OS=Rattus norvegicus GN=Rtn3 PE=1 SV=1 - [RTN3_RAT]	3.51	1	2	3	44	0.6619
Q6IFW6	Keratin, type I cytoskeletal 10 OS=Rattus norvegicus GN=Krt10 PE=3 SV=1 - [K1C10_RAT]	6.65	1	3	4	8	0.6674
Q4KLF8	Actin-related protein 2/3 complex subunit 5 OS=Rattus norvegicus GN=Arpc5 PE=1 SV=3 - [ARPC5_RAT]	16.56	1	2	2	11	0.6719
F1LMY4	Ryanodine receptor 1 OS=Rattus norvegicus GN=Ryr1 PE=1 SV=1 - [RYR1_RAT]	0.83	1	2	3	11	0.6799
P27615	Lysosome membrane protein 2 OS=Rattus norvegicus GN=Scarb2 PE=1 SV=2 - [SCRB2_RAT]	7.53	1	2	2	5	0.6802
Q80U96	Exportin-1 OS=Rattus norvegicus GN=Xpo1 PE=1 SV=1 - [XPO1_RAT]	8.12	1	4	5	13	0.6815
Q9WUH4	Four and a half LIM domains protein 1 OS=Rattus norvegicus GN=Fhl1 PE=2 SV=1 - [FHL1_RAT]	25.00	1	6	6	32	0.6816
P62959	Histidine triad nucleotide-binding protein 1 OS=Rattus	37.30	1	3	3	15	0.6834

	norvegicus GN=Hint1 PE=1 SV=5 - [HINT1_RAT]						
P19132	Ferritin heavy chain OS=Rattus norvegicus GN=Fth1 PE=1 SV=3 - [FRIH_RAT]	57.14	1	10	10	144	0.6842
M0RC99	Ras-related protein Rab-5A OS=Rattus norvegicus GN=Rab5a PE=2 SV=1 - [RAB5A_RAT]	14.88	1	3	3	4	0.6863
P05545	Serine protease inhibitor A3K OS=Rattus norvegicus GN=Serpina3k PE=1 SV=3 - [SPA3K_RAT]	61.06	1	16	21	936	0.6905
P19804	Nucleoside diphosphate kinase B OS=Rattus norvegicus GN=Nme2 PE=1 SV=1 - [NDKB_RAT]	75.00	1	4	10	469	0.6910
P62963	Profilin-1 OS=Rattus norvegicus GN=Pfn1 PE=1 SV=2 - [PROF1_RAT]	72.14	1	10	10	533	0.6920
Q9EQX9	Ubiquitin-conjugating enzyme E2 N OS=Rattus norvegicus GN=Ube2n PE=1 SV=1 - [UBE2N_RAT]	42.11	1	5	5	107	0.6937
Q9R1T3	Cathepsin Z OS=Rattus norvegicus GN=Ctsz PE=1 SV=2 - [CATZ_RAT]	18.95	1	4	4	40	0.6961
P07687	Epoxide hydrolase 1 OS=Rattus norvegicus GN=Ephx1 PE=1 SV=1 - [HYEP_RAT]	9.45	1	3	3	7	0.6975
O35854	Branched-chain-amino-acid aminotransferase, mitochondrial OS=Rattus norvegicus GN=Bcat2 PE=1 SV=1 - [BCAT2_RAT]	9.41	1	3	3	7	0.6991
Q7M0E3	Destrin OS=Rattus norvegicus GN=Dstn PE=1 SV=3 - [DEST_RAT]	36.97	1	5	5	155	0.6997
O08590	Membrane primary amine oxidase OS=Rattus norvegicus GN=Aoc3 PE=1 SV=4 - [AOC3_RAT]	40.24	1	22	22	1528	0.7008
Q5M7U6	Actin-related protein 2 OS=Rattus norvegicus GN=Actr2 PE=2 SV=1 - [ARP2_RAT]	21.83	1	7	7	27	0.7009
P27791	cAMP-dependent protein kinase catalytic subunit alpha OS=Rattus norvegicus GN=Prkaca PE=1 SV=2 - [KAPCA_RAT]	7.12	1	2	3	14	0.7027
P62630	Elongation factor 1-alpha 1 OS=Rattus norvegicus GN=Eef1a1 PE=2 SV=1 - [EF1A1_RAT]	56.28	1	21	21	1875	0.7044
P60901	Proteasome subunit alpha type-6 OS=Rattus norvegicus GN=Psma6 PE=1 SV=1 - [PSA6_RAT]	38.62	1	8	8	68	0.7068
Q5XIC0	Enoyl-CoA delta isomerase 2, mitochondrial OS=Rattus norvegicus GN=Eci2 PE=1 SV=1 - [ECI2_RAT]	6.14	1	2	2	4	0.7103
Q04462	Valine--tRNA ligase OS=Rattus norvegicus GN=Vars PE=2 SV=2 - [SYVC_RAT]	12.26	1	8	8	32	0.7103
P30009	Myristoylated alanine-rich C-kinase substrate OS=Rattus norvegicus GN=Marcks PE=1 SV=2 - [MARCS_RAT]	32.04	1	6	6	50	0.7108
Q9WVR7	Protein phosphatase 1F OS=Rattus norvegicus GN=Ppm1f PE=2 SV=1 - [PPM1F_RAT]	11.78	1	2	2	2	0.7124
B0BNA5	Coactosin-like protein OS=Rattus norvegicus GN=Cotl1 PE=1 SV=1 - [COTL1_RAT]	49.30	1	8	8	18	0.7147
P01026	Complement C3 OS=Rattus norvegicus GN=C3 PE=1 SV=3 - [CO3_RAT]	64.94	1	83	86	2415	0.7150
P55161	Nck-associated protein 1 OS=Rattus norvegicus GN=Nckap1 PE=2 SV=1 - [NCKP1_RAT]	1.68	1	1	2	2	0.7162
Q2TL32	E3 ubiquitin-protein ligase UBR4 OS=Rattus norvegicus GN=Ubr4 PE=1 SV=2 - [UBR4_RAT]	1.19	1	4	4	10	0.7193
P49911	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Rattus norvegicus GN=Anp32a PE=2 SV=1 - [AN32A_RAT]	21.05	1	3	5	41	0.7200
Q6URK4	Heterogeneous nuclear ribonucleoprotein A3 OS=Rattus norvegicus GN=Hnrnpa3 PE=1 SV=1 - [ROA3_RAT]	10.29	1	3	3	47	0.7216
P97629	Leucyl-cystinyl aminopeptidase OS=Rattus norvegicus GN=Lnpep PE=1 SV=1 - [LCAP_RAT]	7.80	1	8	8	23	0.7244
Q6DGG0	Peptidyl-prolyl cis-trans isomerase D OS=Rattus norvegicus GN=Ppid PE=1 SV=3 - [PPID_RAT]	14.32	1	3	3	12	0.7271
Q6IMF3	Keratin, type II cytoskeletal 1 OS=Rattus norvegicus GN=Krt1 PE=2 SV=1 - [K2C1_RAT]	5.28	1	4	4	31	0.7293
Q63610	Tropomyosin alpha-3 chain OS=Rattus norvegicus GN=Tpm3 PE=1 SV=2 - [TPM3_RAT]	50.40	1	8	16	179	0.7316
Q9ESS6	Basal cell adhesion molecule OS=Rattus norvegicus GN=Bcam PE=2 SV=1 - [BCAM_RAT]	4.49	1	2	2	5	0.7326
P85834	Elongation factor Tu, mitochondrial OS=Rattus norvegicus GN=Tufm PE=1 SV=1 - [EFTU_RAT]	4.87	1	2	2	4	0.7371

P13084	Nucleophosmin OS=Rattus norvegicus GN=Npm1 PE=1 SV=1 - [NPM_RAT]	25.00	1	5	5	12	0.7372
P70580	Membrane-associated progesterone receptor component 1 OS=Rattus norvegicus GN=Pgrmc1 PE=1 SV=3 - [PGRC1_RAT]	7.69	1	2	2	5	0.7474
Q6P7S1	Acid ceramidase OS=Rattus norvegicus GN=Asah1 PE=2 SV=1 - [ASAH1_RAT]	24.62	1	6	6	26	0.7505
P32755	4-hydroxyphenylpyruvate dioxygenase OS=Rattus norvegicus GN=Hpd PE=1 SV=3 - [HPPD_RAT]	8.65	1	2	2	3	0.7510
Q5I0D1	Glyoxalase domain-containing protein 4 OS=Rattus norvegicus GN=Glod4 PE=1 SV=1 - [GLOD4_RAT]	43.62	1	8	9	35	0.7540
Q2MHH0	Tumor suppressor candidate 5 homolog OS=Rattus norvegicus GN=Tusc5 PE=1 SV=1 - [TUSC5_RAT]	24.86	1	3	3	114	0.7542
P58775	Tropomyosin beta chain OS=Rattus norvegicus GN=Tpm2 PE=1 SV=1 - [TPM2_RAT]	28.52	1	1	9	93	0.7569
Q5I0G4	Glycine--tRNA ligase (Fragment) OS=Rattus norvegicus GN=Gars PE=1 SV=1 - [SYG_RAT]	8.48	1	3	3	6	0.7585
P11762	Galectin-1 OS=Rattus norvegicus GN=Lgals1 PE=1 SV=2 - [LEG1_RAT]	61.48	1	10	10	612	0.7601
Q6AYQ4	Transmembrane protein 109 OS=Rattus norvegicus GN=Tmem109 PE=2 SV=1 - [TM109_RAT]	12.35	1	3	3	4	0.7635
B0BNM1	NAD(P)H-hydrate epimerase OS=Rattus norvegicus GN=Apoa1bp PE=2 SV=1 - [NNRE_RAT]	21.28	1	3	3	12	0.7651
O35795	Ectonucleoside triphosphate diphosphohydrolase 2 OS=Rattus norvegicus GN=Entpd2 PE=1 SV=1 - [ENTP2_RAT]	6.87	1	2	2	5	0.7652
P43884	Perilipin-1 OS=Rattus norvegicus GN=Plin1 PE=1 SV=1 - [PLIN1_RAT]	70.21	1	23	24	1194	0.7652
P27952	40S ribosomal protein S2 OS=Rattus norvegicus GN=Rps2 PE=1 SV=1 - [RS2_RAT]	16.04	1	4	4	33	0.7686
P68255	14-3-3 protein theta OS=Rattus norvegicus GN=Ywhaq PE=1 SV=1 - [1433T_RAT]	72.24	1	14	20	495	0.7698
Q6Q0N1	Cytosolic non-specific dipeptidase OS=Rattus norvegicus GN=Cndp2 PE=1 SV=1 - [CNDP2_RAT]	37.89	1	15	15	130	0.7707
Q921A4	Cytoglobin OS=Rattus norvegicus GN=Cygb PE=1 SV=1 - [CYGB_RAT]	46.84	1	8	8	24	0.7707
P02091	Hemoglobin subunit beta-1 OS=Rattus norvegicus GN=Hbb PE=1 SV=3 - [HBB1_RAT]	89.80	1	4	16	15347	0.7708
P62870	Transcription elongation factor B polypeptide 2 OS=Rattus norvegicus GN=Tceb2 PE=1 SV=1 - [ELOB_RAT]	42.37	1	3	3	6	0.7710
Q63569	26S protease regulatory subunit 6A OS=Rattus norvegicus GN=Psmc3 PE=2 SV=1 - [PRS6A_RAT]	5.92	1	2	2	2	0.7721
Q6B345	Protein S100-A11 OS=Rattus norvegicus GN=S100a11 PE=3 SV=1 - [S10AB_RAT]	46.94	1	4	4	73	0.7729
P35213	14-3-3 protein beta/alpha OS=Rattus norvegicus GN=Ywhab PE=1 SV=3 - [1433B_RAT]	71.54	1	9	16	480	0.7741
P21531	60S ribosomal protein L3 OS=Rattus norvegicus GN=Rpl3 PE=1 SV=3 - [RL3_RAT]	19.11	1	5	5	31	0.7751
P27867	Sorbitol dehydrogenase OS=Rattus norvegicus GN=Sord PE=1 SV=4 - [DHSO_RAT]	9.80	1	2	2	6	0.7758
Q00715	Histone H2B type 1 OS=Rattus norvegicus PE=1 SV=2 - [H2B1_RAT]	39.20	1	5	5	260	0.7769
Q4V8F7	Coiled-coil domain-containing protein 63 OS=Rattus norvegicus GN=Ccdc63 PE=2 SV=1 - [CCD63_RAT]	5.55	1	2	2	2	0.7769
P62703	40S ribosomal protein S4, X isoform OS=Rattus norvegicus GN=Rps4x PE=2 SV=2 - [RS4X_RAT]	31.18	1	7	8	27	0.7769
Q4FZT9	26S proteasome non-ATPase regulatory subunit 2 OS=Rattus norvegicus GN=Psmd2 PE=1 SV=1 - [PSMD2_RAT]	21.15	1	13	13	70	0.7841
Q68FQ0	T-complex protein 1 subunit epsilon OS=Rattus norvegicus GN=Cct5 PE=1 SV=1 - [TCPE_RAT]	7.21	1	2	2	4	0.7846
P04916	Retinol-binding protein 4 OS=Rattus norvegicus GN=Rbp4 PE=1 SV=1 - [RET4_RAT]	23.88	1	4	4	45	0.7857
P70623	Fatty acid-binding protein, adipocyte OS=Rattus norvegicus GN=Fabp4 PE=1 SV=3 - [FABP4_RAT]	74.24	1	13	13	6757	0.7858
Q68FR9	Elongation factor 1-delta OS=Rattus norvegicus GN=Eef1d PE=1 SV=2 - [EF1D_RAT]	21.71	1	4	4	28	0.7862

P05544	Serine protease inhibitor A3L OS=Rattus norvegicus GN=Serpina3l PE=1 SV=3 - [SPA3L_RAT]	60.29	1	15	20	696	0.7870
Q8R4Z9	Mitofusin-1 OS=Rattus norvegicus GN=Mfn1 PE=1 SV=1 - [MFN1_RAT]	3.78	1	2	2	2	0.7921
P43244	Matrin-3 OS=Rattus norvegicus GN=Matr3 PE=1 SV=2 - [MATR3_RAT]	4.62	1	2	2	20	0.7921
P04897	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Rattus norvegicus GN=Gnai2 PE=1 SV=3 - [GNAI2_RAT]	58.87	1	10	16	180	0.7958
Q641Y0	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Rattus norvegicus GN=Ddost PE=2 SV=1 - [OST48_RAT]	25.17	1	7	7	31	0.7970
P10688	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1 OS=Rattus norvegicus GN=Plcd1 PE=1 SV=1 - [PLCD1_RAT]	7.41	1	2	3	6	0.7984
P62804	Histone H4 OS=Rattus norvegicus GN=Hist1h4b PE=1 SV=2 - [H4_RAT]	53.40	1	8	8	273	0.7989
P54311	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Rattus norvegicus GN=Gnb1 PE=1 SV=4 - [GBB1_RAT]	59.41	1	7	14	179	0.8010
Q10758	Keratin, type II cytoskeletal 8 OS=Rattus norvegicus GN=Krt8 PE=1 SV=3 - [K2C8_RAT]	16.56	1	4	9	80	0.8029
Q9R063	Peroxiredoxin-5, mitochondrial OS=Rattus norvegicus GN=Prdx5 PE=1 SV=1 - [PRDX5_RAT]	54.93	1	11	11	263	0.8057
P15999	ATP synthase subunit alpha, mitochondrial OS=Rattus norvegicus GN=Atp5a1 PE=1 SV=2 - [ATPA_RAT]	49.37	1	22	22	1146	0.8090
Q91Y81	Septin-2 OS=Rattus norvegicus GN=Sept2 PE=1 SV=1 - [SEPT2_RAT]	39.89	1	9	9	40	0.8113
D3ZHV2	Microtubule-actin cross-linking factor 1 OS=Rattus norvegicus GN=Macf1 PE=1 SV=1 - [MACF1_RAT]	1.01	1	2	4	5	0.8120
O35828	Coronin-7 OS=Rattus norvegicus GN=Coro7 PE=1 SV=2 - [CORO7_RAT]	11.61	1	4	4	4	0.8196
P83868	Prostaglandin E synthase 3 OS=Rattus norvegicus GN=Ptges3 PE=1 SV=2 - [TEBP_RAT]	32.50	1	4	4	22	0.8240
P52303	AP-1 complex subunit beta-1 OS=Rattus norvegicus GN=Ap1b1 PE=1 SV=1 - [AP1B1_RAT]	25.08	1	4	13	124	0.8244
P69897	Tubulin beta-5 chain OS=Rattus norvegicus GN=Tubb5 PE=1 SV=1 - [TBB5_RAT]	74.10	1	4	26	2253	0.8247
Q01177	Plasminogen OS=Rattus norvegicus GN=Plg PE=2 SV=2 - [PLMN_RAT]	55.42	1	32	32	171	0.8249
Q9JLJ3	4-trimethylaminobutyraldehyde dehydrogenase OS=Rattus norvegicus GN=Aldh9a1 PE=1 SV=1 - [AL9A1_RAT]	53.24	1	13	15	193	0.8287
O54975	Xaa-Pro aminopeptidase 1 OS=Rattus norvegicus GN=Xpnpep1 PE=1 SV=1 - [XPP1_RAT]	11.88	1	3	4	7	0.8288
P85108	Tubulin beta-2A chain OS=Rattus norvegicus GN=Tubb2a PE=1 SV=1 - [TBB2A_RAT]	73.93	2	4	25	2039	0.8295
Q6P9T8	Tubulin beta-4B chain OS=Rattus norvegicus GN=Tubb4b PE=1 SV=1 - [TBB4B_RAT]	68.31	1	3	25	2258	0.8295
P63324	40S ribosomal protein S12 OS=Rattus norvegicus GN=Rps12 PE=1 SV=2 - [RS12_RAT]	22.73	1	3	3	44	0.8298
Q6RUV5	Ras-related C3 botulinum toxin substrate 1 OS=Rattus norvegicus GN=Rac1 PE=1 SV=1 - [RAC1_RAT]	39.58	1	7	8	46	0.8368
P41498	Low molecular weight phosphotyrosine protein phosphatase OS=Rattus norvegicus GN=Acp1 PE=1 SV=3 - [PPAC_RAT]	24.05	1	3	3	16	0.8393
P62198	26S protease regulatory subunit 8 OS=Rattus norvegicus GN=Psmc5 PE=1 SV=1 - [PRS8_RAT]	9.36	1	3	3	8	0.8407
P10824	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Rattus norvegicus GN=Gnai1 PE=1 SV=3 - [GNAI1_RAT]	34.46	1	3	9	105	0.8433
Q2PQA9	Kinesin-1 heavy chain OS=Rattus norvegicus GN=Kif5b PE=1 SV=1 - [KINH_RAT]	3.63	1	2	2	2	0.8444
Q5RKI0	WD repeat-containing protein 1 OS=Rattus norvegicus GN=Wdr1 PE=1 SV=3 - [WDR1_RAT]	9.90	1	5	5	9	0.8474
P38650	Cytoplasmic dynein 1 heavy chain 1 OS=Rattus norvegicus GN=Dync1h1 PE=1 SV=1 - [DYHC1_RAT]	34.15	1	117	120	639	0.8489

Q6GQP4	Ras-related protein Rab-31 OS=Rattus norvegicus GN=Rab31 PE=1 SV=2 - [RAB31_RAT]	18.04	1	3	3	6	0.8489
P04692	Tropomyosin alpha-1 chain OS=Rattus norvegicus GN=Tpm1 PE=1 SV=3 - [TPM1_RAT]	33.10	1	1	11	109	0.8492
Q9ES21	Phosphatidylinositide phosphatase SAC1 OS=Rattus norvegicus GN=Sacm1l PE=1 SV=1 - [SAC1_RAT]	15.84	1	7	7	35	0.8499
Q5U318	Astrocytic phosphoprotein PEA-15 OS=Rattus norvegicus GN=Pea15 PE=1 SV=1 - [PEA15_RAT]	16.15	1	2	2	5	0.8509
Q6UPE1	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Rattus norvegicus GN=Etfdh PE=1 SV=1 - [ETFD_RAT]	3.73	1	2	2	2	0.8536
P68370	Tubulin alpha-1A chain OS=Rattus norvegicus GN=Tuba1a PE=1 SV=1 - [TBA1A_RAT]	66.52	1	2	22	1599	0.8552
Q6P9V9	Tubulin alpha-1B chain OS=Rattus norvegicus GN=Tuba1b PE=1 SV=1 - [TBA1B_RAT]	66.52	1	3	23	1719	0.8552
Q4KM73	UMP-CMP kinase OS=Rattus norvegicus GN=Cmpk1 PE=1 SV=2 - [KCY_RAT]	54.08	1	9	9	41	0.8597
Q62745	CD81 antigen OS=Rattus norvegicus GN=Cd81 PE=1 SV=1 - [CD81_RAT]	15.25	1	2	2	4	0.8616
P62250	40S ribosomal protein S16 OS=Rattus norvegicus GN=Rps16 PE=1 SV=2 - [RS16_RAT]	32.88	1	4	4	45	0.8659
Q03626	Murinoglobulin-1 OS=Rattus norvegicus GN=Mug1 PE=2 SV=1 - [MUG1_RAT]	53.67	1	24	57	2739	0.8662
P14046	Alpha-1-inhibitor 3 OS=Rattus norvegicus GN=A1i3 PE=1 SV=1 - [A1I3_RAT]	52.67	1	24	57	2835	0.8662
P61354	60S ribosomal protein L27 OS=Rattus norvegicus GN=Rpl27 PE=2 SV=2 - [RL27_RAT]	22.06	1	2	2	2	0.8677
Q63556	Serine protease inhibitor A3M (Fragment) OS=Rattus norvegicus GN=Serpina3m PE=2 SV=1 - [SPA3M_RAT]	14.56	1	2	5	30	0.8686
P97852	Peroxisomal multifunctional enzyme type 2 OS=Rattus norvegicus GN=Hsd17b4 PE=1 SV=3 - [DHB4_RAT]	16.87	1	8	10	107	0.8701
P30839	Fatty aldehyde dehydrogenase OS=Rattus norvegicus GN=Aldh3a2 PE=1 SV=1 - [AL3A2_RAT]	14.46	1	5	5	28	0.8707
P34067	Proteasome subunit beta type-4 OS=Rattus norvegicus GN=Psmb4 PE=1 SV=2 - [PSB4_RAT]	29.66	1	5	5	12	0.8721
P14630	Apolipoprotein M OS=Rattus norvegicus GN=Apom PE=1 SV=2 - [APOM_RAT]	13.16	1	2	2	3	0.8745
Q9Z0W7	Chloride intracellular channel protein 4 OS=Rattus norvegicus GN=Clic4 PE=1 SV=3 - [CLIC4_RAT]	34.78	1	6	7	29	0.8755
P30904	Macrophage migration inhibitory factor OS=Rattus norvegicus GN=Mif PE=1 SV=4 - [MIF_RAT]	13.91	1	2	2	3	0.8775
Q9ES40	PRA1 family protein 3 OS=Rattus norvegicus GN=Arl6ip5 PE=1 SV=1 - [PRAF3_RAT]	15.96	1	2	2	4	0.8785
F1MA98	Nucleoprotein TPR OS=Rattus norvegicus GN=Tpr PE=1 SV=1 - [TPR_RAT]	4.07	1	4	5	11	0.8802
P61751	ADP-ribosylation factor 4 OS=Rattus norvegicus GN=Arf4 PE=2 SV=2 - [ARF4_RAT]	52.78	1	3	6	91	0.8818
O55096	Dipeptidyl peptidase 3 OS=Rattus norvegicus GN=Dpp3 PE=1 SV=2 - [DPP3_RAT]	19.38	1	7	7	29	0.8821
D3Z8L7	Ras-related protein R-Ras OS=Rattus norvegicus GN=Rras PE=1 SV=1 - [RRAS_RAT]	24.77	1	4	4	45	0.8850
P17046	Lysosome-associated membrane glycoprotein 2 OS=Rattus norvegicus GN=Lamp2 PE=1 SV=2 - [LAMP2_RAT]	7.30	1	2	2	8	0.8864
Q6IG12	Keratin, type II cytoskeletal 7 OS=Rattus norvegicus GN=Krt7 PE=3 SV=1 - [K2C7_RAT]	13.35	1	3	7	49	0.8867
P18292	Prothrombin OS=Rattus norvegicus GN=F2 PE=1 SV=1 - [THRB_RAT]	21.72	1	8	8	52	0.8882
Q4QRB4	Tubulin beta-3 chain OS=Rattus norvegicus GN=Tubb3 PE=1 SV=1 - [TBB3_RAT]	36.22	1	2	15	1118	0.8894
P04182	Ornithine aminotransferase, mitochondrial OS=Rattus norvegicus GN=Oat PE=1 SV=1 - [OAT_RAT]	26.20	1	6	7	15	0.8910
B5DEH2	Erlin-2 OS=Rattus norvegicus GN=Erlin2 PE=1 SV=1 - [ERLN2_RAT]	8.55	1	2	2	2	0.8991
Q6DGG1	Alpha/beta hydrolase domain-containing protein 14B OS=Rattus norvegicus GN=Abhd14b PE=2 SV=1 - [ABHEB_RAT]	15.71	1	2	2	2	0.8996

O88600	Heat shock 70 kDa protein 4 OS=Rattus norvegicus GN=Hspa4 PE=1 SV=1 - [HSP74_RAT]	30.24	1	15	16	119	0.9007
B0BNE5	S-formylglutathione hydrolase OS=Rattus norvegicus GN=Esd PE=2 SV=1 - [ESTD_RAT]	44.33	1	6	6	20	0.9041
P62425	60S ribosomal protein L7a OS=Rattus norvegicus GN=Rpl7a PE=1 SV=2 - [RL7A_RAT]	13.16	1	4	4	32	0.9046
Q711G3	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Rattus norvegicus GN=Iah1 PE=2 SV=2 - [IAH1_RAT]	15.26	1	2	2	5	0.9084
P85973	Purine nucleoside phosphorylase OS=Rattus norvegicus GN=Pnp PE=1 SV=1 - [PNPH_RAT]	73.36	1	14	14	458	0.9088
P63245	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Rattus norvegicus GN=Gnb2l1 PE=1 SV=3 - [GBLP_RAT]	52.37	1	10	10	66	0.9112
P98158	Low-density lipoprotein receptor-related protein 2 OS=Rattus norvegicus GN=Lrp2 PE=1 SV=1 - [LRP2_RAT]	0.60	1	2	2	2	0.9117
P14740	Dipeptidyl peptidase 4 OS=Rattus norvegicus GN=Dpp4 PE=1 SV=2 - [DPP4_RAT]	19.17	1	10	11	83	0.9121
P41350	Caveolin-1 OS=Rattus norvegicus GN=Cav1 PE=1 SV=3 - [CAV1_RAT]	52.81	1	8	8	443	0.9123
Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	3.12	1	2	2	5	0.9154
P06399	Fibrinogen alpha chain OS=Rattus norvegicus GN=Fga PE=1 SV=3 - [FIBA_RAT]	27.88	1	18	18	405	0.9179
Q99PF5	Far upstream element-binding protein 2 OS=Rattus norvegicus GN=Khsrp PE=1 SV=1 - [FUBP2_RAT]	4.99	1	3	3	5	0.9230
P34058	Heat shock protein HSP 90-beta OS=Rattus norvegicus GN=Hsp90ab1 PE=1 SV=4 - [HS90B_RAT]	66.44	1	25	41	1119	0.9232
Q6P734	Plasma protease C1 inhibitor OS=Rattus norvegicus GN=Serping1 PE=2 SV=1 - [IC1_RAT]	38.29	1	14	14	42	0.9242
P07632	Superoxide dismutase [Cu-Zn] OS=Rattus norvegicus GN=Sod1 PE=1 SV=2 - [SODC_RAT]	58.44	1	8	8	219	0.9248
P01946	Hemoglobin subunit alpha-1/2 OS=Rattus norvegicus GN=Hba1 PE=1 SV=3 - [HBA_RAT]	95.77	1	14	14	15416	0.9325
A2RUV9	Adipocyte enhancer-binding protein 1 OS=Rattus norvegicus GN=Aebp1 PE=2 SV=1 - [AEBP1_RAT]	3.63	1	3	3	4	0.9348
O88664	Serine/threonine-protein kinase TAO1 OS=Rattus norvegicus GN=Taok1 PE=1 SV=1 - [TAOK1_RAT]	2.00	1	2	2	2	0.9349
P14562	Lysosome-associated membrane glycoprotein 1 OS=Rattus norvegicus GN=Lamp1 PE=1 SV=1 - [LAMP1_RAT]	17.44	1	6	6	34	0.9362
P50503	Hsc70-interacting protein OS=Rattus norvegicus GN=St13 PE=1 SV=1 - [F10A1_RAT]	13.04	1	4	4	22	0.9379
P04256	Heterogeneous nuclear ribonucleoprotein A1 OS=Rattus norvegicus GN=Hnrnpa1 PE=1 SV=3 - [ROA1_RAT]	25.31	1	5	6	48	0.9425
P13383	Nucleolin OS=Rattus norvegicus GN=Ncl PE=1 SV=3 - [NUCL_RAT]	22.86	1	14	14	101	0.9431
O88761	26S proteasome non-ATPase regulatory subunit 1 OS=Rattus norvegicus GN=Psmd1 PE=1 SV=1 - [PSMD1_RAT]	7.56	1	4	4	25	0.9456
Q9WU49	Calcium-regulated heat stable protein 1 OS=Rattus norvegicus GN=Carhsp1 PE=1 SV=1 - [CHSP1_RAT]	18.37	1	2	2	8	0.9479
Q1JU68	Eukaryotic translation initiation factor 3 subunit A OS=Rattus norvegicus GN=Eif3a PE=2 SV=2 - [EIF3A_RAT]	6.72	1	6	6	46	0.9492
Q5RJP0	Aldose reductase-related protein 1 OS=Rattus norvegicus GN=Akr1b7 PE=1 SV=1 - [ALD1_RAT]	21.20	1	3	6	9	0.9505
Q6AXQ0	SUMO-activating enzyme subunit 1 OS=Rattus norvegicus GN=Sae1 PE=2 SV=1 - [SAE1_RAT]	9.17	1	2	2	2	0.9574
P68511	14-3-3 protein eta OS=Rattus norvegicus GN=Ywhah PE=1 SV=2 - [1433F_RAT]	56.91	1	10	16	324	0.9602
P97576	GrpE protein homolog 1, mitochondrial OS=Rattus norvegicus GN=Grpel1 PE=1 SV=2 - [GRPE1_RAT]	11.52	1	3	3	7	0.9606
B4F7E8	Niban-like protein 1 OS=Rattus norvegicus GN=Fam129b PE=1 SV=1 - [NIBL1_RAT]	7.90	1	3	3	4	0.9607
P04276	Vitamin D-binding protein OS=Rattus norvegicus	71.43	1	24	24	351	0.9611

	GN=Gc PE=1 SV=3 - [VTDB_RAT]						
P02466	Collagen alpha-2(I) chain OS=Rattus norvegicus GN=Col1a2 PE=1 SV=3 - [CO1A2_RAT]	2.55	1	2	2	10	0.9616
Q9WVC0	Septin-7 OS=Rattus norvegicus GN=Sept7 PE=1 SV=1 - [SEPT7_RAT]	19.72	1	6	7	48	0.9622
P61206	ADP-ribosylation factor 3 OS=Rattus norvegicus GN=Arf3 PE=2 SV=2 - [ARF3_RAT]	54.70	2	5	8	183	0.9643
Q07066	Peroxisomal membrane protein 2 OS=Rattus norvegicus GN=Pxmp2 PE=1 SV=2 - [PXMP2_RAT]	21.13	1	2	3	11	0.9663
P82995	Heat shock protein HSP 90-alpha OS=Rattus norvegicus GN=Hsp90aa1 PE=1 SV=3 - [HS90A_RAT]	60.98	1	23	37	839	0.9667
P0CC09	Histone H2A type 2-A OS=Rattus norvegicus GN=Hist2h2aa3 PE=1 SV=1 - [H2A2A_RAT]	57.69	8	4	6	285	0.9675
P52296	Importin subunit beta-1 OS=Rattus norvegicus GN=Kpnb1 PE=1 SV=1 - [IMB1_RAT]	37.83	1	18	21	201	0.9683
P07824	Arginase-1 OS=Rattus norvegicus GN=Arg1 PE=1 SV=2 - [ARGI1_RAT]	11.76	1	2	2	6	0.9686
P18484	AP-2 complex subunit alpha-2 OS=Rattus norvegicus GN=Ap2a2 PE=1 SV=3 - [AP2A2_RAT]	20.36	1	12	12	122	0.9726
P54313	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Rattus norvegicus GN=Gnb2 PE=1 SV=4 - [GBB2_RAT]	61.76	2	7	14	166	0.9741
P11517	Hemoglobin subunit beta-2 OS=Rattus norvegicus PE=1 SV=2 - [HBB2_RAT]	88.44	1	3	15	10485	0.9741
Q9JK11	Reticulon-4 OS=Rattus norvegicus GN=Rtn4 PE=1 SV=1 - [RTN4_RAT]	4.21	1	4	4	24	0.9749
Q64119	Myosin light polypeptide 6 OS=Rattus norvegicus GN=Myl6 PE=1 SV=3 - [MYL6_RAT]	58.28	1	7	7	133	0.9807
Q68A21	Transcriptional activator protein Pur-beta OS=Rattus norvegicus GN=Purb PE=1 SV=3 - [PURB_RAT]	15.24	1	2	2	4	0.9844
P43278	Histone H1.0 OS=Rattus norvegicus GN=H1f0 PE=2 SV=2 - [H10_RAT]	22.16	1	4	4	16	0.9874
Q05982	Nucleoside diphosphate kinase A OS=Rattus norvegicus GN=Nme1 PE=1 SV=1 - [NDKA_RAT]	63.16	1	3	9	291	0.9935
P11951	Cytochrome c oxidase subunit 6C-2 OS=Rattus norvegicus GN=Cox6c2 PE=1 SV=3 - [CX6C2_RAT]	36.84	1	3	3	20	0.9960
P48679	Prelamin-A/C OS=Rattus norvegicus GN=Lmna PE=1 SV=1 - [LMNA_RAT]	32.03	1	17	19	120	0.9988
P60711	Actin, cytoplasmic 1 OS=Rattus norvegicus GN=Actb PE=1 SV=1 - [ACTB_RAT]	82.67	2	12	25	5778	

2-cycles chemotherapy (Fish oil-diet) versus tumor

Accession	Description	Σ Coverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	P-value
P07379	Phosphoenolpyruvate carboxykinase, cytosolic [GTP] OS=Rattus norvegicus GN=Pck1 PE=1 SV=1 - [PCKGC_RAT]	15.59	1	5	6	24	0.0001
P29410	Adenylate kinase 2, mitochondrial OS=Rattus norvegicus GN=Ak2 PE=2 SV=2 - [KAD2_RAT]	54.39	1	11	11	163	0.0002
O88644	Grifin OS=Rattus norvegicus GN=Grifin PE=1 SV=1 - [GRIFN_RAT]	15.28	1	2	2	35	0.0003
P07871	3-ketoacyl-CoA thiolase B, peroxisomal OS=Rattus norvegicus GN=Acaa1b PE=1 SV=2 - [THIKB_RAT]	13.68	2	5	5	22	0.0005
P05065	Fructose-bisphosphate aldolase A OS=Rattus norvegicus GN=Aldoa PE=1 SV=2 - [ALDOA_RAT]	81.04	1	23	24	1274	0.0005
P25409	Alanine aminotransferase 1 OS=Rattus norvegicus GN=Gpt PE=1 SV=2 - [ALAT1_RAT]	51.81	1	14	14	101	0.0006
P00406	Cytochrome c oxidase subunit 2 OS=Rattus norvegicus GN=Mtco2 PE=1 SV=3 - [COX2_RAT]	18.94	1	4	4	152	0.0006
Q920J4	Thioredoxin-like protein 1 OS=Rattus norvegicus GN=Txnl1 PE=1 SV=3 - [TXNL1_RAT]	13.15	1	2	2	2	0.0007
P07633	Propionyl-CoA carboxylase beta chain, mitochondrial	18.11	1	5	6	12	0.0013

	OS=Rattus norvegicus GN=Pccb PE=2 SV=1 - [PCCB_RAT]						
Q5XI22	Acetyl-CoA acetyltransferase, cytosolic OS=Rattus norvegicus GN=Acat2 PE=1 SV=1 - [THIC_RAT]	16.88	1	3	3	6	0.0015
P08460	Nidogen-1 (Fragment) OS=Rattus norvegicus GN=Nid1 PE=1 SV=2 - [NID1_RAT]	29.94	1	5	5	46	0.0017
P11497	Acetyl-CoA carboxylase 1 OS=Rattus norvegicus GN=Acaca PE=1 SV=1 - [ACACA_RAT]	54.71	1	87	87	908	0.0019
P04797	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus GN=Gapdh PE=1 SV=3 - [G3P_RAT]	75.98	1	18	18	1638	0.0020
P04762	Catalase OS=Rattus norvegicus GN=Cat PE=1 SV=3 - [CATA_RAT]	55.79	1	22	22	432	0.0021
P62898	Cytochrome c, somatic OS=Rattus norvegicus GN=Cycs PE=1 SV=2 - [CYC_RAT]	62.86	1	7	8	152	0.0028
P20788	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Rattus norvegicus GN=Uqcrfs1 PE=1 SV=2 - [UCRI_RAT]	22.63	1	3	4	20	0.0028
P25113	Phosphoglycerate mutase 1 OS=Rattus norvegicus GN=Pgam1 PE=1 SV=4 - [PGAM1_RAT]	74.41	1	18	18	359	0.0030
Q6AYG5	Ethylmalonyl-CoA decarboxylase OS=Rattus norvegicus GN=Echdc1 PE=1 SV=1 - [ECHD1_RAT]	49.83	1	9	10	77	0.0031
P05369	Farnesyl pyrophosphate synthase OS=Rattus norvegicus GN=Fdps PE=2 SV=2 - [FPPS_RAT]	15.58	1	5	5	15	0.0032
Q64591	2,4-dienoyl-CoA reductase, mitochondrial OS=Rattus norvegicus GN=Decr1 PE=1 SV=2 - [DECR_RAT]	44.18	1	10	10	132	0.0035
B5DFC9	Nidogen-2 OS=Rattus norvegicus GN=Nid2 PE=2 SV=1 - [NID2_RAT]	15.76	1	14	14	71	0.0038
P11240	Cytochrome c oxidase subunit 5A, mitochondrial OS=Rattus norvegicus GN=Cox5a PE=1 SV=1 - [COX5A_RAT]	54.79	1	7	7	92	0.0039
P45953	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acadvl PE=1 SV=1 - [ACADV_RAT]	25.50	1	10	10	68	0.0039
Q66HG6	Carbonic anhydrase 5B, mitochondrial OS=Rattus norvegicus GN=Ca5b PE=2 SV=1 - [CAH5B_RAT]	19.24	1	4	4	18	0.0040
Q66H12	Alpha-N-acetylgalactosaminidase OS=Rattus norvegicus GN=Naga PE=2 SV=1 - [NAGAB_RAT]	9.40	1	3	3	5	0.0048
P12785	Fatty acid synthase OS=Rattus norvegicus GN=Fasn PE=1 SV=3 - [FAS_RAT]	74.93	1	129	130	6301	0.0051
Q02253	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Rattus norvegicus GN=Aldh6a1 PE=1 SV=1 - [MMSA_RAT]	42.80	1	14	14	105	0.0052
P26644	Beta-2-glycoprotein 1 OS=Rattus norvegicus GN=Apoh PE=2 SV=2 - [APOH_RAT]	15.15	1	5	5	25	0.0057
P19234	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Rattus norvegicus GN=Ndufv2 PE=1 SV=2 - [NDUV2_RAT]	21.77	1	4	4	47	0.0059
P48721	Stress-70 protein, mitochondrial OS=Rattus norvegicus GN=Hspa9 PE=1 SV=3 - [GRP75_RAT]	40.21	1	22	22	326	0.0060
Q9Z0V6	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Rattus norvegicus GN=Prdx3 PE=1 SV=2 - [PRDX3_RAT]	36.96	1	6	6	120	0.0060
P10888	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Rattus norvegicus GN=Cox4i1 PE=1 SV=1 - [COX41_RAT]	31.36	1	5	5	141	0.0069
P32089	Tricarboxylate transport protein, mitochondrial OS=Rattus norvegicus GN=Slc25a1 PE=1 SV=1 - [TXTP_RAT]	34.41	1	7	8	163	0.0069
Q5U2Q3	Ester hydrolase C11orf54 homolog OS=Rattus norvegicus PE=1 SV=1 - [CK054_RAT]	24.13	1	6	6	109	0.0074
P21913	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Rattus norvegicus GN=Sdhb PE=2 SV=2 - [SDHB_RAT]	23.05	1	6	6	24	0.0078
P52873	Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus GN=Pc PE=1 SV=2 - [PYC_RAT]	70.03	1	53	54	1850	0.0079
P11348	Dihydropteridine reductase OS=Rattus norvegicus GN=Qdpr PE=1 SV=1 - [DHPR_RAT]	50.21	1	8	8	56	0.0081
Q99NA5	Isocitrate dehydrogenase [NAD] subunit alpha,	29.23	1	8	8	154	0.0084

	mitochondrial OS=Rattus norvegicus GN=Idh3a PE=1 SV=1 - [IDH3A_RAT]						
P26284	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Rattus norvegicus GN=Pdha1 PE=1 SV=2 - [ODPA_RAT]	49.49	1	17	17	158	0.0087
Q6AYC4	Macrophage-capping protein OS=Rattus norvegicus GN=Capg PE=1 SV=1 - [CAPG_RAT]	44.41	1	9	9	86	0.0087
Q68FY0	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Rattus norvegicus GN=Uqcrc1 PE=1 SV=1 - [QCR1_RAT]	33.75	1	10	10	186	0.0093
P04143	Thyroid hormone-inducible hepatic protein OS=Rattus norvegicus GN=Thrsp PE=1 SV=1 - [THRSP_RAT]	24.00	1	2	2	27	0.0095
P08461	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Rattus norvegicus GN=Dlat PE=1 SV=3 - [ODP2_RAT]	34.02	1	13	13	70	0.0096
P04642	L-lactate dehydrogenase A chain OS=Rattus norvegicus GN=Ldha PE=1 SV=1 - [LDHA_RAT]	85.54	1	23	26	850	0.0096
P04905	Glutathione S-transferase Mu 1 OS=Rattus norvegicus GN=Gstm1 PE=1 SV=2 - [GSTM1_RAT]	51.38	1	6	9	63	0.0096
P20761	Ig gamma-2B chain C region OS=Rattus norvegicus GN=Igh-1a PE=1 SV=1 - [IGG2B_RAT]	34.83	1	6	6	437	0.0104
P08503	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acadm PE=1 SV=1 - [ACADM_RAT]	20.19	1	6	6	36	0.0106
P06399	Fibrinogen alpha chain OS=Rattus norvegicus GN=Fga PE=1 SV=3 - [FIBA_RAT]	37.34	1	27	27	870	0.0106
P04764	Alpha-enolase OS=Rattus norvegicus GN=Eno1 PE=1 SV=4 - [ENOA_RAT]	69.82	1	19	23	1182	0.0107
P32551	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Rattus norvegicus GN=Uqcrc2 PE=1 SV=2 - [QCR2_RAT]	67.48	1	17	17	233	0.0111
P56574	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus GN=Idh2 PE=1 SV=2 - [IDHP_RAT]	35.62	1	12	14	104	0.0113
Q8VHF5	Citrate synthase, mitochondrial OS=Rattus norvegicus GN=Cs PE=1 SV=1 - [CISY_RAT]	41.63	1	14	14	199	0.0115
P05712	Ras-related protein Rab-2A OS=Rattus norvegicus GN=Rab2a PE=2 SV=1 - [RAB2A_RAT]	50.47	1	6	7	40	0.0121
Q9Z2L0	Voltage-dependent anion-selective channel protein 1 OS=Rattus norvegicus GN=Vdac1 PE=1 SV=4 - [VDAC1_RAT]	51.59	1	10	10	85	0.0123
P19357	Solute carrier family 2, facilitated glucose transporter member 4 OS=Rattus norvegicus GN=Slc2a4 PE=1 SV=1 - [GTR4_RAT]	8.06	1	3	3	15	0.0124
P20760	Ig gamma-2A chain C region OS=Rattus norvegicus GN=Igg-2a PE=1 SV=1 - [IGG2A_RAT]	63.35	1	14	16	1156	0.0133
Q68FU3	Electron transfer flavoprotein subunit beta OS=Rattus norvegicus GN=Etfb PE=2 SV=3 - [ETFB_RAT]	46.67	1	10	10	184	0.0135
P26772	10 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspe1 PE=1 SV=3 - [CH10_RAT]	52.94	1	7	7	78	0.0137
P05371	Clusterin OS=Rattus norvegicus GN=Clu PE=1 SV=2 - [CLUS_RAT]	6.26	1	2	2	9	0.0137
P11915	Non-specific lipid-transfer protein OS=Rattus norvegicus GN=Scp2 PE=1 SV=3 - [NLTP_RAT]	16.64	1	10	11	161	0.0141
P19511	ATP synthase F(0) complex subunit B1, mitochondrial OS=Rattus norvegicus GN=Atp5f1 PE=1 SV=1 - [AT5F1_RAT]	38.28	1	9	10	139	0.0141
Q99PS8	Histidine-rich glycoprotein OS=Rattus norvegicus GN=Hrg PE=1 SV=1 - [HRG_RAT]	13.71	1	5	5	25	0.0142
O08651	D-3-phosphoglycerate dehydrogenase OS=Rattus norvegicus GN=Phgdh PE=1 SV=3 - [SERA_RAT]	26.64	1	10	10	216	0.0146
P13437	3-ketoacyl-CoA thiolase, mitochondrial OS=Rattus norvegicus GN=Acaa2 PE=2 SV=1 - [THIM_RAT]	61.46	1	17	17	353	0.0158
P07153	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Rattus norvegicus GN=Rpn1 PE=2 SV=1 - [RPN1_RAT]	22.81	1	10	10	70	0.0161
O35077	Glycerol-3-phosphate dehydrogenase [NAD(+)],	91.40	1	27	27	2765	0.0162

	cytoplasmic OS=Rattus norvegicus GN=Gpd1 PE=1 SV=4 - [GPDA_RAT]						
Q6P7R8	Very-long-chain 3-oxoacyl-CoA reductase OS=Rattus norvegicus GN=Hsd17b12 PE=2 SV=1 - [DHB12_RAT]	19.55	1	4	4	59	0.0164
P49432	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Rattus norvegicus GN=Pdhb PE=1 SV=2 - [ODPB_RAT]	42.62	1	11	11	255	0.0166
P50137	Transketolase OS=Rattus norvegicus GN=Tkt PE=1 SV=1 - [TKT_RAT]	61.64	1	26	26	816	0.0169
Q63413	Spliceosome RNA helicase Ddx39b OS=Rattus norvegicus GN=Ddx39b PE=2 SV=3 - [DX39B_RAT]	7.01	1	2	2	2	0.0169
P29411	GTP:AMP phosphotransferase AK3, mitochondrial OS=Rattus norvegicus GN=Ak3 PE=2 SV=2 - [KAD3_RAT]	58.15	1	11	11	94	0.0170
P17988	Sulfotransferase 1A1 OS=Rattus norvegicus GN=Sult1a1 PE=1 SV=1 - [ST1A1_RAT]	26.46	1	5	5	8	0.0172
P09606	Glutamine synthetase OS=Rattus norvegicus GN=Glul PE=1 SV=3 - [GLNA_RAT]	43.97	1	12	12	231	0.0174
P14604	Enoyl-CoA hydratase, mitochondrial OS=Rattus norvegicus GN=Echs1 PE=1 SV=1 - [ECHM_RAT]	48.97	1	9	9	251	0.0175
P10111	Peptidyl-prolyl cis-trans isomerase A OS=Rattus norvegicus GN=Ppia PE=1 SV=2 - [PPIA_RAT]	59.76	1	11	11	843	0.0180
P18886	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Rattus norvegicus GN=Cpt2 PE=1 SV=1 - [CPT2_RAT]	21.28	1	8	8	19	0.0180
P09811	Glycogen phosphorylase, liver form OS=Rattus norvegicus GN=Pygl PE=1 SV=5 - [PYGL_RAT]	33.29	1	17	19	127	0.0184
Q6AYS7	Aminoacylase-1A OS=Rattus norvegicus GN=Acy1a PE=1 SV=1 - [ACY1A_RAT]	36.76	2	9	10	34	0.0191
P31044	Phosphatidylethanolamine-binding protein 1 OS=Rattus norvegicus GN=Pebp1 PE=1 SV=3 - [PEBP1_RAT]	53.48	1	6	6	117	0.0192
P13697	NADP-dependent malic enzyme OS=Rattus norvegicus GN=Me1 PE=1 SV=2 - [MAOX_RAT]	78.67	1	30	31	1005	0.0199
P11030	Acyl-CoA-binding protein OS=Rattus norvegicus GN=Dbi PE=1 SV=3 - [ACBP_RAT]	54.02	1	5	5	101	0.0211
P24329	Thiosulfate sulfurtransferase OS=Rattus norvegicus GN=Tst PE=1 SV=3 - [THTR_RAT]	29.63	1	5	6	39	0.0211
P62243	40S ribosomal protein S8 OS=Rattus norvegicus GN=Rps8 PE=1 SV=2 - [RS8_RAT]	9.62	1	2	2	2	0.0216
P08009	Glutathione S-transferase Yb-3 OS=Rattus norvegicus GN=Gstm3 PE=1 SV=2 - [GSTM4_RAT]	38.99	1	1	8	155	0.0221
O89049	Thioredoxin reductase 1, cytoplasmic OS=Rattus norvegicus GN=Txnrd1 PE=1 SV=5 - [TRXR1_RAT]	16.63	1	4	4	10	0.0226
P97532	3-mercaptopyruvate sulfurtransferase OS=Rattus norvegicus GN=Mpst PE=1 SV=3 - [THTM_RAT]	40.40	1	9	9	97	0.0229
Q63598	Plastin-3 OS=Rattus norvegicus GN=Pls3 PE=1 SV=2 - [PLST_RAT]	24.29	1	8	9	50	0.0233
P20070	NADH-cytochrome b5 reductase 3 OS=Rattus norvegicus GN=Cyb5r3 PE=1 SV=2 - [NB5R3_RAT]	77.08	1	15	15	314	0.0237
Q66HF1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus GN=Ndufs1 PE=1 SV=1 - [NDUS1_RAT]	37.28	1	17	17	109	0.0238
Q64611	Cysteine sulfinic acid decarboxylase OS=Rattus norvegicus GN=Csad PE=1 SV=1 - [CSAD_RAT]	40.16	1	13	13	230	0.0241
Q5BK63	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Rattus norvegicus GN=Ndufa9 PE=1 SV=2 - [NDUA9_RAT]	22.55	1	5	5	44	0.0253
P41562	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Rattus norvegicus GN=Idh1 PE=1 SV=1 - [IDHC_RAT]	63.77	1	22	23	373	0.0261
P13803	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Rattus norvegicus GN=Etfa PE=1 SV=4 - [ETFA_RAT]	56.76	1	12	12	303	0.0270
P18292	Prothrombin OS=Rattus norvegicus GN=F2 PE=1 SV=1 - [THRB_RAT]	16.21	1	6	6	42	0.0275
P57113	Maleylacetoacetate isomerase OS=Rattus norvegicus GN=Gstz1 PE=1 SV=2 - [MAAI_RAT]	63.89	1	9	9	128	0.0289

Q6P7P5	Basic leucine zipper and W2 domain-containing protein 1 OS=Rattus norvegicus GN=Bzw1 PE=1 SV=1 - [BZW1_RAT]	7.88	1	2	2	2	0.0297
P13635	Ceruloplasmin OS=Rattus norvegicus GN=Cp PE=1 SV=3 - [CERU_RAT]	51.65	1	44	45	1143	0.0301
P12007	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ivd PE=1 SV=2 - [IVD_RAT]	43.16	1	11	11	78	0.0302
P52759	Ribonuclease UK114 OS=Rattus norvegicus GN=Hrsp12 PE=1 SV=3 - [UK114_RAT]	52.55	1	5	5	20	0.0305
P15429	Beta-enolase OS=Rattus norvegicus GN=Eno3 PE=1 SV=3 - [ENOB_RAT]	26.96	1	3	7	244	0.0309
P05370	Glucose-6-phosphate 1-dehydrogenase OS=Rattus norvegicus GN=G6pdx PE=1 SV=3 - [G6PD_RAT]	18.45	1	7	7	43	0.0322
P20759	Ig gamma-1 chain C region OS=Rattus norvegicus PE=1 SV=1 - [IGHG1_RAT]	20.55	1	3	5	269	0.0331
P20767	Ig lambda-2 chain C region OS=Rattus norvegicus PE=4 SV=1 - [LAC2_RAT]	76.92	1	5	5	100	0.0347
P42123	L-lactate dehydrogenase B chain OS=Rattus norvegicus GN=Ldhb PE=1 SV=2 - [LDHB_RAT]	69.46	1	19	22	734	0.0353
P80254	D-dopachrome decarboxylase OS=Rattus norvegicus GN=Ddt PE=1 SV=3 - [DOPD_RAT]	77.97	1	7	7	146	0.0354
P61751	ADP-ribosylation factor 4 OS=Rattus norvegicus GN=Arf4 PE=2 SV=2 - [ARF4_RAT]	60.56	1	4	8	125	0.0360
Q4KM35	Proteasome subunit beta type-10 OS=Rattus norvegicus GN=Psmb10 PE=2 SV=1 - [PSB10_RAT]	20.15	1	4	4	9	0.0362
Q920L2	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Rattus norvegicus GN=Sdha PE=1 SV=1 - [SDHA_RAT]	21.95	1	10	10	85	0.0365
P04636	Malate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Mdh2 PE=1 SV=2 - [MDHM_RAT]	64.20	1	18	18	642	0.0365
P28037	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Rattus norvegicus GN=Aldh1l1 PE=1 SV=3 - [AL1L1_RAT]	33.59	1	21	21	81	0.0370
O88989	Malate dehydrogenase, cytoplasmic OS=Rattus norvegicus GN=Mdh1 PE=1 SV=3 - [MDHC_RAT]	48.80	1	15	15	1099	0.0372
P14408	Fumarate hydratase, mitochondrial OS=Rattus norvegicus GN=Fh PE=1 SV=1 - [FUMH_RAT]	30.18	1	8	8	46	0.0380
Q5BJY9	Keratin, type I cytoskeletal 18 OS=Rattus norvegicus GN=Krt18 PE=1 SV=3 - [K1C18_RAT]	13.71	1	4	5	11	0.0386
Q66H98	Serum deprivation-response protein OS=Rattus norvegicus GN=Sdpr PE=1 SV=3 - [SDPR_RAT]	45.08	1	13	13	341	0.0392
P29266	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Hibadh PE=1 SV=3 - [3HIDH_RAT]	30.75	1	7	7	50	0.0405
P38718	Mitochondrial pyruvate carrier 2 OS=Rattus norvegicus GN=Mpc2 PE=2 SV=1 - [MPC2_RAT]	25.98	1	3	3	9	0.0408
P16638	ATP-citrate synthase OS=Rattus norvegicus GN=Acly PE=1 SV=1 - [ACLY_RAT]	59.09	1	51	51	1717	0.0409
O35567	Bifunctional purine biosynthesis protein PURH OS=Rattus norvegicus GN=Atic PE=1 SV=2 - [PUR9_RAT]	25.84	1	9	9	30	0.0411
Q5PPN5	Tubulin polymerization-promoting protein family member 3 OS=Rattus norvegicus GN=Tppp3 PE=2 SV=1 - [TPPP3_RAT]	31.82	1	5	5	17	0.0422
P46844	Biliverdin reductase A OS=Rattus norvegicus GN=Blvra PE=1 SV=1 - [BIEA_RAT]	41.02	1	9	9	48	0.0423
O88767	Protein deglycase DJ-1 OS=Rattus norvegicus GN=Park7 PE=1 SV=1 - [PARK7_RAT]	87.30	1	12	12	201	0.0435
P23965	Enoyl-CoA delta isomerase 1, mitochondrial OS=Rattus norvegicus GN=Eci1 PE=1 SV=1 - [ECI1_RAT]	42.91	1	9	9	173	0.0437
Q05962	ADP/ATP translocase 1 OS=Rattus norvegicus GN=Slc25a4 PE=1 SV=3 - [ADT1_RAT]	40.94	1	4	11	354	0.0446
P10719	ATP synthase subunit beta, mitochondrial OS=Rattus norvegicus GN=Atp5b PE=1 SV=2 - [ATPB_RAT]	77.88	1	26	26	1560	0.0450
P15999	ATP synthase subunit alpha, mitochondrial OS=Rattus norvegicus GN=Atp5a1 PE=1 SV=2 - [ATPA_RAT]	49.55	1	23	23	1180	0.0457
Q0ZHH6	Atlastin-3 OS=Rattus norvegicus GN=Atl3 PE=2 SV=2	21.44	1	6	6	94	0.0460

	- [ATLA3_RAT]						
P07150	Annexin A1 OS=Rattus norvegicus GN=Anxa1 PE=1 SV=2 - [ANXA1_RAT]	75.14	1	29	29	2393	0.0461
P63170	Dynein light chain 1, cytoplasmic OS=Rattus norvegicus GN=Dynll1 PE=1 SV=1 - [DYL1_RAT]	49.44	1	3	3	9	0.0470
P11951	Cytochrome c oxidase subunit 6C-2 OS=Rattus norvegicus GN=Cox6c2 PE=1 SV=3 - [CX6C2_RAT]	36.84	1	3	3	19	0.0485
P09117	Fructose-bisphosphate aldolase C OS=Rattus norvegicus GN=Aldoc PE=1 SV=3 - [ALDOC_RAT]	11.85	1	3	5	167	0.0490
P07338	Chymotrypsinogen B OS=Rattus norvegicus GN=Ctrb1 PE=1 SV=1 - [CTRB1_RAT]	14.45	1	2	2	2	0.0495
P48004	Proteasome subunit alpha type-7 OS=Rattus norvegicus GN=Psma7 PE=1 SV=1 - [PSA7_RAT]	29.53	1	5	6	28	0.0510
Q09073	ADP/ATP translocase 2 OS=Rattus norvegicus GN=Slc25a5 PE=1 SV=3 - [ADT2_RAT]	44.30	1	5	12	341	0.0511
Q5EB81	NADH-cytochrome b5 reductase 1 OS=Rattus norvegicus GN=Cyb5r1 PE=2 SV=1 - [NB5R1_RAT]	6.56	1	2	2	2	0.0515
P85968	6-phosphogluconate dehydrogenase, decarboxylating OS=Rattus norvegicus GN=Pgd PE=1 SV=1 - [6PGD_RAT]	54.66	1	18	18	508	0.0523
P07861	Neprilysin OS=Rattus norvegicus GN=Mme PE=1 SV=2 - [NEP_RAT]	3.87	1	2	2	3	0.0529
Q9QY44	ATP-binding cassette sub-family D member 2 OS=Rattus norvegicus GN=Abcd2 PE=1 SV=1 - [ABCD2_RAT]	16.33	1	6	7	26	0.0529
P10760	Adenosylhomocysteinase OS=Rattus norvegicus GN=Ahcy PE=1 SV=3 - [SAHH_RAT]	38.43	1	13	13	151	0.0529
Q8CG45	Aflatoxin B1 aldehyde reductase member 2 OS=Rattus norvegicus GN=Akr7a2 PE=1 SV=2 - [ARK72_RAT]	20.44	1	6	6	19	0.0532
Q3MIE4	Synaptic vesicle membrane protein VAT-1 homolog OS=Rattus norvegicus GN=Vat1 PE=1 SV=1 - [VAT1_RAT]	50.99	1	13	13	119	0.0536
P12075	Cytochrome c oxidase subunit 5B, mitochondrial OS=Rattus norvegicus GN=Cox5b PE=1 SV=2 - [COX5B_RAT]	36.43	1	5	5	9	0.0536
P02401	60S acidic ribosomal protein P2 OS=Rattus norvegicus GN=Rplp2 PE=1 SV=2 - [RLA2_RAT]	66.96	1	4	4	66	0.0541
B0LPN4	Ryanodine receptor 2 OS=Rattus norvegicus GN=Ryr2 PE=1 SV=2 - [RYR2_RAT]	1.03	1	3	3	5	0.0552
Q7TP48	Adipocyte plasma membrane-associated protein OS=Rattus norvegicus GN=Apmap PE=2 SV=2 - [APMAP_RAT]	65.43	1	15	15	376	0.0555
O54921	Exocyst complex component 2 OS=Rattus norvegicus GN=Exoc2 PE=1 SV=1 - [EXOC2_RAT]	1.84	1	2	2	2	0.0563
P14669	Annexin A3 OS=Rattus norvegicus GN=Anxa3 PE=1 SV=4 - [ANXA3_RAT]	64.51	1	17	18	246	0.0575
Q9WUH4	Four and a half LIM domains protein 1 OS=Rattus norvegicus GN=Fhl1 PE=2 SV=1 - [FHL1_RAT]	12.50	1	3	3	21	0.0589
Q64057	Alpha-aminoadipic semialdehyde dehydrogenase OS=Rattus norvegicus GN=Aldh7a1 PE=1 SV=2 - [AL7A1_RAT]	35.99	1	12	12	39	0.0589
P84817	Mitochondrial fission 1 protein OS=Rattus norvegicus GN=Fis1 PE=1 SV=1 - [FIS1_RAT]	32.24	1	5	5	110	0.0591
Q07936	Annexin A2 OS=Rattus norvegicus GN=Anxa2 PE=1 SV=2 - [ANXA2_RAT]	71.39	1	26	26	2128	0.0597
Q641Z6	EH domain-containing protein 1 OS=Rattus norvegicus GN=Ehd1 PE=1 SV=1 - [EHD1_RAT]	70.79	1	25	26	583	0.0601
Q6IRK9	Carboxypeptidase Q OS=Rattus norvegicus GN=Cpq PE=1 SV=1 - [CBPQ_RAT]	34.96	1	10	10	40	0.0603
P05508	NADH-ubiquinone oxidoreductase chain 4 OS=Rattus norvegicus GN=Mtnd4 PE=3 SV=3 - [NU4M_RAT]	12.42	1	3	3	22	0.0606
P09456	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Rattus norvegicus GN=Prkar1a PE=1 SV=2 - [KAP0_RAT]	10.76	1	2	2	7	0.0611
P18614	Integrin alpha-1 OS=Rattus norvegicus GN=Itga1 PE=1 SV=1 - [ITA1_RAT]	4.15	1	2	2	2	0.0615
Q9R063	Peroxiredoxin-5, mitochondrial OS=Rattus norvegicus GN=Prdx5 PE=1 SV=1 - [PRDX5_RAT]	51.17	1	9	9	299	0.0626

P35435	ATP synthase subunit gamma, mitochondrial OS=Rattus norvegicus GN=Atp5c1 PE=1 SV=2 - [ATPG_RAT]	40.66	1	8	8	61	0.0629
Q2PQA9	Kinesin-1 heavy chain OS=Rattus norvegicus GN=Kif5b PE=1 SV=1 - [KINH_RAT]	5.30	1	2	3	6	0.0640
P58775	Tropomyosin beta chain OS=Rattus norvegicus GN=Tpm2 PE=1 SV=1 - [TPM2_RAT]	27.82	1	1	11	106	0.0640
Q63041	Alpha-1-macroglobulin OS=Rattus norvegicus GN=A1m PE=1 SV=1 - [A1M_RAT]	67.33	1	67	68	2385	0.0643
Q62826	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=1 SV=4 - [HNRPM_RAT]	3.04	1	2	2	8	0.0644
P85125	Polymerase I and transcript release factor OS=Rattus norvegicus GN=Ptrf PE=1 SV=1 - [PTRF_RAT]	42.09	1	18	18	1844	0.0644
P25093	Fumarylacetoacetase OS=Rattus norvegicus GN=Fah PE=1 SV=1 - [FAAA_RAT]	43.44	1	11	11	188	0.0645
Q5XIE6	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Rattus norvegicus GN=Hibch PE=1 SV=2 - [HIBCH_RAT]	18.18	1	4	4	7	0.0654
P35171	Cytochrome c oxidase subunit 7A2, mitochondrial OS=Rattus norvegicus GN=Cox7a2 PE=1 SV=1 - [CX7A2_RAT]	27.71	1	2	2	6	0.0664
Q6MG60	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Rattus norvegicus GN=Ddah2 PE=1 SV=1 - [DDAH2_RAT]	52.98	1	8	8	94	0.0672
P23764	Glutathione peroxidase 3 OS=Rattus norvegicus GN=Gpx3 PE=2 SV=2 - [GPX3_RAT]	32.30	1	6	6	124	0.0690
P62914	60S ribosomal protein L11 OS=Rattus norvegicus GN=Rpl11 PE=1 SV=2 - [RL11_RAT]	16.85	1	3	3	58	0.0695
P31721	Complement C1q subcomponent subunit B OS=Rattus norvegicus GN=C1qb PE=1 SV=2 - [C1QB_RAT]	9.88	1	2	2	9	0.0708
P86252	Transcriptional activator protein Pur-alpha (Fragments) OS=Rattus norvegicus GN=Pura PE=1 SV=1 - [PURA_RAT]	63.77	1	4	4	33	0.0709
P61621	Protein transport protein Sec61 subunit alpha isoform 1 OS=Rattus norvegicus GN=Sec61a1 PE=2 SV=2 - [S61A1_RAT]	15.76	1	4	4	33	0.0711
Q3T1J1	Eukaryotic translation initiation factor 5A-1 OS=Rattus norvegicus GN=Eif5a PE=1 SV=3 - [IF5A1_RAT]	46.10	1	8	8	108	0.0711
Q64537	Calpain small subunit 1 OS=Rattus norvegicus GN=Capns1 PE=1 SV=3 - [CPNS1_RAT]	64.07	1	9	9	70	0.0717
Q9EQS0	Transaldolase OS=Rattus norvegicus GN=Taldo1 PE=1 SV=2 - [TALDO_RAT]	39.17	1	13	13	96	0.0727
P23514	Coatomer subunit beta OS=Rattus norvegicus GN=Copb1 PE=1 SV=1 - [COPB_RAT]	11.44	1	5	6	76	0.0727
Q6PDU7	ATP synthase subunit g, mitochondrial OS=Rattus norvegicus GN=Atp5l PE=1 SV=2 - [ATP5L_RAT]	53.40	1	4	4	19	0.0727
A2RRU1	Glycogen [starch] synthase, muscle OS=Rattus norvegicus GN=Gys1 PE=1 SV=1 - [GYS1_RAT]	5.96	1	2	2	2	0.0728
Q9EPH1	Alpha-1B-glycoprotein OS=Rattus norvegicus GN=A1bg PE=2 SV=2 - [A1BG_RAT]	29.82	1	11	11	124	0.0734
P53534	Glycogen phosphorylase, brain form (Fragment) OS=Rattus norvegicus GN=Pygb PE=1 SV=3 - [PYGB_RAT]	13.72	1	6	8	33	0.0739
P38983	40S ribosomal protein SA OS=Rattus norvegicus GN=Rpsa PE=1 SV=3 - [RSSA_RAT]	42.37	1	8	8	134	0.0751
P04906	Glutathione S-transferase P OS=Rattus norvegicus GN=Gstp1 PE=1 SV=2 - [GSTP1_RAT]	59.52	1	8	8	295	0.0753
Q9ER34	Aconitate hydratase, mitochondrial OS=Rattus norvegicus GN=Aco2 PE=1 SV=2 - [ACON_RAT]	54.74	1	33	33	740	0.0764
P55053	Fatty acid-binding protein, epidermal OS=Rattus norvegicus GN=Fabp5 PE=1 SV=3 - [FABP5_RAT]	69.63	1	9	9	234	0.0768
Q3KR86	MICOS complex subunit Mic60 (Fragment) OS=Rattus norvegicus GN=Immt PE=1 SV=1 - [MIC60_RAT]	17.90	1	8	8	24	0.0773
Q9JJ31	Cullin-5 OS=Rattus norvegicus GN=Cul5 PE=1 SV=3 - [CUL5_RAT]	4.49	1	2	2	3	0.0777
Q06647	ATP synthase subunit O, mitochondrial OS=Rattus norvegicus GN=Atp5o PE=1 SV=1 - [ATPO_RAT]	66.20	1	11	12	196	0.0785

P02793	Ferritin light chain 1 OS=Rattus norvegicus GN=Ftl1 PE=1 SV=3 - [FRIL1_RAT]	72.13	1	1	12	399	0.0803
P97675	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3 OS=Rattus norvegicus GN=Enpp3 PE=1 SV=2 - [ENPP3_RAT]	21.26	1	12	12	100	0.0817
Q9Z2G8	Nucleosome assembly protein 1-like 1 OS=Rattus norvegicus GN=Nap1l1 PE=1 SV=1 - [NP1L1_RAT]	7.18	1	2	2	16	0.0818
Q9Z1A6	Vigilin OS=Rattus norvegicus GN=Hdlbp PE=1 SV=1 - [VIGLN_RAT]	9.62	1	10	10	31	0.0826
Q68FT1	Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Rattus norvegicus GN=Coq9 PE=1 SV=2 - [COQ9_RAT]	6.09	1	2	2	4	0.0832
P21396	Amine oxidase [flavin-containing] A OS=Rattus norvegicus GN=Maoa PE=1 SV=1 - [AOFA_RAT]	6.84	1	3	3	4	0.0844
P14562	Lysosome-associated membrane glycoprotein 1 OS=Rattus norvegicus GN=Lamp1 PE=1 SV=1 - [LAMP1_RAT]	14.74	1	5	5	26	0.0851
P17764	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus GN=Acat1 PE=1 SV=1 - [THIL_RAT]	51.89	1	14	14	132	0.0851
P07756	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Rattus norvegicus GN=Cps1 PE=1 SV=1 - [CPSM_RAT]	20.27	1	20	20	110	0.0855
Q03626	Murinoglobulin-1 OS=Rattus norvegicus GN=Mug1 PE=2 SV=1 - [MUG1_RAT]	53.13	1	24	57	3089	0.0857
P14046	Alpha-1-inhibitor 3 OS=Rattus norvegicus GN=A1i3 PE=1 SV=1 - [A1I3_RAT]	52.13	1	25	58	3285	0.0857
P16391	RT1 class I histocompatibility antigen, AA alpha chain OS=Rattus norvegicus PE=1 SV=2 - [HA12_RAT]	11.32	1	4	4	24	0.0858
P70619	Glutathione reductase (Fragment) OS=Rattus norvegicus GN=Gsr PE=2 SV=2 - [GSHR_RAT]	8.02	1	2	2	2	0.0859
Q62847	Gamma-adducin OS=Rattus norvegicus GN=Add3 PE=1 SV=2 - [ADDG_RAT]	5.39	1	2	2	3	0.0862
P01836	Ig kappa chain C region, A allele OS=Rattus norvegicus PE=1 SV=1 - [KACA_RAT]	76.42	1	7	7	800	0.0863
P02692	Fatty acid-binding protein, liver OS=Rattus norvegicus GN=Fabp1 PE=1 SV=1 - [FABPL_RAT]	62.20	1	6	6	74	0.0863
P63039	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspd1 PE=1 SV=1 - [CH60_RAT]	65.45	1	30	30	1046	0.0877
Q6P6V0	Glucose-6-phosphate isomerase OS=Rattus norvegicus GN=Gpi PE=1 SV=1 - [G6PI_RAT]	52.69	1	23	23	468	0.0878
P06214	Delta-aminolevulinic acid dehydratase OS=Rattus norvegicus GN=Alad PE=1 SV=1 - [HEM2_RAT]	35.45	1	6	6	51	0.0882
Q66HA6	ADP-ribosylation factor-like protein 8B OS=Rattus norvegicus GN=Arl8b PE=2 SV=1 - [ARL8B_RAT]	24.73	1	3	3	4	0.0889
P43884	Perilipin-1 OS=Rattus norvegicus GN=Plin1 PE=1 SV=1 - [PLIN1_RAT]	65.38	1	22	22	1216	0.0914
Q9JLJ3	4-trimethylaminobutyraldehyde dehydrogenase OS=Rattus norvegicus GN=Aldh9a1 PE=1 SV=1 - [AL9A1_RAT]	53.24	1	13	15	213	0.0929
Q6P734	Plasma protease C1 inhibitor OS=Rattus norvegicus GN=Serping1 PE=2 SV=1 - [IC1_RAT]	47.82	1	18	18	86	0.0939
Q5XIH7	Prohibitin-2 OS=Rattus norvegicus GN=Phb2 PE=1 SV=1 - [PHB2_RAT]	53.85	1	11	12	122	0.0941
P10860	Glutamate dehydrogenase 1, mitochondrial OS=Rattus norvegicus GN=Glud1 PE=1 SV=2 - [DHE3_RAT]	48.03	1	18	19	150	0.0945
P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	58.81	1	32	32	646	0.0946
Q63691	Monocyte differentiation antigen CD14 OS=Rattus norvegicus GN=Cd14 PE=2 SV=2 - [CD14_RAT]	26.34	1	6	6	84	0.0953
P38652	Phosphoglucomutase-1 OS=Rattus norvegicus GN=Pgm1 PE=1 SV=2 - [PGM1_RAT]	35.05	1	11	11	128	0.0973
Q8R431	Monoglyceride lipase OS=Rattus norvegicus GN=Mgll PE=1 SV=1 - [MGLL_RAT]	67.66	1	17	17	768	0.0974
P85973	Purine nucleoside phosphorylase OS=Rattus norvegicus GN=Pnp PE=1 SV=1 - [PNPH_RAT]	73.36	1	14	14	520	0.0982
P70645	Bleomycin hydrolase OS=Rattus norvegicus GN=Blmh PE=1 SV=1 - [BLMH_RAT]	8.37	1	2	2	2	0.0990

Q63945	Protein SET OS=Rattus norvegicus GN=Set PE=2 SV=2 - [SET_RAT]	27.68	1	5	5	12	0.1003
P04041	Glutathione peroxidase 1 OS=Rattus norvegicus GN=Gpx1 PE=1 SV=4 - [GPX1_RAT]	75.12	1	11	12	230	0.1004
P07895	Superoxide dismutase [Mn], mitochondrial OS=Rattus norvegicus GN=Sod2 PE=1 SV=2 - [SODM_RAT]	35.59	1	7	7	93	0.1016
P06866	Haptoglobin OS=Rattus norvegicus GN=Hp PE=1 SV=3 - [HPT_RAT]	63.11	1	21	22	623	0.1017
P31720	Complement C1q subcomponent subunit A OS=Rattus norvegicus GN=C1qa PE=1 SV=2 - [C1QA_RAT]	20.41	1	3	3	8	0.1021
Q6P0K8	Junction plakoglobin OS=Rattus norvegicus GN=Jup PE=1 SV=1 - [PLAK_RAT]	5.10	1	2	2	2	0.1031
O70351	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Rattus norvegicus GN=Hsd17b10 PE=1 SV=3 - [HCD2_RAT]	72.41	1	10	11	182	0.1031
P08430	UDP-glucuronosyltransferase 1-6 OS=Rattus norvegicus GN=Ugt1a6 PE=1 SV=1 - [UD16_RAT]	20.79	6	4	7	70	0.1032
P17475	Alpha-1-antiproteinase OS=Rattus norvegicus GN=Serpina1 PE=1 SV=2 - [A1AT_RAT]	53.77	1	21	21	1566	0.1056
P43244	Matrin-3 OS=Rattus norvegicus GN=Matr3 PE=1 SV=2 - [MATR3_RAT]	8.05	1	4	4	17	0.1057
P36876	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Rattus norvegicus GN=Ppp2r2a PE=2 SV=1 - [2ABA_RAT]	6.94	1	2	2	6	0.1071
P06238	Alpha-2-macroglobulin OS=Rattus norvegicus GN=A2m PE=2 SV=2 - [A2MG_RAT]	56.05	1	63	64	1143	0.1076
P04692	Tropomyosin alpha-1 chain OS=Rattus norvegicus GN=Tpm1 PE=1 SV=3 - [TPM1_RAT]	38.38	1	1	13	135	0.1077
P02680	Fibrinogen gamma chain OS=Rattus norvegicus GN=Fgg PE=1 SV=3 - [FIBG_RAT]	63.82	1	24	24	880	0.1091
P20059	Hemopexin OS=Rattus norvegicus GN=Hpx PE=1 SV=3 - [HEMO_RAT]	64.35	1	30	30	2205	0.1091
Q63716	Peroxiredoxin-1 OS=Rattus norvegicus GN=Prdx1 PE=1 SV=1 - [PRDX1_RAT]	74.37	1	13	15	648	0.1106
Q6P6R2	Dihydrolipoyl dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Dld PE=1 SV=1 - [DLDH_RAT]	42.04	1	14	14	283	0.1118
P00786	Pro-cathepsin H OS=Rattus norvegicus GN=Ctsh PE=1 SV=1 - [CATH_RAT]	6.31	1	2	2	3	0.1128
Q8VD48	Dehydrogenase/reductase SDR family member 9 OS=Rattus norvegicus GN=Dhrs9 PE=2 SV=1 - [DHRS9_RAT]	9.40	1	2	2	2	0.1133
Q924S5	Lon protease homolog, mitochondrial OS=Rattus norvegicus GN=Lonp1 PE=2 SV=1 - [LONM_RAT]	4.63	1	2	2	2	0.1145
P27952	40S ribosomal protein S2 OS=Rattus norvegicus GN=Rps2 PE=1 SV=1 - [RS2_RAT]	19.80	1	5	5	24	0.1161
Q6AXX6	Redox-regulatory protein FAM213A OS=Rattus norvegicus GN=Fam213a PE=1 SV=1 - [F213A_RAT]	15.72	1	3	3	18	0.1167
P12369	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus GN=Prkar2b PE=1 SV=3 - [KAP3_RAT]	57.45	1	15	15	165	0.1172
P50503	Hsc70-interacting protein OS=Rattus norvegicus GN=St13 PE=1 SV=1 - [F10A1_RAT]	10.33	1	3	3	21	0.1178
P41350	Caveolin-1 OS=Rattus norvegicus GN=Cav1 PE=1 SV=3 - [CAV1_RAT]	63.48	1	10	10	483	0.1179
P14141	Carbonic anhydrase 3 OS=Rattus norvegicus GN=Ca3 PE=1 SV=3 - [CAH3_RAT]	87.31	1	22	22	15804	0.1185
Q63965	Sideroflexin-1 OS=Rattus norvegicus GN=Sfxn1 PE=2 SV=4 - [SFXN1_RAT]	20.19	1	3	3	5	0.1189
Q5I0P2	Glycine cleavage system H protein, mitochondrial OS=Rattus norvegicus GN=Gcsh PE=2 SV=1 - [GCSH_RAT]	33.53	1	3	3	12	0.1190
P01048	T-kininogen 1 OS=Rattus norvegicus GN=Map1 PE=1 SV=2 - [KNT1_RAT]	50.23	1	8	20	1120	0.1194
P09006	Serine protease inhibitor A3N OS=Rattus norvegicus GN=Serpina3n PE=1 SV=3 - [SPA3N_RAT]	68.18	1	24	24	753	0.1211
O35763	Moesin OS=Rattus norvegicus GN=Msn PE=1 SV=3 - [MOES_RAT]	33.80	1	11	18	237	0.1214
Q7TP54	Protein FAM65B OS=Rattus norvegicus GN=Fam65b	11.45	1	2	13	396	0.1217

	PE=1 SV=1 - [FA65B_RAT]						
P14668	Annexin A5 OS=Rattus norvegicus GN=Anxa5 PE=1 SV=3 - [ANXA5_RAT]	73.04	1	23	23	1185	0.1225
P0C2X9	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Aldh4a1 PE=1 SV=1 - [AL4A1_RAT]	6.57	1	2	2	3	0.1235
P14480	Fibrinogen beta chain OS=Rattus norvegicus GN=Fgb PE=1 SV=4 - [FIBB_RAT]	71.40	1	34	34	956	0.1244
P23457	3-alpha-hydroxysteroid dehydrogenase OS=Rattus norvegicus GN=Akr1c9 PE=1 SV=1 - [DIDH_RAT]	47.52	1	10	12	164	0.1245
P48500	Triosephosphate isomerase OS=Rattus norvegicus GN=Tpi1 PE=1 SV=2 - [TPIS_RAT]	85.54	1	16	16	712	0.1262
Q6PCU2	V-type proton ATPase subunit E 1 OS=Rattus norvegicus GN=Atp6v1e1 PE=1 SV=1 - [VATE1_RAT]	13.27	1	2	2	25	0.1267
P62832	60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1 - [RL23_RAT]	32.14	1	3	3	27	0.1272
P61589	Transforming protein RhoA OS=Rattus norvegicus GN=Rhoa PE=1 SV=1 - [RHOA_RAT]	67.36	1	10	10	129	0.1277
P48199	C-reactive protein OS=Rattus norvegicus GN=Crp PE=1 SV=1 - [CRP_RAT]	32.61	1	5	5	270	0.1299
P15651	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acads PE=1 SV=2 - [ACADS_RAT]	27.18	1	7	8	24	0.1306
P23358	60S ribosomal protein L12 OS=Rattus norvegicus GN=Rpl12 PE=2 SV=1 - [RL12_RAT]	59.39	1	7	7	92	0.1316
Q9WVK7	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Hadh PE=2 SV=1 - [HCDH_RAT]	67.52	1	12	12	415	0.1321
P85971	6-phosphogluconolactonase OS=Rattus norvegicus GN=Pgls PE=1 SV=1 - [6PGL_RAT]	30.74	1	4	4	106	0.1322
P08932	T-kininogen 2 OS=Rattus norvegicus PE=1 SV=2 - [KNT2_RAT]	63.49	1	7	22	862	0.1324
P61983	14-3-3 protein gamma OS=Rattus norvegicus GN=Ywhag PE=1 SV=2 - [1433G_RAT]	80.97	1	12	19	673	0.1345
Q63610	Tropomyosin alpha-3 chain OS=Rattus norvegicus GN=Tpm3 PE=1 SV=2 - [TPM3_RAT]	53.63	1	9	17	198	0.1349
P67779	Prohibitin OS=Rattus norvegicus GN=Phb PE=1 SV=1 - [PHB_RAT]	80.15	1	15	15	140	0.1351
P47942	Dihydropyrimidinase-related protein 2 OS=Rattus norvegicus GN=Dpysl2 PE=1 SV=1 - [DPYL2_RAT]	44.76	1	12	15	245	0.1352
B2RZ37	Receptor expression-enhancing protein 5 OS=Rattus norvegicus GN=Reep5 PE=1 SV=1 - [REEP5_RAT]	25.93	1	8	8	327	0.1353
B0K020	CDGSH iron-sulfur domain-containing protein 1 OS=Rattus norvegicus GN=Cisd1 PE=3 SV=1 - [CISD1_RAT]	34.26	1	3	3	8	0.1356
Q4V8F9	Hydroxysteroid dehydrogenase-like protein 2 OS=Rattus norvegicus GN=Hsdl2 PE=2 SV=1 - [HSDL2_RAT]	5.53	1	2	2	9	0.1358
P19356	Porphobilinogen deaminase OS=Rattus norvegicus GN=Hmbs PE=1 SV=2 - [HEM3_RAT]	11.08	1	2	2	7	0.1360
P02764	Alpha-1-acid glycoprotein OS=Rattus norvegicus GN=Orm1 PE=2 SV=1 - [A1AG_RAT]	29.76	1	9	9	75	0.1386
P61980	Heterogeneous nuclear ribonucleoprotein K OS=Rattus norvegicus GN=Hnrnpk PE=1 SV=1 - [HNRPK_RAT]	27.00	1	8	9	80	0.1388
Q6AY20	Cation-dependent mannose-6-phosphate receptor OS=Rattus norvegicus GN=M6pr PE=1 SV=1 - [MPRD_RAT]	8.27	1	2	2	2	0.1392
P63326	40S ribosomal protein S10 OS=Rattus norvegicus GN=Rps10 PE=2 SV=1 - [RS10_RAT]	14.55	1	2	2	8	0.1397
P34067	Proteasome subunit beta type-4 OS=Rattus norvegicus GN=Psmb4 PE=1 SV=2 - [PSB4_RAT]	29.66	1	5	5	9	0.1408
Q62736	Non-muscle caldesmon OS=Rattus norvegicus GN=Cald1 PE=1 SV=1 - [CALD1_RAT]	19.40	1	8	8	41	0.1429
Q63663	Guanylate-binding protein 1 OS=Rattus norvegicus GN=Gbp2 PE=1 SV=2 - [GBP2_RAT]	2.72	1	2	2	2	0.1440
P08934	Kininogen-1 OS=Rattus norvegicus GN=Kng1 PE=2 SV=1 - [KNG1_RAT]	18.47	1	7	10	58	0.1442

Q2TL32	E3 ubiquitin-protein ligase UBR4 OS=Rattus norvegicus GN=Ubr4 PE=1 SV=2 - [UBR4_RAT]	2.95	1	8	8	22	0.1453
P30427	Plectin OS=Rattus norvegicus GN=Plec PE=1 SV=2 - [PLEC_RAT]	18.58	1	60	62	194	0.1455
Q9WTV5	26S proteasome non-ATPase regulatory subunit 9 OS=Rattus norvegicus GN=Psmd9 PE=1 SV=1 - [PSMD9_RAT]	9.01	1	2	2	2	0.1458
P07824	Arginase-1 OS=Rattus norvegicus GN=Arg1 PE=1 SV=2 - [ARGI1_RAT]	11.76	1	2	2	3	0.1462
O35331	Pyridoxal kinase OS=Rattus norvegicus GN=Pdxk PE=1 SV=1 - [PDXK_RAT]	5.13	1	2	2	2	0.1464
Q6UPE1	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Rattus norvegicus GN=Etfdh PE=1 SV=1 - [ETFD_RAT]	3.73	1	2	2	2	0.1464
Q64550	UDP-glucuronosyltransferase 1-1 OS=Rattus norvegicus GN=Ugt1a1 PE=1 SV=1 - [UD11_RAT]	13.27	1	1	4	64	0.1470
P31722	Complement C1q subcomponent subunit C OS=Rattus norvegicus GN=C1qc PE=1 SV=2 - [C1QC_RAT]	16.73	1	3	3	5	0.1475
P08010	Glutathione S-transferase Mu 2 OS=Rattus norvegicus GN=Gstm2 PE=1 SV=2 - [GSTM2_RAT]	73.39	1	10	17	304	0.1476
P62909	40S ribosomal protein S3 OS=Rattus norvegicus GN=Rps3 PE=1 SV=1 - [RS3_RAT]	53.09	1	10	10	97	0.1496
P52555	Endoplasmic reticulum resident protein 29 OS=Rattus norvegicus GN=Erp29 PE=1 SV=2 - [ERP29_RAT]	51.54	1	9	9	95	0.1501
P11884	Aldehyde dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Aldh2 PE=1 SV=1 - [ALDH2_RAT]	56.26	1	20	20	567	0.1512
P11960	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial (Fragment) OS=Rattus norvegicus GN=Bckdha PE=1 SV=1 - [ODBA_RAT]	13.15	1	3	3	8	0.1527
P97687	Ectonucleoside triphosphate diphosphohydrolase 1 OS=Rattus norvegicus GN=Entpd1 PE=1 SV=1 - [ENTP1_RAT]	5.48	1	2	2	2	0.1536
O09171	Betaine--homocysteine S-methyltransferase 1 OS=Rattus norvegicus GN=Bhmt PE=1 SV=1 - [BHMT1_RAT]	11.06	1	4	4	7	0.1543
Q63525	Nuclear migration protein nudC OS=Rattus norvegicus GN=Nudc PE=1 SV=1 - [NUDC_RAT]	6.02	1	2	2	2	0.1546
P47875	Cysteine and glycine-rich protein 1 OS=Rattus norvegicus GN=Csrp1 PE=1 SV=2 - [CSRP1_RAT]	30.57	1	5	5	99	0.1559
P13832	Myosin regulatory light chain RLC-A OS=Rattus norvegicus GN=Rlc-a PE=2 SV=2 - [MRLCA_RAT]	34.30	2	5	5	51	0.1561
Q63514	C4b-binding protein alpha chain OS=Rattus norvegicus GN=C4bpa PE=2 SV=1 - [C4BPA_RAT]	19.53	1	9	9	34	0.1561
Q9EPB1	Dipeptidyl peptidase 2 OS=Rattus norvegicus GN=Dpp7 PE=1 SV=1 - [DPP2_RAT]	4.20	1	2	2	2	0.1574
P04937	Fibronectin OS=Rattus norvegicus GN=Fn1 PE=1 SV=2 - [FINC_RAT]	23.46	1	35	35	173	0.1575
P48037	Annexin A6 OS=Rattus norvegicus GN=Anxa6 PE=1 SV=2 - [ANXA6_RAT]	68.50	1	44	44	1194	0.1582
Q63584	Transmembrane emp24 domain-containing protein 10 OS=Rattus norvegicus GN=Tmed10 PE=1 SV=2 - [TMEDA_RAT]	17.81	1	3	3	36	0.1584
P97849	Long-chain fatty acid transport protein 1 OS=Rattus norvegicus GN=Slc27a1 PE=2 SV=1 - [S27A1_RAT]	17.49	1	7	7	99	0.1591
Q5HZA4	LysM and putative peptidoglycan-binding domain-containing protein 1 OS=Rattus norvegicus GN=Lysmd1 PE=1 SV=1 - [LYSM1_RAT]	11.01	1	2	2	2	0.1598
Q9EQP5	Prolargin OS=Rattus norvegicus GN=Prelp PE=2 SV=1 - [PRELP_RAT]	42.44	1	12	12	92	0.1608
Q5I0E7	Transmembrane emp24 domain-containing protein 9 OS=Rattus norvegicus GN=Tmed9 PE=1 SV=1 - [TMED9_RAT]	19.15	1	4	4	18	0.1614
P04166	Cytochrome b5 type B OS=Rattus norvegicus GN=Cyb5b PE=1 SV=2 - [CYB5B_RAT]	51.37	1	4	4	61	0.1622
P01041	Cystatin-B OS=Rattus norvegicus GN=Cstb PE=1 SV=1 - [CYTB_RAT]	34.69	1	3	3	23	0.1631
Q75WE7	von Willebrand factor A domain-containing protein 5A OS=Rattus norvegicus GN=Vwa5a PE=2 SV=1 -	5.96	1	4	4	5	0.1642

	[VWA5A_RAT]						
Q8R4Z9	Mitofusin-1 OS=Rattus norvegicus GN=Mfn1 PE=1 SV=1 - [MFN1_RAT]	3.78	1	2	2	2	0.1648
Q62930	Complement component C9 OS=Rattus norvegicus GN=C9 PE=2 SV=1 - [CO9_RAT]	51.44	1	22	22	182	0.1654
P31399	ATP synthase subunit d, mitochondrial OS=Rattus norvegicus GN=Atp5h PE=1 SV=3 - [ATP5H_RAT]	34.16	1	5	5	31	0.1654
P15304	Hormone-sensitive lipase OS=Rattus norvegicus GN=Lipe PE=1 SV=3 - [LIPS_RAT]	45.60	1	31	31	970	0.1673
P19945	60S acidic ribosomal protein P0 OS=Rattus norvegicus GN=Rplp0 PE=1 SV=2 - [RLA0_RAT]	43.85	1	8	9	151	0.1675
B0BNF1	Septin-8 OS=Rattus norvegicus GN=Sept8 PE=1 SV=1 - [SEPT8_RAT]	4.07	1	1	2	6	0.1692
Q99PF5	Far upstream element-binding protein 2 OS=Rattus norvegicus GN=Khsrp PE=1 SV=1 - [FUBP2_RAT]	4.99	1	3	3	7	0.1696
O35244	Peroxiredoxin-6 OS=Rattus norvegicus GN=Prdx6 PE=1 SV=3 - [PRDX6_RAT]	67.86	1	13	13	231	0.1701
Q4KLF8	Actin-related protein 2/3 complex subunit 5 OS=Rattus norvegicus GN=Arpc5 PE=1 SV=3 - [ARPC5_RAT]	16.56	1	2	2	19	0.1707
Q5XI78	2-oxoglutarate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ogdh PE=1 SV=1 - [ODO1_RAT]	40.57	1	28	28	412	0.1711
P09330	Ribose-phosphate pyrophosphokinase 2 OS=Rattus norvegicus GN=Prps2 PE=1 SV=3 - [PRPS2_RAT]	10.06	2	2	2	2	0.1731
P04904	Glutathione S-transferase alpha-3 OS=Rattus norvegicus GN=Gsta3 PE=1 SV=3 - [GSTA3_RAT]	63.80	1	10	10	143	0.1733
Q64232	Very-long-chain enoyl-CoA reductase OS=Rattus norvegicus GN=Tecr PE=1 SV=1 - [TECR_RAT]	21.10	1	7	7	36	0.1735
P16617	Phosphoglycerate kinase 1 OS=Rattus norvegicus GN=Pgk1 PE=1 SV=2 - [PGK1_RAT]	74.10	1	24	24	437	0.1739
P27139	Carbonic anhydrase 2 OS=Rattus norvegicus GN=Ca2 PE=1 SV=2 - [CAH2_RAT]	64.62	1	12	12	391	0.1757
Q9EPF2	Cell surface glycoprotein MUC18 OS=Rattus norvegicus GN=Mcam PE=1 SV=2 - [MUC18_RAT]	43.06	1	21	21	337	0.1764
O08619	Coagulation factor XIII A chain OS=Rattus norvegicus GN=F13a1 PE=2 SV=3 - [F13A_RAT]	20.90	1	12	12	203	0.1767
P05942	Protein S100-A4 OS=Rattus norvegicus GN=S100a4 PE=2 SV=1 - [S10A4_RAT]	27.72	1	3	3	66	0.1770
P25235	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Rattus norvegicus GN=Rpn2 PE=2 SV=2 - [RPN2_RAT]	43.58	1	13	13	170	0.1773
Q794E4	Heterogeneous nuclear ribonucleoprotein F OS=Rattus norvegicus GN=Hnrnpf PE=1 SV=3 - [HNRPF_RAT]	10.36	1	2	3	29	0.1779
P00388	NADPH--cytochrome P450 reductase OS=Rattus norvegicus GN=Por PE=1 SV=3 - [NCPR_RAT]	33.48	1	15	15	104	0.1798
Q9JJ22	Endoplasmic reticulum aminopeptidase 1 OS=Rattus norvegicus GN=Erap1 PE=2 SV=2 - [ERAP1_RAT]	10.75	1	6	7	30	0.1818
P07687	Epoxide hydrolase 1 OS=Rattus norvegicus GN=Ephx1 PE=1 SV=1 - [HYEP_RAT]	7.03	1	2	2	3	0.1824
O35854	Branched-chain-amino-acid aminotransferase, mitochondrial OS=Rattus norvegicus GN=Bcat2 PE=1 SV=1 - [BCAT2_RAT]	12.47	1	4	4	5	0.1842
Q6P7Q4	Lactoylglutathione lyase OS=Rattus norvegicus GN=Glo1 PE=1 SV=3 - [LGUL_RAT]	41.30	1	7	7	76	0.1850
P55260	Annexin A4 OS=Rattus norvegicus GN=Anxa4 PE=1 SV=3 - [ANXA4_RAT]	53.61	1	14	14	123	0.1853
P07335	Creatine kinase B-type OS=Rattus norvegicus GN=Ckb PE=1 SV=2 - [KCRB_RAT]	59.32	1	16	16	287	0.1898
P84092	AP-2 complex subunit mu OS=Rattus norvegicus GN=Ap2m1 PE=1 SV=1 - [AP2M1_RAT]	12.18	1	5	5	8	0.1905
Q63270	Cytoplasmic aconitate hydratase OS=Rattus norvegicus GN=Aco1 PE=1 SV=1 - [ACOC_RAT]	40.04	1	24	24	515	0.1906
Q6IFU8	Keratin, type I cytoskeletal 17 OS=Rattus norvegicus GN=Krt17 PE=1 SV=1 - [K1C17_RAT]	20.79	1	6	8	16	0.1910
P58365	Cadherin-23 OS=Rattus norvegicus GN=Cdh23 PE=2 SV=1 - [CAD23_RAT]	1.12	1	2	2	2	0.1931
Q62975	Protein Z-dependent protease inhibitor OS=Rattus norvegicus GN=Serpina10 PE=2 SV=2 - [ZPI_RAT]	11.01	1	3	3	3	0.1973

Q9Z311	Trans-2-enoyl-CoA reductase, mitochondrial OS=Rattus norvegicus GN=Mecr PE=1 SV=1 - [MECR_RAT]	20.64	1	2	2	12	0.1984
P16303	Carboxylesterase 1D OS=Rattus norvegicus GN=Ces1d PE=1 SV=2 - [CES1D_RAT]	53.63	1	28	28	3036	0.1999
Q9JLA3	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Rattus norvegicus GN=Uggt1 PE=1 SV=2 - [UGGG1_RAT]	22.82	1	20	22	137	0.2004
Q6P5P5	Mesoderm-specific transcript homolog protein OS=Rattus norvegicus GN=Mest PE=2 SV=1 - [MEST_RAT]	26.87	1	5	5	95	0.2020
P70615	Lamin-B1 OS=Rattus norvegicus GN=Lmnb1 PE=1 SV=3 - [LMNB1_RAT]	19.76	1	6	8	21	0.2023
Q4V7A0	WD repeat-containing protein 61 OS=Rattus norvegicus GN=Wdr61 PE=1 SV=1 - [WDR61_RAT]	11.80	1	2	2	7	0.2031
Q5XI32	F-actin-capping protein subunit beta OS=Rattus norvegicus GN=Capzb PE=1 SV=1 - [CAPZB_RAT]	19.85	1	4	5	32	0.2032
P17077	60S ribosomal protein L9 OS=Rattus norvegicus GN=Rpl9 PE=1 SV=1 - [RL9_RAT]	35.42	1	5	5	10	0.2032
P04355	Metallothionein-2 OS=Rattus norvegicus GN=Mt2 PE=1 SV=1 - [MT2_RAT]	21.31	1	2	2	8	0.2046
Q9JHW0	Proteasome subunit beta type-7 OS=Rattus norvegicus GN=Psmb7 PE=1 SV=1 - [PSB7_RAT]	13.72	1	3	3	6	0.2046
Q63416	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Rattus norvegicus GN=Itih3 PE=2 SV=1 - [ITIH3_RAT]	33.93	1	19	20	441	0.2047
Q00657	Chondroitin sulfate proteoglycan 4 OS=Rattus norvegicus GN=Cspg4 PE=1 SV=2 - [CSPG4_RAT]	1.33	1	2	2	2	0.2061
P63095	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Rattus norvegicus GN=Gnas PE=1 SV=1 - [GNAS2_RAT]	27.16	2	6	7	116	0.2072
Q63355	Unconventional myosin-Ic OS=Rattus norvegicus GN=Myo1c PE=1 SV=2 - [MYO1C_RAT]	53.54	1	48	50	1492	0.2090
P81128	Rho GTPase-activating protein 35 OS=Rattus norvegicus GN=Arhgap35 PE=1 SV=2 - [RHG35_RAT]	2.38	1	2	2	2	0.2122
P51886	Lumican OS=Rattus norvegicus GN=Lum PE=1 SV=1 - [LUM_RAT]	36.09	1	11	11	380	0.2128
Q4QQT4	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Rattus norvegicus GN=Ppp2r1b PE=2 SV=1 - [2AAB_RAT]	6.99	1	3	3	33	0.2130
P85834	Elongation factor Tu, mitochondrial OS=Rattus norvegicus GN=Tufm PE=1 SV=1 - [EFTU_RAT]	4.87	1	2	2	4	0.2138
P06757	Alcohol dehydrogenase 1 OS=Rattus norvegicus GN=Adh1 PE=1 SV=3 - [ADH1_RAT]	9.04	1	3	3	6	0.2139
P31977	Ezrin OS=Rattus norvegicus GN=Ezr PE=1 SV=3 - [EZRI_RAT]	16.72	1	3	9	135	0.2142
P09495	Tropomyosin alpha-4 chain OS=Rattus norvegicus GN=Tpm4 PE=1 SV=3 - [TPM4_RAT]	52.42	1	7	16	210	0.2149
P30713	Glutathione S-transferase theta-2 OS=Rattus norvegicus GN=Gstt2 PE=1 SV=3 - [GSTT2_RAT]	9.84	1	2	2	2	0.2170
P18418	Calreticulin OS=Rattus norvegicus GN=Calr PE=1 SV=1 - [CALR_RAT]	66.83	1	21	21	325	0.2180
Q5XIC0	Enoyl-CoA delta isomerase 2, mitochondrial OS=Rattus norvegicus GN=Eci2 PE=1 SV=1 - [ECI2_RAT]	9.72	1	3	3	6	0.2182
P38656	Lupus La protein homolog OS=Rattus norvegicus GN=Ssb PE=1 SV=1 - [LA_RAT]	11.57	1	2	3	3	0.2188
P97576	GrpE protein homolog 1, mitochondrial OS=Rattus norvegicus GN=Grpel1 PE=1 SV=2 - [GRPE1_RAT]	11.52	1	2	2	4	0.2205
Q9QX27	Suppression of tumorigenicity 18 protein OS=Rattus norvegicus GN=St18 PE=2 SV=2 - [ST18_RAT]	2.52	1	2	2	2	0.2224
Q64240	Protein AMBP OS=Rattus norvegicus GN=Ambp PE=1 SV=1 - [AMBP_RAT]	15.47	1	4	4	61	0.2226
P00507	Aspartate aminotransferase, mitochondrial OS=Rattus norvegicus GN=Got2 PE=1 SV=2 - [AATM_RAT]	34.88	1	11	11	82	0.2227
P24268	Cathepsin D OS=Rattus norvegicus GN=Ctsd PE=1 SV=1 - [CATD_RAT]	29.73	1	7	8	43	0.2227
P36972	Adenine phosphoribosyltransferase OS=Rattus norvegicus GN=Aprt PE=1 SV=1 - [APT_RAT]	79.44	1	11	11	222	0.2249

Q9WTT6	Guanine deaminase OS=Rattus norvegicus GN=Gda PE=1 SV=1 - [GUAD_RAT]	72.47	1	27	27	1116	0.2252
P18163	Long-chain-fatty-acid--CoA ligase 1 OS=Rattus norvegicus GN=Acsl1 PE=1 SV=1 - [ACSL1_RAT]	71.67	1	39	41	3291	0.2255
P30904	Macrophage migration inhibitory factor OS=Rattus norvegicus GN=Mif PE=1 SV=4 - [MIF_RAT]	13.91	1	2	2	3	0.2287
Q9Z2Q1	Protein transport protein Sec31A OS=Rattus norvegicus GN=Sec31a PE=1 SV=2 - [SC31A_RAT]	13.53	1	10	10	95	0.2289
Q8VI04	Isoaspartyl peptidase/L-asparaginase OS=Rattus norvegicus GN=Asrgl1 PE=1 SV=1 - [ASGL1_RAT]	25.53	1	6	6	12	0.2298
P00884	Fructose-bisphosphate aldolase B OS=Rattus norvegicus GN=Aldob PE=1 SV=2 - [ALDOB_RAT]	22.80	1	6	6	9	0.2313
P62703	40S ribosomal protein S4, X isoform OS=Rattus norvegicus GN=Rps4x PE=2 SV=2 - [RS4X_RAT]	22.43	1	6	6	17	0.2318
Q6Q0N1	Cytosolic non-specific dipeptidase OS=Rattus norvegicus GN=Cndp2 PE=1 SV=1 - [CNDP2_RAT]	44.84	1	16	16	133	0.2319
Q920A6	Retinoid-inducible serine carboxypeptidase OS=Rattus norvegicus GN=Scpep1 PE=2 SV=1 - [RISC_RAT]	17.48	1	5	6	109	0.2320
Q63279	Keratin, type I cytoskeletal 19 OS=Rattus norvegicus GN=Krt19 PE=1 SV=2 - [K1C19_RAT]	38.21	1	9	11	39	0.2322
B2GV38	Ubiquitin-like protein 4A OS=Rattus norvegicus GN=Ubl4a PE=2 SV=1 - [UBL4A_RAT]	19.75	1	2	2	2	0.2328
P30835	ATP-dependent 6-phosphofructokinase, liver type OS=Rattus norvegicus GN=Pfkl PE=1 SV=3 - [PFKAL_RAT]	3.85	1	3	3	5	0.2332
P62278	40S ribosomal protein S13 OS=Rattus norvegicus GN=Rps13 PE=1 SV=2 - [RS13_RAT]	45.03	1	6	7	21	0.2352
Q9JJ79	Cytoplasmic dynein 2 heavy chain 1 OS=Rattus norvegicus GN=Dync2h1 PE=1 SV=1 - [DYHC2_RAT]	4.11	1	6	11	14	0.2357
Q4FZU2	Keratin, type II cytoskeletal 6A OS=Rattus norvegicus GN=Krt6a PE=1 SV=1 - [K2C6A_RAT]	7.43	1	1	5	60	0.2358
P10688	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1 OS=Rattus norvegicus GN=Plcd1 PE=1 SV=1 - [PLCD1_RAT]	7.41	1	2	3	7	0.2359
Q6IG05	Keratin, type II cytoskeletal 75 OS=Rattus norvegicus GN=Krt75 PE=3 SV=2 - [K2C75_RAT]	12.18	1	3	9	56	0.2365
Q5XFX0	Transgelin-2 OS=Rattus norvegicus GN=Tagln2 PE=1 SV=1 - [TAGL2_RAT]	85.93	1	17	17	585	0.2372
P00173	Cytochrome b5 OS=Rattus norvegicus GN=Cyb5a PE=1 SV=2 - [CYB5_RAT]	41.04	1	4	4	74	0.2387
Q63644	Rho-associated protein kinase 1 OS=Rattus norvegicus GN=Rock1 PE=1 SV=1 - [ROCK1_RAT]	2.26	1	2	2	3	0.2395
Q5U300	Ubiquitin-like modifier-activating enzyme 1 OS=Rattus norvegicus GN=Uba1 PE=1 SV=1 - [UBA1_RAT]	47.35	1	31	31	465	0.2402
D3ZHV2	Microtubule-actin cross-linking factor 1 OS=Rattus norvegicus GN=Macf1 PE=1 SV=1 - [MACF1_RAT]	0.77	1	2	3	6	0.2417
Q8VBU2	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1 - [NDRG2_RAT]	30.73	1	5	6	66	0.2422
P62804	Histone H4 OS=Rattus norvegicus GN=Hist1h4b PE=1 SV=2 - [H4_RAT]	53.40	1	8	8	285	0.2423
P51635	Alcohol dehydrogenase [NADP(+)] OS=Rattus norvegicus GN=Akr1a1 PE=1 SV=2 - [AK1A1_RAT]	46.15	1	13	13	127	0.2437
Q5BK81	Prostaglandin reductase 2 OS=Rattus norvegicus GN=Ptgr2 PE=2 SV=2 - [PTGR2_RAT]	36.18	1	7	7	21	0.2447
P84245	Histone H3.3 OS=Rattus norvegicus GN=H3f3b PE=1 SV=2 - [H33_RAT]	40.44	2	4	4	17	0.2464
P21531	60S ribosomal protein L3 OS=Rattus norvegicus GN=Rpl3 PE=1 SV=3 - [RL3_RAT]	17.12	1	4	4	32	0.2488
P14841	Cystatin-C OS=Rattus norvegicus GN=Cst3 PE=1 SV=2 - [CYTC_RAT]	29.29	1	3	3	32	0.2501
Q6NYB7	Ras-related protein Rab-1A OS=Rattus norvegicus GN=Rab1A PE=1 SV=3 - [RAB1A_RAT]	56.10	1	4	8	246	0.2505
Q07009	Calpain-2 catalytic subunit OS=Rattus norvegicus GN=Capn2 PE=1 SV=3 - [CAN2_RAT]	30.57	1	14	14	105	0.2511
P27881	Hexokinase-2 OS=Rattus norvegicus GN=Hk2 PE=1 SV=1 - [HXK2_RAT]	5.67	1	3	4	6	0.2520
P13086	Succinyl-CoA ligase [ADP/GDP-forming] subunit	40.46	1	8	9	67	0.2528

	alpha, mitochondrial OS=Rattus norvegicus GN=Suclg1 PE=2 SV=2 - [SUCA_RAT]						
P49911	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Rattus norvegicus GN=Anp32a PE=2 SV=1 - [AN32A_RAT]	34.41	1	5	6	42	0.2531
P19944	60S acidic ribosomal protein P1 OS=Rattus norvegicus GN=Rplp1 PE=3 SV=1 - [RLA1_RAT]	51.75	1	2	2	58	0.2560
P62161	Calmodulin OS=Rattus norvegicus GN=Calm1 PE=1 SV=2 - [CALM_RAT]	34.23	1	5	5	82	0.2562
P13221	Aspartate aminotransferase, cytoplasmic OS=Rattus norvegicus GN=Got1 PE=1 SV=3 - [AATC_RAT]	7.99	1	2	2	2	0.2590
F1MA98	Nucleoprotein TPR OS=Rattus norvegicus GN=Tpr PE=1 SV=1 - [TPR_RAT]	5.34	1	5	7	20	0.2596
P07943	Aldose reductase OS=Rattus norvegicus GN=Akr1b1 PE=1 SV=3 - [ALDR_RAT]	59.49	1	14	16	314	0.2599
P42667	Signal peptidase complex catalytic subunit SEC11A OS=Rattus norvegicus GN=Sec11a PE=2 SV=1 - [SC11A_RAT]	9.50	1	2	2	2	0.2650
P28073	Proteasome subunit beta type-6 OS=Rattus norvegicus GN=Psmb6 PE=1 SV=3 - [PSB6_RAT]	29.41	1	4	4	43	0.2654
P18484	AP-2 complex subunit alpha-2 OS=Rattus norvegicus GN=Ap2a2 PE=1 SV=3 - [AP2A2_RAT]	21.96	1	12	12	134	0.2670
P27653	C-1-tetrahydrofolate synthase, cytoplasmic OS=Rattus norvegicus GN=Mthfd1 PE=1 SV=3 - [C1TC_RAT]	2.99	1	2	2	2	0.2684
P62775	Myotrophin OS=Rattus norvegicus GN=Mtpn PE=1 SV=2 - [MTPN_RAT]	25.42	1	2	2	27	0.2690
P33124	Long-chain-fatty-acid--CoA ligase 6 OS=Rattus norvegicus GN=Acsl6 PE=1 SV=1 - [ACSL6_RAT]	2.73	1	1	2	294	0.2692
P02091	Hemoglobin subunit beta-1 OS=Rattus norvegicus GN=Hbb PE=1 SV=3 - [HBB1_RAT]	89.80	1	5	16	15616	0.2710
P63159	High mobility group protein B1 OS=Rattus norvegicus GN=Hmgb1 PE=1 SV=2 - [HMGB1_RAT]	25.58	1	5	5	19	0.2720
Q5U1Z2	Trafficking protein particle complex subunit 3 OS=Rattus norvegicus GN=Trappc3 PE=2 SV=1 - [TPPC3_RAT]	18.33	1	3	3	4	0.2739
Q9WVC0	Septin-7 OS=Rattus norvegicus GN=Sept7 PE=1 SV=1 - [SEPT7_RAT]	17.43	1	5	6	55	0.2748
P47245	Nardilysin OS=Rattus norvegicus GN=Nrd1 PE=1 SV=1 - [NRDC_RAT]	6.46	1	4	4	16	0.2760
Q6AY09	Heterogeneous nuclear ribonucleoprotein H2 OS=Rattus norvegicus GN=Hnrnph2 PE=1 SV=1 - [HNRH2_RAT]	9.58	1	2	3	8	0.2781
P12346	Serotransferrin OS=Rattus norvegicus GN=Tf PE=1 SV=3 - [TRFE_RAT]	73.93	1	46	46	5865	0.2806
P04644	40S ribosomal protein S17 OS=Rattus norvegicus GN=Rps17 PE=1 SV=3 - [RS17_RAT]	58.52	1	7	7	62	0.2857
Q9QX79	Fetuin-B OS=Rattus norvegicus GN=Fetub PE=2 SV=2 - [FETUB_RAT]	58.47	1	17	17	385	0.2870
P62859	40S ribosomal protein S28 OS=Rattus norvegicus GN=Rps28 PE=1 SV=1 - [RS28_RAT]	30.43	1	2	2	15	0.2910
P52296	Importin subunit beta-1 OS=Rattus norvegicus GN=Kpnb1 PE=1 SV=1 - [IMB1_RAT]	36.69	1	18	20	192	0.2923
P35565	Calnexin OS=Rattus norvegicus GN=Canx PE=1 SV=1 - [CALX_RAT]	37.56	1	18	18	210	0.2923
P20762	Ig gamma-2C chain C region OS=Rattus norvegicus PE=2 SV=1 - [IGG2C_RAT]	35.26	1	7	7	38	0.2923
Q5I0D1	Glyoxalase domain-containing protein 4 OS=Rattus norvegicus GN=Glod4 PE=1 SV=1 - [GLOD4_RAT]	36.91	1	7	8	40	0.2929
Q9Z0V5	Peroxiredoxin-4 OS=Rattus norvegicus GN=Prdx4 PE=2 SV=1 - [PRDX4_RAT]	29.30	1	4	6	207	0.2930
P61805	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Rattus norvegicus GN=Dad1 PE=3 SV=3 - [DAD1_RAT]	17.70	1	2	2	10	0.2938
Q62651	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Rattus norvegicus GN=Ech1 PE=1 SV=2 - [ECH1_RAT]	46.79	1	10	10	48	0.2960
P62828	GTP-binding nuclear protein Ran OS=Rattus norvegicus GN=Ran PE=1 SV=3 - [RAN_RAT]	31.02	2	6	6	54	0.2966

O35814	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1 - [STIP1_RAT]	6.81	1	2	2	14	0.2983
Q5QD51	A-kinase anchor protein 12 OS=Rattus norvegicus GN=Akap12 PE=1 SV=1 - [AKA12_RAT]	6.99	1	8	9	81	0.3001
P24368	Peptidyl-prolyl cis-trans isomerase B OS=Rattus norvegicus GN=Ppib PE=1 SV=3 - [PPIB_RAT]	51.39	1	12	12	218	0.3002
O55012	Phosphatidylinositol-binding clathrin assembly protein OS=Rattus norvegicus GN=Picalm PE=1 SV=1 - [PICAL_RAT]	13.75	1	4	5	18	0.3025
Q6AYQ4	Transmembrane protein 109 OS=Rattus norvegicus GN=Tmem109 PE=2 SV=1 - [TM109_RAT]	8.64	1	2	2	2	0.3035
Q63507	60S ribosomal protein L14 OS=Rattus norvegicus GN=Rpl14 PE=1 SV=3 - [RL14_RAT]	10.28	1	2	2	10	0.3037
P62198	26S protease regulatory subunit 8 OS=Rattus norvegicus GN=Psmc5 PE=1 SV=1 - [PRS8_RAT]	17.24	1	4	4	6	0.3043
P05765	40S ribosomal protein S21 OS=Rattus norvegicus GN=Rps21 PE=1 SV=1 - [RS21_RAT]	28.92	1	2	2	16	0.3046
P36372	Antigen peptide transporter 2 OS=Rattus norvegicus GN=Tap2 PE=2 SV=1 - [TAP2_RAT]	4.55	1	2	3	9	0.3066
P10824	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Rattus norvegicus GN=Gnai1 PE=1 SV=3 - [GNAI1_RAT]	35.31	1	3	9	108	0.3071
P62959	Histidine triad nucleotide-binding protein 1 OS=Rattus norvegicus GN=Hint1 PE=1 SV=5 - [HINT1_RAT]	37.30	1	3	3	15	0.3072
Q64428	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus GN=Hadha PE=1 SV=2 - [ECHA_RAT]	51.64	1	27	27	769	0.3082
P47727	Carbonyl reductase [NADPH] 1 OS=Rattus norvegicus GN=Cbr1 PE=1 SV=2 - [CBR1_RAT]	76.17	1	19	19	1414	0.3104
Q63544	Gamma-synuclein OS=Rattus norvegicus GN=Sncg PE=1 SV=2 - [SYUG_RAT]	74.80	1	11	11	559	0.3106
Q794F9	4F2 cell-surface antigen heavy chain OS=Rattus norvegicus GN=Slc3a2 PE=1 SV=1 - [4F2_RAT]	18.03	1	6	6	13	0.3144
P15684	Aminopeptidase N OS=Rattus norvegicus GN=Anpep PE=1 SV=2 - [AMPN_RAT]	25.80	1	16	17	76	0.3148
Q05175	Brain acid soluble protein 1 OS=Rattus norvegicus GN=Basp1 PE=1 SV=2 - [BASP1_RAT]	13.64	1	2	2	3	0.3183
P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	51.98	1	33	33	881	0.3193
Q5EB77	Ras-related protein Rab-18 OS=Rattus norvegicus GN=Rab18 PE=2 SV=1 - [RAB18_RAT]	50.49	1	8	8	66	0.3194
Q4V8H8	EH domain-containing protein 2 OS=Rattus norvegicus GN=Ehd2 PE=1 SV=1 - [EHD2_RAT]	73.30	1	31	32	2335	0.3199
Q9JJ54	Heterogeneous nuclear ribonucleoprotein D0 OS=Rattus norvegicus GN=Hnrnpd PE=1 SV=2 - [HNRPD_RAT]	6.23	1	2	2	2	0.3211
D4AE41	RNA binding motif protein, X-linked-like-1 OS=Rattus norvegicus GN=Rbmxl1 PE=3 SV=1 - [RMXL1_RAT]	10.31	3	3	3	4	0.3250
Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	25.97	1	9	9	41	0.3257
Q6P6Q2	Keratin, type II cytoskeletal 5 OS=Rattus norvegicus GN=Krt5 PE=1 SV=1 - [K2C5_RAT]	16.84	1	3	10	68	0.3274
B0BNN3	Carbonic anhydrase 1 OS=Rattus norvegicus GN=Ca1 PE=1 SV=1 - [CAH1_RAT]	85.82	1	13	13	634	0.3277
P41542	General vesicular transport factor p115 OS=Rattus norvegicus GN=Uso1 PE=1 SV=1 - [USO1_RAT]	8.45	1	6	7	36	0.3298
P21708	Mitogen-activated protein kinase 3 OS=Rattus norvegicus GN=Mapk3 PE=1 SV=5 - [MK03_RAT]	12.89	1	2	3	3	0.3322
B3DMA2	Acyl-CoA dehydrogenase family member 11 OS=Rattus norvegicus GN=Acad11 PE=1 SV=1 - [ACD11_RAT]	10.27	1	6	6	24	0.3333
O88656	Actin-related protein 2/3 complex subunit 1B OS=Rattus norvegicus GN=Arpc1b PE=1 SV=3 - [ARC1B_RAT]	13.17	1	4	4	12	0.3398
Q64573	Liver carboxylesterase 4 OS=Rattus norvegicus PE=2 SV=2 - [EST4_RAT]	10.87	1	1	3	49	0.3405
P19132	Ferritin heavy chain OS=Rattus norvegicus GN=Fth1 PE=1 SV=3 - [FRIH_RAT]	57.14	1	10	10	138	0.3405

P62083	40S ribosomal protein S7 OS=Rattus norvegicus GN=Rps7 PE=1 SV=1 - [RS7_RAT]	47.42	1	4	5	70	0.3405
P01026	Complement C3 OS=Rattus norvegicus GN=C3 PE=1 SV=3 - [CO3_RAT]	68.19	1	90	93	3006	0.3409
P63174	60S ribosomal protein L38 OS=Rattus norvegicus GN=Rpl38 PE=1 SV=2 - [RL38_RAT]	35.71	1	2	2	2	0.3409
P00697	Lysozyme C-1 OS=Rattus norvegicus GN=Lyz1 PE=1 SV=2 - [LYSC1_RAT]	28.38	1	2	2	2	0.3409
Q6AXZ4	Centrosomal protein CEP57L1 OS=Rattus norvegicus GN=Cep57l1 PE=2 SV=1 - [CE57L_RAT]	7.91	1	2	2	2	0.3409
P14272	Plasma kallikrein OS=Rattus norvegicus GN=Klkb1 PE=1 SV=1 - [KLKB1_RAT]	5.02	1	2	3	3	0.3409
Q5U1Z0	Rab3 GTPase-activating protein non-catalytic subunit OS=Rattus norvegicus GN=Rab3gap2 PE=1 SV=2 - [RBGPR_RAT]	4.26	1	2	2	6	0.3409
Q9Z1W6	Protein LYRIC OS=Rattus norvegicus GN=Mtdh PE=1 SV=2 - [LYRIC_RAT]	3.79	1	2	2	2	0.3409
Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	3.12	1	2	2	5	0.3409
P98158	Low-density lipoprotein receptor-related protein 2 OS=Rattus norvegicus GN=Lrp2 PE=1 SV=1 - [LRP2_RAT]	0.60	1	2	2	2	0.3409
P52303	AP-1 complex subunit beta-1 OS=Rattus norvegicus GN=Ap1b1 PE=1 SV=1 - [AP1B1_RAT]	24.24	1	4	12	135	0.3413
Q63570	26S protease regulatory subunit 6B OS=Rattus norvegicus GN=Psmc4 PE=1 SV=1 - [PRS6B_RAT]	17.70	1	3	3	83	0.3418
P04785	Protein disulfide-isomerase OS=Rattus norvegicus GN=P4hb PE=1 SV=2 - [PDIA1_RAT]	58.55	1	22	23	587	0.3457
Q62745	CD81 antigen OS=Rattus norvegicus GN=Cd81 PE=1 SV=1 - [CD81_RAT]	15.25	1	2	2	4	0.3464
Q9EQX9	Ubiquitin-conjugating enzyme E2 N OS=Rattus norvegicus GN=Ube2n PE=1 SV=1 - [UBE2N_RAT]	42.11	1	5	5	128	0.3466
P49242	40S ribosomal protein S3a OS=Rattus norvegicus GN=Rps3a PE=1 SV=2 - [RS3A_RAT]	21.59	1	4	5	13	0.3474
Q3KRD8	Eukaryotic translation initiation factor 6 OS=Rattus norvegicus GN=Eif6 PE=1 SV=1 - [IF6_RAT]	17.14	1	2	2	3	0.3478
Q9WU82	Catenin beta-1 OS=Rattus norvegicus GN=Ctnnb1 PE=1 SV=1 - [CTNB1_RAT]	4.10	1	2	2	3	0.3496
P10686	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 OS=Rattus norvegicus GN=Plcg1 PE=1 SV=1 - [PLCG1_RAT]	2.33	1	2	2	6	0.3500
Q62940	E3 ubiquitin-protein ligase NEDD4 OS=Rattus norvegicus GN=Nedd4 PE=1 SV=1 - [NEDD4_RAT]	18.38	1	11	11	96	0.3519
Q64542	Plasma membrane calcium-transporting ATPase 4 OS=Rattus norvegicus GN=Atp2b4 PE=1 SV=1 - [AT2B4_RAT]	3.91	1	2	3	7	0.3607
Q6QA69	1-acylglycerol-3-phosphate O-acyltransferase ABHD5 OS=Rattus norvegicus GN=Abhd5 PE=1 SV=1 - [ABHD5_RAT]	36.18	1	6	7	160	0.3612
G3V7P1	Syntaxin-12 OS=Rattus norvegicus GN=Stx12 PE=1 SV=1 - [STX12_RAT]	20.80	1	4	4	11	0.3615
P62907	60S ribosomal protein L10a OS=Rattus norvegicus GN=Rpl10a PE=1 SV=2 - [RL10A_RAT]	18.89	1	3	4	26	0.3629
P35434	ATP synthase subunit delta, mitochondrial OS=Rattus norvegicus GN=Atp5d PE=1 SV=2 - [ATPD_RAT]	13.69	1	2	2	21	0.3649
Q9QXQ0	Alpha-actinin-4 OS=Rattus norvegicus GN=Actn4 PE=1 SV=2 - [ACTN4_RAT]	48.30	1	19	32	306	0.3659
P11442	Clathrin heavy chain 1 OS=Rattus norvegicus GN=Cltc PE=1 SV=3 - [CLH1_RAT]	58.63	1	76	76	1172	0.3661
Q62812	Myosin-9 OS=Rattus norvegicus GN=Myh9 PE=1 SV=3 - [MYH9_RAT]	36.10	1	49	57	872	0.3663
P50878	60S ribosomal protein L4 OS=Rattus norvegicus GN=Rpl4 PE=1 SV=3 - [RL4_RAT]	11.88	1	3	4	16	0.3684
O35264	Platelet-activating factor acetylhydrolase IB subunit beta OS=Rattus norvegicus GN=Pafah1b2 PE=1 SV=1 - [PA1B2_RAT]	12.23	1	2	2	32	0.3695
Q9WVR7	Protein phosphatase 1F OS=Rattus norvegicus GN=Ppm1f PE=2 SV=1 - [PPM1F_RAT]	11.78	1	2	2	2	0.3696

Q9QZA2	Programmed cell death 6-interacting protein OS=Rattus norvegicus GN=Pdcd6ip PE=1 SV=2 - [PDC6I_RAT]	13.75	1	6	6	91	0.3715
P24090	Alpha-2-HS-glycoprotein OS=Rattus norvegicus GN=Ahsg PE=1 SV=2 - [FETUA_RAT]	38.92	1	8	8	500	0.3717
P27791	cAMP-dependent protein kinase catalytic subunit alpha OS=Rattus norvegicus GN=Prkaca PE=1 SV=2 - [KAPCA_RAT]	13.96	1	3	4	29	0.3718
Q63347	26S protease regulatory subunit 7 OS=Rattus norvegicus GN=Psmc2 PE=1 SV=3 - [PRS7_RAT]	5.31	1	2	2	2	0.3725
P30839	Fatty aldehyde dehydrogenase OS=Rattus norvegicus GN=Aldh3a2 PE=1 SV=1 - [AL3A2_RAT]	16.94	1	6	6	35	0.3728
Q5HZY2	GTP-binding protein SAR1b OS=Rattus norvegicus GN=Sar1b PE=2 SV=1 - [SAR1B_RAT]	25.25	1	3	3	3	0.3732
P16975	SPARC OS=Rattus norvegicus GN=Sparc PE=1 SV=4 - [SPRC_RAT]	11.63	1	3	3	5	0.3733
Q63617	Hypoxia up-regulated protein 1 OS=Rattus norvegicus GN=Hyou1 PE=1 SV=1 - [HYOU1_RAT]	27.43	1	17	19	179	0.3754
D3Z8L7	Ras-related protein R-Ras OS=Rattus norvegicus GN=Rras PE=1 SV=1 - [RRAS_RAT]	24.77	1	4	4	53	0.3787
P17046	Lysosome-associated membrane glycoprotein 2 OS=Rattus norvegicus GN=Lamp2 PE=1 SV=2 - [LAMP2_RAT]	7.30	1	2	2	11	0.3788
P28480	T-complex protein 1 subunit alpha OS=Rattus norvegicus GN=Tcp1 PE=1 SV=1 - [TCPA_RAT]	15.47	1	3	3	23	0.3790
P20171	GTPase HRas OS=Rattus norvegicus GN=Hras PE=1 SV=2 - [RASH_RAT]	20.11	2	3	3	9	0.3791
Q60587	Trifunctional enzyme subunit beta, mitochondrial OS=Rattus norvegicus GN=Hadhb PE=1 SV=1 - [ECHB_RAT]	46.11	1	17	17	196	0.3811
P17074	40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3 - [RS19_RAT]	44.14	1	7	7	97	0.3837
Q66H89	Centrosomal protein of 83 kDa OS=Rattus norvegicus GN=Cep83 PE=2 SV=1 - [CEP83_RAT]	3.47	1	3	3	7	0.3843
P10960	Prosaposin OS=Rattus norvegicus GN=Psap PE=1 SV=1 - [SAP_RAT]	3.79	1	2	2	3	0.3845
Q5M7W5	Microtubule-associated protein 4 OS=Rattus norvegicus GN=Map4 PE=1 SV=1 - [MAP4_RAT]	28.86	1	18	18	78	0.3862
P26453	Basigin OS=Rattus norvegicus GN=Bsg PE=1 SV=2 - [BASI_RAT]	21.39	1	8	8	63	0.3894
P11762	Galectin-1 OS=Rattus norvegicus GN=Lgals1 PE=1 SV=2 - [LEG1_RAT]	61.48	1	10	10	750	0.3894
P07151	Beta-2-microglobulin OS=Rattus norvegicus GN=B2m PE=1 SV=1 - [B2MG_RAT]	34.45	1	6	6	59	0.3903
P10252	CD48 antigen OS=Rattus norvegicus GN=Cd48 PE=1 SV=1 - [CD48_RAT]	15.83	1	3	3	5	0.3915
P54313	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Rattus norvegicus GN=Gnb2 PE=1 SV=4 - [GBB2_RAT]	56.18	1	7	13	168	0.3924
Q9Z1P2	Alpha-actinin-1 OS=Rattus norvegicus GN=Actn1 PE=1 SV=1 - [ACTN1_RAT]	41.48	1	12	25	218	0.3924
P27605	Hypoxanthine-guanine phosphoribosyltransferase OS=Rattus norvegicus GN=Hprt1 PE=1 SV=1 - [HPRT_RAT]	44.95	1	8	8	63	0.3994
P62716	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Rattus norvegicus GN=Ppp2cb PE=2 SV=1 - [PP2AB_RAT]	11.65	2	2	2	12	0.3998
Q641Y8	ATP-dependent RNA helicase DDX1 OS=Rattus norvegicus GN=Ddx1 PE=1 SV=1 - [DDX1_RAT]	5.14	1	2	2	3	0.3999
Q07969	Platelet glycoprotein 4 OS=Rattus norvegicus GN=Cd36 PE=1 SV=3 - [CD36_RAT]	36.86	1	11	11	676	0.4005
P27615	Lysosome membrane protein 2 OS=Rattus norvegicus GN=Scarb2 PE=1 SV=2 - [SCRB2_RAT]	7.95	1	2	2	4	0.4011
Q8VHE9	All-trans-retinol 13,14-reductase OS=Rattus norvegicus GN=Retsat PE=2 SV=1 - [RETST_RAT]	36.78	1	13	13	326	0.4052
P61023	Calcineurin B homologous protein 1 OS=Rattus norvegicus GN=Chp1 PE=1 SV=2 - [CHP1_RAT]	58.46	1	9	9	62	0.4057
Q7TQ94	Nitrilase homolog 1 OS=Rattus norvegicus GN=Nit1 PE=2 SV=1 - [NIT1_RAT]	38.70	1	5	6	40	0.4061

P07483	Fatty acid-binding protein, heart OS=Rattus norvegicus GN=Fabp3 PE=1 SV=2 - [FABPH_RAT]	34.59	1	4	4	5	0.4081
P32755	4-hydroxyphenylpyruvate dioxygenase OS=Rattus norvegicus GN=Hpd PE=1 SV=3 - [HPPD_RAT]	8.65	1	2	2	3	0.4107
Q6PCT3	Tumor protein D54 OS=Rattus norvegicus GN=Tpd52l2 PE=1 SV=1 - [TPD54_RAT]	14.55	1	2	2	4	0.4109
P19804	Nucleoside diphosphate kinase B OS=Rattus norvegicus GN=Nme2 PE=1 SV=1 - [NDKB_RAT]	75.00	1	5	11	575	0.4141
Q9Z1X1	Extended synaptotagmin-1 OS=Rattus norvegicus GN=Esyt1 PE=1 SV=1 - [ESYT1_RAT]	46.88	1	34	34	590	0.4163
P09527	Ras-related protein Rab-7a OS=Rattus norvegicus GN=Rab7a PE=1 SV=2 - [RAB7A_RAT]	66.18	1	10	10	140	0.4186
Q6B345	Protein S100-A11 OS=Rattus norvegicus GN=S100a11 PE=3 SV=1 - [S10AB_RAT]	46.94	1	4	4	100	0.4209
Q9WUW3	Complement factor I OS=Rattus norvegicus GN=Cfi PE=2 SV=1 - [CFAI_RAT]	7.62	1	2	3	5	0.4224
P62271	40S ribosomal protein S18 OS=Rattus norvegicus GN=Rps18 PE=1 SV=3 - [RS18_RAT]	48.68	1	10	10	117	0.4239
P01015	Angiotensinogen OS=Rattus norvegicus GN=Agt PE=1 SV=1 - [ANGT_RAT]	29.35	1	6	7	45	0.4252
Q63028	Alpha-adducin OS=Rattus norvegicus GN=Add1 PE=1 SV=2 - [ADDA_RAT]	14.69	1	4	5	22	0.4256
B0BNE5	S-formylglutathione hydrolase OS=Rattus norvegicus GN=Esd PE=2 SV=1 - [ESTD_RAT]	40.07	1	5	5	16	0.4260
P24942	Excitatory amino acid transporter 1 OS=Rattus norvegicus GN=Slc1a3 PE=1 SV=2 - [EAA1_RAT]	7.18	1	2	2	24	0.4261
P11980	Pyruvate kinase PKM OS=Rattus norvegicus GN=Pkm PE=1 SV=3 - [KPYM_RAT]	51.04	1	24	24	692	0.4272
Q64640	Adenosine kinase OS=Rattus norvegicus GN=Adk PE=1 SV=3 - [ADK_RAT]	20.50	1	3	3	10	0.4328
Q5XIU9	Membrane-associated progesterone receptor component 2 OS=Rattus norvegicus GN=Pgrmc2 PE=1 SV=1 - [PGRC2_RAT]	34.10	1	6	6	35	0.4363
Q68FS4	Cytosol aminopeptidase OS=Rattus norvegicus GN=Lap3 PE=1 SV=1 - [AMPL_RAT]	39.31	1	12	12	97	0.4369
Q9Z1H9	Protein kinase C delta-binding protein OS=Rattus norvegicus GN=Prkcdbp PE=1 SV=1 - [PRDBP_RAT]	41.83	1	12	12	84	0.4418
O35796	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Rattus norvegicus GN=C1qbp PE=1 SV=2 - [C1QBP_RAT]	22.58	1	3	3	8	0.4418
Q63798	Proteasome activator complex subunit 2 OS=Rattus norvegicus GN=Psme2 PE=2 SV=3 - [PSME2_RAT]	26.89	1	5	5	48	0.4436
P04916	Retinol-binding protein 4 OS=Rattus norvegicus GN=Rbp4 PE=1 SV=1 - [RET4_RAT]	25.87	1	4	5	43	0.4439
Q01205	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Rattus norvegicus GN=Dlst PE=1 SV=2 - [ODO2_RAT]	14.32	1	4	4	16	0.4488
Q6DGG1	Alpha/beta hydrolase domain-containing protein 14B OS=Rattus norvegicus GN=Abhd14b PE=2 SV=1 - [ABHEB_RAT]	15.71	1	2	2	2	0.4491
Q811M5	Complement component C6 OS=Rattus norvegicus GN=C6 PE=2 SV=1 - [CO6_RAT]	23.55	1	15	15	91	0.4509
B2GV06	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Rattus norvegicus GN=Oxct1 PE=1 SV=1 - [SCOT1_RAT]	43.46	1	13	14	133	0.4509
P29994	Inositol 1,4,5-trisphosphate receptor type 1 OS=Rattus norvegicus GN=Itpr1 PE=1 SV=2 - [ITPR1_RAT]	1.02	1	2	2	4	0.4520
Q63377	Sodium/potassium-transporting ATPase subunit beta-3 OS=Rattus norvegicus GN=Atp1b3 PE=2 SV=1 - [AT1B3_RAT]	17.92	1	3	3	11	0.4537
Q8CFN2	Cell division control protein 42 homolog OS=Rattus norvegicus GN=Cdc42 PE=1 SV=2 - [CDC42_RAT]	26.70	1	3	4	105	0.4538
Q01177	Plasminogen OS=Rattus norvegicus GN=Plg PE=2 SV=2 - [PLMN_RAT]	40.64	1	24	24	131	0.4543
P29314	40S ribosomal protein S9 OS=Rattus norvegicus GN=Rps9 PE=1 SV=4 - [RS9_RAT]	12.89	1	3	4	18	0.4544
P54921	Alpha-soluble NSF attachment protein OS=Rattus	12.54	1	3	3	4	0.4551

	norvegicus GN=Napa PE=1 SV=2 - [SNAA_RAT]						
P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	72.29	1	11	11	283	0.4555
Q5XIP9	Transmembrane protein 43 OS=Rattus norvegicus GN=Tmem43 PE=2 SV=1 - [TMM43_RAT]	34.25	1	8	8	67	0.4560
Q9JHY2	Sideroflexin-3 OS=Rattus norvegicus GN=Sfxn3 PE=2 SV=1 - [SFXN3_RAT]	14.02	1	2	2	2	0.4627
P04631	Protein S100-B OS=Rattus norvegicus GN=S100b PE=1 SV=2 - [S100B_RAT]	40.22	1	3	3	43	0.4633
P61206	ADP-ribosylation factor 3 OS=Rattus norvegicus GN=Arf3 PE=2 SV=2 - [ARF3_RAT]	54.70	2	5	9	235	0.4635
Q4V8F7	Coiled-coil domain-containing protein 63 OS=Rattus norvegicus GN=Ccdc63 PE=2 SV=1 - [CCD63_RAT]	5.55	1	2	2	2	0.4675
P07632	Superoxide dismutase [Cu-Zn] OS=Rattus norvegicus GN=Sod1 PE=1 SV=2 - [SODC_RAT]	49.35	1	7	7	249	0.4677
Q6AYH5	Dynactin subunit 2 OS=Rattus norvegicus GN=Dctn2 PE=1 SV=1 - [DCTN2_RAT]	7.46	1	2	2	2	0.4680
Q99J82	Integrin-linked protein kinase OS=Rattus norvegicus GN=Ilk PE=2 SV=1 - [ILK_RAT]	15.71	1	6	6	17	0.4696
P21588	5'-nucleotidase OS=Rattus norvegicus GN=Nt5e PE=1 SV=1 - [5NTD_RAT]	11.11	1	4	4	14	0.4726
P43278	Histone H1.0 OS=Rattus norvegicus GN=H1f0 PE=2 SV=2 - [H10_RAT]	22.16	1	5	5	23	0.4732
P05964	Protein S100-A6 OS=Rattus norvegicus GN=S100a6 PE=1 SV=3 - [S10A6_RAT]	19.10	1	3	3	38	0.4754
P04897	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Rattus norvegicus GN=Gnai2 PE=1 SV=3 - [GNAI2_RAT]	52.68	1	9	14	181	0.4757
P15865	Histone H1.4 OS=Rattus norvegicus GN=Hist1h1e PE=1 SV=3 - [H14_RAT]	17.35	1	7	7	303	0.4766
Q6IMF3	Keratin, type II cytoskeletal 1 OS=Rattus norvegicus GN=Krt1 PE=2 SV=1 - [K2C1_RAT]	6.88	1	4	5	61	0.4778
Q5RJR8	Leucine-rich repeat-containing protein 59 OS=Rattus norvegicus GN=Lrrc59 PE=1 SV=1 - [LRC59_RAT]	6.84	1	2	2	14	0.4781
P85515	Alpha-centractin OS=Rattus norvegicus GN=Actr1a PE=1 SV=1 - [ACTZ_RAT]	19.41	1	5	5	18	0.4842
P02650	Apolipoprotein E OS=Rattus norvegicus GN=Apoe PE=1 SV=2 - [APOE_RAT]	52.56	1	14	14	357	0.4859
B0BNA5	Coactosin-like protein OS=Rattus norvegicus GN=Cotl1 PE=1 SV=1 - [COTL1_RAT]	68.31	1	9	9	41	0.4882
Q5U211	Sorting nexin-3 OS=Rattus norvegicus GN=Snx3 PE=1 SV=1 - [SNX3_RAT]	56.79	1	7	7	30	0.4884
P16257	Translocator protein OS=Rattus norvegicus GN=Tspo PE=1 SV=1 - [TSPO_RAT]	27.22	1	2	2	4	0.4901
Q9Z339	Glutathione S-transferase omega-1 OS=Rattus norvegicus GN=Gsto1 PE=1 SV=2 - [GSTO1_RAT]	39.00	1	6	6	51	0.4917
P10536	Ras-related protein Rab-1B OS=Rattus norvegicus GN=Rab1b PE=1 SV=1 - [RAB1B_RAT]	48.26	1	3	7	244	0.4943
Q4V7C7	Actin-related protein 3 OS=Rattus norvegicus GN=Actr3 PE=1 SV=1 - [ARP3_RAT]	45.22	1	10	11	96	0.4986
Q62952	Dihydropyrimidinase-related protein 3 OS=Rattus norvegicus GN=Dpysl3 PE=1 SV=2 - [DPYL3_RAT]	31.58	1	11	13	69	0.4990
P02767	Transthyretin OS=Rattus norvegicus GN=Ttr PE=1 SV=1 - [TTHY_RAT]	62.59	1	6	6	146	0.4993
Q63862	Myosin-11 (Fragments) OS=Rattus norvegicus GN=Myh11 PE=1 SV=3 - [MYH11_RAT]	29.69	1	21	31	353	0.5024
P29315	Ribonuclease inhibitor OS=Rattus norvegicus GN=Rnh1 PE=1 SV=2 - [RINI_RAT]	26.10	1	6	6	27	0.5029
Q91Y78	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Rattus norvegicus GN=Uchl3 PE=1 SV=1 - [UCHL3_RAT]	12.61	1	2	2	2	0.5036
D3ZAF6	ATP synthase subunit f, mitochondrial OS=Rattus norvegicus GN=Atp5j2 PE=1 SV=1 - [ATPK_RAT]	23.86	1	2	2	16	0.5041
P04550	Parathymosin OS=Rattus norvegicus GN=Ptms PE=1 SV=2 - [PTMS_RAT]	22.55	1	2	2	2	0.5050
P62630	Elongation factor 1-alpha 1 OS=Rattus norvegicus GN=Eef1a1 PE=2 SV=1 - [EF1A1_RAT]	56.28	1	21	21	1882	0.5110
Q62638	Golgi apparatus protein 1 OS=Rattus norvegicus	6.32	1	5	5	10	0.5110

	GN=Glg1 PE=1 SV=1 - [GSLG1_RAT]						
P62902	60S ribosomal protein L31 OS=Rattus norvegicus GN=Rpl31 PE=2 SV=1 - [RL31_RAT]	18.40	1	2	2	16	0.5124
P61107	Ras-related protein Rab-14 OS=Rattus norvegicus GN=Rab14 PE=1 SV=3 - [RAB14_RAT]	33.95	1	5	6	60	0.5181
P63245	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Rattus norvegicus GN=Gnb2l1 PE=1 SV=3 - [GBLP_RAT]	51.10	1	10	10	61	0.5194
Q9EPH8	Polyadenylate-binding protein 1 OS=Rattus norvegicus GN=Pabpc1 PE=1 SV=1 - [PABP1_RAT]	4.40	1	2	2	2	0.5216
P02466	Collagen alpha-2(I) chain OS=Rattus norvegicus GN=Col1a2 PE=1 SV=3 - [CO1A2_RAT]	2.04	1	2	2	3	0.5241
P41498	Low molecular weight phosphotyrosine protein phosphatase OS=Rattus norvegicus GN=Acp1 PE=1 SV=3 - [PPAC_RAT]	24.05	1	3	3	20	0.5249
P31430	Dipeptidase 1 OS=Rattus norvegicus GN=Dpep1 PE=2 SV=2 - [DPEP1_RAT]	36.83	1	8	8	85	0.5259
P08011	Microsomal glutathione S-transferase 1 OS=Rattus norvegicus GN=Mgst1 PE=1 SV=3 - [MGST1_RAT]	80.65	1	9	9	1362	0.5271
Q63258	Integrin alpha-7 OS=Rattus norvegicus GN=Itga7 PE=1 SV=2 - [ITA7_RAT]	10.04	1	5	7	12	0.5329
P06685	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Rattus norvegicus GN=Atp1a1 PE=1 SV=1 - [AT1A1_RAT]	13.59	1	9	9	142	0.5338
P63088	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Rattus norvegicus GN=Ppp1cc PE=1 SV=1 - [PP1G_RAT]	23.53	3	3	5	22	0.5375
P00787	Cathepsin B OS=Rattus norvegicus GN=Ctsb PE=1 SV=2 - [CATB_RAT]	32.45	1	9	9	154	0.5382
P32038	Complement factor D OS=Rattus norvegicus GN=Cfd PE=1 SV=2 - [CFAD_RAT]	48.29	1	6	6	54	0.5395
Q6GQP4	Ras-related protein Rab-31 OS=Rattus norvegicus GN=Rab31 PE=1 SV=2 - [RAB31_RAT]	12.37	1	2	2	2	0.5405
Q01129	Decorin OS=Rattus norvegicus GN=Dcn PE=1 SV=1 - [PGS2_RAT]	32.77	1	11	12	487	0.5405
M0RC99	Ras-related protein Rab-5A OS=Rattus norvegicus GN=Rab5a PE=2 SV=1 - [RAB5A_RAT]	10.23	1	2	2	6	0.5425
P06761	78 kDa glucose-regulated protein OS=Rattus norvegicus GN=Hspa5 PE=1 SV=1 - [GRP78_RAT]	48.78	1	26	28	917	0.5443
Q9HB97	Alpha-parvin OS=Rattus norvegicus GN=Parva PE=1 SV=2 - [PARVA_RAT]	20.43	1	5	5	22	0.5451
Q62636	Ras-related protein Rap-1b OS=Rattus norvegicus GN=Rap1b PE=1 SV=2 - [RAP1B_RAT]	73.37	1	5	10	176	0.5500
Q63170	Dynein heavy chain 7, axonemal OS=Rattus norvegicus GN=Dnah7 PE=2 SV=2 - [DYH7_RAT]	1.65	1	3	4	5	0.5511
P04638	Apolipoprotein A-II OS=Rattus norvegicus GN=Apoa2 PE=2 SV=1 - [APOA2_RAT]	19.61	1	2	2	7	0.5513
Q07066	Peroxisomal membrane protein 2 OS=Rattus norvegicus GN=Pxmp2 PE=1 SV=2 - [PXMP2_RAT]	21.13	1	2	3	8	0.5521
Q6URK4	Heterogeneous nuclear ribonucleoprotein A3 OS=Rattus norvegicus GN=Hnrnpa3 PE=1 SV=1 - [ROA3_RAT]	14.25	1	4	4	50	0.5561
Q63010	Liver carboxylesterase B-1 OS=Rattus norvegicus PE=1 SV=1 - [EST5_RAT]	10.87	1	1	3	53	0.5562
P62890	60S ribosomal protein L30 OS=Rattus norvegicus GN=Rpl30 PE=3 SV=2 - [RL30_RAT]	24.35	1	2	2	31	0.5569
B2GUZ5	F-actin-capping protein subunit alpha-1 OS=Rattus norvegicus GN=Capza1 PE=1 SV=1 - [CAZA1_RAT]	20.28	1	3	4	36	0.5572
Q3T1K5	F-actin-capping protein subunit alpha-2 OS=Rattus norvegicus GN=Capza2 PE=1 SV=1 - [CAZA2_RAT]	27.97	1	4	5	47	0.5573
O08662	Phosphatidylinositol 4-kinase alpha OS=Rattus norvegicus GN=Pi4ka PE=1 SV=1 - [PI4KA_RAT]	7.30	1	5	8	17	0.5578
Q08163	Adenylyl cyclase-associated protein 1 OS=Rattus norvegicus GN=Cap1 PE=1 SV=3 - [CAP1_RAT]	42.62	1	11	12	283	0.5589
P97697	Inositol monophosphatase 1 OS=Rattus norvegicus GN=Impa1 PE=1 SV=2 - [IMPA1_RAT]	15.88	1	3	3	5	0.5609
D4ABY2	Coatomer subunit gamma-2 OS=Rattus norvegicus GN=Copg2 PE=3 SV=2 - [COPG2_RAT]	4.20	1	1	2	21	0.5610

P05943	Protein S100-A10 OS=Rattus norvegicus GN=S100a10 PE=1 SV=2 - [S10AA_RAT]	17.89	1	2	2	20	0.5633
O08629	Transcription intermediary factor 1-beta OS=Rattus norvegicus GN=Trim28 PE=1 SV=2 - [TIF1B_RAT]	8.14	1	4	5	7	0.5717
P11232	Thioredoxin OS=Rattus norvegicus GN=Txn PE=1 SV=2 - [THIO_RAT]	31.43	1	5	5	95	0.5727
P23680	Serum amyloid P-component OS=Rattus norvegicus GN=Apcs PE=2 SV=2 - [SAMP_RAT]	14.04	1	2	2	2	0.5728
P42930	Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1 - [HSPB1_RAT]	59.22	1	11	11	342	0.5737
Q5XIM9	T-complex protein 1 subunit beta OS=Rattus norvegicus GN=Cct2 PE=1 SV=3 - [TCPB_RAT]	14.39	1	4	4	19	0.5738
P16036	Phosphate carrier protein, mitochondrial OS=Rattus norvegicus GN=Slc25a3 PE=1 SV=1 - [MPCP_RAT]	42.42	1	10	10	188	0.5763
Q9WU49	Calcium-regulated heat stable protein 1 OS=Rattus norvegicus GN=Carhsp1 PE=1 SV=1 - [CHSP1_RAT]	18.37	1	2	2	3	0.5766
Q00438	Polypyrimidine tract-binding protein 1 OS=Rattus norvegicus GN=Ptbp1 PE=1 SV=1 - [PTBP1_RAT]	33.87	1	8	8	38	0.5777
O88761	26S proteasome non-ATPase regulatory subunit 1 OS=Rattus norvegicus GN=Psmd1 PE=1 SV=1 - [PSMD1_RAT]	7.56	1	4	4	26	0.5799
O55096	Dipeptidyl peptidase 3 OS=Rattus norvegicus GN=Dpp3 PE=1 SV=2 - [DPP3_RAT]	20.46	1	7	7	27	0.5805
Q05982	Nucleoside diphosphate kinase A OS=Rattus norvegicus GN=Nme1 PE=1 SV=1 - [NDKA_RAT]	75.66	1	4	10	341	0.5860
P28077	Proteasome subunit beta type-9 OS=Rattus norvegicus GN=Psmb9 PE=1 SV=2 - [PSB9_RAT]	23.74	1	4	4	20	0.5871
P56571	ES1 protein homolog, mitochondrial OS=Rattus norvegicus PE=1 SV=2 - [ES1_RAT]	35.71	1	7	7	39	0.5873
Q4KM74	Vesicle-trafficking protein SEC22b OS=Rattus norvegicus GN=Sec22b PE=1 SV=3 - [SC22B_RAT]	36.74	1	6	7	59	0.5880
Q6P9T8	Tubulin beta-4B chain OS=Rattus norvegicus GN=Tubb4b PE=1 SV=1 - [TBB4B_RAT]	68.31	1	4	24	2192	0.5884
P85108	Tubulin beta-2A chain OS=Rattus norvegicus GN=Tubb2a PE=1 SV=1 - [TBB2A_RAT]	73.93	2	6	25	2002	0.5887
P55159	Serum paraoxonase/arylesterase 1 OS=Rattus norvegicus GN=Pon1 PE=1 SV=3 - [PON1_RAT]	9.58	1	2	2	2	0.5896
P69897	Tubulin beta-5 chain OS=Rattus norvegicus GN=Tubb5 PE=1 SV=1 - [TBB5_RAT]	74.10	1	4	25	2178	0.5932
P62944	AP-2 complex subunit beta OS=Rattus norvegicus GN=Ap2b1 PE=1 SV=1 - [AP2B1_RAT]	21.34	1	8	14	263	0.5939
P68370	Tubulin alpha-1A chain OS=Rattus norvegicus GN=Tuba1a PE=1 SV=1 - [TBA1A_RAT]	66.52	1	2	22	1628	0.5943
Q6P9V9	Tubulin alpha-1B chain OS=Rattus norvegicus GN=Tuba1b PE=1 SV=1 - [TBA1B_RAT]	66.52	1	3	23	1746	0.5943
Q80U96	Exportin-1 OS=Rattus norvegicus GN=Xpo1 PE=1 SV=1 - [XPO1_RAT]	8.12	1	4	5	22	0.5961
P15650	Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acadl PE=1 SV=1 - [ACADL_RAT]	21.86	1	8	8	49	0.5971
P27867	Sorbitol dehydrogenase OS=Rattus norvegicus GN=Sord PE=1 SV=4 - [DHSO_RAT]	9.80	1	2	2	8	0.5972
P05708	Hexokinase-1 OS=Rattus norvegicus GN=Hk1 PE=1 SV=4 - [HXK1_RAT]	12.96	1	8	9	46	0.5983
Q6UVM4	Potassium channel subfamily T member 2 OS=Rattus norvegicus GN=Kcnt2 PE=1 SV=1 - [KCNT2_RAT]	4.12	1	2	2	2	0.5987
P13471	40S ribosomal protein S14 OS=Rattus norvegicus GN=Rps14 PE=2 SV=3 - [RS14_RAT]	29.80	1	3	3	72	0.5994
P63018	Heat shock cognate 71 kDa protein OS=Rattus norvegicus GN=Hspa8 PE=1 SV=1 - [HSP7C_RAT]	75.54	1	35	40	1312	0.6012
Q66HD0	Endoplasmin OS=Rattus norvegicus GN=Hsp90b1 PE=1 SV=2 - [ENPL_RAT]	55.35	1	36	38	754	0.6017
P34064	Proteasome subunit alpha type-5 OS=Rattus norvegicus GN=Psma5 PE=1 SV=1 - [PSA5_RAT]	18.26	1	4	4	12	0.6053
A7VJC2	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1 - [ROA2_RAT]	41.36	1	12	13	138	0.6076
Q62667	Major vault protein OS=Rattus norvegicus GN=Mvp	30.89	1	15	16	42	0.6082

	PE=1 SV=4 - [MVP_RAT]						
P00564	Creatine kinase M-type OS=Rattus norvegicus GN=Ckm PE=1 SV=2 - [KCRM_RAT]	24.93	1	7	7	15	0.6091
Q7TMA5	Apolipoprotein B-100 OS=Rattus norvegicus GN=Apob PE=1 SV=1 - [APOB_RAT]	3.94	1	13	13	16	0.6099
Q9EST6	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Rattus norvegicus GN=Anp32b PE=1 SV=1 - [AN32B_RAT]	18.75	1	3	4	21	0.6104
P11517	Hemoglobin subunit beta-2 OS=Rattus norvegicus PE=1 SV=2 - [HBB2_RAT]	88.44	1	3	14	10549	0.6104
P60868	40S ribosomal protein S20 OS=Rattus norvegicus GN=Rps20 PE=3 SV=1 - [RS20_RAT]	25.21	1	3	3	37	0.6148
P40112	Proteasome subunit beta type-3 OS=Rattus norvegicus GN=Psmb3 PE=1 SV=1 - [PSB3_RAT]	26.83	1	4	4	62	0.6160
O88600	Heat shock 70 kDa protein 4 OS=Rattus norvegicus GN=Hspa4 PE=1 SV=1 - [HSP74_RAT]	29.76	1	16	17	107	0.6162
P54311	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Rattus norvegicus GN=Gnb1 PE=1 SV=4 - [GBB1_RAT]	52.35	1	6	13	194	0.6165
Q63556	Serine protease inhibitor A3M (Fragment) OS=Rattus norvegicus GN=Serpina3m PE=2 SV=1 - [SPA3M_RAT]	14.56	1	2	5	36	0.6170
P29975	Aquaporin-1 OS=Rattus norvegicus GN=Aqp1 PE=1 SV=4 - [AQP1_RAT]	26.77	1	4	4	5	0.6188
P31000	Vimentin OS=Rattus norvegicus GN=Vim PE=1 SV=2 - [VIME_RAT]	79.18	1	36	42	1931	0.6209
Q66HG4	Aldose 1-epimerase OS=Rattus norvegicus GN=Galm PE=1 SV=1 - [GALM_RAT]	28.07	1	6	6	35	0.6209
P35704	Peroxiredoxin-2 OS=Rattus norvegicus GN=Prdx2 PE=1 SV=3 - [PRDX2_RAT]	57.58	1	9	9	432	0.6227
P38659	Protein disulfide-isomerase A4 OS=Rattus norvegicus GN=Pdia4 PE=1 SV=2 - [PDIA4_RAT]	35.61	1	18	18	72	0.6244
Q5RJP0	Aldose reductase-related protein 1 OS=Rattus norvegicus GN=Akr1b7 PE=1 SV=1 - [ALD1_RAT]	12.66	1	1	3	3	0.6279
Q9Z0W7	Chloride intracellular channel protein 4 OS=Rattus norvegicus GN=Clic4 PE=1 SV=3 - [CLIC4_RAT]	29.64	1	4	5	44	0.6288
Q7TPJ0	Translocon-associated protein subunit alpha OS=Rattus norvegicus GN=Ssr1 PE=1 SV=1 - [SSRA_RAT]	8.15	1	2	2	2	0.6302
P18420	Proteasome subunit alpha type-1 OS=Rattus norvegicus GN=Psma1 PE=1 SV=2 - [PSA1_RAT]	29.28	1	8	8	16	0.6324
Q921A4	Cytoglobin OS=Rattus norvegicus GN=Cygb PE=1 SV=1 - [CYGB_RAT]	54.74	1	8	8	18	0.6349
Q63356	Unconventional myosin-Ie OS=Rattus norvegicus GN=Myo1e PE=1 SV=1 - [MYO1E_RAT]	2.26	1	1	2	5	0.6351
Q08290	Calponin-1 OS=Rattus norvegicus GN=Cnn1 PE=1 SV=1 - [CNN1_RAT]	19.87	1	5	5	14	0.6352
Q00715	Histone H2B type 1 OS=Rattus norvegicus PE=1 SV=2 - [H2B1_RAT]	39.20	1	5	5	257	0.6363
P01946	Hemoglobin subunit alpha-1/2 OS=Rattus norvegicus GN=Hba1 PE=1 SV=3 - [HBA_RAT]	95.77	1	13	13	14945	0.6394
P68511	14-3-3 protein eta OS=Rattus norvegicus GN=Ywhah PE=1 SV=2 - [1433F_RAT]	52.85	1	8	14	339	0.6438
P21263	Nestin OS=Rattus norvegicus GN=Nes PE=1 SV=2 - [NEST_RAT]	1.27	1	2	2	2	0.6441
P18421	Proteasome subunit beta type-1 OS=Rattus norvegicus GN=Psmb1 PE=1 SV=3 - [PSB1_RAT]	39.17	1	7	7	60	0.6448
P62246	40S ribosomal protein S15a OS=Rattus norvegicus GN=Rps15a PE=1 SV=2 - [RS15A_RAT]	17.69	1	2	2	5	0.6464
Q9R1T3	Cathepsin Z OS=Rattus norvegicus GN=Ctsz PE=1 SV=2 - [CATZ_RAT]	18.95	1	4	4	29	0.6471
Q5RKI1	Eukaryotic initiation factor 4A-II OS=Rattus norvegicus GN=Eif4a2 PE=1 SV=1 - [IF4A2_RAT]	35.63	1	11	11	149	0.6484
P04256	Heterogeneous nuclear ribonucleoprotein A1 OS=Rattus norvegicus GN=Hnrnpa1 PE=1 SV=3 - [ROA1_RAT]	23.13	1	4	6	45	0.6495
P50475	Alanine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Aars PE=1 SV=3 - [SYAC_RAT]	6.71	1	4	4	20	0.6504
P09895	60S ribosomal protein L5 OS=Rattus norvegicus	10.77	1	2	2	4	0.6516

	GN=Rpl5 PE=1 SV=3 - [RL5_RAT]						
P12001	60S ribosomal protein L18 OS=Rattus norvegicus GN=Rpl18 PE=1 SV=2 - [RL18_RAT]	29.79	1	5	5	57	0.6522
Q8VIF7	Selenium-binding protein 1 OS=Rattus norvegicus GN=Selenbp1 PE=1 SV=1 - [SBP1_RAT]	61.44	1	21	23	151	0.6525
Q68FQ0	T-complex protein 1 subunit epsilon OS=Rattus norvegicus GN=Cct5 PE=1 SV=1 - [TCPE_RAT]	12.75	1	3	3	6	0.6534
Q6PEC4	S-phase kinase-associated protein 1 OS=Rattus norvegicus GN=Skp1 PE=1 SV=3 - [SKP1_RAT]	20.86	1	3	3	4	0.6538
P26376	Interferon-induced transmembrane protein 3 OS=Rattus norvegicus GN=ifitm3 PE=2 SV=1 - [IFM3_RAT]	32.12	1	3	3	27	0.6554
P04276	Vitamin D-binding protein OS=Rattus norvegicus GN=Gc PE=1 SV=3 - [VTDB_RAT]	50.00	1	17	17	368	0.6558
Q9ESW0	DNA damage-binding protein 1 OS=Rattus norvegicus GN=Ddb1 PE=1 SV=1 - [DDB1_RAT]	2.98	1	2	2	3	0.6597
P06302	Prothymosin alpha OS=Rattus norvegicus GN=Ptma PE=1 SV=2 - [PTMA_RAT]	22.32	1	4	4	11	0.6679
P02454	Collagen alpha-1(I) chain OS=Rattus norvegicus GN=Col1a1 PE=1 SV=5 - [CO1A1_RAT]	2.34	1	2	2	2	0.6745
P17220	Proteasome subunit alpha type-2 OS=Rattus norvegicus GN=Psma2 PE=1 SV=3 - [PSA2_RAT]	45.30	1	9	9	88	0.6766
Q6AY30	Saccharopine dehydrogenase-like oxidoreductase OS=Rattus norvegicus GN=Sccpdh PE=1 SV=1 - [SCPDL_RAT]	12.12	1	2	2	8	0.6792
P82471	Guanine nucleotide-binding protein G(q) subunit alpha OS=Rattus norvegicus GN=Gnaq PE=2 SV=2 - [GNAQ_RAT]	25.07	1	6	6	34	0.6796
P38650	Cytoplasmic dynein 1 heavy chain 1 OS=Rattus norvegicus GN=Dync1h1 PE=1 SV=1 - [DYHC1_RAT]	32.77	1	115	118	740	0.6816
Q68FR9	Elongation factor 1-delta OS=Rattus norvegicus GN=Eef1d PE=1 SV=2 - [EF1D_RAT]	21.71	1	4	4	27	0.6826
Q5I0D7	Xaa-Pro dipeptidase OS=Rattus norvegicus GN=Pepd PE=2 SV=1 - [PEPD_RAT]	10.57	1	4	4	85	0.6864
P62853	40S ribosomal protein S25 OS=Rattus norvegicus GN=Rps25 PE=2 SV=1 - [RS25_RAT]	22.40	1	3	3	4	0.6895
P63324	40S ribosomal protein S12 OS=Rattus norvegicus GN=Rps12 PE=1 SV=2 - [RS12_RAT]	28.79	1	4	4	45	0.6913
P22985	Xanthine dehydrogenase/oxidase OS=Rattus norvegicus GN=Xdh PE=1 SV=3 - [XDH_RAT]	44.10	1	34	34	1035	0.6920
Q62969	Prostacyclin synthase OS=Rattus norvegicus GN=Ptgis PE=2 SV=1 - [PTGIS_RAT]	14.37	1	4	4	16	0.6927
Q80Z29	Nicotinamide phosphoribosyltransferase OS=Rattus norvegicus GN=Nampt PE=1 SV=1 - [NAMPT_RAT]	14.46	1	3	3	5	0.6930
P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	66.14	1	126	129	1903	0.6954
Q9QWE9	Gamma-glutamyltransferase 5 OS=Rattus norvegicus GN=Ggt5 PE=2 SV=1 - [GGT5_RAT]	7.34	1	2	2	2	0.6958
Q04462	Valine--tRNA ligase OS=Rattus norvegicus GN=Vars PE=2 SV=2 - [SYVC_RAT]	12.26	1	8	8	22	0.6977
P02563	Myosin-6 OS=Rattus norvegicus GN=Myh6 PE=1 SV=2 - [MYH6_RAT]	2.37	1	2	2	3	0.7030
P85972	Vinculin OS=Rattus norvegicus GN=Vcl PE=1 SV=1 - [VINC_RAT]	64.54	1	53	56	1405	0.7040
P30009	Myristoylated alanine-rich C-kinase substrate OS=Rattus norvegicus GN=Marcks PE=1 SV=2 - [MARCS_RAT]	28.48	1	5	5	41	0.7047
P62836	Ras-related protein Rap-1A OS=Rattus norvegicus GN=Rap1a PE=1 SV=1 - [RAP1A_RAT]	59.24	1	4	9	160	0.7064
Q6VBQ5	Myeloid-associated differentiation marker OS=Rattus norvegicus GN=Myadm PE=1 SV=1 - [MYADM_RAT]	21.70	1	4	4	53	0.7075
P62870	Transcription elongation factor B polypeptide 2 OS=Rattus norvegicus GN=Tceb2 PE=1 SV=1 - [ELOB_RAT]	42.37	1	3	3	8	0.7102
Q6RUV5	Ras-related C3 botulinum toxin substrate 1 OS=Rattus norvegicus GN=Rac1 PE=1 SV=1 - [RAC1_RAT]	36.46	1	6	7	44	0.7117
Q5SGE0	Leucine-rich PPR motif-containing protein,	15.30	1	12	13	53	0.7119

	mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=1 SV=1 - [LPPRC_RAT]						
Q6AXM8	Serum paraoxonase/arylesterase 2 OS=Rattus norvegicus GN=Pon2 PE=2 SV=1 - [PON2_RAT]	19.77	1	4	4	5	0.7133
P83868	Prostaglandin E synthase 3 OS=Rattus norvegicus GN=Ptges3 PE=1 SV=2 - [TEBP_RAT]	32.50	1	4	4	27	0.7141
P63255	Cysteine-rich protein 1 OS=Rattus norvegicus GN=Crip1 PE=1 SV=2 - [CRIP1_RAT]	61.04	1	3	3	9	0.7146
Q5RKI0	WD repeat-containing protein 1 OS=Rattus norvegicus GN=Wdr1 PE=1 SV=3 - [WDR1_RAT]	4.79	1	2	2	5	0.7175
Q66H80	Coatomer subunit delta OS=Rattus norvegicus GN=Arcn1 PE=2 SV=1 - [COPD_RAT]	11.94	1	4	4	35	0.7175
Q64119	Myosin light polypeptide 6 OS=Rattus norvegicus GN=Myl6 PE=1 SV=3 - [MYL6_RAT]	58.28	2	9	9	166	0.7201
Q711G3	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Rattus norvegicus GN=Iah1 PE=2 SV=2 - [IAH1_RAT]	15.26	1	2	2	4	0.7229
P50398	Rab GDP dissociation inhibitor alpha OS=Rattus norvegicus GN=Gdi1 PE=1 SV=1 - [GDIA_RAT]	42.28	1	8	14	185	0.7239
P63025	Vesicle-associated membrane protein 3 OS=Rattus norvegicus GN=Vamp3 PE=1 SV=1 - [VAMP3_RAT]	38.83	2	3	3	24	0.7282
Q9ES40	PRA1 family protein 3 OS=Rattus norvegicus GN=Arl6ip5 PE=1 SV=1 - [PRAF3_RAT]	15.96	1	2	2	10	0.7301
P22734	Catechol O-methyltransferase OS=Rattus norvegicus GN=Comt PE=1 SV=2 - [COMT_RAT]	24.62	1	4	4	12	0.7323
O35828	Coronin-7 OS=Rattus norvegicus GN=Coro7 PE=1 SV=2 - [CORO7_RAT]	3.80	1	2	2	2	0.7336
P41123	60S ribosomal protein L13 OS=Rattus norvegicus GN=Rpl13 PE=1 SV=2 - [RL13_RAT]	19.43	1	4	4	35	0.7358
Q2MHH0	Tumor suppressor candidate 5 homolog OS=Rattus norvegicus GN=Tusc5 PE=1 SV=1 - [TUSC5_RAT]	24.86	1	3	3	116	0.7359
P29457	Serpin H1 OS=Rattus norvegicus GN=Serpinh1 PE=1 SV=1 - [SERPH_RAT]	60.19	1	17	17	590	0.7382
P81155	Voltage-dependent anion-selective channel protein 2 OS=Rattus norvegicus GN=Vdac2 PE=1 SV=2 - [VDAC2_RAT]	21.36	1	5	5	39	0.7392
Q6P6T1	Complement C1s subcomponent OS=Rattus norvegicus GN=C1s PE=2 SV=2 - [C1S_RAT]	12.35	1	3	3	3	0.7392
Q68FR6	Elongation factor 1-gamma OS=Rattus norvegicus GN=Eef1g PE=2 SV=3 - [EF1G_RAT]	37.07	1	8	10	81	0.7398
P05545	Serine protease inhibitor A3K OS=Rattus norvegicus GN=Serpina3k PE=1 SV=3 - [SPA3K_RAT]	61.06	1	16	21	978	0.7398
F1LMZ8	26S proteasome non-ATPase regulatory subunit 11 OS=Rattus norvegicus GN=Psmd11 PE=1 SV=2 - [PSD11_RAT]	5.92	1	2	2	2	0.7437
Q4KM73	UMP-CMP kinase OS=Rattus norvegicus GN=Cmpk1 PE=1 SV=2 - [KCY_RAT]	54.08	1	8	9	38	0.7443
B2RZ78	Vacuolar protein sorting-associated protein 29 OS=Rattus norvegicus GN=Vps29 PE=1 SV=2 - [VPS29_RAT]	21.98	1	4	4	18	0.7508
P53987	Monocarboxylate transporter 1 OS=Rattus norvegicus GN=Slc16a1 PE=1 SV=1 - [MOT1_RAT]	12.15	1	4	4	99	0.7515
P62963	Profilin-1 OS=Rattus norvegicus GN=Pfn1 PE=1 SV=2 - [PROF1_RAT]	72.14	1	10	10	639	0.7549
Q9ES21	Phosphatidylinositide phosphatase SAC1 OS=Rattus norvegicus GN=Sacm1l PE=1 SV=1 - [SAC1_RAT]	15.84	1	6	7	35	0.7552
Q9WVB1	Ras-related protein Rab-6A OS=Rattus norvegicus GN=Rab6a PE=1 SV=2 - [RAB6A_RAT]	21.63	1	3	4	32	0.7566
Q07984	Translocon-associated protein subunit delta OS=Rattus norvegicus GN=Ssr4 PE=2 SV=1 - [SSRD_RAT]	30.64	1	4	4	11	0.7568
P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	20.57	1	16	17	188	0.7614
Q6AYD3	Proliferation-associated protein 2G4 OS=Rattus norvegicus GN=Pa2g4 PE=1 SV=1 - [PA2G4_RAT]	10.91	1	3	4	15	0.7617
Q4AEF8	Coatomer subunit gamma-1 OS=Rattus norvegicus GN=Copg1 PE=2 SV=1 - [COPG1_RAT]	16.93	1	7	9	41	0.7681
B0BNM1	NAD(P)H-hydrate epimerase OS=Rattus norvegicus	26.95	1	4	4	9	0.7707

	GN=Apoa1bp PE=2 SV=1 - [NNRE_RAT]						
Q4FZT9	26S proteasome non-ATPase regulatory subunit 2 OS=Rattus norvegicus GN=Psmd2 PE=1 SV=1 - [PSMD2_RAT]	18.72	1	11	11	62	0.7719
Q66X93	Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus GN=Snd1 PE=1 SV=1 - [SND1_RAT]	16.50	1	7	9	35	0.7758
P70623	Fatty acid-binding protein, adipocyte OS=Rattus norvegicus GN=Fabp4 PE=1 SV=3 - [FABP4_RAT]	74.24	1	13	13	6816	0.7769
P68255	14-3-3 protein theta OS=Rattus norvegicus GN=Ywhaq PE=1 SV=1 - [1433T_RAT]	72.24	1	14	20	548	0.7811
P14740	Dipeptidyl peptidase 4 OS=Rattus norvegicus GN=Dpp4 PE=1 SV=2 - [DPP4_RAT]	17.47	1	9	10	82	0.7843
P15178	Aspartate--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Dars PE=2 SV=1 - [SYDC_RAT]	7.98	1	3	3	9	0.7896
P05544	Serine protease inhibitor A3L OS=Rattus norvegicus GN=Serpina3l PE=1 SV=3 - [SPA3L_RAT]	58.84	1	14	20	719	0.7934
P18422	Proteasome subunit alpha type-3 OS=Rattus norvegicus GN=Psma3 PE=1 SV=3 - [PSA3_RAT]	14.12	1	3	3	28	0.7946
P24050	40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=1 SV=3 - [RS5_RAT]	28.92	1	6	6	17	0.7946
Q5U318	Astrocytic phosphoprotein PEA-15 OS=Rattus norvegicus GN=Pea15 PE=1 SV=1 - [PEA15_RAT]	29.23	1	3	3	6	0.7982
Q9ESS6	Basal cell adhesion molecule OS=Rattus norvegicus GN=Bcam PE=2 SV=1 - [BCAM_RAT]	4.49	1	2	2	5	0.7997
P27274	CD59 glycoprotein OS=Rattus norvegicus GN=Cd59 PE=1 SV=2 - [CD59_RAT]	30.16	1	4	4	74	0.8000
P68035	Actin, alpha cardiac muscle 1 OS=Rattus norvegicus GN=Actc1 PE=2 SV=1 - [ACTC_RAT]	83.82	2	10	23	3161	0.8009
Q6AY84	Secernin-1 OS=Rattus norvegicus GN=Scrn1 PE=1 SV=1 - [SCRN1_RAT]	6.28	1	2	2	2	0.8025
Q9Z270	Vesicle-associated membrane protein-associated protein A OS=Rattus norvegicus GN=Vapa PE=1 SV=3 - [VAPA_RAT]	28.92	1	7	7	56	0.8037
Q5M7U6	Actin-related protein 2 OS=Rattus norvegicus GN=Actr2 PE=2 SV=1 - [ARP2_RAT]	27.41	1	7	7	24	0.8074
P35213	14-3-3 protein beta/alpha OS=Rattus norvegicus GN=Ywhab PE=1 SV=3 - [1433B_RAT]	71.54	1	9	16	521	0.8074
Q6IG02	Keratin, type II cytoskeletal 2 epidermal OS=Rattus norvegicus GN=Krt2 PE=3 SV=1 - [K22E_RAT]	4.67	1	2	4	9	0.8079
P0C5H9	Mesencephalic astrocyte-derived neurotrophic factor OS=Rattus norvegicus GN=Manf PE=1 SV=1 - [MANF_RAT]	21.79	1	4	4	22	0.8091
Q9Z0U5	Aldehyde oxidase 1 OS=Rattus norvegicus GN=Aox1 PE=1 SV=1 - [AOXA_RAT]	2.63	1	2	2	4	0.8092
O35142	Coatomer subunit beta' OS=Rattus norvegicus GN=Copb2 PE=1 SV=3 - [COPB2_RAT]	12.93	1	7	8	59	0.8111
Q1JU68	Eukaryotic translation initiation factor 3 subunit A OS=Rattus norvegicus GN=Eif3a PE=2 SV=2 - [EIF3A_RAT]	9.23	1	8	8	45	0.8150
P28023	Dynactin subunit 1 OS=Rattus norvegicus GN=Dctn1 PE=1 SV=2 - [DCTN1_RAT]	7.42	1	6	6	13	0.8163
P17078	60S ribosomal protein L35 OS=Rattus norvegicus GN=Rpl35 PE=1 SV=3 - [RL35_RAT]	18.70	1	2	2	5	0.8168
Q7M0E3	Destrin OS=Rattus norvegicus GN=Dstn PE=1 SV=3 - [DEST_RAT]	63.03	1	9	9	209	0.8197
P08649	Complement C4 OS=Rattus norvegicus GN=C4 PE=1 SV=3 - [CO4_RAT]	55.96	1	62	63	1441	0.8203
Q497B0	Omega-amidase NIT2 OS=Rattus norvegicus GN=Nit2 PE=1 SV=1 - [NIT2_RAT]	39.13	1	6	6	20	0.8237
P97852	Peroxisomal multifunctional enzyme type 2 OS=Rattus norvegicus GN=Hsd17b4 PE=1 SV=3 - [DHB4_RAT]	17.01	1	8	10	132	0.8243
Q9QWN8	Spectrin beta chain, non-erythrocytic 2 OS=Rattus norvegicus GN=Sptbn2 PE=1 SV=2 - [SPTN2_RAT]	2.47	1	5	6	32	0.8289
O08678	Serine/threonine-protein kinase MARK1 OS=Rattus norvegicus GN=Mark1 PE=1 SV=1 - [MARK1_RAT]	3.28	2	2	2	2	0.8290
P48679	Prelamin-A/C OS=Rattus norvegicus GN=Lmna PE=1 SV=1 - [LMNA_RAT]	28.42	1	15	16	77	0.8292

P13084	Nucleophosmin OS=Rattus norvegicus GN=Npm1 PE=1 SV=1 - [NPM_RAT]	16.44	1	3	3	10	0.8346
Q62658	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Rattus norvegicus GN=Fkbp1a PE=1 SV=3 - [FKB1A_RAT]	29.63	1	3	3	24	0.8347
P0CG51	Polyubiquitin-B OS=Rattus norvegicus GN=Ubb PE=1 SV=1 - [UBB_RAT]	61.64	4	5	5	461	0.8369
P63322	Ras-related protein Ral-A OS=Rattus norvegicus GN=Rala PE=1 SV=1 - [RALA_RAT]	22.82	1	4	4	19	0.8398
Q91Y80	SH3 domain-binding protein 5 OS=Rattus norvegicus GN=Sh3bp5 PE=1 SV=2 - [3BP5_RAT]	2.63	1	2	2	2	0.8445
P49134	Integrin beta-1 OS=Rattus norvegicus GN=Itgb1 PE=2 SV=1 - [ITB1_RAT]	30.79	1	17	17	230	0.8473
Q9JLZ1	Glutaredoxin-3 OS=Rattus norvegicus GN=Glrx3 PE=1 SV=2 - [GLRX3_RAT]	10.39	1	3	3	4	0.8475
O35303	Dynamin-1-like protein OS=Rattus norvegicus GN=Dnm1l PE=1 SV=1 - [DNM1L_RAT]	8.61	1	3	3	12	0.8477
Q63228	Glia maturation factor beta OS=Rattus norvegicus GN=Gmfb PE=1 SV=2 - [GMFB_RAT]	30.28	1	4	4	9	0.8489
P63029	Translationally-controlled tumor protein OS=Rattus norvegicus GN=Tpt1 PE=1 SV=1 - [TCTP_RAT]	40.12	1	7	7	96	0.8506
P04182	Ornithine aminotransferase, mitochondrial OS=Rattus norvegicus GN=Oat PE=1 SV=1 - [OAT_RAT]	20.27	1	5	5	8	0.8530
Q923V8	15 kDa selenoprotein OS=Rattus norvegicus GN=Sep15 PE=1 SV=3 - [SEP15_RAT]	25.31	1	3	3	6	0.8553
P70580	Membrane-associated progesterone receptor component 1 OS=Rattus norvegicus GN=Pgrmc1 PE=1 SV=3 - [PGRC1_RAT]	33.85	1	4	4	7	0.8556
Q91Y81	Septin-2 OS=Rattus norvegicus GN=Sept2 PE=1 SV=1 - [SEPT2_RAT]	35.46	1	8	8	32	0.8564
Q7M767	Ubiquitin-conjugating enzyme E2 variant 2 OS=Rattus norvegicus GN=Ube2v2 PE=1 SV=3 - [UB2V2_RAT]	34.48	1	4	4	8	0.8609
P63102	14-3-3 protein zeta/delta OS=Rattus norvegicus GN=Ywhaz PE=1 SV=1 - [1433Z_RAT]	72.24	1	13	18	633	0.8621
P97629	Leucyl-cystinyl aminopeptidase OS=Rattus norvegicus GN=Lnpep PE=1 SV=1 - [LCAP_RAT]	4.59	1	4	4	16	0.8630
P62425	60S ribosomal protein L7a OS=Rattus norvegicus GN=Rpl7a PE=1 SV=2 - [RL7A_RAT]	15.04	1	3	3	28	0.8663
P18297	Sepiapterin reductase OS=Rattus norvegicus GN=Spr PE=1 SV=1 - [SPRE_RAT]	21.76	1	2	2	3	0.8665
Q63081	Protein disulfide-isomerase A6 OS=Rattus norvegicus GN=Pdia6 PE=1 SV=2 - [PDIA6_RAT]	42.73	1	13	14	417	0.8674
P11507	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Rattus norvegicus GN=Atp2a2 PE=1 SV=1 - [AT2A2_RAT]	14.48	1	11	11	119	0.8697
P07872	Peroxisomal acyl-coenzyme A oxidase 1 OS=Rattus norvegicus GN=Acox1 PE=1 SV=1 - [ACOX1_RAT]	19.36	1	6	7	16	0.8756
P36370	Antigen peptide transporter 1 OS=Rattus norvegicus GN=Tap1 PE=1 SV=2 - [TAP1_RAT]	9.66	1	4	5	16	0.8757
P21533	60S ribosomal protein L6 OS=Rattus norvegicus GN=Rpl6 PE=1 SV=5 - [RL6_RAT]	29.19	1	7	8	42	0.8785
P60901	Proteasome subunit alpha type-6 OS=Rattus norvegicus GN=Psma6 PE=1 SV=1 - [PSA6_RAT]	38.62	1	8	8	71	0.8800
Q5XHZ0	Heat shock protein 75 kDa, mitochondrial OS=Rattus norvegicus GN=Trap1 PE=1 SV=1 - [TRAP1_RAT]	6.09	1	1	2	12	0.8815
Q6RJR6	Reticulon-3 OS=Rattus norvegicus GN=Rtn3 PE=1 SV=1 - [RTN3_RAT]	2.02	1	2	2	28	0.8819
P36953	Afamin OS=Rattus norvegicus GN=Afm PE=3 SV=1 - [AFAM_RAT]	34.38	1	15	15	80	0.8829
Q6DGG0	Peptidyl-prolyl cis-trans isomerase D OS=Rattus norvegicus GN=Ppid PE=1 SV=3 - [PPID_RAT]	14.05	1	3	3	7	0.8847
P03311	Genome polyprotein OS=Foot-and-mouth disease virus (isolate -/Spain/S8c1SantaPau/1970 serotype C) PE=1 SV=2 - [POLG_FMDVS]	2.23	5	2	2	2	0.8850
P80067	Dipeptidyl peptidase 1 OS=Rattus norvegicus GN=Ctsc PE=1 SV=3 - [CATC_RAT]	4.55	1	2	2	2	0.8866
P31232	Transgelin OS=Rattus norvegicus GN=Tagln PE=1 SV=2 - [TAGL_RAT]	73.13	1	15	15	831	0.8869
P47853	Biglycan OS=Rattus norvegicus GN=Bgn PE=2 SV=1 -	52.57	1	13	15	204	0.8893

	[PGS1_RAT]						
P0DMW0	Heat shock 70 kDa protein 1A OS=Rattus norvegicus GN=Hspa1a PE=2 SV=1 - [HS71A_RAT]	16.38	1	4	8	367	0.8899
P08699	Galectin-3 OS=Rattus norvegicus GN=Lgals3 PE=1 SV=4 - [LEG3_RAT]	27.10	1	5	5	13	0.8908
P02651	Apolipoprotein A-IV OS=Rattus norvegicus GN=Apoa4 PE=1 SV=2 - [APOA4_RAT]	58.82	1	17	17	143	0.8954
O35952	Hydroxyacylglutathione hydrolase, mitochondrial OS=Rattus norvegicus GN=Hagh PE=1 SV=2 - [GLO2_RAT]	16.50	1	3	3	10	0.8959
P34058	Heat shock protein HSP 90-beta OS=Rattus norvegicus GN=Hsp90ab1 PE=1 SV=4 - [HS90B_RAT]	67.13	1	25	41	1188	0.8964
P04639	Apolipoprotein A-I OS=Rattus norvegicus GN=Apoa1 PE=1 SV=2 - [APOA1_RAT]	64.48	1	16	16	556	0.8973
D3ZHA0	Filamin-C OS=Rattus norvegicus GN=Flnc PE=1 SV=1 - [FLNC_RAT]	5.17	1	8	10	89	0.8989
P00762	Anionic trypsin-1 OS=Rattus norvegicus GN=Prss1 PE=1 SV=1 - [TRY1_RAT]	14.23	1	2	2	102	0.8996
Q6P7S1	Acid ceramidase OS=Rattus norvegicus GN=Asah1 PE=2 SV=1 - [ASAH1_RAT]	24.62	1	6	6	43	0.9080
P13383	Nucleolin OS=Rattus norvegicus GN=Ncl PE=1 SV=3 - [NUCL_RAT]	18.93	1	10	10	87	0.9090
P05426	60S ribosomal protein L7 OS=Rattus norvegicus GN=Rpl7 PE=1 SV=2 - [RL7_RAT]	16.92	1	3	3	9	0.9109
P0CC09	Histone H2A type 2-A OS=Rattus norvegicus GN=Hist2h2aa3 PE=1 SV=1 - [H2A2A_RAT]	57.69	8	4	6	299	0.9136
Q5XI73	Rho GDP-dissociation inhibitor 1 OS=Rattus norvegicus GN=Arhgdia PE=1 SV=1 - [GDIR1_RAT]	59.31	1	11	11	250	0.9143
Q9JK11	Reticulon-4 OS=Rattus norvegicus GN=Rtn4 PE=1 SV=1 - [RTN4_RAT]	6.53	1	4	5	25	0.9150
P16446	Phosphatidylinositol transfer protein alpha isoform OS=Rattus norvegicus GN=Pitpna PE=1 SV=2 - [PIPNA_RAT]	12.18	1	2	2	3	0.9157
P85970	Actin-related protein 2/3 complex subunit 2 OS=Rattus norvegicus GN=Arpc2 PE=1 SV=1 - [ARPC2_RAT]	53.00	1	10	10	29	0.9163
P62260	14-3-3 protein epsilon OS=Rattus norvegicus GN=Ywhae PE=1 SV=1 - [1433E_RAT]	76.08	1	20	23	524	0.9181
F1LNJ2	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Rattus norvegicus GN=Snrnp200 PE=1 SV=1 - [U520_RAT]	3.09	1	4	4	8	0.9198
Q63797	Proteasome activator complex subunit 1 OS=Rattus norvegicus GN=Psme1 PE=2 SV=1 - [PSME1_RAT]	57.43	1	12	12	107	0.9216
P23562	Band 3 anion transport protein OS=Rattus norvegicus GN=Slc4a1 PE=1 SV=3 - [B3AT_RAT]	28.69	1	16	16	342	0.9347
P11598	Protein disulfide-isomerase A3 OS=Rattus norvegicus GN=Pdia3 PE=1 SV=2 - [PDIA3_RAT]	58.61	1	31	32	622	0.9374
Q6IFW6	Keratin, type I cytoskeletal 10 OS=Rattus norvegicus GN=Krt10 PE=3 SV=1 - [K1C10_RAT]	15.40	1	8	8	26	0.9378
O35509	Ras-related protein Rab-11B OS=Rattus norvegicus GN=Rab11b PE=1 SV=4 - [RB11B_RAT]	48.17	1	9	9	87	0.9385
P40307	Proteasome subunit beta type-2 OS=Rattus norvegicus GN=Psmb2 PE=1 SV=1 - [PSB2_RAT]	26.37	1	4	4	61	0.9395
P02770	Serum albumin OS=Rattus norvegicus GN=Alb PE=1 SV=2 - [ALBU_RAT]	80.26	1	54	54	32949	0.9409
P62250	40S ribosomal protein S16 OS=Rattus norvegicus GN=Rps16 PE=1 SV=2 - [RS16_RAT]	38.36	1	5	5	37	0.9436
O88664	Serine/threonine-protein kinase TAO1 OS=Rattus norvegicus GN=Taok1 PE=1 SV=1 - [TAOK1_RAT]	2.00	1	2	2	2	0.9475
P21670	Proteasome subunit alpha type-4 OS=Rattus norvegicus GN=Psma4 PE=1 SV=1 - [PSA4_RAT]	41.00	1	6	6	60	0.9520
O35795	Ectonucleoside triphosphate diphosphohydrolase 2 OS=Rattus norvegicus GN=Entpd2 PE=1 SV=1 - [ENTP2_RAT]	6.87	1	2	2	7	0.9522
Q6MG61	Chloride intracellular channel protein 1 OS=Rattus norvegicus GN=Clic1 PE=1 SV=1 - [CLIC1_RAT]	50.62	1	8	8	63	0.9524
Q10758	Keratin, type II cytoskeletal 8 OS=Rattus norvegicus GN=Krt8 PE=1 SV=3 - [K2C8_RAT]	20.29	1	4	10	63	0.9532
P29419	ATP synthase subunit e, mitochondrial OS=Rattus	56.34	1	4	4	36	0.9543

	norvegicus GN=Atp5i PE=1 SV=3 - [ATP5I_RAT]						
P50399	Rab GDP dissociation inhibitor beta OS=Rattus norvegicus GN=Gdi2 PE=1 SV=2 - [GDIB_RAT]	57.98	1	16	22	479	0.9578
O08590	Membrane primary amine oxidase OS=Rattus norvegicus GN=Aoc3 PE=1 SV=4 - [AOC3_RAT]	44.04	1	23	23	1611	0.9583
P31211	Corticosteroid-binding globulin OS=Rattus norvegicus GN=Serpina6 PE=1 SV=2 - [CBG_RAT]	21.21	1	6	6	35	0.9600
P15800	Laminin subunit beta-2 OS=Rattus norvegicus GN=Lamb2 PE=2 SV=1 - [LAMB2_RAT]	22.38	1	28	30	182	0.9614
Q641Y0	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Rattus norvegicus GN=Ddost PE=2 SV=1 - [OST48_RAT]	13.61	1	4	4	29	0.9640
P82995	Heat shock protein HSP 90-alpha OS=Rattus norvegicus GN=Hsp90aa1 PE=1 SV=3 - [HS90A_RAT]	61.12	1	24	38	871	0.9659
P0C0S7	Histone H2A.Z OS=Rattus norvegicus GN=H2afz PE=1 SV=2 - [H2AZ_RAT]	31.25	1	2	4	88	0.9722
Q68FP1	Gelsolin OS=Rattus norvegicus GN=Gsn PE=1 SV=1 - [GELS_RAT]	45.64	1	22	22	457	0.9740
Q7TP52	Carboxymethylenebutenolidase homolog OS=Rattus norvegicus GN=Cmbl PE=2 SV=1 - [CMBL_RAT]	22.45	1	5	5	10	0.9745
Q63569	26S protease regulatory subunit 6A OS=Rattus norvegicus GN=Psmc3 PE=2 SV=1 - [PRS6A_RAT]	5.92	1	2	2	2	0.9816
A1L1J9	Lipase maturation factor 2 OS=Rattus norvegicus GN=Lmf2 PE=2 SV=1 - [LMF2_RAT]	10.11	1	5	5	11	0.9823
Q13409	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3 - [DC1I2_HUMAN]	10.97	1	4	4	19	0.9827
Q68A21	Transcriptional activator protein Pur-beta OS=Rattus norvegicus GN=Purb PE=1 SV=3 - [PURB_RAT]	15.24	1	2	2	4	0.9900
P10959	Carboxylesterase 1C OS=Rattus norvegicus GN=Ces1c PE=1 SV=3 - [EST1C_RAT]	20.58	1	7	8	35	0.9911
P61959	Small ubiquitin-related modifier 2 OS=Rattus norvegicus GN=Sumo2 PE=1 SV=1 - [SUMO2_RAT]	23.16	1	2	2	7	0.9963
P20650	Protein phosphatase 1A OS=Rattus norvegicus GN=Ppm1a PE=1 SV=1 - [PPM1A_RAT]	5.50	2	2	2	2	0.9997
A0JPJ7	Obg-like ATPase 1 OS=Rattus norvegicus GN=Ola1 PE=2 SV=1 - [OLA1_RAT]	10.35	1	3	3	23	0.9999
P60711	Actin, cytoplasmic 1 OS=Rattus norvegicus GN=Actb PE=1 SV=1 - [ACTB_RAT]	82.67	2	12	25	5087	

2-cycles (fish-oil diet) versus 2-cycles (control diet)

Accession	Description	Σ Coverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	P-value
P09456	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Rattus norvegicus GN=Prkar1a PE=1 SV=2 - [KAP0_RAT]	10.76	1	2	2	7	0.0009
P31232	Transgelin OS=Rattus norvegicus GN=Tagln PE=1 SV=2 - [TAGL_RAT]	73.13	1	15	15	697	0.0018
Q63798	Proteasome activator complex subunit 2 OS=Rattus norvegicus GN=Psme2 PE=2 SV=3 - [PSME2_RAT]	32.77	1	6	6	37	0.0054
Q99J82	Integrin-linked protein kinase OS=Rattus norvegicus GN=Ilk PE=2 SV=1 - [ILK_RAT]	13.72	1	5	5	9	0.0058
Q920A6	Retinoid-inducible serine carboxypeptidase OS=Rattus norvegicus GN=Scpep1 PE=2 SV=1 - [RISC_RAT]	17.48	1	5	6	107	0.0067
P00787	Cathepsin B OS=Rattus norvegicus GN=Ctsb PE=1 SV=2 - [CATB_RAT]	28.32	1	8	8	140	0.0076
P06399	Fibrinogen alpha chain OS=Rattus norvegicus GN=Fga PE=1 SV=3 - [FIBA_RAT]	37.34	1	27	27	1135	0.0094
P47875	Cysteine and glycine-rich protein 1 OS=Rattus norvegicus GN=Csrp1 PE=1 SV=2 - [CSRP1_RAT]	30.57	1	5	5	94	0.0122
P07335	Creatine kinase B-type OS=Rattus norvegicus GN=Ckb PE=1 SV=2 - [KCRB_RAT]	52.76	1	15	15	224	0.0125
Q9JHY2	Sideroflexin-3 OS=Rattus norvegicus GN=Sfxn3 PE=2 SV=1 - [SFXN3_RAT]	14.02	1	2	2	2	0.0129

P16446	Phosphatidylinositol transfer protein alpha isoform OS=Rattus norvegicus GN=Pitpna PE=1 SV=2 - [PIPNA_RAT]	12.18	1	2	2	2	0.0141
Q9WUW3	Complement factor I OS=Rattus norvegicus GN=Cfi PE=2 SV=1 - [CFAI_RAT]	5.96	1	2	2	3	0.0158
P11951	Cytochrome c oxidase subunit 6C-2 OS=Rattus norvegicus GN=Cox6c2 PE=1 SV=3 - [CX6C2_RAT]	36.84	1	3	3	15	0.0228
P31430	Dipeptidase 1 OS=Rattus norvegicus GN=Dpep1 PE=2 SV=2 - [DPEP1_RAT]	30.73	1	6	6	51	0.0242
P18292	Prothrombin OS=Rattus norvegicus GN=F2 PE=1 SV=1 - [THRB_RAT]	21.72	1	8	8	68	0.0258
O08619	Coagulation factor XIII A chain OS=Rattus norvegicus GN=F13a1 PE=2 SV=3 - [F13A_RAT]	22.27	1	13	13	240	0.0265
O08662	Phosphatidylinositol 4-kinase alpha OS=Rattus norvegicus GN=Pi4ka PE=1 SV=1 - [PI4KA_RAT]	6.96	1	6	8	23	0.0267
P58775	Tropomyosin beta chain OS=Rattus norvegicus GN=Tpm2 PE=1 SV=1 - [TPM2_RAT]	30.99	1	1	12	101	0.0278
P24942	Excitatory amino acid transporter 1 OS=Rattus norvegicus GN=Slc1a3 PE=1 SV=2 - [EAA1_RAT]	7.18	1	2	2	36	0.0293
Q08290	Calponin-1 OS=Rattus norvegicus GN=Cnn1 PE=1 SV=1 - [CNN1_RAT]	16.16	1	4	4	10	0.0314
Q8CFN2	Cell division control protein 42 homolog OS=Rattus norvegicus GN=Cdc42 PE=1 SV=2 - [CDC42_RAT]	32.46	1	4	5	111	0.0326
Q5M7W5	Microtubule-associated protein 4 OS=Rattus norvegicus GN=Map4 PE=1 SV=1 - [MAP4_RAT]	30.84	1	20	20	82	0.0339
P36876	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Rattus norvegicus GN=Ppp2r2a PE=2 SV=1 - [2ABA_RAT]	6.94	1	2	2	6	0.0384
P50398	Rab GDP dissociation inhibitor alpha OS=Rattus norvegicus GN=Gdi1 PE=1 SV=1 - [GDIA_RAT]	34.45	1	6	10	127	0.0397
P85972	Vinculin OS=Rattus norvegicus GN=Vcl PE=1 SV=1 - [VINC_RAT]	63.41	1	53	55	1393	0.0410
Q6P7P5	Basic leucine zipper and W2 domain-containing protein 1 OS=Rattus norvegicus GN=Bzw1 PE=1 SV=1 - [BZW1_RAT]	7.88	1	2	2	2	0.0419
Q62736	Non-muscle caldesmon OS=Rattus norvegicus GN=Cald1 PE=1 SV=1 - [CALD1_RAT]	14.50	1	5	5	28	0.0425
Q6AY30	Saccharopine dehydrogenase-like oxidoreductase OS=Rattus norvegicus GN=Sccpdh PE=1 SV=1 - [SCPDL_RAT]	12.12	1	2	2	13	0.0437
Q9JJ22	Endoplasmic reticulum aminopeptidase 1 OS=Rattus norvegicus GN=Erap1 PE=2 SV=2 - [ERAP1_RAT]	11.83	1	7	8	38	0.0465
Q64640	Adenosine kinase OS=Rattus norvegicus GN=Adk PE=1 SV=3 - [ADK_RAT]	13.57	1	2	2	5	0.0472
P17077	60S ribosomal protein L9 OS=Rattus norvegicus GN=Rpl9 PE=1 SV=1 - [RL9_RAT]	35.42	1	5	5	17	0.0478
Q03626	Murinoglobulin-1 OS=Rattus norvegicus GN=Mug1 PE=2 SV=1 - [MUG1_RAT]	50.84	1	23	55	3236	0.0493
P14046	Alpha-1-inhibitor 3 OS=Rattus norvegicus GN=A1i3 PE=1 SV=1 - [A1I3_RAT]	50.71	1	23	56	3386	0.0493
P07895	Superoxide dismutase [Mn], mitochondrial OS=Rattus norvegicus GN=Sod2 PE=1 SV=2 - [SODM_RAT]	35.59	1	7	7	94	0.0502
P18614	Integrin alpha-1 OS=Rattus norvegicus GN=Itga1 PE=1 SV=1 - [ITA1_RAT]	4.15	1	2	2	2	0.0514
Q8R431	Monoglyceride lipase OS=Rattus norvegicus GN=Mgll PE=1 SV=1 - [MGLL_RAT]	67.66	1	17	17	630	0.0530
P52759	Ribonuclease UK114 OS=Rattus norvegicus GN=Hrsp12 PE=1 SV=3 - [UK114_RAT]	18.98	1	2	2	3	0.0556
Q9Z2Q1	Protein transport protein Sec31A OS=Rattus norvegicus GN=Sec31a PE=1 SV=2 - [SC31A_RAT]	13.13	1	10	10	126	0.0596
Q4G075	Leukocyte elastase inhibitor A OS=Rattus norvegicus GN=Serpinb1a PE=1 SV=1 - [ILEUA_RAT]	10.55	1	3	3	3	0.0604
Q2PQA9	Kinesin-1 heavy chain OS=Rattus norvegicus GN=Kif5b PE=1 SV=1 - [KINH_RAT]	5.30	1	2	3	8	0.0608
P05765	40S ribosomal protein S21 OS=Rattus norvegicus GN=Rps21 PE=1 SV=1 - [RS21_RAT]	28.92	1	2	2	16	0.0627
P35565	Calnexin OS=Rattus norvegicus GN=Canx PE=1 SV=1 - [CALX_RAT]	32.99	1	15	15	195	0.0638

P04644	40S ribosomal protein S17 OS=Rattus norvegicus GN=Rps17 PE=1 SV=3 - [RS17_RAT]	58.52	1	7	7	57	0.0666
Q62969	Prostacyclin synthase OS=Rattus norvegicus GN=Ptgis PE=2 SV=1 - [PTGIS_RAT]	15.57	1	4	4	21	0.0669
Q3T1K5	F-actin-capping protein subunit alpha-2 OS=Rattus norvegicus GN=Capza2 PE=1 SV=1 - [CAZA2_RAT]	27.97	1	4	5	54	0.0670
Q641Y8	ATP-dependent RNA helicase DDX1 OS=Rattus norvegicus GN=Ddx1 PE=1 SV=1 - [DDX1_RAT]	5.14	1	2	2	3	0.0670
P28480	T-complex protein 1 subunit alpha OS=Rattus norvegicus GN=Tcp1 PE=1 SV=1 - [TCPA_RAT]	18.35	1	4	5	25	0.0671
Q5XI73	Rho GDP-dissociation inhibitor 1 OS=Rattus norvegicus GN=Arhgdia PE=1 SV=1 - [GDIR1_RAT]	59.31	1	11	11	244	0.0676
Q63610	Tropomyosin alpha-3 chain OS=Rattus norvegicus GN=Tpm3 PE=1 SV=2 - [TPM3_RAT]	53.63	1	8	18	211	0.0686
P04692	Tropomyosin alpha-1 chain OS=Rattus norvegicus GN=Tpm1 PE=1 SV=3 - [TPM1_RAT]	39.44	1	1	14	130	0.0687
P21533	60S ribosomal protein L6 OS=Rattus norvegicus GN=Rpl6 PE=1 SV=5 - [RL6_RAT]	29.19	1	7	8	63	0.0692
P18420	Proteasome subunit alpha type-1 OS=Rattus norvegicus GN=Psma1 PE=1 SV=2 - [PSA1_RAT]	26.62	1	7	7	16	0.0693
P14562	Lysosome-associated membrane glycoprotein 1 OS=Rattus norvegicus GN=Lamp1 PE=1 SV=1 - [LAMP1_RAT]	17.44	1	6	6	26	0.0713
P29411	GTP:AMP phosphotransferase AK3, mitochondrial OS=Rattus norvegicus GN=Ak3 PE=2 SV=2 - [KAD3_RAT]	54.19	1	10	10	78	0.0729
P04631	Protein S100-B OS=Rattus norvegicus GN=S100b PE=1 SV=2 - [S100B_RAT]	40.22	1	3	3	26	0.0730
Q920L2	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Rattus norvegicus GN=Sdha PE=1 SV=1 - [SDHA_RAT]	28.81	1	11	12	56	0.0732
P50399	Rab GDP dissociation inhibitor beta OS=Rattus norvegicus GN=Gdi2 PE=1 SV=2 - [GDIB_RAT]	57.98	1	16	20	424	0.0761
P14630	Apolipoprotein M OS=Rattus norvegicus GN=Apom PE=1 SV=2 - [APOM_RAT]	13.16	1	2	2	3	0.0779
Q497B0	Omega-amidase NIT2 OS=Rattus norvegicus GN=Nit2 PE=1 SV=1 - [NIT2_RAT]	35.51	1	5	5	13	0.0781
P27952	40S ribosomal protein S2 OS=Rattus norvegicus GN=Rps2 PE=1 SV=1 - [RS2_RAT]	19.80	1	5	5	33	0.0783
Q8VHE9	All-trans-retinol 13,14-reductase OS=Rattus norvegicus GN=Retsat PE=2 SV=1 - [RETST_RAT]	28.41	1	11	11	250	0.0784
P13635	Ceruloplasmin OS=Rattus norvegicus GN=Cp PE=1 SV=3 - [CERU_RAT]	50.61	1	43	44	1470	0.0787
P06685	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Rattus norvegicus GN=Atp1a1 PE=1 SV=1 - [AT1A1_RAT]	15.64	1	11	11	135	0.0795
P51886	Lumican OS=Rattus norvegicus GN=Lum PE=1 SV=1 - [LUM_RAT]	36.09	1	11	11	371	0.0852
Q63797	Proteasome activator complex subunit 1 OS=Rattus norvegicus GN=Psme1 PE=2 SV=1 - [PSME1_RAT]	54.62	1	12	12	110	0.0873
P09495	Tropomyosin alpha-4 chain OS=Rattus norvegicus GN=Tpm4 PE=1 SV=3 - [TPM4_RAT]	60.89	1	9	19	216	0.0881
Q63041	Alpha-1-macroglobulin OS=Rattus norvegicus GN=A1m PE=1 SV=1 - [A1M_RAT]	65.53	1	65	66	2833	0.0889
Q9WTT6	Guanine deaminase OS=Rattus norvegicus GN=Gda PE=1 SV=1 - [GUAD_RAT]	72.47	1	27	27	1181	0.0898
P49134	Integrin beta-1 OS=Rattus norvegicus GN=Itgb1 PE=2 SV=1 - [ITB1_RAT]	35.92	1	19	20	225	0.0908
Q9JLA3	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Rattus norvegicus GN=Uggt1 PE=1 SV=2 - [UGGG1_RAT]	25.34	1	25	25	149	0.0912
P49242	40S ribosomal protein S3a OS=Rattus norvegicus GN=Rps3a PE=1 SV=2 - [RS3A_RAT]	16.29	1	3	4	7	0.0945
Q9QX27	Suppression of tumorigenicity 18 protein OS=Rattus norvegicus GN=St18 PE=2 SV=2 - [ST18_RAT]	2.52	1	2	2	2	0.0974
Q63617	Hypoxia up-regulated protein 1 OS=Rattus norvegicus GN=Hyou1 PE=1 SV=1 - [HYOU1_RAT]	30.53	1	19	22	195	0.0986
Q6P734	Plasma protease C1 inhibitor OS=Rattus norvegicus	45.44	1	17	17	102	0.0990

	GN=Serping1 PE=2 SV=1 - [IC1_RAT]						
P34067	Proteasome subunit beta type-4 OS=Rattus norvegicus GN=Psmb4 PE=1 SV=2 - [PSB4_RAT]	20.53	1	4	4	9	0.0992
P50878	60S ribosomal protein L4 OS=Rattus norvegicus GN=Rpl4 PE=1 SV=3 - [RL4_RAT]	11.88	1	3	4	26	0.0995
Q9QWE9	Gamma-glutamyltransferase 5 OS=Rattus norvegicus GN=Ggt5 PE=2 SV=1 - [GGT5_RAT]	8.74	1	3	3	6	0.1006
P19945	60S acidic ribosomal protein P0 OS=Rattus norvegicus GN=Rplp0 PE=1 SV=2 - [RLA0_RAT]	44.79	1	8	9	162	0.1012
P27605	Hypoxanthine-guanine phosphoribosyltransferase OS=Rattus norvegicus GN=Hprt1 PE=1 SV=1 - [HPRT_RAT]	49.54	1	9	9	76	0.1037
O35303	Dynamin-1-like protein OS=Rattus norvegicus GN=Dnm1l PE=1 SV=1 - [DNM1L_RAT]	6.49	1	2	2	15	0.1046
P08649	Complement C4 OS=Rattus norvegicus GN=C4 PE=1 SV=3 - [CO4_RAT]	54.40	1	62	62	1469	0.1074
P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	59.64	1	10	10	244	0.1080
F1LNJ2	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Rattus norvegicus GN=Snrnp200 PE=1 SV=1 - [U520_RAT]	2.99	1	3	4	8	0.1094
Q8VBU2	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1 - [NDRG2_RAT]	18.33	1	3	3	34	0.1106
Q5U211	Sorting nexin-3 OS=Rattus norvegicus GN=Snx3 PE=1 SV=1 - [SNX3_RAT]	56.79	1	7	7	34	0.1130
P02692	Fatty acid-binding protein, liver OS=Rattus norvegicus GN=Fabp1 PE=1 SV=1 - [FABPL_RAT]	62.20	1	6	6	29	0.1133
Q9Z270	Vesicle-associated membrane protein-associated protein A OS=Rattus norvegicus GN=Vapa PE=1 SV=3 - [VAPA_RAT]	28.92	1	7	7	51	0.1141
P85515	Alpha-centractin OS=Rattus norvegicus GN=Actr1a PE=1 SV=1 - [ACTZ_RAT]	19.41	1	5	5	21	0.1149
Q6AXM8	Serum paraoxonase/arylesterase 2 OS=Rattus norvegicus GN=Pon2 PE=2 SV=1 - [PON2_RAT]	19.77	1	4	4	5	0.1158
P36372	Antigen peptide transporter 2 OS=Rattus norvegicus GN=Tap2 PE=2 SV=1 - [TAP2_RAT]	4.55	1	2	3	9	0.1168
P43244	Matrin-3 OS=Rattus norvegicus GN=Matr3 PE=1 SV=2 - [MATR3_RAT]	8.05	1	4	4	37	0.1171
Q2TL32	E3 ubiquitin-protein ligase UBR4 OS=Rattus norvegicus GN=Ubr4 PE=1 SV=2 - [UBR4_RAT]	2.95	1	8	8	26	0.1193
Q99PF5	Far upstream element-binding protein 2 OS=Rattus norvegicus GN=Khsrp PE=1 SV=1 - [FUBP2_RAT]	3.19	1	2	2	6	0.1215
P10959	Carboxylesterase 1C OS=Rattus norvegicus GN=Ces1c PE=1 SV=3 - [EST1C_RAT]	22.40	1	8	9	51	0.1215
G3V7P1	Syntaxin-12 OS=Rattus norvegicus GN=Stx12 PE=1 SV=1 - [STX12_RAT]	10.22	1	2	2	5	0.1217
Q64240	Protein AMBP OS=Rattus norvegicus GN=Ambp PE=1 SV=1 - [AMBP_RAT]	15.47	1	4	4	89	0.1225
P06238	Alpha-2-macroglobulin OS=Rattus norvegicus GN=A2m PE=2 SV=2 - [A2MG_RAT]	56.05	1	63	64	1176	0.1284
Q6PEC4	S-phase kinase-associated protein 1 OS=Rattus norvegicus GN=Skp1 PE=1 SV=3 - [SKP1_RAT]	15.34	1	2	2	2	0.1293
Q63416	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Rattus norvegicus GN=Itih3 PE=2 SV=1 - [ITIH3_RAT]	29.20	1	18	18	488	0.1311
P55159	Serum paraoxonase/arylesterase 1 OS=Rattus norvegicus GN=Pon1 PE=1 SV=3 - [PON1_RAT]	9.58	1	2	2	2	0.1342
P04638	Apolipoprotein A-II OS=Rattus norvegicus GN=Apoa2 PE=2 SV=1 - [APOA2_RAT]	30.39	1	3	3	7	0.1351
P62959	Histidine triad nucleotide-binding protein 1 OS=Rattus norvegicus GN=Hint1 PE=1 SV=5 - [HINT1_RAT]	17.46	1	2	2	18	0.1358
Q5XIP9	Transmembrane protein 43 OS=Rattus norvegicus GN=Tmem43 PE=2 SV=1 - [TMM43_RAT]	30.50	1	7	7	51	0.1416
P85971	6-phosphogluconolactonase OS=Rattus norvegicus GN=Pgls PE=1 SV=1 - [6PGL_RAT]	36.96	1	5	5	86	0.1440
P62246	40S ribosomal protein S15a OS=Rattus norvegicus GN=Rps15a PE=1 SV=2 - [RS15A_RAT]	23.85	1	3	3	6	0.1443
Q6AY20	Cation-dependent mannose-6-phosphate receptor OS=Rattus norvegicus GN=M6pr PE=1 SV=1 -	19.78	1	4	4	5	0.1449

	[MPRD_RAT]						
P85845	Fascin OS=Rattus norvegicus GN=Fscn1 PE=1 SV=2 - [FSCN1_RAT]	6.90	1	2	2	2	0.1469
P06762	Heme oxygenase 1 OS=Rattus norvegicus GN=Hmox1 PE=1 SV=1 - [HMOX1_RAT]	16.61	1	3	4	4	0.1492
P22985	Xanthine dehydrogenase/oxidase OS=Rattus norvegicus GN=Xdh PE=1 SV=3 - [XDH_RAT]	42.37	1	34	34	1112	0.1495
P04639	Apolipoprotein A-I OS=Rattus norvegicus GN=Apoa1 PE=1 SV=2 - [APOA1_RAT]	64.48	1	16	16	640	0.1498
O35796	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Rattus norvegicus GN=C1qbp PE=1 SV=2 - [C1QBP_RAT]	11.83	1	2	2	2	0.1499
Q6UVM4	Potassium channel subfamily T member 2 OS=Rattus norvegicus GN=Kcnt2 PE=1 SV=1 - [KCNT2_RAT]	4.12	1	2	2	2	0.1500
Q5RKI1	Eukaryotic initiation factor 4A-II OS=Rattus norvegicus GN=Eif4a2 PE=1 SV=1 - [IF4A2_RAT]	30.71	1	9	9	161	0.1517
P01041	Cystatin-B OS=Rattus norvegicus GN=Cstb PE=1 SV=1 - [CYTB_RAT]	34.69	1	3	3	37	0.1533
P42930	Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1 - [HSPB1_RAT]	63.11	1	11	11	377	0.1544
Q9WVC0	Septin-7 OS=Rattus norvegicus GN=Sept7 PE=1 SV=1 - [SEPT7_RAT]	19.72	1	6	7	53	0.1548
P02764	Alpha-1-acid glycoprotein OS=Rattus norvegicus GN=Orm1 PE=2 SV=1 - [A1AG_RAT]	29.76	1	9	9	88	0.1548
Q9R063	Peroxiredoxin-5, mitochondrial OS=Rattus norvegicus GN=Prdx5 PE=1 SV=1 - [PRDX5_RAT]	54.93	1	11	11	282	0.1553
P02770	Serum albumin OS=Rattus norvegicus GN=Alb PE=1 SV=2 - [ALBU_RAT]	79.28	1	51	51	36778	0.1555
P15800	Laminin subunit beta-2 OS=Rattus norvegicus GN=Lamb2 PE=2 SV=1 - [LAMB2_RAT]	16.10	1	20	22	117	0.1556
O35142	Coatomer subunit beta' OS=Rattus norvegicus GN=Copb2 PE=1 SV=3 - [COPB2_RAT]	11.93	1	7	9	68	0.1563
Q923V8	15 kDa selenoprotein OS=Rattus norvegicus GN=Sep15 PE=1 SV=3 - [SEP15_RAT]	25.31	1	3	3	6	0.1564
Q05962	ADP/ATP translocase 1 OS=Rattus norvegicus GN=Slc25a4 PE=1 SV=3 - [ADT1_RAT]	40.94	1	4	10	303	0.1577
P02680	Fibrinogen gamma chain OS=Rattus norvegicus GN=Fgg PE=1 SV=3 - [FIBG_RAT]	63.82	1	24	24	1151	0.1579
P07824	Arginase-1 OS=Rattus norvegicus GN=Arg1 PE=1 SV=2 - [ARGI1_RAT]	11.76	1	2	2	3	0.1581
P09606	Glutamine synthetase OS=Rattus norvegicus GN=Glul PE=1 SV=3 - [GLNA_RAT]	43.97	1	12	12	245	0.1593
P36370	Antigen peptide transporter 1 OS=Rattus norvegicus GN=Tap1 PE=1 SV=2 - [TAP1_RAT]	8.00	1	3	4	14	0.1593
P20059	Hemopexin OS=Rattus norvegicus GN=Hpx PE=1 SV=3 - [HEMO_RAT]	64.35	1	30	30	2717	0.1596
P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	22.28	1	17	18	184	0.1603
P62271	40S ribosomal protein S18 OS=Rattus norvegicus GN=Rps18 PE=1 SV=3 - [RS18_RAT]	48.68	1	9	9	121	0.1607
Q64542	Plasma membrane calcium-transporting ATPase 4 OS=Rattus norvegicus GN=Atp2b4 PE=1 SV=1 - [AT2B4_RAT]	3.91	1	2	3	7	0.1621
Q6P6T1	Complement C1s subcomponent OS=Rattus norvegicus GN=C1s PE=2 SV=2 - [C1S_RAT]	12.35	1	3	3	3	0.1634
P42667	Signal peptidase complex catalytic subunit SEC11A OS=Rattus norvegicus GN=Sec11a PE=2 SV=1 - [SC11A_RAT]	9.50	1	2	2	2	0.1642
A1L1J9	Lipase maturation factor 2 OS=Rattus norvegicus GN=Lmf2 PE=2 SV=1 - [LMF2_RAT]	7.55	1	4	4	6	0.1664
Q09073	ADP/ATP translocase 2 OS=Rattus norvegicus GN=Slc25a5 PE=1 SV=3 - [ADT2_RAT]	44.30	1	5	11	297	0.1685
O35244	Peroxiredoxin-6 OS=Rattus norvegicus GN=Prdx6 PE=1 SV=3 - [PRDX6_RAT]	60.27	1	12	12	194	0.1688
Q66H89	Centrosomal protein of 83 kDa OS=Rattus norvegicus GN=Cep83 PE=2 SV=1 - [CEP83_RAT]	4.48	1	3	3	7	0.1700
Q9WUH4	Four and a half LIM domains protein 1 OS=Rattus	25.00	1	6	6	23	0.1704

	norvegicus GN=Fhl1 PE=2 SV=1 - [FHL1_RAT]						
Q63228	Glia maturation factor beta OS=Rattus norvegicus GN=Gmfb PE=1 SV=2 - [GMFB_RAT]	30.28	1	4	4	9	0.1708
Q63010	Liver carboxylesterase B-1 OS=Rattus norvegicus PE=1 SV=1 - [EST5_RAT]	7.84	2	2	3	32	0.1723
Q4KM35	Proteasome subunit beta type-10 OS=Rattus norvegicus GN=Psmb10 PE=2 SV=1 - [PSB10_RAT]	20.15	1	4	4	13	0.1728
Q8CG45	Aflatoxin B1 aldehyde reductase member 2 OS=Rattus norvegicus GN=Akr7a2 PE=1 SV=2 - [ARK72_RAT]	11.72	1	3	3	3	0.1740
Q9WVR7	Protein phosphatase 1F OS=Rattus norvegicus GN=Ppm1f PE=2 SV=1 - [PPM1F_RAT]	11.78	1	2	2	4	0.1743
B2GUZ5	F-actin-capping protein subunit alpha-1 OS=Rattus norvegicus GN=Capza1 PE=1 SV=1 - [CAZA1_RAT]	25.87	1	4	5	41	0.1749
P18421	Proteasome subunit beta type-1 OS=Rattus norvegicus GN=Psmb1 PE=1 SV=3 - [PSB1_RAT]	39.17	1	7	7	70	0.1768
P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	65.74	1	127	129	1913	0.1771
Q62740	Secreted phosphoprotein 24 OS=Rattus norvegicus GN=Spp2 PE=1 SV=2 - [SPP24_RAT]	11.82	1	2	2	5	0.1782
Q6MG61	Chloride intracellular channel protein 1 OS=Rattus norvegicus GN=Clic1 PE=1 SV=1 - [CLIC1_RAT]	62.66	1	11	11	77	0.1788
P04797	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus GN=Gapdh PE=1 SV=3 - [G3P_RAT]	75.98	1	17	17	1320	0.1788
Q9Z1X1	Extended synaptotagmin-1 OS=Rattus norvegicus GN=Esyt1 PE=1 SV=1 - [ESYT1_RAT]	46.23	1	32	32	628	0.1805
P11507	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Rattus norvegicus GN=Atp2a2 PE=1 SV=1 - [AT2A2_RAT]	14.00	1	10	10	111	0.1807
P48199	C-reactive protein OS=Rattus norvegicus GN=Crp PE=1 SV=1 - [CRP_RAT]	32.61	1	5	5	269	0.1809
P17475	Alpha-1-antiproteinase OS=Rattus norvegicus GN=Serpina1 PE=1 SV=2 - [A1AT_RAT]	53.77	1	21	21	1695	0.1830
Q62658	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Rattus norvegicus GN=Fkbp1a PE=1 SV=3 - [FKB1A_RAT]	29.63	1	3	3	46	0.1830
P14480	Fibrinogen beta chain OS=Rattus norvegicus GN=Fgb PE=1 SV=4 - [FIBB_RAT]	71.40	1	34	34	1169	0.1835
P70615	Lamin-B1 OS=Rattus norvegicus GN=Lmnb1 PE=1 SV=3 - [LMNB1_RAT]	15.84	1	6	8	31	0.1838
Q01129	Decorin OS=Rattus norvegicus GN=Dcn PE=1 SV=1 - [PGS2_RAT]	34.46	1	12	12	494	0.1848
P06866	Haptoglobin OS=Rattus norvegicus GN=Hp PE=1 SV=3 - [HPT_RAT]	63.11	1	21	22	763	0.1856
P31720	Complement C1q subcomponent subunit A OS=Rattus norvegicus GN=C1qa PE=1 SV=2 - [C1QA_RAT]	20.41	1	3	3	15	0.1860
Q66HG4	Aldose 1-epimerase OS=Rattus norvegicus GN=Galm PE=1 SV=1 - [GALM_RAT]	23.39	1	5	5	31	0.1867
P0CG51	Polyubiquitin-B OS=Rattus norvegicus GN=Ubb PE=1 SV=1 - [UBB_RAT]	70.82	4	7	7	451	0.1869
P38983	40S ribosomal protein SA OS=Rattus norvegicus GN=Rpsa PE=1 SV=3 - [RSSA_RAT]	52.20	1	9	9	129	0.1910
P27615	Lysosome membrane protein 2 OS=Rattus norvegicus GN=Scarb2 PE=1 SV=2 - [SCRB2_RAT]	11.51	1	3	3	9	0.1921
Q9EQP5	Prolargin OS=Rattus norvegicus GN=Prelp PE=2 SV=1 - [PRELP_RAT]	40.32	1	11	11	79	0.1928
Q8VHV7	Heterogeneous nuclear ribonucleoprotein H OS=Rattus norvegicus GN=Hnrnph1 PE=1 SV=2 - [HNRH1_RAT]	11.14	1	2	3	50	0.1930
P29314	40S ribosomal protein S9 OS=Rattus norvegicus GN=Rps9 PE=1 SV=4 - [RS9_RAT]	18.56	1	4	5	12	0.1932
Q5U300	Ubiquitin-like modifier-activating enzyme 1 OS=Rattus norvegicus GN=Uba1 PE=1 SV=1 - [UBA1_RAT]	44.33	1	30	31	462	0.1954
P05369	Farnesyl pyrophosphate synthase OS=Rattus norvegicus GN=Fdps PE=2 SV=2 - [FPPS_RAT]	6.80	1	2	2	2	0.1955
Q66H12	Alpha-N-acetylgalactosaminidase OS=Rattus norvegicus GN=Naga PE=2 SV=1 - [NAGAB_RAT]	6.75	1	2	2	4	0.1957
D3ZHV2	Microtubule-actin cross-linking factor 1 OS=Rattus norvegicus GN=Macf1 PE=1 SV=1 - [MACF1_RAT]	1.49	1	3	6	11	0.1967
P62944	AP-2 complex subunit beta OS=Rattus norvegicus	24.87	1	9	15	284	0.1984

	GN=Ap2b1 PE=1 SV=1 - [AP2B1_RAT]						
P51635	Alcohol dehydrogenase [NADP(+)] OS=Rattus norvegicus GN=Akr1a1 PE=1 SV=2 - [AK1A1_RAT]	48.31	1	13	13	129	0.1986
P04355	Metallothionein-2 OS=Rattus norvegicus GN=Mt2 PE=1 SV=1 - [MT2_RAT]	21.31	1	2	2	8	0.1988
P07153	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Rattus norvegicus GN=Rpn1 PE=2 SV=1 - [RPN1_RAT]	26.78	1	11	11	74	0.1997
P09006	Serine protease inhibitor A3N OS=Rattus norvegicus GN=Serpina3n PE=1 SV=3 - [SPA3N_RAT]	68.18	1	24	24	930	0.2021
Q01177	Plasminogen OS=Rattus norvegicus GN=Plg PE=2 SV=2 - [PLMN_RAT]	55.42	1	32	32	192	0.2021
Q08163	Adenylyl cyclase-associated protein 1 OS=Rattus norvegicus GN=Cap1 PE=1 SV=3 - [CAP1_RAT]	44.94	1	12	12	246	0.2023
P05371	Clusterin OS=Rattus norvegicus GN=Clu PE=1 SV=2 - [CLUS_RAT]	12.30	1	4	4	22	0.2024
Q63413	Spliceosome RNA helicase Ddx39b OS=Rattus norvegicus GN=Ddx39b PE=2 SV=3 - [DX39B_RAT]	9.35	1	3	3	6	0.2027
Q8VD48	Dehydrogenase/reductase SDR family member 9 OS=Rattus norvegicus GN=Dhrs9 PE=2 SV=1 - [DHRS9_RAT]	9.40	1	2	2	2	0.2031
Q99PS8	Histidine-rich glycoprotein OS=Rattus norvegicus GN=Hrg PE=1 SV=1 - [HRG_RAT]	21.90	1	9	9	48	0.2032
P0C5H9	Mesencephalic astrocyte-derived neurotrophic factor OS=Rattus norvegicus GN=Manf PE=1 SV=1 - [MANF_RAT]	13.97	1	3	3	11	0.2046
P12369	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus GN=Prkar2b PE=1 SV=3 - [KAP3_RAT]	31.97	1	9	9	119	0.2050
Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	1.76	1	2	2	2	0.2056
Q5QD51	A-kinase anchor protein 12 OS=Rattus norvegicus GN=Akap12 PE=1 SV=1 - [AKA12_RAT]	5.33	1	7	9	94	0.2069
Q80Z29	Nicotinamide phosphoribosyltransferase OS=Rattus norvegicus GN=Nampt PE=1 SV=1 - [NAMPT_RAT]	14.46	1	3	3	5	0.2112
P85973	Purine nucleoside phosphorylase OS=Rattus norvegicus GN=Pnp PE=1 SV=1 - [PNPH_RAT]	73.36	1	14	14	574	0.2128
P31721	Complement C1q subcomponent subunit B OS=Rattus norvegicus GN=C1qb PE=1 SV=2 - [C1QB_RAT]	9.88	1	2	2	12	0.2136
P23680	Serum amyloid P-component OS=Rattus norvegicus GN=Apcs PE=2 SV=2 - [SAMP_RAT]	14.04	1	2	2	2	0.2152
P24050	40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=1 SV=3 - [RS5_RAT]	13.73	1	4	4	12	0.2152
Q63258	Integrin alpha-7 OS=Rattus norvegicus GN=Itga7 PE=1 SV=2 - [ITA7_RAT]	10.04	1	5	7	12	0.2155
Q99MZ8	LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1 - [LASP1_RAT]	8.37	1	2	3	3	0.2176
O08629	Transcription intermediary factor 1-beta OS=Rattus norvegicus GN=Trim28 PE=1 SV=2 - [TIF1B_RAT]	8.14	1	4	5	7	0.2195
Q05175	Brain acid soluble protein 1 OS=Rattus norvegicus GN=Basp1 PE=1 SV=2 - [BASP1_RAT]	13.64	1	2	2	3	0.2204
Q4KLH6	Centrosomal protein of 162 kDa OS=Rattus norvegicus GN=Cep162 PE=1 SV=2 - [CE162_RAT]	1.14	1	2	2	3	0.2207
P11598	Protein disulfide-isomerase A3 OS=Rattus norvegicus GN=Pdia3 PE=1 SV=2 - [PDIA3_RAT]	60.00	1	31	32	640	0.2213
P63095	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Rattus norvegicus GN=Gnas PE=1 SV=1 - [GNAS2_RAT]	29.44	2	7	8	99	0.2213
P16391	RT1 class I histocompatibility antigen, AA alpha chain OS=Rattus norvegicus PE=1 SV=2 - [HA12_RAT]	11.32	1	4	4	30	0.2237
Q63081	Protein disulfide-isomerase A6 OS=Rattus norvegicus GN=Pdia6 PE=1 SV=2 - [PDIA6_RAT]	39.77	1	11	12	396	0.2251
P63025	Vesicle-associated membrane protein 3 OS=Rattus norvegicus GN=Vamp3 PE=1 SV=1 - [VAMP3_RAT]	23.30	2	2	2	13	0.2271
P50503	Hsc70-interacting protein OS=Rattus norvegicus GN=St13 PE=1 SV=1 - [F10A1_RAT]	8.97	1	3	3	17	0.2275
P67779	Prohibitin OS=Rattus norvegicus GN=Phb PE=1 SV=1 - [PHB_RAT]	62.87	1	12	12	118	0.2276

P62198	26S protease regulatory subunit 8 OS=Rattus norvegicus GN=Psmc5 PE=1 SV=1 - [PRS8_RAT]	21.18	1	5	5	10	0.2287
Q63584	Transmembrane emp24 domain-containing protein 10 OS=Rattus norvegicus GN=Tmed10 PE=1 SV=2 - [TMEDA_RAT]	18.26	1	3	3	37	0.2289
M0RC99	Ras-related protein Rab-5A OS=Rattus norvegicus GN=Rab5a PE=2 SV=1 - [RAB5A_RAT]	14.88	1	3	3	10	0.2291
P52303	AP-1 complex subunit beta-1 OS=Rattus norvegicus GN=Ap1b1 PE=1 SV=1 - [AP1B1_RAT]	20.97	1	4	11	155	0.2310
Q6P0K8	Junction plakoglobin OS=Rattus norvegicus GN=Jup PE=1 SV=1 - [PLAK_RAT]	5.10	1	2	2	2	0.2319
P10824	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Rattus norvegicus GN=Gnai1 PE=1 SV=3 - [GNAI1_RAT]	41.53	1	3	11	123	0.2336
P62804	Histone H4 OS=Rattus norvegicus GN=Hist1h4b PE=1 SV=2 - [H4_RAT]	52.43	1	7	7	300	0.2347
Q3MIE4	Synaptic vesicle membrane protein VAT-1 homolog OS=Rattus norvegicus GN=Vat1 PE=1 SV=1 - [VAT1_RAT]	40.84	1	11	11	137	0.2367
P04904	Glutathione S-transferase alpha-3 OS=Rattus norvegicus GN=Gsta3 PE=1 SV=3 - [GSTA3_RAT]	63.80	1	10	10	114	0.2400
Q5RK27	Solute carrier family 12 member 7 OS=Rattus norvegicus GN=Slc12a7 PE=2 SV=2 - [S12A7_RAT]	1.29	1	2	2	2	0.2401
Q64537	Calpain small subunit 1 OS=Rattus norvegicus GN=Capns1 PE=1 SV=3 - [CPNS1_RAT]	64.07	1	8	8	74	0.2407
Q9QZA2	Programmed cell death 6-interacting protein OS=Rattus norvegicus GN=Pdcd6ip PE=1 SV=2 - [PDC6I_RAT]	16.61	1	7	7	79	0.2416
P21396	Amine oxidase [flavin-containing] A OS=Rattus norvegicus GN=Maoa PE=1 SV=1 - [AOFA_RAT]	5.13	1	2	2	4	0.2444
P19511	ATP synthase F(0) complex subunit B1, mitochondrial OS=Rattus norvegicus GN=Atp5f1 PE=1 SV=1 - [AT5F1_RAT]	38.28	1	9	10	90	0.2447
Q9Z1A6	Vigilin OS=Rattus norvegicus GN=Hdlbp PE=1 SV=1 - [VIGLN_RAT]	14.98	1	16	16	79	0.2450
P01026	Complement C3 OS=Rattus norvegicus GN=C3 PE=1 SV=3 - [CO3_RAT]	66.69	1	87	89	3687	0.2481
P27274	CD59 glycoprotein OS=Rattus norvegicus GN=Cd59 PE=1 SV=2 - [CD59_RAT]	30.16	1	4	4	73	0.2484
Q4V886	RNA polymerase II-associated factor 1 homolog OS=Rattus norvegicus GN=Paf1 PE=2 SV=1 - [PAF1_RAT]	9.16	1	2	2	2	0.2485
P02563	Myosin-6 OS=Rattus norvegicus GN=Myh6 PE=1 SV=2 - [MYH6_RAT]	2.37	1	2	2	3	0.2492
Q9R1Z0	Voltage-dependent anion-selective channel protein 3 OS=Rattus norvegicus GN=Vdac3 PE=1 SV=2 - [VDAC3_RAT]	8.13	1	1	2	19	0.2499
Q811A3	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Rattus norvegicus GN=Plod2 PE=2 SV=1 - [PLOD2_RAT]	22.66	1	13	13	48	0.2503
Q7TQ94	Nitrilase homolog 1 OS=Rattus norvegicus GN=Nit1 PE=2 SV=1 - [NIT1_RAT]	31.16	1	5	5	26	0.2526
P23358	60S ribosomal protein L12 OS=Rattus norvegicus GN=Rpl12 PE=2 SV=1 - [RL12_RAT]	59.39	1	7	7	92	0.2531
Q62745	CD81 antigen OS=Rattus norvegicus GN=Cd81 PE=1 SV=1 - [CD81_RAT]	15.25	1	2	2	4	0.2540
P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	52.91	1	34	34	836	0.2542
P18484	AP-2 complex subunit alpha-2 OS=Rattus norvegicus GN=Ap2a2 PE=1 SV=3 - [AP2A2_RAT]	24.31	1	14	14	168	0.2546
P17220	Proteasome subunit alpha type-2 OS=Rattus norvegicus GN=Psma2 PE=1 SV=3 - [PSA2_RAT]	51.28	1	10	10	78	0.2599
Q8VIF7	Selenium-binding protein 1 OS=Rattus norvegicus GN=Selenbp1 PE=1 SV=1 - [SBP1_RAT]	55.08	1	19	22	128	0.2606
P31722	Complement C1q subcomponent subunit C OS=Rattus norvegicus GN=C1qc PE=1 SV=2 - [C1QC_RAT]	16.73	1	3	3	5	0.2643
P10688	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1 OS=Rattus norvegicus GN=Plcd1 PE=1 SV=1 - [PLCD1_RAT]	7.41	1	2	3	5	0.2676

Q5XIM9	T-complex protein 1 subunit beta OS=Rattus norvegicus GN=Cct2 PE=1 SV=3 - [TCPB_RAT]	14.39	1	4	4	16	0.2679
P17046	Lysosome-associated membrane glycoprotein 2 OS=Rattus norvegicus GN=Lamp2 PE=1 SV=2 - [LAMP2_RAT]	7.30	1	2	2	7	0.2682
P60892	Ribose-phosphate pyrophosphokinase 1 OS=Rattus norvegicus GN=Prps1 PE=1 SV=2 - [PRPS1_RAT]	12.89	1	3	3	5	0.2713
P07150	Annexin A1 OS=Rattus norvegicus GN=Anxa1 PE=1 SV=2 - [ANXA1_RAT]	75.14	1	28	28	2258	0.2719
P06214	Delta-aminolevulinic acid dehydratase OS=Rattus norvegicus GN=Alad PE=1 SV=1 - [HEM2_RAT]	28.79	1	5	5	30	0.2721
P30835	ATP-dependent 6-phosphofructokinase, liver type OS=Rattus norvegicus GN=Pfkl PE=1 SV=3 - [PFKAL_RAT]	2.69	1	2	2	2	0.2722
Q13409	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3 - [DC1I2_HUMAN]	13.17	1	5	5	23	0.2725
P06761	78 kDa glucose-regulated protein OS=Rattus norvegicus GN=Hspa5 PE=1 SV=1 - [GRP78_RAT]	48.93	1	27	29	833	0.2733
Q63355	Unconventional myosin-Ic OS=Rattus norvegicus GN=Myo1c PE=1 SV=2 - [MYO1C_RAT]	53.16	1	45	47	1483	0.2746
P62703	40S ribosomal protein S4, X isoform OS=Rattus norvegicus GN=Rps4x PE=2 SV=2 - [RS4X_RAT]	37.64	1	8	9	18	0.2747
Q63663	Guanylate-binding protein 1 OS=Rattus norvegicus GN=Gbp2 PE=1 SV=2 - [GBP2_RAT]	2.72	1	2	2	2	0.2756
P61621	Protein transport protein Sec61 subunit alpha isoform 1 OS=Rattus norvegicus GN=Sec61a1 PE=2 SV=2 - [S61A1_RAT]	15.76	1	4	4	36	0.2770
P70645	Bleomycin hydrolase OS=Rattus norvegicus GN=Blmh PE=1 SV=1 - [BLMH_RAT]	8.37	1	2	2	2	0.2770
P20759	Ig gamma-1 chain C region OS=Rattus norvegicus PE=1 SV=1 - [IGHG1_RAT]	20.55	1	2	5	425	0.2776
P50475	Alanine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Aars PE=1 SV=3 - [SYAC_RAT]	8.57	1	5	5	20	0.2778
P52555	Endoplasmic reticulum resident protein 29 OS=Rattus norvegicus GN=Erp29 PE=1 SV=2 - [ERP29_RAT]	55.38	1	10	10	98	0.2782
Q62930	Complement component C9 OS=Rattus norvegicus GN=C9 PE=2 SV=1 - [CO9_RAT]	56.50	1	25	25	294	0.2803
P23514	Coatomer subunit beta OS=Rattus norvegicus GN=Copb1 PE=1 SV=1 - [COPB_RAT]	13.85	1	7	7	74	0.2805
Q62636	Ras-related protein Rap-1b OS=Rattus norvegicus GN=Rap1b PE=1 SV=2 - [RAP1B_RAT]	73.37	1	5	10	165	0.2809
P85968	6-phosphogluconate dehydrogenase, decarboxylating OS=Rattus norvegicus GN=Pgd PE=1 SV=1 - [6PGD_RAT]	41.20	1	15	15	347	0.2823
P50115	Protein S100-A8 OS=Rattus norvegicus GN=S100a8 PE=1 SV=3 - [S10A8_RAT]	22.47	1	2	2	2	0.2833
F1MA98	Nucleoprotein TPR OS=Rattus norvegicus GN=Tpr PE=1 SV=1 - [TPR_RAT]	2.71	1	3	4	9	0.2844
Q62826	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=1 SV=4 - [HNRPM_RAT]	5.36	1	3	3	21	0.2855
Q4KM74	Vesicle-trafficking protein SEC22b OS=Rattus norvegicus GN=Sec22b PE=1 SV=3 - [SC22B_RAT]	36.74	1	6	7	66	0.2871
P82471	Guanine nucleotide-binding protein G(q) subunit alpha OS=Rattus norvegicus GN=Gnaq PE=2 SV=2 - [GNAQ_RAT]	25.07	1	6	6	36	0.2914
Q68FR9	Elongation factor 1-delta OS=Rattus norvegicus GN=Eef1d PE=1 SV=2 - [EF1D_RAT]	21.71	1	4	4	25	0.2928
Q66HA6	ADP-ribosylation factor-like protein 8B OS=Rattus norvegicus GN=Arl8b PE=2 SV=1 - [ARL8B_RAT]	24.73	1	3	3	4	0.2936
P0DMW0	Heat shock 70 kDa protein 1A OS=Rattus norvegicus GN=Hspa1a PE=2 SV=1 - [HS71A_RAT]	16.38	1	4	8	362	0.2937
P19356	Porphobilinogen deaminase OS=Rattus norvegicus GN=Hmbs PE=1 SV=2 - [HEM3_RAT]	11.08	1	2	2	7	0.2950
P21531	60S ribosomal protein L3 OS=Rattus norvegicus GN=Rpl3 PE=1 SV=3 - [RL3_RAT]	13.65	1	4	4	37	0.2956
P53565	Homeobox protein cut-like 1 OS=Rattus norvegicus	1.80	1	2	2	2	0.2984

	GN=Cux1 PE=1 SV=2 - [CUX1_RAT]						
P08011	Microsomal glutathione S-transferase 1 OS=Rattus norvegicus GN=Mgst1 PE=1 SV=3 - [MGST1_RAT]	54.19	1	6	6	1081	0.3007
P07687	Epoxide hydrolase 1 OS=Rattus norvegicus GN=Ephx1 PE=1 SV=1 - [HYEP_RAT]	6.81	1	2	2	4	0.3010
Q4QQT4	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Rattus norvegicus GN=Ppp2r1b PE=2 SV=1 - [2AAB_RAT]	5.99	1	3	3	16	0.3017
P07379	Phosphoenolpyruvate carboxykinase, cytosolic [GTP] OS=Rattus norvegicus GN=Pck1 PE=1 SV=1 - [PCKGC_RAT]	9.65	1	3	3	12	0.3042
P63088	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Rattus norvegicus GN=Ppp1cc PE=1 SV=1 - [PP1G_RAT]	23.53	3	3	5	32	0.3047
P01048	T-kininogen 1 OS=Rattus norvegicus GN=Map1 PE=1 SV=2 - [KNT1_RAT]	50.23	1	8	20	1348	0.3063
Q4AEF8	Coatomer subunit gamma-1 OS=Rattus norvegicus GN=Copg1 PE=2 SV=1 - [COPG1_RAT]	26.54	1	11	13	73	0.3064
Q9WTV5	26S proteasome non-ATPase regulatory subunit 9 OS=Rattus norvegicus GN=Psmd9 PE=1 SV=1 - [PSMD9_RAT]	9.01	1	2	2	2	0.3081
Q6QA69	1-acylglycerol-3-phosphate O-acyltransferase ABHD5 OS=Rattus norvegicus GN=Abhd5 PE=1 SV=1 - [ABHD5_RAT]	30.77	1	5	6	153	0.3091
Q8VI04	Isoaspartyl peptidase/L-asparaginase OS=Rattus norvegicus GN=Asrgl1 PE=1 SV=1 - [ASGL1_RAT]	13.51	1	4	4	7	0.3113
P05943	Protein S100-A10 OS=Rattus norvegicus GN=S100a10 PE=1 SV=2 - [S10AA_RAT]	28.42	1	3	3	20	0.3122
P53987	Monocarboxylate transporter 1 OS=Rattus norvegicus GN=Slc16a1 PE=1 SV=1 - [MOT1_RAT]	18.02	1	4	5	84	0.3156
P00564	Creatine kinase M-type OS=Rattus norvegicus GN=Ckm PE=1 SV=2 - [KCRM_RAT]	6.30	1	2	2	3	0.3158
P08932	T-kininogen 2 OS=Rattus norvegicus PE=1 SV=2 - [KNT2_RAT]	63.49	1	7	22	1117	0.3171
P49911	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Rattus norvegicus GN=Anp32a PE=2 SV=1 - [AN32A_RAT]	38.06	1	5	7	51	0.3175
Q9Z0U5	Aldehyde oxidase 1 OS=Rattus norvegicus GN=Aox1 PE=1 SV=1 - [AOXA_RAT]	3.83	1	3	3	7	0.3178
P04916	Retinol-binding protein 4 OS=Rattus norvegicus GN=Rbp4 PE=1 SV=1 - [RET4_RAT]	25.87	1	4	5	48	0.3186
P61751	ADP-ribosylation factor 4 OS=Rattus norvegicus GN=Arf4 PE=2 SV=2 - [ARF4_RAT]	60.56	1	4	8	88	0.3191
Q7M767	Ubiquitin-conjugating enzyme E2 variant 2 OS=Rattus norvegicus GN=Ube2v2 PE=1 SV=3 - [UB2V2_RAT]	30.34	1	4	4	9	0.3191
P07323	Gamma-enolase OS=Rattus norvegicus GN=Eno2 PE=1 SV=2 - [ENOG_RAT]	20.97	1	3	5	201	0.3208
Q63356	Unconventional myosin-Ie OS=Rattus norvegicus GN=Myo1e PE=1 SV=1 - [MYO1E_RAT]	2.26	1	1	2	5	0.3224
Q63507	60S ribosomal protein L14 OS=Rattus norvegicus GN=Rpl14 PE=1 SV=3 - [RL14_RAT]	10.28	1	2	2	13	0.3232
A0JPJ7	Obg-like ATPase 1 OS=Rattus norvegicus GN=Ola1 PE=2 SV=1 - [OLA1_RAT]	17.42	1	4	4	17	0.3248
P21708	Mitogen-activated protein kinase 3 OS=Rattus norvegicus GN=Mapk3 PE=1 SV=5 - [MK03_RAT]	17.37	1	3	4	5	0.3254
Q3KR86	MICOS complex subunit Mic60 (Fragment) OS=Rattus norvegicus GN=Immt PE=1 SV=1 - [MIC60_RAT]	7.55	1	3	4	4	0.3279
P62836	Ras-related protein Rap-1A OS=Rattus norvegicus GN=Rap1a PE=1 SV=1 - [RAP1A_RAT]	59.24	1	4	9	145	0.3301
B5DFC9	Nidogen-2 OS=Rattus norvegicus GN=Nid2 PE=2 SV=1 - [NID2_RAT]	7.16	1	7	7	27	0.3308
P23928	Alpha-crystallin B chain OS=Rattus norvegicus GN=Cryab PE=1 SV=1 - [CRYAB_RAT]	18.29	1	3	3	7	0.3326
Q63347	26S protease regulatory subunit 7 OS=Rattus norvegicus GN=Psmc2 PE=1 SV=3 - [PRS7_RAT]	5.31	1	2	2	2	0.3328
Q9WU82	Catenin beta-1 OS=Rattus norvegicus GN=Ctnnb1 PE=1 SV=1 - [CTNB1_RAT]	4.10	1	2	2	3	0.3330
P15178	Aspartate--tRNA ligase, cytoplasmic OS=Rattus	7.98	1	3	3	3	0.3335

	norvegicus GN=Dars PE=2 SV=1 - [SYDC_RAT]						
P21670	Proteasome subunit alpha type-4 OS=Rattus norvegicus GN=Psma4 PE=1 SV=1 - [PSA4_RAT]	41.00	1	6	6	58	0.3338
Q9JJ79	Cytoplasmic dynein 2 heavy chain 1 OS=Rattus norvegicus GN=Dync2h1 PE=1 SV=1 - [DYHC2_RAT]	2.62	1	4	7	10	0.3364
B0BNE5	S-formylglutathione hydrolase OS=Rattus norvegicus GN=Esd PE=2 SV=1 - [ESTD_RAT]	44.33	1	6	6	18	0.3366
Q4V8H8	EH domain-containing protein 2 OS=Rattus norvegicus GN=Ehd2 PE=1 SV=1 - [EHD2_RAT]	74.59	1	31	32	2042	0.3368
Q63514	C4b-binding protein alpha chain OS=Rattus norvegicus GN=C4bpa PE=2 SV=1 - [C4BPA_RAT]	19.53	1	9	9	47	0.3374
Q641Z6	EH domain-containing protein 1 OS=Rattus norvegicus GN=Ehd1 PE=1 SV=1 - [EHD1_RAT]	66.29	1	23	24	432	0.3378
P08503	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acadm PE=1 SV=1 - [ACADM_RAT]	20.19	1	6	6	23	0.3381
Q06647	ATP synthase subunit O, mitochondrial OS=Rattus norvegicus GN=Atp5o PE=1 SV=1 - [ATPO_RAT]	66.20	1	11	12	173	0.3387
P97576	GrpE protein homolog 1, mitochondrial OS=Rattus norvegicus GN=Grpel1 PE=1 SV=2 - [GRPE1_RAT]	11.52	1	2	3	3	0.3389
Q9R1T3	Cathepsin Z OS=Rattus norvegicus GN=Ctsz PE=1 SV=2 - [CATZ_RAT]	11.76	1	3	3	27	0.3393
Q9EPH8	Polyadenylate-binding protein 1 OS=Rattus norvegicus GN=Pabpc1 PE=1 SV=1 - [PABP1_RAT]	10.69	1	4	5	15	0.3404
P43278	Histone H1.0 OS=Rattus norvegicus GN=H1f0 PE=2 SV=2 - [H10_RAT]	16.49	1	3	3	23	0.3405
P55797	Apolipoprotein C-IV OS=Rattus norvegicus GN=Apoc4 PE=2 SV=2 - [APOC4_RAT]	25.00	1	2	2	3	0.3409
P24051	40S ribosomal protein S27-like OS=Rattus norvegicus GN=Rps27l PE=1 SV=3 - [RS27L_RAT]	25.00	2	2	2	3	0.3409
Q91Y78	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Rattus norvegicus GN=Uchl3 PE=1 SV=1 - [UCHL3_RAT]	12.61	1	2	2	2	0.3409
Q5EB81	NADH-cytochrome b5 reductase 1 OS=Rattus norvegicus GN=Cyb5r1 PE=2 SV=1 - [NB5R1_RAT]	9.84	1	3	3	3	0.3409
B2RYG6	Ubiquitin thioesterase OTUB1 OS=Rattus norvegicus GN=Otub1 PE=1 SV=1 - [OTUB1_RAT]	8.86	1	2	2	2	0.3409
Q5XIE6	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Rattus norvegicus GN=Hibch PE=1 SV=2 - [HIBCH_RAT]	7.53	1	2	2	2	0.3409
Q6AYH5	Dynactin subunit 2 OS=Rattus norvegicus GN=Dctn2 PE=1 SV=1 - [DCTN2_RAT]	7.46	1	2	2	2	0.3409
Q63525	Nuclear migration protein nudC OS=Rattus norvegicus GN=Nudc PE=1 SV=1 - [NUDC_RAT]	6.02	1	2	2	2	0.3409
P26051	CD44 antigen OS=Rattus norvegicus GN=Cd44 PE=1 SV=2 - [CD44_RAT]	4.97	1	2	2	3	0.3409
Q9Z1W6	Protein LYRIC OS=Rattus norvegicus GN=Mtdh PE=1 SV=2 - [LYRIC_RAT]	3.79	1	2	2	2	0.3409
P14272	Plasma kallikrein OS=Rattus norvegicus GN=Klkb1 PE=1 SV=1 - [KLKB1_RAT]	3.45	1	2	2	2	0.3409
Q9R1J8	Prolyl 3-hydroxylase 1 OS=Rattus norvegicus GN=P3h1 PE=1 SV=1 - [P3H1_RAT]	3.02	1	2	2	2	0.3409
Q499R0	Zinc finger protein 518A OS=Rattus norvegicus GN=Znf518a PE=2 SV=1 - [Z518A_RAT]	2.91	1	3	3	4	0.3409
P13941	Collagen alpha-1(III) chain OS=Rattus norvegicus GN=Col3a1 PE=2 SV=3 - [CO3A1_RAT]	2.19	1	3	3	3	0.3409
P55161	Nck-associated protein 1 OS=Rattus norvegicus GN=Nckap1 PE=2 SV=1 - [NCKP1_RAT]	1.68	1	1	2	2	0.3409
P15684	Aminopeptidase N OS=Rattus norvegicus GN=Anpep PE=1 SV=2 - [AMPN_RAT]	29.84	1	18	19	122	0.3421
Q66HD0	Endoplasmin OS=Rattus norvegicus GN=Hsp90b1 PE=1 SV=2 - [ENPL_RAT]	53.86	1	34	36	825	0.3428
P40307	Proteasome subunit beta type-2 OS=Rattus norvegicus GN=Psmb2 PE=1 SV=1 - [PSB2_RAT]	26.37	1	4	4	64	0.3430
Q9Z1P2	Alpha-actinin-1 OS=Rattus norvegicus GN=Actn1 PE=1 SV=1 - [ACTN1_RAT]	48.21	1	16	33	271	0.3434
P62630	Elongation factor 1-alpha 1 OS=Rattus norvegicus	56.28	1	20	20	1885	0.3474

	GN=Eef1a1 PE=2 SV=1 - [EF1A1_RAT]						
O88767	Protein deglycase DJ-1 OS=Rattus norvegicus GN=Park7 PE=1 SV=1 - [PARK7_RAT]	87.30	1	12	12	187	0.3483
P07151	Beta-2-microglobulin OS=Rattus norvegicus GN=B2m PE=1 SV=1 - [B2MG_RAT]	27.73	1	5	5	70	0.3496
P63170	Dynein light chain 1, cytoplasmic OS=Rattus norvegicus GN=Dynll1 PE=1 SV=1 - [DYL1_RAT]	49.44	1	3	3	9	0.3506
P63029	Translationally-controlled tumor protein OS=Rattus norvegicus GN=Tpt1 PE=1 SV=1 - [TCTP_RAT]	40.12	1	7	7	90	0.3517
P86252	Transcriptional activator protein Pur-alpha (Fragments) OS=Rattus norvegicus GN=Pura PE=1 SV=1 - [PURA_RAT]	56.52	1	3	3	25	0.3524
Q4KLF8	Actin-related protein 2/3 complex subunit 5 OS=Rattus norvegicus GN=Arpc5 PE=1 SV=3 - [ARPC5_RAT]	16.56	1	2	2	18	0.3545
P07872	Peroxisomal acyl-coenzyme A oxidase 1 OS=Rattus norvegicus GN=Acox1 PE=1 SV=1 - [ACOX1_RAT]	9.08	1	4	4	6	0.3549
P43884	Perilipin-1 OS=Rattus norvegicus GN=Plin1 PE=1 SV=1 - [PLIN1_RAT]	67.31	1	22	23	1162	0.3597
Q62651	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Rattus norvegicus GN=Ech1 PE=1 SV=2 - [ECH1_RAT]	40.67	1	10	10	50	0.3604
P62859	40S ribosomal protein S28 OS=Rattus norvegicus GN=Rps28 PE=1 SV=1 - [RS28_RAT]	30.43	1	2	2	14	0.3612
P14668	Annexin A5 OS=Rattus norvegicus GN=Anxa5 PE=1 SV=3 - [ANXA5_RAT]	75.55	1	24	24	1143	0.3614
P30839	Fatty aldehyde dehydrogenase OS=Rattus norvegicus GN=Aldh3a2 PE=1 SV=1 - [AL3A2_RAT]	13.43	1	5	5	27	0.3648
Q68FR6	Elongation factor 1-gamma OS=Rattus norvegicus GN=Eef1g PE=2 SV=3 - [EF1G_RAT]	37.07	1	8	10	80	0.3650
P62083	40S ribosomal protein S7 OS=Rattus norvegicus GN=Rps7 PE=1 SV=1 - [RS7_RAT]	43.81	1	6	6	58	0.3651
Q62638	Golgi apparatus protein 1 OS=Rattus norvegicus GN=Glg1 PE=1 SV=1 - [GSLG1_RAT]	4.70	1	4	4	12	0.3669
Q9EPB1	Dipeptidyl peptidase 2 OS=Rattus norvegicus GN=Dpp7 PE=1 SV=1 - [DPP2_RAT]	4.20	1	2	2	2	0.3676
Q5I0D1	Glyoxalase domain-containing protein 4 OS=Rattus norvegicus GN=Glod4 PE=1 SV=1 - [GLOD4_RAT]	43.62	1	8	9	41	0.3682
Q6VBQ5	Myeloid-associated differentiation marker OS=Rattus norvegicus GN=Myadm PE=1 SV=1 - [MYADM_RAT]	12.58	1	3	3	55	0.3695
P16036	Phosphate carrier protein, mitochondrial OS=Rattus norvegicus GN=Slc25a3 PE=1 SV=1 - [MPCP_RAT]	26.97	1	8	8	168	0.3708
P14669	Annexin A3 OS=Rattus norvegicus GN=Anxa3 PE=1 SV=4 - [ANXA3_RAT]	64.81	1	18	20	225	0.3710
P20788	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Rattus norvegicus GN=Uqcrfs1 PE=1 SV=2 - [UCRI_RAT]	22.63	1	3	4	8	0.3729
P30427	Plectin OS=Rattus norvegicus GN=Plec PE=1 SV=2 - [PLEC_RAT]	27.74	1	96	100	421	0.3743
P97532	3-mercaptopyruvate sulfurtransferase OS=Rattus norvegicus GN=Mpst PE=1 SV=3 - [THTM_RAT]	31.99	1	7	7	77	0.3790
P00406	Cytochrome c oxidase subunit 2 OS=Rattus norvegicus GN=Mtco2 PE=1 SV=3 - [COX2_RAT]	18.94	1	4	4	127	0.3797
Q66X93	Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus GN=Snd1 PE=1 SV=1 - [SND1_RAT]	30.91	1	18	19	64	0.3819
P85970	Actin-related protein 2/3 complex subunit 2 OS=Rattus norvegicus GN=Arpc2 PE=1 SV=1 - [ARPC2_RAT]	57.33	1	12	12	42	0.3835
Q6AYD3	Proliferation-associated protein 2G4 OS=Rattus norvegicus GN=Pa2g4 PE=1 SV=1 - [PA2G4_RAT]	8.12	1	3	3	7	0.3838
Q6AYQ4	Transmembrane protein 109 OS=Rattus norvegicus GN=Tmem109 PE=2 SV=1 - [TM109_RAT]	8.64	1	2	2	2	0.3854
Q62975	Protein Z-dependent protease inhibitor OS=Rattus norvegicus GN=Serpina10 PE=2 SV=2 - [ZPI_RAT]	16.06	1	5	5	13	0.3855
Q6P6Q2	Keratin, type II cytoskeletal 5 OS=Rattus norvegicus GN=Krt5 PE=1 SV=1 - [K2C5_RAT]	12.67	1	3	8	52	0.3878
Q9QXQ0	Alpha-actinin-4 OS=Rattus norvegicus GN=Actn4 PE=1 SV=2 - [ACTN4_RAT]	60.70	1	27	44	370	0.3915

Q64232	Very-long-chain enoyl-CoA reductase OS=Rattus norvegicus GN=Tecr PE=1 SV=1 - [TECR_RAT]	15.58	1	4	4	12	0.3920
D3Z8L7	Ras-related protein R-Ras OS=Rattus norvegicus GN=Rras PE=1 SV=1 - [RRAS_RAT]	24.77	1	4	4	60	0.3923
P63018	Heat shock cognate 71 kDa protein OS=Rattus norvegicus GN=Hspa8 PE=1 SV=1 - [HSP7C_RAT]	71.52	1	33	38	1275	0.3924
P13832	Myosin regulatory light chain RLC-A OS=Rattus norvegicus GN=Rlc-a PE=2 SV=2 - [MRLCA_RAT]	34.30	2	5	5	51	0.3930
Q91ZN1	Coronin-1A OS=Rattus norvegicus GN=Coro1a PE=1 SV=3 - [COR1A_RAT]	13.67	1	2	2	3	0.3934
P61354	60S ribosomal protein L27 OS=Rattus norvegicus GN=Rpl27 PE=2 SV=2 - [RL27_RAT]	22.06	1	2	2	2	0.3941
Q62847	Gamma-adducin OS=Rattus norvegicus GN=Add3 PE=1 SV=2 - [ADDG_RAT]	5.39	1	2	2	3	0.3950
P08934	Kininogen-1 OS=Rattus norvegicus GN=Kng1 PE=2 SV=1 - [KNG1_RAT]	23.00	1	8	11	89	0.3956
P02696	Retinol-binding protein 1 OS=Rattus norvegicus GN=Rbp1 PE=1 SV=2 - [RET1_RAT]	17.78	1	2	2	2	0.3957
P36953	Afamin OS=Rattus norvegicus GN=Afm PE=3 SV=1 - [AFAM_RAT]	32.24	1	15	15	89	0.3961
Q9JLT0	Myosin-10 OS=Rattus norvegicus GN=Myh10 PE=1 SV=1 - [MYH10_RAT]	7.64	1	3	12	153	0.3965
P26453	Basigin OS=Rattus norvegicus GN=Bsg PE=1 SV=2 - [BASI_RAT]	16.75	1	6	6	33	0.3978
O35952	Hydroxyacylglutathione hydrolase, mitochondrial OS=Rattus norvegicus GN=Hagh PE=1 SV=2 - [GLO2_RAT]	9.06	1	2	2	4	0.3979
P97697	Inositol monophosphatase 1 OS=Rattus norvegicus GN=Impa1 PE=1 SV=2 - [IMPA1_RAT]	11.55	1	2	2	3	0.3999
P02651	Apolipoprotein A-IV OS=Rattus norvegicus GN=Apoa4 PE=1 SV=2 - [APOA4_RAT]	61.89	1	18	18	160	0.4002
Q6MG60	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Rattus norvegicus GN=Ddah2 PE=1 SV=1 - [DDAH2_RAT]	34.04	1	7	7	87	0.4026
Q9QWN8	Spectrin beta chain, non-erythrocytic 2 OS=Rattus norvegicus GN=Sptbn2 PE=1 SV=2 - [SPTN2_RAT]	6.11	1	9	11	40	0.4030
P97675	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3 OS=Rattus norvegicus GN=Enpp3 PE=1 SV=2 - [ENPP3_RAT]	23.66	1	14	14	155	0.4035
P29457	Serpin H1 OS=Rattus norvegicus GN=Serpinh1 PE=1 SV=1 - [SERPH_RAT]	58.03	1	18	18	562	0.4043
P15304	Hormone-sensitive lipase OS=Rattus norvegicus GN=Lipe PE=1 SV=3 - [LIPS_RAT]	41.67	1	30	30	792	0.4056
P46844	Biliverdin reductase A OS=Rattus norvegicus GN=Blvra PE=1 SV=1 - [BIEA_RAT]	38.31	1	8	8	50	0.4060
P63102	14-3-3 protein zeta/delta OS=Rattus norvegicus GN=Ywhaz PE=1 SV=1 - [1433Z_RAT]	72.24	1	12	17	639	0.4071
P05426	60S ribosomal protein L7 OS=Rattus norvegicus GN=Rpl7 PE=1 SV=2 - [RL7_RAT]	31.92	1	6	6	31	0.4086
P26644	Beta-2-glycoprotein 1 OS=Rattus norvegicus GN=Apoh PE=2 SV=2 - [APOH_RAT]	26.26	1	7	7	32	0.4100
P08010	Glutathione S-transferase Mu 2 OS=Rattus norvegicus GN=Gstm2 PE=1 SV=2 - [GSTM2_RAT]	73.39	1	10	17	286	0.4116
P02793	Ferritin light chain 1 OS=Rattus norvegicus GN=Ftl1 PE=1 SV=3 - [FRIL1_RAT]	72.13	1	2	12	448	0.4123
Q9JLJ3	4-trimethylaminobutyraldehyde dehydrogenase OS=Rattus norvegicus GN=Aldh9a1 PE=1 SV=1 - [AL9A1_RAT]	39.68	1	11	12	156	0.4141
O35854	Branched-chain-amino-acid aminotransferase, mitochondrial OS=Rattus norvegicus GN=Bcat2 PE=1 SV=1 - [BCAT2_RAT]	9.92	1	3	3	6	0.4171
P23562	Band 3 anion transport protein OS=Rattus norvegicus GN=Slc4a1 PE=1 SV=3 - [B3AT_RAT]	24.38	1	15	15	349	0.4175
P62909	40S ribosomal protein S3 OS=Rattus norvegicus GN=Rps3 PE=1 SV=1 - [RS3_RAT]	53.09	1	11	11	105	0.4183
Q7TP52	Carboxymethylenebutenolidase homolog OS=Rattus norvegicus GN=Cmbl PE=2 SV=1 - [CMBL_RAT]	22.45	1	5	5	13	0.4185
P03311	Genome polyprotein OS=Foot-and-mouth disease virus	2.23	5	2	2	2	0.4199

	(isolate -/Spain/S8c1SantaPau/1970 serotype C) PE=1 SV=2 - [POLG_FMDVS]						
Q6REY9	Rho GTPase-activating protein 20 OS=Rattus norvegicus GN=Arhgap20 PE=1 SV=2 - [RHG20_RAT]	3.30	1	2	2	3	0.4219
Q5M7U6	Actin-related protein 2 OS=Rattus norvegicus GN=Actr2 PE=2 SV=1 - [ARP2_RAT]	30.96	1	8	8	29	0.4226
Q00438	Polypyrimidine tract-binding protein 1 OS=Rattus norvegicus GN=Ptbp1 PE=1 SV=1 - [PTBP1_RAT]	33.87	1	8	8	32	0.4240
Q5XFX0	Transgelin-2 OS=Rattus norvegicus GN=Tagln2 PE=1 SV=1 - [TAGL2_RAT]	85.93	1	17	17	594	0.4244
P56571	ES1 protein homolog, mitochondrial OS=Rattus norvegicus PE=1 SV=2 - [ES1_RAT]	31.95	1	6	6	30	0.4267
P52296	Importin subunit beta-1 OS=Rattus norvegicus GN=Kpnb1 PE=1 SV=1 - [IMB1_RAT]	22.51	1	13	14	171	0.4274
P07633	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Rattus norvegicus GN=Pccb PE=2 SV=1 - [PCCB_RAT]	7.58	1	3	3	3	0.4303
Q4QRB4	Tubulin beta-3 chain OS=Rattus norvegicus GN=Tubb3 PE=1 SV=1 - [TBB3_RAT]	36.00	1	2	14	1006	0.4310
Q794E4	Heterogeneous nuclear ribonucleoprotein F OS=Rattus norvegicus GN=Hnrnpf PE=1 SV=3 - [HNRPF_RAT]	10.36	1	2	3	52	0.4312
P07943	Aldose reductase OS=Rattus norvegicus GN=Akr1b1 PE=1 SV=3 - [ALDR_RAT]	51.27	1	12	14	280	0.4335
P16617	Phosphoglycerate kinase 1 OS=Rattus norvegicus GN=Pgk1 PE=1 SV=2 - [PGK1_RAT]	69.30	1	20	20	420	0.4354
P20760	Ig gamma-2A chain C region OS=Rattus norvegicus GN=Igg-2a PE=1 SV=1 - [IGG2A_RAT]	63.98	1	14	17	1776	0.4369
P97943	Scavenger receptor class B member 1 OS=Rattus norvegicus GN=Scarb1 PE=1 SV=1 - [SCRB1_RAT]	10.02	1	2	2	2	0.4370
Q5XIC0	Enoyl-CoA delta isomerase 2, mitochondrial OS=Rattus norvegicus GN=Eci2 PE=1 SV=1 - [ECI2_RAT]	6.65	1	2	2	2	0.4377
O35077	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Rattus norvegicus GN=Gpd1 PE=1 SV=4 - [GPDA_RAT]	91.40	1	26	26	1741	0.4381
P20762	Ig gamma-2C chain C region OS=Rattus norvegicus PE=2 SV=1 - [IGG2C_RAT]	38.30	1	8	8	45	0.4405
P60868	40S ribosomal protein S20 OS=Rattus norvegicus GN=Rps20 PE=3 SV=1 - [RS20_RAT]	28.57	1	4	4	43	0.4408
O88761	26S proteasome non-ATPase regulatory subunit 1 OS=Rattus norvegicus GN=Psmd1 PE=1 SV=1 - [PSMD1_RAT]	7.56	1	4	4	35	0.4418
B0K020	CDGSH iron-sulfur domain-containing protein 1 OS=Rattus norvegicus GN=Cisd1 PE=3 SV=1 - [CISD1_RAT]	22.22	1	2	2	2	0.4419
P12346	Serotransferrin OS=Rattus norvegicus GN=Tf PE=1 SV=3 - [TRFE_RAT]	70.92	1	45	45	6564	0.4454
P02466	Collagen alpha-2(I) chain OS=Rattus norvegicus GN=Col1a2 PE=1 SV=3 - [CO1A2_RAT]	3.21	1	3	3	13	0.4459
P14408	Fumarate hydratase, mitochondrial OS=Rattus norvegicus GN=Fh PE=1 SV=1 - [FUMH_RAT]	31.76	1	9	9	31	0.4471
Q6P9T8	Tubulin beta-4B chain OS=Rattus norvegicus GN=Tubb4b PE=1 SV=1 - [TBB4B_RAT]	68.09	1	3	24	2054	0.4476
P85108	Tubulin beta-2A chain OS=Rattus norvegicus GN=Tubb2a PE=1 SV=1 - [TBB2A_RAT]	73.71	2	6	24	1845	0.4478
Q62940	E3 ubiquitin-protein ligase NEDD4 OS=Rattus norvegicus GN=Nedd4 PE=1 SV=1 - [NEDD4_RAT]	18.38	1	11	11	87	0.4494
P69897	Tubulin beta-5 chain OS=Rattus norvegicus GN=Tubb5 PE=1 SV=1 - [TBB5_RAT]	73.87	1	4	25	2083	0.4497
Q7TP54	Protein FAM65B OS=Rattus norvegicus GN=Fam65b PE=1 SV=1 - [FA65B_RAT]	11.45	1	3	13	442	0.4528
P20070	NADH-cytochrome b5 reductase 3 OS=Rattus norvegicus GN=Cyb5r3 PE=1 SV=2 - [NB5R3_RAT]	77.08	1	15	15	248	0.4532
Q6IRK9	Carboxypeptidase Q OS=Rattus norvegicus GN=Cpq PE=1 SV=1 - [CBPQ_RAT]	32.63	1	9	9	55	0.4545
P21588	5'-nucleotidase OS=Rattus norvegicus GN=Nt5e PE=1 SV=1 - [5NTD_RAT]	9.20	1	3	3	13	0.4559
P60901	Proteasome subunit alpha type-6 OS=Rattus norvegicus	38.62	1	8	8	81	0.4572

	GN=Psma6 PE=1 SV=1 - [PSA6_RAT]						
P19132	Ferritin heavy chain OS=Rattus norvegicus GN=Fth1 PE=1 SV=3 - [FRIH_RAT]	57.14	1	10	10	174	0.4583
P62260	14-3-3 protein epsilon OS=Rattus norvegicus GN=Ywhae PE=1 SV=1 - [1433E_RAT]	72.16	1	19	22	521	0.4594
Q5XIU9	Membrane-associated progesterone receptor component 2 OS=Rattus norvegicus GN=Pgrmc2 PE=1 SV=1 - [PGRC2_RAT]	34.10	1	6	6	23	0.4611
Q6Q0N1	Cytosolic non-specific dipeptidase OS=Rattus norvegicus GN=Cndp2 PE=1 SV=1 - [CNDP2_RAT]	40.63	1	15	15	135	0.4622
Q5I0E7	Transmembrane emp24 domain-containing protein 9 OS=Rattus norvegicus GN=Tmed9 PE=1 SV=1 - [TMED9_RAT]	26.38	1	5	5	26	0.4635
A2RUV9	Adipocyte enhancer-binding protein 1 OS=Rattus norvegicus GN=Aebp1 PE=2 SV=1 - [AEBP1_RAT]	3.63	1	3	3	4	0.4637
P15999	ATP synthase subunit alpha, mitochondrial OS=Rattus norvegicus GN=Atp5a1 PE=1 SV=2 - [ATPA_RAT]	46.84	1	21	21	968	0.4640
P17078	60S ribosomal protein L35 OS=Rattus norvegicus GN=Rpl35 PE=1 SV=3 - [RL35_RAT]	18.70	1	2	2	5	0.4651
P18422	Proteasome subunit alpha type-3 OS=Rattus norvegicus GN=Psma3 PE=1 SV=3 - [PSA3_RAT]	14.12	1	3	3	26	0.4655
P15865	Histone H1.4 OS=Rattus norvegicus GN=Hist1h1e PE=1 SV=3 - [H14_RAT]	17.35	1	7	7	360	0.4680
P25113	Phosphoglycerate mutase 1 OS=Rattus norvegicus GN=Pgam1 PE=1 SV=4 - [PGAM1_RAT]	73.62	1	15	15	300	0.4705
Q68FS4	Cytosol aminopeptidase OS=Rattus norvegicus GN=Lap3 PE=1 SV=1 - [AMPL_RAT]	34.10	1	10	10	74	0.4712
Q5I0G4	Glycine--tRNA ligase (Fragment) OS=Rattus norvegicus GN=Gars PE=1 SV=1 - [SYG_RAT]	8.48	1	3	3	6	0.4722
Q68FT1	Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Rattus norvegicus GN=Coq9 PE=1 SV=2 - [COQ9_RAT]	6.09	1	2	2	2	0.4739
O08678	Serine/threonine-protein kinase MARK1 OS=Rattus norvegicus GN=Mark1 PE=1 SV=1 - [MARK1_RAT]	5.04	2	3	3	8	0.4744
P62963	Profilin-1 OS=Rattus norvegicus GN=Pfn1 PE=1 SV=2 - [PROF1_RAT]	72.14	1	10	10	598	0.4745
P10760	Adenosylhomocysteinase OS=Rattus norvegicus GN=Ahcy PE=1 SV=3 - [SAHH_RAT]	38.43	1	13	13	156	0.4756
O55012	Phosphatidylinositol-binding clathrin assembly protein OS=Rattus norvegicus GN=Picalm PE=1 SV=1 - [PICAL_RAT]	11.56	1	4	4	24	0.4758
P55260	Annexin A4 OS=Rattus norvegicus GN=Anxa4 PE=1 SV=3 - [ANXA4_RAT]	53.61	1	14	14	121	0.4795
Q6P7Q4	Lactoylglutathione lyase OS=Rattus norvegicus GN=Glo1 PE=1 SV=3 - [LGUL_RAT]	41.30	1	7	7	67	0.4796
D3ZAF6	ATP synthase subunit f, mitochondrial OS=Rattus norvegicus GN=Atp5j2 PE=1 SV=1 - [ATPK_RAT]	23.86	1	2	2	9	0.4800
P29419	ATP synthase subunit e, mitochondrial OS=Rattus norvegicus GN=Atp5i PE=1 SV=3 - [ATP5I_RAT]	56.34	1	4	4	25	0.4842
P11232	Thioredoxin OS=Rattus norvegicus GN=Txn PE=1 SV=2 - [THIO_RAT]	31.43	1	5	5	105	0.4882
Q9JHW0	Proteasome subunit beta type-7 OS=Rattus norvegicus GN=Psmb7 PE=1 SV=1 - [PSB7_RAT]	10.47	1	2	2	2	0.4891
Q02253	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Rattus norvegicus GN=Aldh6a1 PE=1 SV=1 - [MMSA_RAT]	37.38	1	13	13	63	0.4893
Q64428	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus GN=Hadha PE=1 SV=2 - [ECHA_RAT]	48.49	1	24	25	627	0.4900
B3DMA2	Acyl-CoA dehydrogenase family member 11 OS=Rattus norvegicus GN=Acad11 PE=1 SV=1 - [ACD11_RAT]	3.85	1	3	3	6	0.4904
Q7TPJ0	Translocon-associated protein subunit alpha OS=Rattus norvegicus GN=Ssr1 PE=1 SV=1 - [SSRA_RAT]	8.15	1	2	2	4	0.4909
P63326	40S ribosomal protein S10 OS=Rattus norvegicus GN=Rps10 PE=2 SV=1 - [RS10_RAT]	14.55	1	2	2	5	0.4921
P81155	Voltage-dependent anion-selective channel protein 2 OS=Rattus norvegicus GN=Vdac2 PE=1 SV=2 -	18.64	1	3	4	31	0.4934

	[VDAC2_RAT]						
F1LMY4	Ryanodine receptor 1 OS=Rattus norvegicus GN=Ryr1 PE=1 SV=1 - [RYR1_RAT]	0.83	1	2	3	11	0.4935
Q63377	Sodium/potassium-transporting ATPase subunit beta-3 OS=Rattus norvegicus GN=Atp1b3 PE=2 SV=1 - [AT1B3_RAT]	17.92	1	3	3	6	0.4961
B4F7E8	Niban-like protein 1 OS=Rattus norvegicus GN=Fam129b PE=1 SV=1 - [NIBL1_RAT]	7.90	1	3	3	4	0.4974
P61983	14-3-3 protein gamma OS=Rattus norvegicus GN=Ywhag PE=1 SV=2 - [1433G_RAT]	79.76	1	11	18	611	0.5008
Q5PPN5	Tubulin polymerization-promoting protein family member 3 OS=Rattus norvegicus GN=Tppp3 PE=2 SV=1 - [TPPP3_RAT]	31.82	1	5	5	14	0.5016
P61589	Transforming protein RhoA OS=Rattus norvegicus GN=Rhoa PE=1 SV=1 - [RHOA_RAT]	51.81	1	9	9	136	0.5016
P30009	Myristoylated alanine-rich C-kinase substrate OS=Rattus norvegicus GN=Marcks PE=1 SV=2 - [MARCS_RAT]	24.92	1	5	5	45	0.5038
P06302	Prothymosin alpha OS=Rattus norvegicus GN=Ptma PE=1 SV=2 - [PTMA_RAT]	22.32	1	4	4	16	0.5040
P63322	Ras-related protein Ral-A OS=Rattus norvegicus GN=Rala PE=1 SV=1 - [RALA_RAT]	22.82	1	4	4	16	0.5078
Q62952	Dihydropyrimidinase-related protein 3 OS=Rattus norvegicus GN=Dpysl3 PE=1 SV=2 - [DPYL3_RAT]	28.60	1	9	11	53	0.5081
P07756	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Rattus norvegicus GN=Cps1 PE=1 SV=1 - [CPSM_RAT]	2.73	1	3	3	12	0.5084
Q7TP48	Adipocyte plasma membrane-associated protein OS=Rattus norvegicus GN=Apmap PE=2 SV=2 - [APMAP_RAT]	48.94	1	13	13	293	0.5107
Q80U96	Exportin-1 OS=Rattus norvegicus GN=Xpo1 PE=1 SV=1 - [XPO1_RAT]	8.12	1	4	5	27	0.5125
P38652	Phosphoglucomutase-1 OS=Rattus norvegicus GN=Pgm1 PE=1 SV=2 - [PGM1_RAT]	27.76	1	8	8	82	0.5151
P00786	Pro-cathepsin H OS=Rattus norvegicus GN=Ctsh PE=1 SV=1 - [CATH_RAT]	6.61	1	3	3	6	0.5171
D3ZHA0	Filamin-C OS=Rattus norvegicus GN=Flnc PE=1 SV=1 - [FLNC_RAT]	7.63	1	12	15	112	0.5178
P08699	Galectin-3 OS=Rattus norvegicus GN=Lgals3 PE=1 SV=4 - [LEG3_RAT]	27.10	1	6	6	22	0.5180
P11762	Galectin-1 OS=Rattus norvegicus GN=Lgals1 PE=1 SV=2 - [LEG1_RAT]	61.48	1	10	10	676	0.5195
P28023	Dynactin subunit 1 OS=Rattus norvegicus GN=Dctn1 PE=1 SV=2 - [DCTN1_RAT]	9.53	1	8	8	21	0.5226
Q6P7R8	Very-long-chain 3-oxoacyl-CoA reductase OS=Rattus norvegicus GN=Hsd17b12 PE=2 SV=1 - [DHB12_RAT]	14.42	1	3	3	41	0.5233
Q9WU49	Calcium-regulated heat stable protein 1 OS=Rattus norvegicus GN=Carhsp1 PE=1 SV=1 - [CHSP1_RAT]	18.37	1	2	2	5	0.5241
P63245	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Rattus norvegicus GN=Gnb2l1 PE=1 SV=3 - [GBLP_RAT]	62.46	1	12	12	91	0.5245
D3ZW55	Inosine triphosphate pyrophosphatase OS=Rattus norvegicus GN=Itpa PE=3 SV=1 - [ITPA_RAT]	16.67	1	2	2	3	0.5260
B0BNM1	NAD(P)H-hydrate epimerase OS=Rattus norvegicus GN=Apoa1bp PE=2 SV=1 - [NNRE_RAT]	16.31	1	3	3	11	0.5266
P62870	Transcription elongation factor B polypeptide 2 OS=Rattus norvegicus GN=Tceb2 PE=1 SV=1 - [ELOB_RAT]	42.37	1	3	3	10	0.5268
Q9ER34	Aconitate hydratase, mitochondrial OS=Rattus norvegicus GN=Aco2 PE=1 SV=2 - [ACON_RAT]	53.72	1	29	29	506	0.5278
P10111	Peptidyl-prolyl cis-trans isomerase A OS=Rattus norvegicus GN=Ppia PE=1 SV=2 - [PPIA_RAT]	59.76	1	11	11	718	0.5285
Q64633	UDP-glucuronosyltransferase 1-7 OS=Rattus norvegicus GN=Ugt1a7c PE=2 SV=1 - [UD17_RAT]	18.46	6	1	5	50	0.5306
Q9ES40	PRA1 family protein 3 OS=Rattus norvegicus GN=Arl6ip5 PE=1 SV=1 - [PRAF3_RAT]	15.96	1	2	2	14	0.5327
P08461	Dihydrolipoyllysine-residue acetyltransferase	16.30	1	7	7	21	0.5327

	component of pyruvate dehydrogenase complex, mitochondrial OS=Rattus norvegicus GN=Dlat PE=1 SV=3 - [ODP2_RAT]						
Q9JLZ1	Glutaredoxin-3 OS=Rattus norvegicus GN=Glrx3 PE=1 SV=2 - [GLRX3_RAT]	11.28	1	3	3	6	0.5330
O54921	Exocyst complex component 2 OS=Rattus norvegicus GN=Exoc2 PE=1 SV=1 - [EXOC2_RAT]	1.84	1	2	2	2	0.5332
P48004	Proteasome subunit alpha type-7 OS=Rattus norvegicus GN=Psma7 PE=1 SV=1 - [PSA7_RAT]	38.98	1	8	9	30	0.5334
P97629	Leucyl-cystinyl aminopeptidase OS=Rattus norvegicus GN=Lnpep PE=1 SV=1 - [LCAP_RAT]	7.80	1	7	7	29	0.5338
P05712	Ras-related protein Rab-2A OS=Rattus norvegicus GN=Rab2a PE=2 SV=1 - [RAB2A_RAT]	38.21	1	6	6	57	0.5369
P62828	GTP-binding nuclear protein Ran OS=Rattus norvegicus GN=Ran PE=1 SV=3 - [RAN_RAT]	31.02	2	6	6	64	0.5377
Q07066	Peroxisomal membrane protein 2 OS=Rattus norvegicus GN=Pxmp2 PE=1 SV=2 - [PXMP2_RAT]	21.13	1	2	3	3	0.5381
P28077	Proteasome subunit beta type-9 OS=Rattus norvegicus GN=Psmb9 PE=1 SV=2 - [PSB9_RAT]	23.74	1	4	4	24	0.5387
Q4FZU2	Keratin, type II cytoskeletal 6A OS=Rattus norvegicus GN=Krt6a PE=1 SV=1 - [K2C6A_RAT]	10.14	1	4	7	56	0.5404
P48037	Annexin A6 OS=Rattus norvegicus GN=Anxa6 PE=1 SV=2 - [ANXA6_RAT]	64.93	1	41	41	1174	0.5418
P29266	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Hibadh PE=1 SV=3 - [3HIDH_RAT]	30.45	1	7	7	42	0.5425
P27791	cAMP-dependent protein kinase catalytic subunit alpha OS=Rattus norvegicus GN=Prkaca PE=1 SV=2 - [KAPCA_RAT]	10.54	1	2	3	15	0.5436
Q68FP1	Gelsolin OS=Rattus norvegicus GN=Gsn PE=1 SV=1 - [GELS_RAT]	45.38	1	22	22	478	0.5446
P04256	Heterogeneous nuclear ribonucleoprotein A1 OS=Rattus norvegicus GN=Hnrnpa1 PE=1 SV=3 - [ROA1_RAT]	27.81	1	5	7	53	0.5447
O54975	Xaa-Pro aminopeptidase 1 OS=Rattus norvegicus GN=Xpnpep1 PE=1 SV=1 - [XPP1_RAT]	11.88	1	3	4	7	0.5450
P41350	Caveolin-1 OS=Rattus norvegicus GN=Cav1 PE=1 SV=3 - [CAV1_RAT]	51.69	1	8	8	472	0.5497
P63255	Cysteine-rich protein 1 OS=Rattus norvegicus GN=Crip1 PE=1 SV=2 - [CRIP1_RAT]	71.43	1	4	4	10	0.5504
P04636	Malate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Mdh2 PE=1 SV=2 - [MDHM_RAT]	64.20	1	18	18	506	0.5512
Q5BK81	Prostaglandin reductase 2 OS=Rattus norvegicus GN=Ptgr2 PE=2 SV=2 - [PTGR2_RAT]	31.34	1	6	6	15	0.5516
P83868	Prostaglandin E synthase 3 OS=Rattus norvegicus GN=Ptges3 PE=1 SV=2 - [TEBP_RAT]	32.50	1	4	4	37	0.5531
P85125	Polymerase I and transcript release factor OS=Rattus norvegicus GN=Ptrf PE=1 SV=1 - [PTRF_RAT]	43.88	1	19	19	1788	0.5532
P47853	Biglycan OS=Rattus norvegicus GN=Bgn PE=2 SV=1 - [PGS1_RAT]	50.41	1	13	14	284	0.5546
P02454	Collagen alpha-1(I) chain OS=Rattus norvegicus GN=Col1a1 PE=1 SV=5 - [CO1A1_RAT]	4.20	1	4	4	27	0.5546
P61959	Small ubiquitin-related modifier 2 OS=Rattus norvegicus GN=Sumo2 PE=1 SV=1 - [SUMO2_RAT]	23.16	1	2	2	7	0.5548
Q66H80	Coatomer subunit delta OS=Rattus norvegicus GN=Arcn1 PE=2 SV=1 - [COPD_RAT]	8.81	1	4	4	31	0.5555
P04937	Fibronectin OS=Rattus norvegicus GN=Fn1 PE=1 SV=2 - [FINC_RAT]	26.16	1	39	39	322	0.5558
P13084	Nucleophosmin OS=Rattus norvegicus GN=Npm1 PE=1 SV=1 - [NPM_RAT]	29.79	1	6	6	22	0.5576
P05942	Protein S100-A4 OS=Rattus norvegicus GN=S100a4 PE=2 SV=1 - [S10A4_RAT]	27.72	1	3	3	58	0.5578
P23965	Enoyl-CoA delta isomerase 1, mitochondrial OS=Rattus norvegicus GN=Eci1 PE=1 SV=1 - [ECI1_RAT]	42.91	1	9	9	165	0.5582
Q711G3	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Rattus norvegicus GN=Iah1 PE=2 SV=2 - [IAH1_RAT]	15.26	1	2	2	5	0.5590
Q3KRD8	Eukaryotic translation initiation factor 6 OS=Rattus	17.14	1	2	2	3	0.5600

	norvegicus GN=Eif6 PE=1 SV=1 - [IF6_RAT]						
Q5BK63	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Rattus norvegicus GN=Ndufa9 PE=1 SV=2 - [NDUA9_RAT]	20.69	1	3	4	25	0.5605
Q812D1	PC4 and SFRS1-interacting protein OS=Rattus norvegicus GN=Psip1 PE=1 SV=1 - [PSIP1_RAT]	5.68	1	2	2	2	0.5606
P09811	Glycogen phosphorylase, liver form OS=Rattus norvegicus GN=Pygl PE=1 SV=5 - [PYGL_RAT]	19.18	1	9	11	28	0.5645
Q5I0D7	Xaa-Pro dipeptidase OS=Rattus norvegicus GN=Pepd PE=2 SV=1 - [PEPD_RAT]	12.20	1	5	5	92	0.5661
P63331	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Rattus norvegicus GN=Ppp2ca PE=1 SV=1 - [PP2AA_RAT]	21.04	2	3	4	23	0.5664
Q63598	Plastin-3 OS=Rattus norvegicus GN=Pls3 PE=1 SV=2 - [PLST_RAT]	20.95	1	7	7	38	0.5683
B0BNN3	Carbonic anhydrase 1 OS=Rattus norvegicus GN=Ca1 PE=1 SV=1 - [CAH1_RAT]	70.50	1	12	12	632	0.5693
P11030	Acyl-CoA-binding protein OS=Rattus norvegicus GN=Dbi PE=1 SV=3 - [ACBP_RAT]	51.72	1	4	4	79	0.5702
P17764	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus GN=Acat1 PE=1 SV=1 - [THIL_RAT]	44.81	1	12	12	97	0.5733
Q9HB97	Alpha-parvin OS=Rattus norvegicus GN=Parva PE=1 SV=2 - [PARVA_RAT]	20.43	1	5	5	38	0.5742
O88656	Actin-related protein 2/3 complex subunit 1B OS=Rattus norvegicus GN=Arpc1b PE=1 SV=3 - [ARC1B_RAT]	13.17	1	4	4	26	0.5748
P14141	Carbonic anhydrase 3 OS=Rattus norvegicus GN=Ca3 PE=1 SV=3 - [CAH3_RAT]	87.31	1	21	21	17035	0.5752
P62775	Myotrophin OS=Rattus norvegicus GN=Mtpn PE=1 SV=2 - [MTPN_RAT]	25.42	1	2	2	24	0.5757
Q5XIH7	Prohibitin-2 OS=Rattus norvegicus GN=Phb2 PE=1 SV=1 - [PHB2_RAT]	53.85	1	11	12	101	0.5819
B0BNF1	Septin-8 OS=Rattus norvegicus GN=Sept8 PE=1 SV=1 - [SEPT8_RAT]	4.07	1	1	2	8	0.5826
B0LPN4	Ryanodine receptor 2 OS=Rattus norvegicus GN=Ryr2 PE=1 SV=2 - [RYR2_RAT]	0.67	1	2	2	2	0.5827
P07632	Superoxide dismutase [Cu-Zn] OS=Rattus norvegicus GN=Sod1 PE=1 SV=2 - [SODC_RAT]	58.44	1	8	8	232	0.5836
P08009	Glutathione S-transferase Yb-3 OS=Rattus norvegicus GN=Gstm3 PE=1 SV=2 - [GSTM4_RAT]	38.99	1	1	8	156	0.5843
Q5RJP0	Aldose reductase-related protein 1 OS=Rattus norvegicus GN=Akr1b7 PE=1 SV=1 - [ALD1_RAT]	21.20	1	3	6	6	0.5848
P04762	Catalase OS=Rattus norvegicus GN=Cat PE=1 SV=3 - [CATA_RAT]	52.75	1	20	20	311	0.5853
P38650	Cytoplasmic dynein 1 heavy chain 1 OS=Rattus norvegicus GN=Dync1h1 PE=1 SV=1 - [DYHC1_RAT]	36.33	1	126	129	853	0.5895
Q62667	Major vault protein OS=Rattus norvegicus GN=Mvp PE=1 SV=4 - [MVP_RAT]	36.82	1	20	20	73	0.5904
P05964	Protein S100-A6 OS=Rattus norvegicus GN=S100a6 PE=1 SV=3 - [S10A6_RAT]	19.10	1	3	3	40	0.5924
Q9WVK7	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Hadh PE=2 SV=1 - [HCDH_RAT]	67.52	1	12	12	292	0.5925
P04276	Vitamin D-binding protein OS=Rattus norvegicus GN=Gc PE=1 SV=3 - [VTDB_RAT]	69.54	1	23	23	403	0.5944
O88644	Grifin OS=Rattus norvegicus GN=Grifin PE=1 SV=1 - [GRIFN_RAT]	15.28	1	2	2	33	0.5949
P22734	Catechol O-methyltransferase OS=Rattus norvegicus GN=Comt PE=1 SV=2 - [COMT_RAT]	37.88	1	6	6	14	0.5963
P68255	14-3-3 protein theta OS=Rattus norvegicus GN=Ywhaq PE=1 SV=1 - [1433T_RAT]	62.86	1	12	18	539	0.5969
P62898	Cytochrome c, somatic OS=Rattus norvegicus GN=Cycs PE=1 SV=2 - [CYC_RAT]	62.86	1	7	8	109	0.5975
Q62689	Tyrosine-protein kinase JAK2 OS=Rattus norvegicus GN=Jak2 PE=1 SV=1 - [JAK2_RAT]	4.24	1	2	3	9	0.5978
B2GV06	Succinyl-CoA:3-ketoacid coenzyme A transferase 1,	41.15	1	12	13	122	0.5978

	mitochondrial OS=Rattus norvegicus GN=Oxct1 PE=1 SV=1 - [SCOT1_RAT]						
P70623	Fatty acid-binding protein, adipocyte OS=Rattus norvegicus GN=Fabp4 PE=1 SV=3 - [FABP4_RAT]	74.24	1	13	13	7155	0.5989
Q63279	Keratin, type I cytoskeletal 19 OS=Rattus norvegicus GN=Krt19 PE=1 SV=2 - [K1C19_RAT]	47.64	1	10	15	66	0.5992
P25235	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Rattus norvegicus GN=Rpn2 PE=2 SV=2 - [RPN2_RAT]	35.02	1	11	11	137	0.5999
Q9ESW0	DNA damage-binding protein 1 OS=Rattus norvegicus GN=Ddb1 PE=1 SV=1 - [DDB1_RAT]	2.98	1	2	2	3	0.6016
P09895	60S ribosomal protein L5 OS=Rattus norvegicus GN=Rpl5 PE=1 SV=3 - [RL5_RAT]	10.77	1	2	2	8	0.6020
O35509	Ras-related protein Rab-11B OS=Rattus norvegicus GN=Rab11b PE=1 SV=4 - [RB11B_RAT]	52.29	1	10	10	97	0.6023
P11240	Cytochrome c oxidase subunit 5A, mitochondrial OS=Rattus norvegicus GN=Cox5a PE=1 SV=1 - [COX5A_RAT]	23.29	1	5	5	73	0.6066
O89049	Thioredoxin reductase 1, cytoplasmic OS=Rattus norvegicus GN=Txnrd1 PE=1 SV=5 - [TRXR1_RAT]	9.02	1	2	2	10	0.6101
P61206	ADP-ribosylation factor 3 OS=Rattus norvegicus GN=Arf3 PE=2 SV=2 - [ARF3_RAT]	54.70	2	5	9	214	0.6104
Q62812	Myosin-9 OS=Rattus norvegicus GN=Myh9 PE=1 SV=3 - [MYH9_RAT]	40.95	1	56	68	1079	0.6126
P48500	Triosephosphate isomerase OS=Rattus norvegicus GN=Tpi1 PE=1 SV=2 - [TPIS_RAT]	85.54	1	16	16	697	0.6127
A7VJC2	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1 - [ROA2_RAT]	43.06	1	13	14	170	0.6157
P68035	Actin, alpha cardiac muscle 1 OS=Rattus norvegicus GN=Actc1 PE=2 SV=1 - [ACTC_RAT]	83.82	2	10	23	3192	0.6203
P05544	Serine protease inhibitor A3L OS=Rattus norvegicus GN=Serpina3l PE=1 SV=3 - [SPA3L_RAT]	54.72	1	16	20	719	0.6207
P35435	ATP synthase subunit gamma, mitochondrial OS=Rattus norvegicus GN=Atp5c1 PE=1 SV=2 - [ATPG_RAT]	40.66	1	8	8	51	0.6220
P12001	60S ribosomal protein L18 OS=Rattus norvegicus GN=Rpl18 PE=1 SV=2 - [RL18_RAT]	37.23	1	6	6	77	0.6223
Q6AYG5	Ethylmalonyl-CoA decarboxylase OS=Rattus norvegicus GN=Echdc1 PE=1 SV=1 - [ECHD1_RAT]	42.14	1	6	7	37	0.6230
P13803	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Rattus norvegicus GN=Etfa PE=1 SV=4 - [ETFA_RAT]	56.76	1	12	12	255	0.6237
Q6P5P5	Mesoderm-specific transcript homolog protein OS=Rattus norvegicus GN=Mest PE=2 SV=1 - [MEST_RAT]	26.87	1	5	5	89	0.6293
Q9Z0V5	Peroxiredoxin-4 OS=Rattus norvegicus GN=Prdx4 PE=2 SV=1 - [PRDX4_RAT]	29.30	1	4	6	215	0.6296
P35213	14-3-3 protein beta/alpha OS=Rattus norvegicus GN=Ywhab PE=1 SV=3 - [1433B_RAT]	71.54	1	9	16	509	0.6309
Q9EPH1	Alpha-1B-glycoprotein OS=Rattus norvegicus GN=A1bg PE=2 SV=2 - [A1BG_RAT]	30.02	1	12	12	89	0.6323
P31399	ATP synthase subunit d, mitochondrial OS=Rattus norvegicus GN=Atp5h PE=1 SV=3 - [ATP5H_RAT]	34.16	1	4	4	18	0.6338
P54311	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Rattus norvegicus GN=Gnb1 PE=1 SV=4 - [GBB1_RAT]	56.18	1	7	13	201	0.6348
P04166	Cytochrome b5 type B OS=Rattus norvegicus GN=Cyb5b PE=1 SV=2 - [CYB5B_RAT]	51.37	1	4	4	44	0.6349
P97687	Ectonucleoside triphosphate diphosphohydrolase 1 OS=Rattus norvegicus GN=Entpd1 PE=1 SV=1 - [ENTP1_RAT]	5.48	1	2	2	2	0.6364
P18418	Calreticulin OS=Rattus norvegicus GN=Calr PE=1 SV=1 - [CALR_RAT]	66.35	1	20	20	276	0.6368
P10888	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Rattus norvegicus GN=Cox4i1 PE=1 SV=1 - [COX41_RAT]	36.09	1	6	6	110	0.6384
Q63862	Myosin-11 (Fragments) OS=Rattus norvegicus	27.43	1	18	29	367	0.6387

	GN=Myh11 PE=1 SV=3 - [MYH11_RAT]						
Q05982	Nucleoside diphosphate kinase A OS=Rattus norvegicus GN=Nme1 PE=1 SV=1 - [NDKA_RAT]	65.79	1	3	9	314	0.6399
O35828	Coronin-7 OS=Rattus norvegicus GN=Coro7 PE=1 SV=2 - [CORO7_RAT]	7.81	1	2	2	2	0.6409
Q6AXX6	Redox-regulatory protein FAM213A OS=Rattus norvegicus GN=Fam213a PE=1 SV=1 - [F213A_RAT]	15.72	1	3	3	21	0.6410
P55053	Fatty acid-binding protein, epidermal OS=Rattus norvegicus GN=Fabp5 PE=1 SV=3 - [FABP5_RAT]	69.63	1	9	9	214	0.6418
Q68FS2	COP9 signalosome complex subunit 4 OS=Rattus norvegicus GN=Cops4 PE=1 SV=1 - [CSN4_RAT]	11.08	1	2	2	2	0.6429
Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	24.49	1	8	8	26	0.6449
Q6AYC4	Macrophage-capping protein OS=Rattus norvegicus GN=Capg PE=1 SV=1 - [CAPG_RAT]	44.41	1	9	9	108	0.6463
P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	53.35	1	31	31	656	0.6470
P04897	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Rattus norvegicus GN=Gnai2 PE=1 SV=3 - [GNAI2_RAT]	62.54	1	10	17	203	0.6471
O55171	Acyl-coenzyme A thioesterase 2, mitochondrial OS=Rattus norvegicus GN=Acot2 PE=1 SV=1 - [ACOT2_RAT]	3.97	1	2	2	2	0.6484
P31211	Corticosteroid-binding globulin OS=Rattus norvegicus GN=Serpina6 PE=1 SV=2 - [CBG_RAT]	23.48	1	6	6	28	0.6508
P84245	Histone H3.3 OS=Rattus norvegicus GN=H3f3b PE=1 SV=2 - [H33_RAT]	40.44	2	4	4	12	0.6512
Q91Y81	Septin-2 OS=Rattus norvegicus GN=Sept2 PE=1 SV=1 - [SEPT2_RAT]	35.46	1	8	8	40	0.6525
Q9ES21	Phosphatidylinositide phosphatase SAC1 OS=Rattus norvegicus GN=Sacm1l PE=1 SV=1 - [SAC1_RAT]	15.84	1	7	7	36	0.6541
Q63270	Cytoplasmic aconitate hydratase OS=Rattus norvegicus GN=Aco1 PE=1 SV=1 - [ACOC_RAT]	40.04	1	24	24	452	0.6554
A1L1L2	Transmembrane protein 214 OS=Rattus norvegicus GN=Tmem214 PE=2 SV=1 - [TM214_RAT]	2.77	1	2	2	3	0.6564
P13437	3-ketoacyl-CoA thiolase, mitochondrial OS=Rattus norvegicus GN=Acaa2 PE=2 SV=1 - [THIM_RAT]	61.46	1	17	17	286	0.6606
P05370	Glucose-6-phosphate 1-dehydrogenase OS=Rattus norvegicus GN=G6pdx PE=1 SV=3 - [G6PD_RAT]	8.16	1	3	3	15	0.6619
Q4FZT9	26S proteasome non-ATPase regulatory subunit 2 OS=Rattus norvegicus GN=Psmd2 PE=1 SV=1 - [PSMD2_RAT]	21.37	1	13	13	56	0.6628
P38659	Protein disulfide-isomerase A4 OS=Rattus norvegicus GN=Pdia4 PE=1 SV=2 - [PDIA4_RAT]	36.86	1	19	19	99	0.6641
Q5U318	Astrocytic phosphoprotein PEA-15 OS=Rattus norvegicus GN=Pea15 PE=1 SV=1 - [PEA15_RAT]	29.23	1	3	3	5	0.6650
P52504	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Rattus norvegicus GN=Ndufs6 PE=3 SV=1 - [NDUS6_RAT]	21.55	1	2	2	2	0.6651
Q5RJR8	Leucine-rich repeat-containing protein 59 OS=Rattus norvegicus GN=Lrrc59 PE=1 SV=1 - [LRC59_RAT]	10.10	1	3	3	26	0.6661
Q9EPF2	Cell surface glycoprotein MUC18 OS=Rattus norvegicus GN=Mcam PE=1 SV=2 - [MUC18_RAT]	40.43	1	19	19	298	0.6678
Q9EQS0	Transaldolase OS=Rattus norvegicus GN=Taldo1 PE=1 SV=2 - [TALDO_RAT]	39.47	1	14	14	83	0.6682
P10860	Glutamate dehydrogenase 1, mitochondrial OS=Rattus norvegicus GN=Glud1 PE=1 SV=2 - [DHE3_RAT]	37.81	1	15	15	113	0.6683
O08590	Membrane primary amine oxidase OS=Rattus norvegicus GN=Aoc3 PE=1 SV=4 - [AOC3_RAT]	44.04	1	23	23	1689	0.6690
Q60587	Trifunctional enzyme subunit beta, mitochondrial OS=Rattus norvegicus GN=Hadhb PE=1 SV=1 - [ECHB_RAT]	40.84	1	17	17	164	0.6698
Q6IFW6	Keratin, type I cytoskeletal 10 OS=Rattus norvegicus GN=Krt10 PE=3 SV=1 - [K1C10_RAT]	16.73	1	8	9	20	0.6703
Q63691	Monocyte differentiation antigen CD14 OS=Rattus norvegicus GN=Cd14 PE=2 SV=2 - [CD14_RAT]	26.34	1	6	6	71	0.6713
P63174	60S ribosomal protein L38 OS=Rattus norvegicus GN=Rpl38 PE=1 SV=2 - [RL38_RAT]	35.71	1	2	2	2	0.6716

Q3T1L0	Aldehyde dehydrogenase family 16 member A1 OS=Rattus norvegicus GN=Aldh16a1 PE=2 SV=1 - [A16A1_RAT]	5.74	1	2	2	2	0.6726
P49432	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Rattus norvegicus GN=Pdhb PE=1 SV=2 - [ODPB_RAT]	35.10	1	8	8	116	0.6737
O88600	Heat shock 70 kDa protein 4 OS=Rattus norvegicus GN=Hspa4 PE=1 SV=1 - [HSP74_RAT]	30.00	1	16	17	136	0.6763
P80254	D-dopachrome decarboxylase OS=Rattus norvegicus GN=Ddt PE=1 SV=3 - [DOPD_RAT]	77.97	1	7	7	124	0.6776
P62907	60S ribosomal protein L10a OS=Rattus norvegicus GN=Rpl10a PE=1 SV=2 - [RL10A_RAT]	13.36	1	3	3	28	0.6780
P68511	14-3-3 protein eta OS=Rattus norvegicus GN=Ywhah PE=1 SV=2 - [1433F_RAT]	56.91	1	10	16	367	0.6782
Q9Z2G8	Nucleosome assembly protein 1-like 1 OS=Rattus norvegicus GN=Nap1l1 PE=1 SV=1 - [NP1L1_RAT]	7.18	1	2	2	10	0.6796
P26772	10 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspe1 PE=1 SV=3 - [CH10_RAT]	66.67	1	7	7	72	0.6811
Q07969	Platelet glycoprotein 4 OS=Rattus norvegicus GN=Cd36 PE=1 SV=3 - [CD36_RAT]	30.30	1	10	10	644	0.6816
P54313	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Rattus norvegicus GN=Gnb2 PE=1 SV=4 - [GBB2_RAT]	56.47	2	6	13	182	0.6821
P13471	40S ribosomal protein S14 OS=Rattus norvegicus GN=Rps14 PE=2 SV=3 - [RS14_RAT]	15.89	1	2	2	67	0.6823
Q6P7S1	Acid ceramidase OS=Rattus norvegicus GN=Asah1 PE=2 SV=1 - [ASAH1_RAT]	24.62	1	6	6	31	0.6827
P30713	Glutathione S-transferase theta-2 OS=Rattus norvegicus GN=Gstt2 PE=1 SV=3 - [GSTT2_RAT]	18.85	1	3	4	8	0.6840
P27139	Carbonic anhydrase 2 OS=Rattus norvegicus GN=Ca2 PE=1 SV=2 - [CAH2_RAT]	64.62	1	12	12	360	0.6846
Q63945	Protein SET OS=Rattus norvegicus GN=Set PE=2 SV=2 - [SET_RAT]	31.49	1	6	6	18	0.6848
Q63544	Gamma-synuclein OS=Rattus norvegicus GN=Sncg PE=1 SV=2 - [SYUG_RAT]	74.80	1	11	11	564	0.6880
P84092	AP-2 complex subunit mu OS=Rattus norvegicus GN=Ap2m1 PE=1 SV=1 - [AP2M1_RAT]	12.18	1	5	5	8	0.6908
P01946	Hemoglobin subunit alpha-1/2 OS=Rattus norvegicus GN=Hba1 PE=1 SV=3 - [HBA_RAT]	95.77	1	13	13	16877	0.6909
Q5HZY2	GTP-binding protein SAR1b OS=Rattus norvegicus GN=Sar1b PE=2 SV=1 - [SAR1B_RAT]	25.25	1	3	3	3	0.6917
P25093	Fumarylacetoacetase OS=Rattus norvegicus GN=Fah PE=1 SV=1 - [FAAA_RAT]	36.99	1	11	11	136	0.6953
Q5U1Z0	Rab3 GTPase-activating protein non-catalytic subunit OS=Rattus norvegicus GN=Rab3gap2 PE=1 SV=2 - [RBGPR_RAT]	4.26	1	2	2	6	0.6954
P50137	Transketolase OS=Rattus norvegicus GN=Tkt PE=1 SV=1 - [TKT_RAT]	47.35	1	20	20	413	0.6965
Q6RJR6	Reticulon-3 OS=Rattus norvegicus GN=Rtn3 PE=1 SV=1 - [RTN3_RAT]	3.51	1	2	3	44	0.6967
Q9EQX9	Ubiquitin-conjugating enzyme E2 N OS=Rattus norvegicus GN=Ube2n PE=1 SV=1 - [UBE2N_RAT]	42.11	1	5	5	125	0.6974
P00173	Cytochrome b5 OS=Rattus norvegicus GN=Cyb5a PE=1 SV=2 - [CYB5_RAT]	41.04	1	4	4	64	0.6975
P28037	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Rattus norvegicus GN=Aldh1l1 PE=1 SV=3 - [AL1L1_RAT]	22.62	1	14	15	44	0.6999
P13221	Aspartate aminotransferase, cytoplasmic OS=Rattus norvegicus GN=Got1 PE=1 SV=3 - [AATC_RAT]	13.56	1	4	4	7	0.7020
Q6IG05	Keratin, type II cytoskeletal 75 OS=Rattus norvegicus GN=Krt75 PE=3 SV=2 - [K2C75_RAT]	12.18	1	3	8	48	0.7040
P80067	Dipeptidyl peptidase 1 OS=Rattus norvegicus GN=Ctsc PE=1 SV=3 - [CATC_RAT]	4.55	1	2	2	2	0.7045
Q9Z339	Glutathione S-transferase omega-1 OS=Rattus norvegicus GN=Gsto1 PE=1 SV=2 - [GSTO1_RAT]	24.48	1	4	4	48	0.7051
D4ABY2	Coatomer subunit gamma-2 OS=Rattus norvegicus GN=Copg2 PE=3 SV=2 - [COPG2_RAT]	4.20	1	1	2	29	0.7071
P10960	Prosaposin OS=Rattus norvegicus GN=Psap PE=1	3.79	1	2	2	3	0.7090

	SV=1 - [SAP_RAT]						
Q66H98	Serum deprivation-response protein OS=Rattus norvegicus GN=Sdpr PE=1 SV=3 - [SDPR_RAT]	42.69	1	12	12	267	0.7091
P08460	Nidogen-1 (Fragment) OS=Rattus norvegicus GN=Nid1 PE=1 SV=2 - [NID1_RAT]	18.83	1	4	4	31	0.7099
Q5HZA4	LysM and putative peptidoglycan-binding domain-containing protein 1 OS=Rattus norvegicus GN=Lysmd1 PE=1 SV=1 - [LYSM1_RAT]	11.01	1	2	2	2	0.7122
P42123	L-lactate dehydrogenase B chain OS=Rattus norvegicus GN=Ldhb PE=1 SV=2 - [LDHB_RAT]	69.46	1	19	22	665	0.7155
Q9Z0W7	Chloride intracellular channel protein 4 OS=Rattus norvegicus GN=Clic4 PE=1 SV=3 - [CLIC4_RAT]	35.57	1	7	7	33	0.7163
P02091	Hemoglobin subunit beta-1 OS=Rattus norvegicus GN=Hbb PE=1 SV=3 - [HBB1_RAT]	89.80	1	5	17	16533	0.7170
P62243	40S ribosomal protein S8 OS=Rattus norvegicus GN=Rps8 PE=1 SV=2 - [RS8_RAT]	9.62	1	2	2	5	0.7194
P41123	60S ribosomal protein L13 OS=Rattus norvegicus GN=Rpl13 PE=1 SV=2 - [RL13_RAT]	19.43	1	4	4	26	0.7206
Q9WVB1	Ras-related protein Rab-6A OS=Rattus norvegicus GN=Rab6a PE=1 SV=2 - [RAB6A_RAT]	27.40	1	4	5	52	0.7210
P24090	Alpha-2-HS-glycoprotein OS=Rattus norvegicus GN=Ahsg PE=1 SV=2 - [FETUA_RAT]	43.47	1	8	9	463	0.7222
P48679	Prelamin-A/C OS=Rattus norvegicus GN=Lmna PE=1 SV=1 - [LMNA_RAT]	30.98	1	16	18	115	0.7257
Q6AYS7	Aminoacylase-1A OS=Rattus norvegicus GN=Acy1a PE=1 SV=1 - [ACY1A_RAT]	17.65	2	6	6	17	0.7291
Q10758	Keratin, type II cytoskeletal 8 OS=Rattus norvegicus GN=Krt8 PE=1 SV=3 - [K2C8_RAT]	23.19	1	6	11	95	0.7291
P41562	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Rattus norvegicus GN=Idh1 PE=1 SV=1 - [IDHC_RAT]	66.67	1	23	24	311	0.7323
P09527	Ras-related protein Rab-7a OS=Rattus norvegicus GN=Rab7a PE=1 SV=2 - [RAB7A_RAT]	66.18	1	10	10	147	0.7336
P21913	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Rattus norvegicus GN=Sdhb PE=2 SV=2 - [SDHB_RAT]	18.79	1	5	5	23	0.7345
P68370	Tubulin alpha-1A chain OS=Rattus norvegicus GN=Tuba1a PE=1 SV=1 - [TBA1A_RAT]	66.52	1	2	22	1577	0.7372
Q6P9V9	Tubulin alpha-1B chain OS=Rattus norvegicus GN=Tuba1b PE=1 SV=1 - [TBA1B_RAT]	66.52	1	2	22	1679	0.7372
Q0ZHH6	Atlastin-3 OS=Rattus norvegicus GN=Atl3 PE=2 SV=2 - [ATLA3_RAT]	24.21	1	7	7	64	0.7413
Q6GQP4	Ras-related protein Rab-31 OS=Rattus norvegicus GN=Rab31 PE=1 SV=2 - [RAB31_RAT]	18.04	1	3	3	8	0.7431
Q6IMF3	Keratin, type II cytoskeletal 1 OS=Rattus norvegicus GN=Krt1 PE=2 SV=1 - [K2C1_RAT]	6.88	1	4	5	44	0.7445
O35795	Ectonucleoside triphosphate diphosphohydrolase 2 OS=Rattus norvegicus GN=Entpd2 PE=1 SV=1 - [ENTP2_RAT]	6.87	1	2	2	2	0.7450
P27867	Sorbitol dehydrogenase OS=Rattus norvegicus GN=Sord PE=1 SV=4 - [DHSO_RAT]	9.80	1	2	2	10	0.7453
P50617	Dendrin OS=Rattus norvegicus GN=Ddn PE=1 SV=3 - [DEND_RAT]	7.21	1	2	2	2	0.7462
P47727	Carbonyl reductase [NADPH] 1 OS=Rattus norvegicus GN=Cbr1 PE=1 SV=2 - [CBR1_RAT]	76.17	1	19	19	1236	0.7481
P61023	Calcineurin B homologous protein 1 OS=Rattus norvegicus GN=Chp1 PE=1 SV=2 - [CHP1_RAT]	58.46	1	9	9	56	0.7524
Q4V7C7	Actin-related protein 3 OS=Rattus norvegicus GN=Actr3 PE=1 SV=1 - [ARP3_RAT]	56.94	1	14	14	105	0.7552
P20761	Ig gamma-2B chain C region OS=Rattus norvegicus GN=Igh-1a PE=1 SV=1 - [IGG2B_RAT]	37.54	1	7	7	601	0.7562
Q6B345	Protein S100-A11 OS=Rattus norvegicus GN=S100a11 PE=3 SV=1 - [S10AB_RAT]	46.94	1	4	4	87	0.7574
P11517	Hemoglobin subunit beta-2 OS=Rattus norvegicus PE=1 SV=2 - [HBB2_RAT]	88.44	1	3	15	11440	0.7576
P35171	Cytochrome c oxidase subunit 7A2, mitochondrial OS=Rattus norvegicus GN=Cox7a2 PE=1 SV=1 - [CX7A2_RAT]	27.71	1	2	2	6	0.7598

P02401	60S acidic ribosomal protein P2 OS=Rattus norvegicus GN=Rplp2 PE=1 SV=2 - [RLA2_RAT]	66.96	1	4	4	60	0.7615
P26376	Interferon-induced transmembrane protein 3 OS=Rattus norvegicus GN=ifitm3 PE=2 SV=1 - [IFM3_RAT]	32.12	1	3	3	31	0.7620
O55096	Dipeptidyl peptidase 3 OS=Rattus norvegicus GN=Dpp3 PE=1 SV=2 - [DPP3_RAT]	21.68	1	8	8	28	0.7632
Q6Q760	Sodium leak channel non-selective protein OS=Rattus norvegicus GN=Nalcn PE=1 SV=1 - [NALCN_RAT]	1.55	1	2	3	5	0.7635
P41498	Low molecular weight phosphotyrosine protein phosphatase OS=Rattus norvegicus GN=Acp1 PE=1 SV=3 - [PPAC_RAT]	24.05	1	3	3	16	0.7639
Q9Z1H9	Protein kinase C delta-binding protein OS=Rattus norvegicus GN=Prkcdbp PE=1 SV=1 - [PRDBP_RAT]	41.83	1	12	12	88	0.7645
Q641Y0	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Rattus norvegicus GN=Ddost PE=2 SV=1 - [OST48_RAT]	22.68	1	6	6	48	0.7654
Q5U2Q3	Ester hydrolase C11orf54 homolog OS=Rattus norvegicus PE=1 SV=1 - [CK054_RAT]	20.95	1	4	4	68	0.7657
Q5EB77	Ras-related protein Rab-18 OS=Rattus norvegicus GN=Rab18 PE=2 SV=1 - [RAB18_RAT]	50.49	1	8	8	78	0.7669
Q00715	Histone H2B type 1 OS=Rattus norvegicus PE=1 SV=2 - [H2B1_RAT]	39.20	1	5	5	257	0.7680
P13596	Neural cell adhesion molecule 1 OS=Rattus norvegicus GN=Ncam1 PE=1 SV=1 - [NCAM1_RAT]	4.08	1	2	3	3	0.7697
Q9QY44	ATP-binding cassette sub-family D member 2 OS=Rattus norvegicus GN=Abcd2 PE=1 SV=1 - [ABCD2_RAT]	12.01	1	5	6	12	0.7710
Q9Z2L0	Voltage-dependent anion-selective channel protein 1 OS=Rattus norvegicus GN=Vdac1 PE=1 SV=4 - [VDAC1_RAT]	44.88	1	9	9	64	0.7713
P15429	Beta-enolase OS=Rattus norvegicus GN=Eno3 PE=1 SV=3 - [ENOB_RAT]	27.88	1	2	7	209	0.7741
P12785	Fatty acid synthase OS=Rattus norvegicus GN=Fasn PE=1 SV=3 - [FAS_RAT]	61.80	1	112	112	2252	0.7753
P19804	Nucleoside diphosphate kinase B OS=Rattus norvegicus GN=Nme2 PE=1 SV=1 - [NDKB_RAT]	69.08	1	4	10	472	0.7756
P25409	Alanine aminotransferase 1 OS=Rattus norvegicus GN=Gpt PE=1 SV=2 - [ALAT1_RAT]	23.39	1	6	7	31	0.7785
P24368	Peptidyl-prolyl cis-trans isomerase B OS=Rattus norvegicus GN=Ppib PE=1 SV=3 - [PPIB_RAT]	51.39	1	12	12	244	0.7820
P04182	Ornithine aminotransferase, mitochondrial OS=Rattus norvegicus GN=Oat PE=1 SV=1 - [OAT_RAT]	18.68	1	5	6	13	0.7833
P23764	Glutathione peroxidase 3 OS=Rattus norvegicus GN=Gpx3 PE=2 SV=2 - [GPX3_RAT]	32.30	1	6	6	155	0.7863
Q794F9	4F2 cell-surface antigen heavy chain OS=Rattus norvegicus GN=Slc3a2 PE=1 SV=1 - [4F2_RAT]	5.31	1	2	2	2	0.7866
Q6AY84	Secernin-1 OS=Rattus norvegicus GN=Scrn1 PE=1 SV=1 - [SCRN1_RAT]	6.28	1	2	2	2	0.7868
P02767	Transthyretin OS=Rattus norvegicus GN=Ttr PE=1 SV=1 - [TTHY_RAT]	62.59	1	6	6	114	0.7873
P32038	Complement factor D OS=Rattus norvegicus GN=Cfd PE=1 SV=2 - [CFAD_RAT]	42.97	1	6	6	56	0.7876
B2RZ78	Vacuolar protein sorting-associated protein 29 OS=Rattus norvegicus GN=Vps29 PE=1 SV=2 - [VPS29_RAT]	21.98	1	4	4	19	0.7878
Q6P6R2	Dihydrolipoyl dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Dld PE=1 SV=1 - [DLDH_RAT]	36.54	1	13	13	146	0.7886
P28075	Proteasome subunit beta type-5 OS=Rattus norvegicus GN=Psmb5 PE=1 SV=3 - [PSB5_RAT]	14.83	1	3	3	4	0.7888
O70199	UDP-glucose 6-dehydrogenase OS=Rattus norvegicus GN=Ugdh PE=1 SV=1 - [UGDH_RAT]	10.14	1	3	3	3	0.7897
F1LMZ8	26S proteasome non-ATPase regulatory subunit 11 OS=Rattus norvegicus GN=Psmd11 PE=1 SV=2 - [PSD11_RAT]	6.16	1	2	2	3	0.7909
P56574	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus GN=Idh2 PE=1 SV=2 - [IDHP_RAT]	40.93	1	14	16	81	0.7921

Q64057	Alpha-aminoadipic semialdehyde dehydrogenase OS=Rattus norvegicus GN=Aldh7a1 PE=1 SV=2 - [AL7A1_RAT]	25.05	1	9	9	21	0.7931
P04906	Glutathione S-transferase P OS=Rattus norvegicus GN=Gstp1 PE=1 SV=2 - [GSTP1_RAT]	52.38	1	8	8	278	0.7958
P01015	Angiotensinogen OS=Rattus norvegicus GN=Agt PE=1 SV=1 - [ANGT_RAT]	31.24	1	7	8	34	0.7959
P19234	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Rattus norvegicus GN=Ndufv2 PE=1 SV=2 - [NDUV2_RAT]	9.27	1	2	2	35	0.7963
P29410	Adenylate kinase 2, mitochondrial OS=Rattus norvegicus GN=Ak2 PE=2 SV=2 - [KAD2_RAT]	48.54	1	10	10	98	0.7971
P58365	Cadherin-23 OS=Rattus norvegicus GN=Cdh23 PE=2 SV=1 - [CAD23_RAT]	1.39	1	3	3	7	0.7971
Q63556	Serine protease inhibitor A3M (Fragment) OS=Rattus norvegicus GN=Serpina3m PE=2 SV=1 - [SPA3M_RAT]	11.65	1	2	4	38	0.7975
B5DEH2	Erlin-2 OS=Rattus norvegicus GN=Erlin2 PE=1 SV=1 - [ERLN2_RAT]	8.55	1	2	2	2	0.7981
O35763	Moesin OS=Rattus norvegicus GN=Msn PE=1 SV=3 - [MOES_RAT]	42.81	1	14	21	278	0.8007
P24329	Thiosulfate sulfurtransferase OS=Rattus norvegicus GN=Tst PE=1 SV=3 - [THTR_RAT]	23.57	1	4	5	19	0.8036
O88989	Malate dehydrogenase, cytoplasmic OS=Rattus norvegicus GN=Mdh1 PE=1 SV=3 - [MDHC_RAT]	48.80	1	15	15	838	0.8048
Q63570	26S protease regulatory subunit 6B OS=Rattus norvegicus GN=Psmc4 PE=1 SV=1 - [PRS6B_RAT]	28.23	1	5	5	89	0.8055
Q63210	Guanine nucleotide-binding protein subunit alpha-12 OS=Rattus norvegicus GN=Gna12 PE=1 SV=3 - [GNA12_RAT]	11.61	1	2	3	11	0.8069
Q6NYB7	Ras-related protein Rab-1A OS=Rattus norvegicus GN=Rab1A PE=1 SV=3 - [RAB1A_RAT]	56.10	1	4	8	286	0.8094
O35567	Bifunctional purine biosynthesis protein PURH OS=Rattus norvegicus GN=Atic PE=1 SV=2 - [PUR9_RAT]	27.03	1	7	7	15	0.8123
P31044	Phosphatidylethanolamine-binding protein 1 OS=Rattus norvegicus GN=Pebp1 PE=1 SV=3 - [PEBP1_RAT]	57.22	1	7	7	121	0.8140
P01836	Ig kappa chain C region, A allele OS=Rattus norvegicus PE=1 SV=1 - [KACA_RAT]	76.42	1	7	7	1043	0.8147
Q921A4	Cytoglobin OS=Rattus norvegicus GN=Cygb PE=1 SV=1 - [CYGB_RAT]	64.21	1	10	10	34	0.8149
P04764	Alpha-enolase OS=Rattus norvegicus GN=Eno1 PE=1 SV=4 - [ENOA_RAT]	71.89	1	19	24	949	0.8157
P08430	UDP-glucuronosyltransferase 1-6 OS=Rattus norvegicus GN=Ugt1a6 PE=1 SV=1 - [UD16_RAT]	19.28	6	2	6	51	0.8176
Q7M0E3	Destrin OS=Rattus norvegicus GN=Dstn PE=1 SV=3 - [DEST_RAT]	63.03	1	9	9	192	0.8177
P14604	Enoyl-CoA hydratase, mitochondrial OS=Rattus norvegicus GN=Echs1 PE=1 SV=1 - [ECHM_RAT]	36.55	1	8	8	171	0.8181
P32551	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Rattus norvegicus GN=Uqcrc2 PE=1 SV=2 - [QCR2_RAT]	54.65	1	15	15	142	0.8187
O35264	Platelet-activating factor acetylhydrolase IB subunit beta OS=Rattus norvegicus GN=Pafah1b2 PE=1 SV=1 - [PA1B2_RAT]	12.23	1	2	2	33	0.8231
P07871	3-ketoacyl-CoA thiolase B, peroxisomal OS=Rattus norvegicus GN=Acaa1b PE=1 SV=2 - [THIKB_RAT]	13.21	2	4	4	5	0.8247
P34064	Proteasome subunit alpha type-5 OS=Rattus norvegicus GN=Psma5 PE=1 SV=1 - [PSA5_RAT]	16.18	1	3	3	8	0.8262
Q9QX79	Fetuin-B OS=Rattus norvegicus GN=Fetub PE=2 SV=2 - [FETUB_RAT]	62.17	1	18	18	382	0.8270
P11960	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial (Fragment) OS=Rattus norvegicus GN=Bckdha PE=1 SV=1 - [ODBA_RAT]	9.98	1	2	2	2	0.8283
P53534	Glycogen phosphorylase, brain form (Fragment) OS=Rattus norvegicus GN=Pygb PE=1 SV=3 - [PYGB_RAT]	13.84	1	7	9	19	0.8321
P62250	40S ribosomal protein S16 OS=Rattus norvegicus	38.36	1	5	5	50	0.8322

	GN=Rps16 PE=1 SV=2 - [RS16_RAT]						
P33124	Long-chain-fatty-acid--CoA ligase 6 OS=Rattus norvegicus GN=Acsl6 PE=1 SV=1 - [ACSL6_RAT]	3.73	1	1	3	259	0.8399
Q811M5	Complement component C6 OS=Rattus norvegicus GN=C6 PE=2 SV=1 - [CO6_RAT]	28.48	1	18	18	122	0.8402
P00507	Aspartate aminotransferase, mitochondrial OS=Rattus norvegicus GN=Got2 PE=1 SV=2 - [AATM_RAT]	38.84	1	13	14	93	0.8408
P07483	Fatty acid-binding protein, heart OS=Rattus norvegicus GN=Fabp3 PE=1 SV=2 - [FABPH_RAT]	34.59	1	4	4	8	0.8418
P15651	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acads PE=1 SV=2 - [ACADS_RAT]	22.09	1	6	6	15	0.8442
B2RZ37	Receptor expression-enhancing protein 5 OS=Rattus norvegicus GN=Reep5 PE=1 SV=1 - [REEP5_RAT]	25.93	1	8	8	319	0.8443
P62161	Calmodulin OS=Rattus norvegicus GN=Calm1 PE=1 SV=2 - [CALM_RAT]	32.21	1	5	5	72	0.8444
P62890	60S ribosomal protein L30 OS=Rattus norvegicus GN=Rpl30 PE=3 SV=2 - [RL30_RAT]	40.87	1	4	4	37	0.8448
P11884	Aldehyde dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Aldh2 PE=1 SV=1 - [ALDH2_RAT]	56.26	1	20	20	452	0.8458
Q64119	Myosin light polypeptide 6 OS=Rattus norvegicus GN=Myl6 PE=1 SV=3 - [MYL6_RAT]	58.28	2	9	9	141	0.8474
Q4KM73	UMP-CMP kinase OS=Rattus norvegicus GN=Cmpk1 PE=1 SV=2 - [KCY_RAT]	60.20	1	10	10	41	0.8479
Q6P686	Osteoclast-stimulating factor 1 OS=Rattus norvegicus GN=Ostf1 PE=1 SV=1 - [OSTF1_RAT]	11.21	1	2	2	2	0.8486
Q9EST6	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Rattus norvegicus GN=Anp32b PE=1 SV=1 - [AN32B_RAT]	18.75	1	3	5	34	0.8491
P62902	60S ribosomal protein L31 OS=Rattus norvegicus GN=Rpl31 PE=2 SV=1 - [RL31_RAT]	18.40	1	2	2	17	0.8525
Q5RKI0	WD repeat-containing protein 1 OS=Rattus norvegicus GN=Wdr1 PE=1 SV=3 - [WDR1_RAT]	9.90	1	5	5	10	0.8538
Q64611	Cysteine sulfinic acid decarboxylase OS=Rattus norvegicus GN=Csad PE=1 SV=1 - [CSAD_RAT]	35.09	1	11	11	152	0.8557
Q5FVI6	V-type proton ATPase subunit C 1 OS=Rattus norvegicus GN=Atp6v1c1 PE=2 SV=1 - [VATC1_RAT]	8.90	1	2	2	2	0.8590
P23457	3-alpha-hydroxysteroid dehydrogenase OS=Rattus norvegicus GN=Akr1c9 PE=1 SV=1 - [DIDH_RAT]	55.59	1	12	14	162	0.8604
Q6URK4	Heterogeneous nuclear ribonucleoprotein A3 OS=Rattus norvegicus GN=Hnrnpa3 PE=1 SV=1 - [ROA3_RAT]	14.25	1	4	4	67	0.8623
P48721	Stress-70 protein, mitochondrial OS=Rattus norvegicus GN=Hspa9 PE=1 SV=3 - [GRP75_RAT]	35.79	1	18	19	223	0.8637
Q7TMA5	Apolipoprotein B-100 OS=Rattus norvegicus GN=Apob PE=1 SV=1 - [APOB_RAT]	4.22	1	14	15	19	0.8653
P11980	Pyruvate kinase PKM OS=Rattus norvegicus GN=Pkm PE=1 SV=3 - [KPYM_RAT]	48.21	1	23	23	691	0.8658
P52873	Pyruvate carboxylase, mitochondrial OS=Rattus norvegicus GN=Pc PE=1 SV=2 - [PYC_RAT]	55.52	1	44	45	1068	0.8693
Q66HF1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus GN=Ndufs1 PE=1 SV=1 - [NDUS1_RAT]	28.61	1	12	12	57	0.8694
B0BNA5	Coactosin-like protein OS=Rattus norvegicus GN=Cotl1 PE=1 SV=1 - [COTL1_RAT]	57.75	1	7	7	41	0.8695
P62278	40S ribosomal protein S13 OS=Rattus norvegicus GN=Rps13 PE=1 SV=2 - [RS13_RAT]	45.03	1	6	7	19	0.8731
P61107	Ras-related protein Rab-14 OS=Rattus norvegicus GN=Rab14 PE=1 SV=3 - [RAB14_RAT]	59.07	1	8	9	70	0.8734
Q6P6V0	Glucose-6-phosphate isomerase OS=Rattus norvegicus GN=Gpi PE=1 SV=1 - [G6PI_RAT]	47.49	1	19	19	346	0.8734
Q68FQ0	T-complex protein 1 subunit epsilon OS=Rattus norvegicus GN=Cct5 PE=1 SV=1 - [TCPE_RAT]	7.39	1	2	2	2	0.8739
P05708	Hexokinase-1 OS=Rattus norvegicus GN=Hk1 PE=1 SV=4 - [HXK1_RAT]	11.66	1	8	8	58	0.8743
Q1JU68	Eukaryotic translation initiation factor 3 subunit A OS=Rattus norvegicus GN=Eif3a PE=2 SV=2 -	9.90	1	9	9	59	0.8747

	[EIF3A_RAT]						
Q6PCU2	V-type proton ATPase subunit E 1 OS=Rattus norvegicus GN=Atp6v1e1 PE=1 SV=1 - [VATE1_RAT]	23.45	1	4	4	41	0.8753
P45953	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acadvl PE=1 SV=1 - [ACADV_RAT]	17.71	1	6	6	37	0.8762
O08651	D-3-phosphoglycerate dehydrogenase OS=Rattus norvegicus GN=Phgdh PE=1 SV=3 - [SERA_RAT]	25.14	1	9	9	156	0.8765
P12007	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ivd PE=1 SV=2 - [IVD_RAT]	43.16	1	11	11	51	0.8767
Q924S5	Lon protease homolog, mitochondrial OS=Rattus norvegicus GN=Lonp1 PE=2 SV=1 - [LONM_RAT]	2.95	1	2	2	2	0.8788
P14740	Dipeptidyl peptidase 4 OS=Rattus norvegicus GN=Dpp4 PE=1 SV=2 - [DPP4_RAT]	14.99	1	9	10	79	0.8802
P13086	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Rattus norvegicus GN=Suclg1 PE=2 SV=2 - [SUCA_RAT]	40.75	1	9	10	53	0.8805
Q6RUV5	Ras-related C3 botulinum toxin substrate 1 OS=Rattus norvegicus GN=Rac1 PE=1 SV=1 - [RAC1_RAT]	39.58	1	8	9	46	0.8818
P84817	Mitochondrial fission 1 protein OS=Rattus norvegicus GN=Fis1 PE=1 SV=1 - [FIS1_RAT]	32.24	1	5	5	99	0.8861
P17074	40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3 - [RS19_RAT]	33.79	1	5	5	96	0.8867
Q6IG12	Keratin, type II cytoskeletal 7 OS=Rattus norvegicus GN=Krt7 PE=3 SV=1 - [K2C7_RAT]	11.82	1	3	6	51	0.8902
Q07984	Translocon-associated protein subunit delta OS=Rattus norvegicus GN=Ssr4 PE=2 SV=1 - [SSRD_RAT]	30.64	1	4	4	10	0.8906
P05545	Serine protease inhibitor A3K OS=Rattus norvegicus GN=Serpina3k PE=1 SV=3 - [SPA3K_RAT]	61.06	1	16	20	942	0.8950
P35434	ATP synthase subunit delta, mitochondrial OS=Rattus norvegicus GN=Atp5d PE=1 SV=2 - [ATPD_RAT]	13.69	1	2	2	12	0.8956
Q6DGG0	Peptidyl-prolyl cis-trans isomerase D OS=Rattus norvegicus GN=Ppid PE=1 SV=3 - [PPID_RAT]	17.57	1	4	4	9	0.9013
P32089	Tricarboxylate transport protein, mitochondrial OS=Rattus norvegicus GN=Slc25a1 PE=1 SV=1 - [TXTP_RAT]	26.69	1	5	6	33	0.9014
P10719	ATP synthase subunit beta, mitochondrial OS=Rattus norvegicus GN=Atp5b PE=1 SV=2 - [ATPB_RAT]	77.88	1	26	26	1178	0.9023
P31000	Vimentin OS=Rattus norvegicus GN=Vim PE=1 SV=2 - [VIME_RAT]	79.61	1	37	42	2348	0.9030
Q4V7A0	WD repeat-containing protein 61 OS=Rattus norvegicus GN=Wdr61 PE=1 SV=1 - [WDR61_RAT]	11.80	1	2	2	7	0.9036
Q5BJY9	Keratin, type I cytoskeletal 18 OS=Rattus norvegicus GN=Krt18 PE=1 SV=3 - [K1C18_RAT]	25.06	1	6	8	27	0.9053
P63324	40S ribosomal protein S12 OS=Rattus norvegicus GN=Rps12 PE=1 SV=2 - [RS12_RAT]	28.79	1	4	4	39	0.9063
P13697	NADP-dependent malic enzyme OS=Rattus norvegicus GN=Me1 PE=1 SV=2 - [MAOX_RAT]	64.34	1	20	21	266	0.9078
P11915	Non-specific lipid-transfer protein OS=Rattus norvegicus GN=Scp2 PE=1 SV=3 - [NLTP_RAT]	16.27	1	9	9	138	0.9081
P47942	Dihydropyrimidinase-related protein 2 OS=Rattus norvegicus GN=Dpysl2 PE=1 SV=1 - [DPYL2_RAT]	44.76	1	12	15	234	0.9089
P26284	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Rattus norvegicus GN=Pdha1 PE=1 SV=2 - [ODPA_RAT]	37.44	1	11	11	67	0.9109
Q68FU3	Electron transfer flavoprotein subunit beta OS=Rattus norvegicus GN=Etfb PE=2 SV=3 - [ETFB_RAT]	46.67	1	10	10	177	0.9128
P19944	60S acidic ribosomal protein P1 OS=Rattus norvegicus GN=Rplp1 PE=3 SV=1 - [RLA1_RAT]	51.75	1	2	2	42	0.9128
P0CC09	Histone H2A type 2-A OS=Rattus norvegicus GN=Hist2h2aa3 PE=1 SV=1 - [H2A2A_RAT]	57.69	8	6	6	328	0.9140
P04642	L-lactate dehydrogenase A chain OS=Rattus norvegicus GN=Ldha PE=1 SV=1 - [LDHA_RAT]	82.83	1	22	25	727	0.9160
P10252	CD48 antigen OS=Rattus norvegicus GN=Cd48 PE=1 SV=1 - [CD48_RAT]	15.83	1	3	3	3	0.9161
Q64591	2,4-dienoyl-CoA reductase, mitochondrial OS=Rattus	38.81	1	9	9	128	0.9165

	norvegicus GN=Decr1 PE=1 SV=2 - [DECR_RAT]						
P70580	Membrane-associated progesterone receptor component 1 OS=Rattus norvegicus GN=Pgrmc1 PE=1 SV=3 - [PGRC1_RAT]	33.85	1	4	4	6	0.9165
P16303	Carboxylesterase 1D OS=Rattus norvegicus GN=Ces1d PE=1 SV=2 - [CES1D_RAT]	53.63	1	28	28	2852	0.9174
Q75WE7	von Willebrand factor A domain-containing protein 5A OS=Rattus norvegicus GN=Vwa5a PE=2 SV=1 - [VWA5A_RAT]	10.71	1	6	6	13	0.9187
P62853	40S ribosomal protein S25 OS=Rattus norvegicus GN=Rps25 PE=2 SV=1 - [RS25_RAT]	24.00	1	4	4	9	0.9189
Q9Z0V6	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Rattus norvegicus GN=Prdx3 PE=1 SV=2 - [PRDX3_RAT]	36.96	1	6	6	113	0.9209
Q4V8F9	Hydroxysteroid dehydrogenase-like protein 2 OS=Rattus norvegicus GN=Hsdl2 PE=2 SV=1 - [HSDL2_RAT]	5.53	1	2	2	2	0.9217
Q9JJ54	Heterogeneous nuclear ribonucleoprotein D0 OS=Rattus norvegicus GN=Hnrnpd PE=1 SV=2 - [HNRPD_RAT]	6.23	1	2	2	8	0.9225
P02650	Apolipoprotein E OS=Rattus norvegicus GN=Apoe PE=1 SV=2 - [APOE_RAT]	53.53	1	15	15	497	0.9230
P11442	Clathrin heavy chain 1 OS=Rattus norvegicus GN=Cltc PE=1 SV=3 - [CLH1_RAT]	53.25	1	71	71	1283	0.9232
P04041	Glutathione peroxidase 1 OS=Rattus norvegicus GN=Gpx1 PE=1 SV=4 - [GPX1_RAT]	79.60	1	11	12	220	0.9233
Q63716	Peroxiredoxin-1 OS=Rattus norvegicus GN=Prdx1 PE=1 SV=1 - [PRDX1_RAT]	74.37	1	13	15	634	0.9238
P54921	Alpha-soluble NSF attachment protein OS=Rattus norvegicus GN=Napa PE=1 SV=2 - [SNAA_RAT]	12.88	1	3	3	7	0.9271
Q9JK11	Reticulon-4 OS=Rattus norvegicus GN=Rtn4 PE=1 SV=1 - [RTN4_RAT]	6.53	1	4	5	9	0.9280
Q5XI22	Acetyl-CoA acetyltransferase, cytosolic OS=Rattus norvegicus GN=Acat2 PE=1 SV=1 - [THIC_RAT]	9.32	1	2	2	2	0.9303
Q99NA5	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Rattus norvegicus GN=Idh3a PE=1 SV=1 - [IDH3A_RAT]	24.04	1	6	6	93	0.9308
P61805	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Rattus norvegicus GN=Dad1 PE=3 SV=3 - [DAD1_RAT]	26.55	1	3	3	15	0.9311
P41542	General vesicular transport factor p115 OS=Rattus norvegicus GN=Uso1 PE=1 SV=1 - [USO1_RAT]	8.97	1	6	7	25	0.9344
Q6PCT3	Tumor protein D54 OS=Rattus norvegicus GN=Tpd52l2 PE=1 SV=1 - [TPD54_RAT]	11.36	1	2	2	2	0.9346
P35704	Peroxiredoxin-2 OS=Rattus norvegicus GN=Prdx2 PE=1 SV=3 - [PRDX2_RAT]	57.58	1	9	9	431	0.9347
P13383	Nucleolin OS=Rattus norvegicus GN=Ncl PE=1 SV=3 - [NUCL_RAT]	21.18	1	13	13	106	0.9436
P63039	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspd1 PE=1 SV=1 - [CH60_RAT]	53.75	1	23	23	723	0.9438
P15650	Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Acadl PE=1 SV=1 - [ACADL_RAT]	29.77	1	11	11	56	0.9441
P14841	Cystatin-C OS=Rattus norvegicus GN=Cst3 PE=1 SV=2 - [CYTC_RAT]	29.29	1	3	3	35	0.9455
Q4TU93	C-type mannose receptor 2 OS=Rattus norvegicus GN=Mrc2 PE=1 SV=1 - [MRC2_RAT]	2.03	1	2	2	3	0.9455
P11497	Acetyl-CoA carboxylase 1 OS=Rattus norvegicus GN=Acaca PE=1 SV=1 - [ACACA_RAT]	32.62	1	56	56	263	0.9460
D4AE41	RNA binding motif protein, X-linked-like-1 OS=Rattus norvegicus GN=Rbmxl1 PE=3 SV=1 - [RMXL1_RAT]	10.31	3	3	3	13	0.9473
Q5SGE0	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=1 SV=1 - [LPPRC_RAT]	10.13	1	8	9	33	0.9508
Q6AXQ0	SUMO-activating enzyme subunit 1 OS=Rattus norvegicus GN=Sae1 PE=2 SV=1 - [SAE1_RAT]	9.17	1	2	2	2	0.9514
P04785	Protein disulfide-isomerase OS=Rattus norvegicus GN=P4hb PE=1 SV=2 - [PDIA1_RAT]	57.37	1	22	22	544	0.9519

P61980	Heterogeneous nuclear ribonucleoprotein K OS=Rattus norvegicus GN=Hnrnpk PE=1 SV=1 - [HNRPK_RAT]	25.05	1	7	8	126	0.9521
P00697	Lysozyme C-1 OS=Rattus norvegicus GN=Lyz1 PE=1 SV=2 - [LYSC1_RAT]	28.38	1	2	2	2	0.9534
P24268	Cathepsin D OS=Rattus norvegicus GN=Ctsd PE=1 SV=1 - [CATD_RAT]	21.87	1	6	6	54	0.9539
P28073	Proteasome subunit beta type-6 OS=Rattus norvegicus GN=Psmb6 PE=1 SV=3 - [PSB6_RAT]	8.82	1	2	2	43	0.9552
P27653	C-1-tetrahydrofolate synthase, cytoplasmic OS=Rattus norvegicus GN=Mthfd1 PE=1 SV=3 - [C1TC_RAT]	2.99	1	2	2	2	0.9568
P20171	GTPase HRas OS=Rattus norvegicus GN=Hras PE=1 SV=2 - [RASH_RAT]	12.17	2	2	2	9	0.9574
P62425	60S ribosomal protein L7a OS=Rattus norvegicus GN=Rpl7a PE=1 SV=2 - [RL7A_RAT]	18.05	1	5	5	34	0.9597
P10536	Ras-related protein Rab-1B OS=Rattus norvegicus GN=Rab1b PE=1 SV=1 - [RAB1B_RAT]	48.26	1	3	7	258	0.9604
Q6IFU8	Keratin, type I cytoskeletal 17 OS=Rattus norvegicus GN=Krt17 PE=1 SV=1 - [K1C17_RAT]	24.71	1	6	10	23	0.9627
Q07009	Calpain-2 catalytic subunit OS=Rattus norvegicus GN=Capn2 PE=1 SV=3 - [CAN2_RAT]	29.14	1	12	13	77	0.9628
Q2MHH0	Tumor suppressor candidate 5 homolog OS=Rattus norvegicus GN=Tusc5 PE=1 SV=1 - [TUSC5_RAT]	24.86	1	3	3	112	0.9658
Q63690	Apoptosis regulator BAX OS=Rattus norvegicus GN=Bax PE=1 SV=2 - [BAX_RAT]	12.50	1	2	2	2	0.9672
Q5XI78	2-oxoglutarate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ogdh PE=1 SV=1 - [ODO1_RAT]	38.71	1	27	27	320	0.9708
P11348	Dihydropteridine reductase OS=Rattus norvegicus GN=Qdpr PE=1 SV=1 - [DHPR_RAT]	50.21	1	8	8	47	0.9708
P18163	Long-chain-fatty-acid--CoA ligase 1 OS=Rattus norvegicus GN=Acsl1 PE=1 SV=1 - [ACSL1_RAT]	61.66	1	36	38	2596	0.9722
O70351	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Rattus norvegicus GN=Hsd17b10 PE=1 SV=3 - [HCD2_RAT]	67.05	1	10	10	127	0.9733
Q5XI32	F-actin-capping protein subunit beta OS=Rattus norvegicus GN=Capzb PE=1 SV=1 - [CAPZB_RAT]	25.74	1	6	6	36	0.9759
P97852	Peroxisomal multifunctional enzyme type 2 OS=Rattus norvegicus GN=Hsd17b4 PE=1 SV=3 - [DHB4_RAT]	18.10	1	8	10	105	0.9772
Q68A21	Transcriptional activator protein Pur-beta OS=Rattus norvegicus GN=Purb PE=1 SV=3 - [PURB_RAT]	15.24	1	2	2	4	0.9774
Q63028	Alpha-adducin OS=Rattus norvegicus GN=Add1 PE=1 SV=2 - [ADDA_RAT]	11.97	1	5	5	23	0.9778
P00388	NADPH--cytochrome P450 reductase OS=Rattus norvegicus GN=Por PE=1 SV=3 - [NCPR_RAT]	24.78	1	12	12	78	0.9800
P05065	Fructose-bisphosphate aldolase A OS=Rattus norvegicus GN=Aldoa PE=1 SV=2 - [ALDOA_RAT]	81.04	1	24	24	870	0.9804
Q04462	Valine--tRNA ligase OS=Rattus norvegicus GN=Vars PE=2 SV=2 - [SYVC_RAT]	12.26	1	8	8	42	0.9806
P29975	Aquaporin-1 OS=Rattus norvegicus GN=Aqp1 PE=1 SV=4 - [AQP1_RAT]	7.06	1	2	2	5	0.9813
P97849	Long-chain fatty acid transport protein 1 OS=Rattus norvegicus GN=Slc27a1 PE=2 SV=1 - [S27A1_RAT]	24.61	1	10	10	100	0.9815
P04905	Glutathione S-transferase Mu 1 OS=Rattus norvegicus GN=Gstm1 PE=1 SV=2 - [GSTM1_RAT]	45.87	1	5	8	41	0.9840
P29315	Ribonuclease inhibitor OS=Rattus norvegicus GN=Rnh1 PE=1 SV=2 - [RINI_RAT]	34.21	1	9	9	28	0.9841
P16638	ATP-citrate synthase OS=Rattus norvegicus GN=Acly PE=1 SV=1 - [ACLY_RAT]	50.27	1	43	43	717	0.9865
P57113	Maleylacetoacetate isomerase OS=Rattus norvegicus GN=Gstz1 PE=1 SV=2 - [MAAI_RAT]	56.94	1	8	8	74	0.9891
P34058	Heat shock protein HSP 90-beta OS=Rattus norvegicus GN=Hsp90ab1 PE=1 SV=4 - [HS90B_RAT]	66.02	1	25	41	1225	0.9898
Q07936	Annexin A2 OS=Rattus norvegicus GN=Anxa2 PE=1 SV=2 - [ANXA2_RAT]	75.81	1	28	28	2201	0.9902
P20767	Ig lambda-2 chain C region OS=Rattus norvegicus PE=4 SV=1 - [LAC2_RAT]	76.92	1	5	5	154	0.9917
Q8VHF5	Citrate synthase, mitochondrial OS=Rattus norvegicus GN=Cs PE=1 SV=1 - [CISY_RAT]	38.20	1	13	13	135	0.9932
P31977	Ezrin OS=Rattus norvegicus GN=Ezr PE=1 SV=3 -	22.53	1	6	12	168	0.9938

	[EZRI_RAT]						
P47245	Nardilysin OS=Rattus norvegicus GN=Nrd1 PE=1 SV=1 - [NRDC_RAT]	2.33	1	2	2	2	0.9948
P40112	Proteasome subunit beta type-3 OS=Rattus norvegicus GN=Psmb3 PE=1 SV=1 - [PSB3_RAT]	26.83	1	4	4	60	0.9953
P82995	Heat shock protein HSP 90-alpha OS=Rattus norvegicus GN=Hsp90aa1 PE=1 SV=3 - [HS90A_RAT]	61.12	1	24	38	882	0.9954
Q68FY0	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Rattus norvegicus GN=Uqcrc1 PE=1 SV=1 - [QCR1_RAT]	28.13	1	8	8	99	0.9956
P63159	High mobility group protein B1 OS=Rattus norvegicus GN=Hmgb1 PE=1 SV=2 - [HMGB1_RAT]	40.00	1	8	8	37	0.9961
P62832	60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1 - [RL23_RAT]	32.14	1	3	3	32	0.9964
P62914	60S ribosomal protein L11 OS=Rattus norvegicus GN=Rpl11 PE=1 SV=2 - [RL11_RAT]	16.85	1	3	3	63	0.9967
Q3T1J1	Eukaryotic translation initiation factor 5A-1 OS=Rattus norvegicus GN=Eif5a PE=1 SV=3 - [IF5A1_RAT]	45.45	1	7	7	87	0.9994
P36972	Adenine phosphoribosyltransferase OS=Rattus norvegicus GN=Aprt PE=1 SV=1 - [APT_RAT]	80.56	1	12	12	224	0.9997
P60711	Actin, cytoplasmic 1 OS=Rattus norvegicus GN=Actb PE=1 SV=1 - [ACTB_RAT]	82.67	2	12	25	5499	