A Chemical-proteomic Platform to Monitor Cysteine Sensitivity to Transnitrosation

Author: Yani Zhou

Persistent link: http://hdl.handle.net/2345/bc-ir:106814

This work is posted on eScholarship@BC,
Boston College University Libraries.

Boston College Electronic Thesis or Dissertation, 2016

Copyright is held by the author. This work is licensed under a Creative Commons Attribution 4.0 International License. http://creativecommons.org/licenses/by/4.0/

A CHEMICAL-PROTEOMIC PLATFORM TO MONITOR CYSTEINE SENSITIVITY TO TRANSNITROSATION

Dissertation

by

YANI ZHOU

submitted to the Faculty of

Boston College

The Graduate School of Arts and Science

Department of Chemistry

in partial fulfillment of the requirements for the degree of

Doctor of Philosophy

May 2016

© Copyright by Yani Zhou
2016

A chemical-proteomic platform to monitor cysteine sensitivity to transnitrosation

Yani Zhou

Dissertation advisor: Dr. Eranthie Weerapana

Abstract

S-nitrosation has emerged as a ubiquitous endogenous protein posttranslational modification that significantly impacts cellular protein function through a variety of mechanisms. Despite the advent of chemical and proteomic methods to study *S*-nitrosation, the subset of cellular cysteine residues that show uniquely high reactivity to endogenous transnitrosation donors is poorly characterized. To further these existing global studies, a cysteine-reactivity profiling strategy was applied herein to rank ~600 cysteine residues by sensitivity to *S*-nitrosoglutathione. These proteomic studies revealed several previously uncharacterized sites of *S*-nitrosation, including Cys58 in HADH2. Further characterization revealed that HADH2 catalytic activity is allosterically regulated by *S*-nitrosation, and this modification occurs in cells at (patho)physiological levels of nitrosative stress. Functional role of Cys58 and its regulation by *S*-nitrosation facilitated the identification of RB-21-CA as a potential covalent Cys58 inhibitor. Global analysis of GSNO, *S*-nitroso-Coenzyme A and Thioredoxin-C73-SNO transnitrosation identified 756 cysteines with different sensitivity to each of three SNO donors. Systematic evaluation on transnitrosation selectivity revealed that specific interaction of transnitrosation donor with its protein target is a key component governing the selective transnitrosation of a specific cysteine residue. Together, these studies illustrated the potential of cysteine-reactivity profiling strategy for evaluating the substrate specificity of transnitrosation donors and enable the identification of previously uncharacterized, functionally relevant

sites of *S*-nitrosation.

Another cysteine oxoform, *S*-glutathionylation, is the disulfide formation of a protein cysteine residue with glutathione. Although glucose starvation is known to induce redox-disturbance, global and individual protein *S*-glutathionylation in response to glucose metabolism or mitochondrial activity remains largely unknown. By using a clickable glutathione approach, which forms clickable glutathione by the use of a mutant of glutathione synthetase, we found that protein *S*-glutathionylation is readily induced in response to glucose starvation when mitochondrial reactive oxygen species are elevated in cells, and glucose is the major determinant for inducing reversible glutathionylation. Application of a proteomic mass spectrometry platform identified over 1,300 *S*-glutathionylated. Confirmation of *S*-glutathionylation for selected proteins by in gel analysis further validated the mass spectrometry results, and highlights the dynamic change of *S*-glutathionylation on an individual protein level.

In order to expand on the understanding of the functional role of the cysteine residues in biological systems, we evaluated a panel of 1,3,5-triazine- and 4-aminopiperidine-based cysteine-reactive small-molecules on two proteins, apoptosis signal-regulating kinase 1 (ASK1) and peroxiredoxin 1 (Prdx1), between which a intermolecular disulfide forms and results in the activation of mitogen-activated protein kinase pathway. In-gel fluorescence revealed that RB-11-CA and SMC-1, both of which contain an n-octyl group as a diversity element, showed greatest selectivity and potency to ASK1 and Prdx1, respectively. Further mass spectrometry analysis identified cysteine 225 of ASK1 and cysteine 173 of Prdx1 are the sites of covalent probe modification.

Acknowledgements

I would like to give my first thank-you to my advisor, Professor Eranthie Weerapana. I am so glad and lucky that I had the opportunity to be one of your first graduate students. It was such an invaluable experience to set up a fresh new laboratory with you. And it would surely help me a lot in the rest of my life. I appreciate your inspiration whenever I felt frustrated by an unexpected experimental result, as well as your patience and willingness to answer the countless questions and problems I encountered. You are really amazing as a tutor, a teacher and a friend to be with. I genuinely enjoyed working for you!

I would like to thank my thesis committee, Professor Mary F. Roberts, Professor Jianmin Gao and Professor Abhishek Chatterjee, for reading and correcting my thesis. Thank you for your worm and kind support and advice in my research as well as the life in Boston College during my graduate study.

Thank you all the collaborators I worked with. A special thank goes to Dr. Brian Smith, Dr. Sarah Wynia Smith and Professor Michael Marletta on the protein functional characterization in my project. I would also like to thank our collaborators Professor Vadim N. Gladyshev, Professer Young-Hoon Ahn and their lab members.

I have to thank, from the bottom of my heart, a lot to the entire Weerapana lab, current and former lab members, Julie, Nick, Alex, Shalise, Lisa, Kyle, Tyler, Katie, Aaron, Jia, Ranjan, Helay, Dan and Masahiro. I would not successfully finish my graduate study without your continues and patient help. Every one of you was always ready to answer my questions without hesitation. I really learned much more than what I

expected, from experimental ideals, lab techniques, trouble shootings, to living in Boston, practicing and correcting my langrage, and sharing different kinds of food and opinions. It was my great pleasure to work together with all of you. It was also an unforgettable experience that amazingly colored my life. I would specially thank Julie, Nick and Alex. It was my great pleasure to be one of our "OG Four" team. Thank you for all of your support and help as lab members and as wonderful friends. I would also like to thank Helay and Jia as my special friends in and out of lab, as foreigner students to help each other with positivity and ambition. I need to thank Dan for all kinds of your help and encouragement. I really enjoyed every conversation with you.

Thank you all the Boston College Chemistry Department staff: Dale, Lynne P, Lynne O, Ian, Steve, Howard and Bill. You are a great team to work with. I really appreciated your constant help for these past years.

I need to thank all my friends, Yue, Qingyi, Qiongying, Jin, Zhiyong, Hao, Tianyi, Fang, *et al*.. I will miss every time hanging out with you and all the parties we had.

Last but not least, I have thank a lot to my uncle's family, from the very first day here in Boston. I will not survive without all the support you have given to me. I also need to thank all of my other family members, specially all my cousins. You are my closest sisters, brothers and friends. Thank you for all your endless support. I would like to give my greatest acknowledgement to my family: my father, my mother, my sister and my brother. I remember everything you have done for me with deepest love. It is my greatest pleasure to be one of you as a family, every day of my life. I am so glad you are here together with me, to share the very important moment in my life. I will always love you, just like your everlasting love to me. Thank you from the very bottom of my heart!

Table of Contents

Acknowledgements i

Table of Contents iii

List of Figures vii

List of Tables xiii

List of Abbreviations xv

Chapter 1. Introduction 1

Chemical properties of cysteine 2

Biological functions of cysteine 3

Cysteine *S*-nitrosation 5

1. Nitric oxide and cysteine *S*-nitrosothiol formation 5

2. Biological function of cysteine *S*-nitrosation 8

3. Strategies to detect cysteine *S*-nitrosation 10

3. 1. Detection of NO-related products 11

3. 2. Biotin-switch technique and its improvements 12

3. 3. Direct detection of SNO by phosphine 17

3. 4. Direct detection by organomercury-based method 20

3. 5. Quantitative mass-spectrometry methods 21

Conclusion 25

References 27

Chapter 2. A chemical-proteomic platform to monitor cysteine sensitivity to transnitrosation by *S*-nitrosoglutathione 37

Introduction 38

Results 41

Visualization of protein sensitivity to transitrosation by in-gel fluorescence 41

A competitive cysteine-labeling strategy to quantitatively measure cysteine sensitivity to GSNO 43

Quantitatively measuring cysteine sensitivity to GSNO 46

Functional characterization of Cys58 in HADH2.....57

Conclusion.....67

Acknowledgement.....69

Experimental Procedures.....69

References 83

Chapter 3. Global proteomic analysis of cysteine sensitivity to transnitrosation 92

Introduction 93

Results 99

A competitive cysteine-labeling strategy to quantitatively measure sensitivity to transnitrosating agents 99

Quantitatively measuring cysteine sensitivity to different transnitrosation donors 100

Identifying factors that dictate cysteine sensitivity to transnitrosation 104

Global analysis of binding interaction effects on cysteine sensitivity to transnitrosation.....110

Conclusion.....119

Acknowledgement.....122

Experimental procedures.....122

References 127

Chapter 4. Proteomic mass spectrometry analysis of protein glutathionylation in response to glucose metabolism 132

Introduction 133

Results 135

Clickable glutathione is catalyzed by enzymes implicated in glutathionylation 135

Identification of glutathionylated proteins in response to glucose starvation with mROS production. 138

Confirming the identity and reversibility of individual protein glutathionylation events 142

Conclusion 143

Acknowledgement 144

Experimental Procedures 145

References 146

Chapter 5. Identification of covalent chemical probes to investigate cysteine-mediated protein activities 149

Introduction 150

Results 156

Identification of a cysteine-reactive chemical probe for ASK1-28, Prdx1, and HADH2 156

LC-MS/MS analysis to identify the cysteine targets on ASK1-28 and Prdx1 160

Conclusion 161

Acknowledgement 162

Experimental Procedures.....162

References 168

Appendix I. Mass spectrometry tables 173

List of Figures

Chapter 1.

Figure 1-1. Structures of thiol (protonated, left) and thiolate (deprotonated, right) forms of cysteine residues within proteins with an "unperturbed" pK_a of ~8.5.

Figure 1-2. Common posttranslational modifications of cysteines.

Figure 1-3. Cysteine *S*-nitrosation. (A) *S*-Nitrosation is the transfer of a nitroso-group onto cysteine residues. (B) Formation of *S*-nitrosation can occur through three key pathways: reaction with N_2O_3, reaction with thiyl radicals, or transition metal catalyzed addition of NO to thiols. .

Figure 1-4. The biotin-switch technique (BST) involves capping of reduced thiols with MMTS, followed by selective reduction of *S*-nitrosated cysteines with ascorbate. The resulting newly-formed thiols are then capped with biotin-HPDP for enrichment of *S*-nitrosated proteins.

Figure 1-5. Chemical probes for *S*-nitrosation rely on the use of phosphine esters to form: (1) thio-aza-ylides; (2) sulfenamides; (3) traceless disulfides; (4) traceless sulfonamides; (5) bis-ligation products and (6) adducts with water-soluble TXPTS.

Chapter 2.

Figure 2-1. In-gel fluorescence to visualize protein sensitivity to transnitrosation. (A) Experimental workflow. (B) Structure of GSNO. (C) Structure of the iodoacetamide alkyne probe. (D) Fluorescent gel of A.

Figure 2-2. A competitive cysteine-profiling strategy to quantify sensitivity to transnitrosation. (A) Structure of the Azo-L/Azo-H tags. (B) and (C), Schematic showing the application of the Azo-L and Azo-H tags for quantitative proteomics in control and GSNO treated experiments. .

Figure 2-3. Identifying cysteines sensitive to modification by GSNO. (A) Heavy:Light ratios (R) are shown for 609 cysteine residues identified in GSNO-treated (in red; light: 500 μM GSNO; heavy: buffer;) and control (in black; light: buffer; heavy: buffer) MS analysis. (B) Average R-values are shown for 609 cysteine residues. (C) Distribution of R-values for the control and GSNO-treated samples.

Figure 2-4. Gene ontology (GO) analysis (From data in Appendix I, Table 2A-1). Biological process (A) and molecular function (B) are shown for all proteins (left) and proteins containing the 27 cysteines with greatest GSNO sensitivity (right) (R >3) from the cysteine-reactivity profiling analyses.

Figure 2-5. Measurement of transnitrosation sensitivity at the level of individual cysteine residues within the same protein. (A) Cysteine 54, 109, 158 and 194 of PCBP1. (B) Cysteine 24, 178 and 223 of CLIC1.

Figure 2-6. (A) Manual interrogation of the MS2 fragmentation data assigned Cys152 of GAPDH as the modified residue. (B) IA probe was completely consumed before click chemistry in our analysis platform.

Figure 2-7. Systematic analysis of cysteine-reactivity upon GSNO treatment. (A) Concentration-dependent analysis with 0, 50, 100, 200, or 500 μM GSNO treatment. (B) R values are plotted with increasing GSNO concentration for six cysteine residues (from CLIC4, GSTO1, DCXR, HADH2, CTSD, and GAPDH) with varying sensitivity to GSNO transnitrosation. (C) Corroboration of the MS-based identification of cysteine sensitivity and insensitivity using a gel-based assay for GSTO1 or CTSD. (D) Time-dependent analysis with increasing 500 μM GSNO incubation time for three cysteine residues (from GAPDH Cys152, TUBA4A Cys376 and Trx Cys73) representative of cysteines that are characterized by a variety of kinetic patterns of GSNO transnitrosation and lifetime of the *S*-nitrosated species.

Figure 2-8. HADH2 is selectively *S*-nitrosated at Cys58. (A) Pathway of β–oxidation of fatty acids. (B) Structure of HADH2 (PDB: 2O23) with NAD+ bound in the active site. (C) HADH2 is not glutathionylated when treated with 100 μM GSSG, 100 μM GSH, or 6-100 μM GSNO. (D) Purified HADH2 WT and C58S mutant. (E) *S*-nitrosation of recombinantly expressed and purified HADH2 WT treated with varying concentrations of GSNO or DEA NONOate. (F) *S*-nitrosation of recombinantly expressed and purified HADH2 WT and C58A treated with varying concentrations of GSNO or Cys-SNO. (G) *S*-nitrosation of recombinantly expressed and purified HADH2 WT pretreated with GSNO and then treated with increasing concentration of *S*-methylglutathione. (H) *S*-nitrosation of recombinantly expressed and purified HADH2 WT and C58S treated with 100 μM GSNO. (I) HADH2 *S*-nitrosation in lysates from HEK293T cells overexpressing mock (empty vector), HADH2 WT, or HADH2 C58S treated with 100 μM GSNO. (J) Immunofluorescence staining of the mitochondrial localization of endogenous HADH2 and overexpressed Myc/His tagged HADH2. (K) HADH2 *S*-nitrosation in HEK293T cells overexpressing mock (empty vector), HADH2 WT, or HADH2 C58S were treated with DMSO (control), L-NAME (pan-NOS inhibitor), or 1400W (iNOS-selective inhibitor). (L) HADH2 *S*-nitrosation in A549 cells overexpressing HADH2 WT or HADH2 C58A were treated with cytokines (IFNγ, TNF-α, IL-1β) and/or L-NAME.

.

Figure 2-9. Functional characterization of Cys58 of HADH2. (A) HADH2-catalyzed reduction of acetoacetyl-CoA by NADH monitored *in vitro* by a decrease in absorbance at 340 nm. (B) Catalytic efficiency (k_{cat}/K_M) for WT and C58A-mutant HADH2 with varying acetoacetyl-CoA concentrations in the presence of 100 μM GSNO or GSH. (C) Effect of GSNO on WT HADH2 activity. (D) Catalytic efficiency (k_{cat}/K_M) for WT and C58S mutant HADH2 with varying acetoacetyl-CoA concentrations. (E) Effect of cysteine oxidants on HADH2 activity.

Chapter 3.

Figure 3-1. Protein *S*-nitrosation, transnitrosation and denitrosation systems.

Figure 3-2. Structure of transnitrosation donors: (A) *S*-nitrosoglutathione (GSNO), (B) Thioredoxin-C73-SNO (Trx-SNO), and (C) *S*-nitroso-Coenzyme A (CoA-SNO). (D) Transnitrosation reaction proceeding through a nitroxyl disulfide intermediate.

Figure 3-3. A competitive cysteine-profiling strategy to quantify sensitivity to transnitrosation.

Figure 3-4. Identifying cysteines sensitive to transnitrosation by GSNO, CoA-SNO and Trx-SNO. Quantitative MS analysis of GSNO (A), CoA-SNO (B), and Trx-SNO (C) -treated cell lysates. (D) Distribution of R-values for the GSNO, CoA-SNO and Trx-SNOtreated samples.

Figure 3-5. Biological process (A) and molecular function (B) are shown for all proteins and proteins containing the 50 cysteines with most or least transnitrosation sensitivity from the cysteine-reactivity profiling analyses.

Figure 3-6. Sequence conservation flanking sites of cysteine transnitrosation.

Figure 3-7. Surface-exposure (A) and pK_a (B) analysis of cysteines that were identified as sensitive and insensitive to transnitrosation**.**

Figure 3-8. Correlation of cysteine reactivity with transnitrosation sensitivity.

Figure 3-9. Venn diagram of the proteins carrying 50 most sensitive transnitrosation cysteines to GSNO, CoA-SNO and Trx-SNO.

Figure 3-10. Heatmap of relative sensitivity across all 756 cysteines (left) or the 50 most sensitive cysteines (right) ranked by GSNO transnitrosation**.**

Figure 3-11. MeGSH pre-treatment desensitizes GSNO transnitrosation on cysteine 58 of HADH2. (A). Structures of GSNO (left) and MeGSH (right). (B) Structure of HADH2 (PDB: 2O23) with NAD^+ bound in the active site. (C) R ratios of cysteine 58 of HADH2 in both control and MeGSH-treated sample are plotted. (D) *S*-nitrosation of recombinantly expressed and purified HADH2 WT pretreated with GSNO and then treated with increasing concentration of MeGSH.

Figure 3-12. ATP pre-treatment desensitizes CoA-SNO transnitrosation on cysteine 360 and 641 of PFKP. (A). Structures of CoA-SNO (top) and ATP (bottom). (B) R ratios of cysteine 360 and 641 of PFKP in both control and MeGSH-treated sample are plotted. (C) Structure of PFKP binding with ATP (PDB: 4xyj).

Chapter 4.

Figure 4-1. A workflow using a clickable azido-glutathione approach for detecting protein glutathionylation.

Figure 4-2. Glucose starvation readily induces global glutathionylation in the presence of an electron transport chain blocker in time- (A) and dose- (B) dependent manners, but no treated with glucose starvation alone (C), and antimycin A alone (D).

Figure 4-3. Glutathionylation is reversed by re-addition of glucose.

Figure 4-4. Proteomic analysis of glutathionylated proteins. (A) Approach for pull-down and mass analysis. (B) Analysis of enriched proteins in indicated conditions.

Figure 4-5. Systematic analysis of identified glutahionylated protein**.** (A) The number of glutathionylated proteins in indicated conditions by LC-MS/MS. (B-D) Gene ontology analysis of identified glutathionylated proteome.

Figure 4-6. Proteomic data analysis of glutathionylated proteins. (A) Identified proteins in glucose starvation with or without antimycin A. (B) The range of spectral count for all proteins identified in LC- MS/MS.

Figure 4-7. Determination of glutathionylated proteins by pull-down and Western blotting.

Chapter 5.

Figure 5-1. 1,3,5-triazines and 4-aminopiperidine scaffolds were utilized to generate cysteine-reactive small-molecule libraries. Each scaffold was

functionalized with a cysteine-reactive electrophile (R_1), an alkyne handle (R_2) and a diversity element (R_3). Structures of R_1, R_2 and R_3 groups for a number of the compounds evaluated in this study are shown.

Figure 5-2. In-gel fluorescence and MS proteomic analysis for target identification of Prdx1 and ASK1-28.

Figure 5-3. In-gel fluorescence analysis of small molecule labeling of ASK1-28 and Prdx1. (A) Prdx1 and ASK1 treated by small molecules were resolved by fluorescent gel using IA probe as labeling control. (B) Band intensity relative to IA probe treatment was calculated. (C) Structure of RB-11-CA and SMC-1 that demonstrated greatest labeling for ASK1-28 and Prdx1, respectively.

Figure 5-4. Modification of HADH2 cysteine 58 by RB-21-CA and IA probe. (A) RB- 21-CA labeled HADH WT in a concentration-dependent manner. This labeling diminished for the C58S mutant. (B) Kinetic study of RB-21-CA on HADH2 WT with IC50 of 20.47 μM. (C) Structure of RB-21-CA and IA probe. (D) IA probe labeling events were increased in HADH2 C58A mutant than that of C58S mutant in a concentration- dependent manner.

List of Tables

Chapter 3.

Table 3-1. The 20 most CoA-SNO sensitive cysteine containing proteins that were also detected in a 1 mM ATP pre-treatment mass spectrometry experiment with their annotated cofactors, substrates or binding partners.

Chapter 5.

Table 5-1. LC-MS/MS identification of small molecule cysteine targets.

Appendix.

Table 2A-1. R-values from transnitrosation experiment at 500 μM GSNO.

Table 2A-2. Evaluation of the data obtained by the current cysteine-profiling platform within the context of previously identified sites of *S*-nitrosation.

Table 2A-3. R-values from transnitrosation experiment at 0, 50, 100, 200 and 500 μM GSNO.

Table 2A-4. R-values from time-dependent transnitrosation experiment at 500 μM GSNO (0, 5, 10, 20, 30 and 60 mins treatment).

Table 2A-5. Primers used for sub-cloning and mutagenesis of GSTO1, HADH2 and CTSD.

Table 3A-1. R-values from transnitrosation experiment at 500 μM GSNO.

Table 3A-2. R-values from transnitrosation experiment at 500 μM CoA-SNO.

Table 3A-3. R-values from transnitrosation experiment at 90 μM Trx-SNO.

Table 3A-4. R-values of cysteines (* denotes labeled cysteine) identified from transnitrosation experiments at 500 μM GSNO, 500 μM CoA-SNO, and 90 μM Trx- SNO.

Table 3A-5. PDB codes, solvent-accessible surface area (SASA) and pK_a values for 19 of the most-sensitive and insensitive cysteines to GSNO, CoA-SNO and Trx-SNO transnitrosation respectively.

Table 3A-6. Comparison of cysteine transnitrosatio sensitivity to cysteine reactivity.

Table 3A-7. R-values from 1 mM MeGSH competitive transnitrosation experiment at 500 μM GSNO.

Table 3A-8. R-values from 1 mM ATP competitive transnitrosation experiment at 500 μM CoA-SNO.

Table 4A-1. A list of glutathionylated proteins identified in mass analysis that have a high spectral count and a high enrichment in positive over negative samples.

.

List of Abbreviations

Standard 3-letter and 1-letter codes are used for the 20 natural amino acids

1400W	N-[[3-(aminomethyl)phenyl]methyl]-ethanimidamide, dihydrochloride
Acr	acrylamide
AKT1	protein kinase B
AMPK	AMP-activated kinase
ASK1	apoptosis signal-regulating kinase 1
Azo-H	azobenzene heavy mass spectrometry tag
Azo-L	azobenzene light mass spectrometry tag
BCA	bicinchoninic acid
biotin-HPDP	N-[6-(biotinamido)hexyl]-3'-(2'-pyridyldithio)propionamide
BSA	bovine serium albumin
BST	biotin-switch technique
CA	chloroacetamide
Casp	caspase (Cysteine-dependent aspartate directed proteases)
cGMP	cyclic GMP
CLIC1	chloride intracellular channel protein 1
CLIC4	chloride intracellular channel protein 4
CNB	chloronitrobenzyl
CoA	Coenzyme A
CTSD	cathepsin D
CuAAC	copper (I)-catalyzed azide alkyne cycloaddition

Cys-SNO	*S*-nitrosocysteine
CysNO	*S*-nitrosocysteine
DCXR	L-xylulose reductase
DEA	diethylamine
DMEM	Dulbecco's Modified Eagle Medium
DMSO	dimethylsulfoxide
DNA-PK	DNA-activated protein kinase
DTT	dithiothreitol
EDTA	ethylenediaminetetraacetic acid
eNOS	endothelial NOS
ER	endoplasmic reticulum
GAPDH	glyceraldehyde-3-phosphate dehydrogenase
GCL	γ-glutamylcysteine ligase
GO	gene ontology
GRX	glutaredoxin
Griess	buffer (0.6% w/v sulfanilamide, 30% v/v acetic acid, 0.05% w/v N-1-naphthyl-ethylenediamine-HCl)
GSNOR	GSNO reductase
GS	glutathione synthetase
GSH	glutathione (reduced)
GSNO	*S*-nitrosoglutathione
GSSG	glutathione (oxidezed)
GSTO1	glutathione *S*-transferase omega 1

GSTP	glutathione-*S*-transferase pi
HADH2	3-Hydroxyacyl-CoA dehydrogenase type-2
HDAK2	histone deacetylase 2
HEN	buffer (125 mM HEPES pH 7.7, 1 mM EDTA, 0.1 mM neocuproine)
HEPES	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
HPLC	high-performance liquid chromatography
HRP	horseradish peroxidase
Hsp90	heat shock protein 90
IA-alkyne/IA	iodoacetamide alkyne probe (N-(hex-5-yn-1-yl)-2-iodoacetamide)
IAM	iodoacetamide
ICAT	isotope-coded affinity tags
IKK	IκB kinase
iNOS	inducible NOS
IPTG	isopropyl β-D-1-thiogalactopyranoside
isoTOP-ABPP	isotopic tandem orthogonal proteolysis-activity-base protein profiling
iTRAQ	isobaric tags for relative and absolute quantification
JNK	c-Jun N-terminal kinase
L-NAME	L-N-nitroarginine methyl ester
LC	liquid chromatography
LDE	lipid-derived electrophile
MAP2K	MAPK kinase
MAP3K	MAPK kinase kinase
MAPK	Mitogen-activated protein kinase

MAPK	Mitogen-activated protein kinase
MeGSH	*S*-methylglutathione
MMTS	methyl methanethiosulfonate
mROS	mitochondrial reactive oxygen species
MS	mass spectrometry
MudPIT	Multi-dimensional Protein Identification Technology
^{N3}GSH	azido-glutathione
NAD+	nicotinamide adenine dinucleotide, oxidized
NADH	nicotinamide adenine dinucleotide, reduced
NADP+	nicotinamide-adenine dinucleotide phosphate, oxidized
NADPH	nicotinamide-adenine dinucleotide phosphate, reduced
NEM	N-ethylmaleimide
NLS	nuclear localization signal
nNOS	neuronal NOS
NO	nitric oxide
NOS	NO synthases
PAGE	polyacrylamide gel electrophoresis
PBS	phosphate-buffered saline (137 mM NaCl, 2.7 mM KCl, pH 7.4)
PCBP1	poly(rC)-binding protein 1
PDI	protein disulfide isomerase protein family
Pen/Strep	penicillin/streptomycin
PFKP	6-phosphofructokinase, platelet type
PP2cα	Protein phosphatase 2cα

Prdx	peroxiredoxin
Psmd2	26S proteasome non-ATPase regulatory subunit 2
PTM	posttranslational modification
PTP1B	protein tyrosine phosphatase 1B
R	heavy:light ratio
RBC	red blood cell
Rh	rhodamine
RNS	reactive nitrogen species
ROS	reactive oxygen species
RPMI	Roswell Park Memorial Institute media
S100-A9	protein S100-A9
S100A8	protein S100-A8
SASA	solvent-accessible surface area
SCX	strong cation exchange resin
SDS	sodium dodecyl sulfate
sGC	soluble guanylate cyclase
SHP2	Src-homology phosphatase 2
SILAC	Stable isotope labeling by amino acid in cell culture
SIRT1	sirtuin 1
TBTA	tris[(1-benzyl-1H-1,2,3-triazol-4-yl)methyl]amine
TCA	trichloroacetic acid precipitation
TCEP	tris(2-carboxyethyl)phosphine hydrochloride
TMT	tandem mass tags

TOF	time-of-flight mass analyzer
Tris	tris(hydroxymethyl)aminomethane
Trx	thioredoxin
TrxR	thioredoxin Reductase
WT	wild-type

Chapter 1

Introduction

A significant portion of the work described in this chapter has been published in:

Couvertier S. M., Zhou Y., and Weerapana E., Chemical-proteomic strategies to investigate cysteine posttranslational modifications. *Biochim. Biophys. Acta*., **2014**, 1844, 2315-2330.

Among the twenty common amino acids, cysteine (Cys) is one of two sulfur-containing amino acids. Cysteine is encoded by 3.28% of all codons, yet with typically only 2.2% or less in the proteomic level, which makes it one of the least abundant amino acids incorporated into proteins.[1] The thiol group (R-SH) of cysteine is subject to oxidation to multiple higher oxidation state. It is also reversibly deprotonated generate a thiolate group ($R\text{-}S^-$) with higher nucleophilicity compared with the protonated thiol form.[2] These properties render cysteine diverse roles on its biological function.

Chemical properties of cysteine

Though highly conserved within proteins (typically above 90%), the chemical and physical properties of cysteine allow it to function in diverse biological roles, attributing to its concentration in functional loci within proteins.

Compared to the oxygen on serine, sulfur has a larger atomic radius and is less electronegative. As a result, the free thiol group on cysteine, without involvement of the structural microenvironment, is more acidic and nucleophilic than the hydroxyl group on serine.[1] An "unperturbed" cysteine has a typical pK_a of ~8.5.[3, 4] (Figure 1-1) This value, however, is easily altered by the protein local environment and by other factors. For example, through stabilizing the negatively charged thiolate, a hydrogen bond donor could lower the pK_a, while an electronegative environment destabilizing the thiolate, can lead to an increased pK_a.[5, 6] On the other hand, although both have donor electron pairs, the thiolate form is more nucleophilic than the thiol, which shares this electron pair with hydrogen in a sigma bond. As a result, the nucleophilicity of a cysteine is largely

dependent on the protein local environment that affects its pK_a, and thus the availability and stability of the thiolate forms.

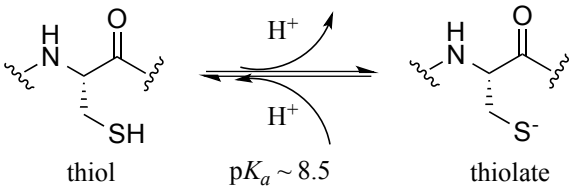


Figure 1-1. Structures of thiol (protonated, left) and thiolate (deprotonated, right) forms of cysteine residues within proteins with an "unperturbed" pK_a of ~8.5.

When it comes into contact with a suitable electron acceptor (oxidant), the sulfur can donate electrons and become oxidized to a range of oxidation states. These oxidized forms of cysteine include intra- or inter-molecular disulfide bonds (RSSR) with protein thiols or low-molecular-weight thiols. The disulfide bond is not "locked", and is capable of undergoing disulfide-exchange with other thiols. This migration of dithiols and disulfides occurs within cellular redox systems, e.g. Thioredoxin/ Thioredoxin Reductase (Trx/TrxR) pairs. Additionally, a strong oxidant can sequentially oxidize a thiol to sulfenic, sulfinic or sulfonic acids.[7] Overall, the cysteine nucleophilicity and redox activity are often correlated with low pK_a of thiolate anion and its microenvironment.

Biological functions of cysteine

The tunable reactivity of cysteine enables it to serve a wide range of roles in protein functions. Cysteines could be in the catalytic sites of enzymes such as oxidoreductases, transferases, hydrolases, isomerases and ligases, and act as essential catalytic residues in both redox and nucleophilic catalysis.[1] In addition, a number of proteins utilize cysteines to coordinate metal ion complexes, such as iron, zinc and

copper. These cysteine complexes with metal ions directly participate in catalysis, regulate protein structure, form binding motifs for nucleic acid, and maintain metal ion homeostasis.[8] Cysteines involved in structural disulfide bonds play essential roles maintaining structural integrity and protein folding.[9] Moreover, the unique chemical property of cysteine thiol enables its roles in regulating protein functions, as most of these regulatory roles are facilitated by cysteine posttranslational modifications (PTMs). In particular, cysteine undergoes a variety of enzymatic and non-enzymatic PTMs to form reversible or irreversible covalent products. Besides oxidation by reactive oxygen species (ROS) and disulfide exchange as mentioned above, cysteine reacts with reactive

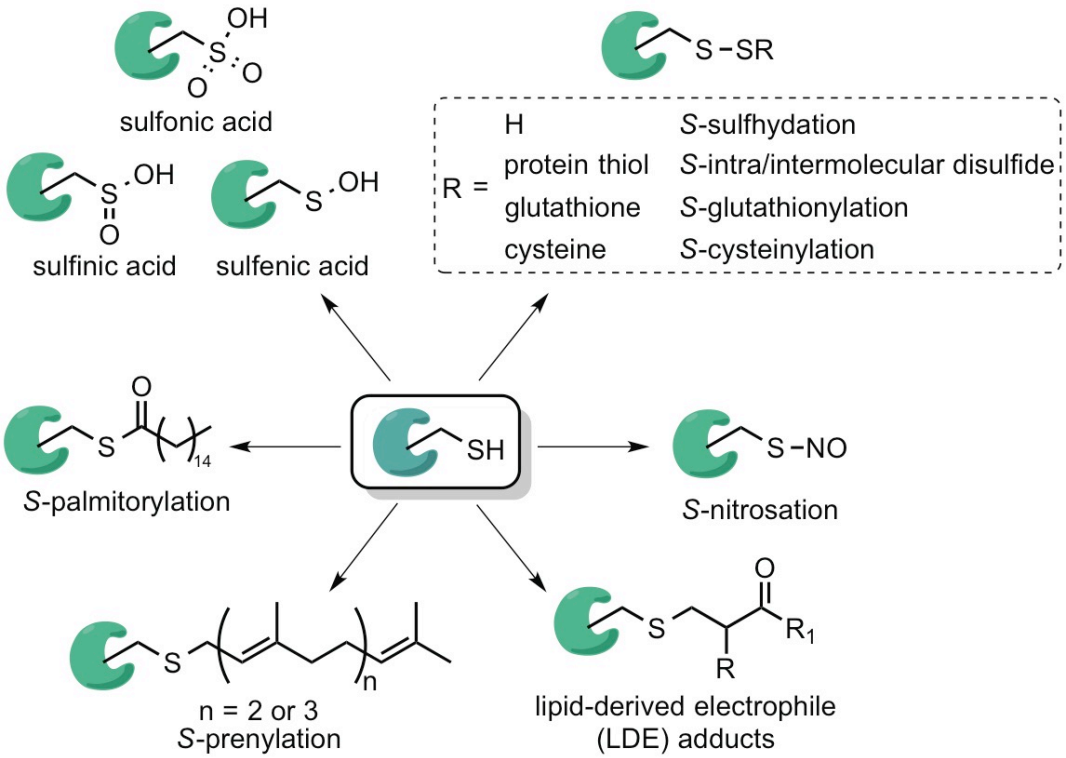


Figure 1-2. Common posttranslational modifications of cysteines.

nitrogen species (RNS), hydrogen sulfide, glutathione (GSH) and lipid-derived electrophiles (LDEs) to produce nitrosothiol,[10] cysteine persulfide,[11] glutathionylated

cysteine[12] and Michael adducts[13] respectively. Cysteine PTMs also include methylation, phosphorylation[14], prenylation[15] and palmitoylation[16], the enzymatic addition of lipid or isoprenoid moiety from an active donor to a cysteine thiol. (Figure 1-2) These diverse cysteine PTMs occur on specific protein targets, and regulate diverse cellular functions like protein activity and localization, and dysregulation of these PTMs are critical in driving a variety of proliferative and degenerative diseases.[17-19]

Cysteine *S*-nitrosation

Cysteine *S*-nitrosation is the conversion of a cysteine thiol to a *S*-nitrosothiol (SNO) by the covalent addition or transfer of a NO moiety to the reactive thiol group on a cysteine residue. (Figure 1-3, A) Currently, over 3000 peptides and proteins have been identified and studied as potential SNO targets.[20, 21] Increasing studies on protein SNO indicate that, besides acting as an endogenous source of NO storage and transport, this dynamic PTM is also involved in protein redox regulation, mediating protein function and activity.

1. Nitric oxide and cysteine *S*-nitrosothiol formation

Recognized as an omnipresent inter- and intra-cellular signaling molecule, nitric oxide (NO) provides the primary source of cysteine *S*-nitrosation. Cellular NO is generated by three types of NO synthases (NOS): endothelial NOS (eNOS), neuronal NOS (nNOS) and inducible NOS (iNOS). NOS oxidize L-arginine to afford NO and L-citrulline.[22] Named from their cell types where they were initially found, eNOS and nNOS synthesize NO in nanomolar concentrations for a short span of time, and in a Ca^{2+} dependent manner. iNOS was first described in mouse macrophages. It is only expressed

in the presence of acute injury and inflammation and is Ca^{2+} independent. During microbial infections, inflammation and some states of physiological stimulation, iNOS is expressed in various cells, leading to a sustained production of micromolar concentrations NO lasting for hours or days. This excessive production of NO plays an important role in antimicrobial defense.

The canonical NO signaling pathway involves NO binding to the heme of soluble guanylate cyclase (sGC) to activate it, which leads to the production of secondary messenger cyclic GMP (cGMP) that participates in downstream signal transduction.[10] The inductive and inhibitive roles of NO in signal transduction have been shown in the regulation of the circulatory and cardiovascular systems, and control of the nervous, respiratory and immune systems.

In parallel, NO serves as a reactive nitrogen species to selectively modify cysteine residues. Besides the radical form of NO, RNS includes nitroxyl radicals (NO^-) and nitrosonium cation (NO^+), formed by NO gaining or losing electrons, and the products of the reaction between NO and ROS, such as peroxynitrite ($ONOO^-$) and the NO_x compounds (e.g. NO_2, N_2O_3, and N_2O_4).[23] SNO synthesis in cells can result from three distinct pathways (Figure 1-3): (1) reaction of cysteine thiols with N_2O_3 resulting from autooxidation of NO; (2) recombination of NO with thiyl radicals; and, (3) transition metal-catalyzed addition of NO to a thiol. In particular, to generate nitrosothiols, NO is first oxidized to nitrogen dioxide radical directly by O_2 or via $ONOO^-$ pathway. The nitrogen dioxide radical recombines another NO radical to form dinitrogen trioxide (N_2O_3), which then reacts with thiolate RS^- to produce nitrosothiol. On the other hand,

thiolate RS^- can transfer an electron to NO_2 radical to generate nitrite and thiyl radical $RS\cdot$, resulting in radical recombination with NO radical and nitrosothiol formation.[23]

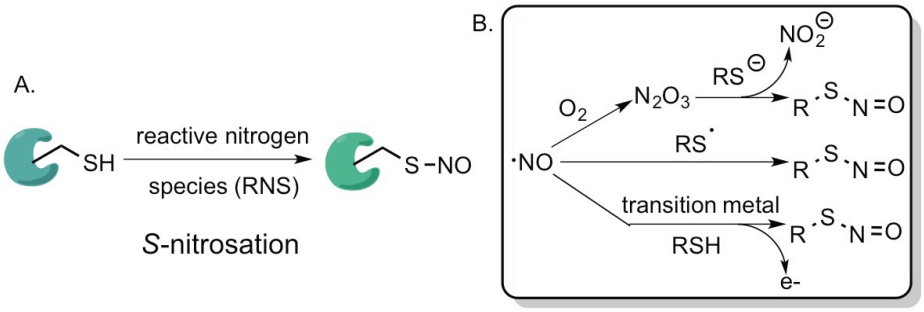


Figure 1-3. Cysteine *S*-nitrosation. (A) *S*-Nitrosation is the transfer of a nitroso-group onto cysteine residues. (B) Formation of *S*-nitrosation can occur through three key pathways: reaction with N_2O_3, reaction with thiyl radicals, or transition metal catalyzed addition of NO to thiols.

SNO formation can also occur by transnitrosation via transfer of a NO group from low-molecular weight SNOs (e.g. *S*-nitrosocysteine (Cys-SNO), *S*-nitrosoglutathione (GSNO)) or other proteins. Such NO exchange reactions demonstrate the cellular dynamic equilibrium of nitrosothiols. The factors driving the transfer of NO in one direction is largely dependent on the direct interaction and appropriate redox potentials between the nitrosothiol and attacking thiol. Specifically, a protein containing a nitrosothiol possesses a higher redox potential compared to a protein with free thiol, and can be reduced by gaining an electron via transferring NO group to an adjacent free thiol.[24, 25]

The reactive and unstable nature of the S-N bond renders *S*-nitrosothiols susceptible to undergo photolytic decomposition via hemolytic cleavage, highlighting the reversible nature of *S*-nitrosation. Transnitrosation, featured by NO exchange between

two cysteine residues, is a proof of this biological reversibility. Reducing species in biological environment such as GSH and reduced metals would facilitate SNO cleavage.[26] At concentration ~10^{-6} M, Cu (I) ions can catalyze homolytic decomposition of RSNO to NO. Heterolytic cleavage of RSNO is facilitated by metal ions like Hg^{+2} to generate the free thiol and nitrous acid. High cellular concentration of GSH (millimolar level) maintains an intracellular reducing environment and results in RSNO decomposition by transnitrosation to generate GSNO, which can be subsequently reduced by GSNO reductase (GSNOR) and carbonyl reductase 1 (CBR1).[25]

The abundance of cysteine residues on proteins is comparatively low (~2% of all amino acids in the proteomes). A study to measure the *S*-nitrosation occupancy level in an ischemic reperfusion injury model identified that, under physiological conditions, 1-10% of the proteome are occupied by *S*-nitrosothiol at a specific cysteine site.[27] Thus, only selected free thiol cysteine residues are *S*-nitrosated, indicating the low level of SNO and its specific selectivity. Protein stability, denitrosation, compartmentalization of SNO proteins and limitations of detection methods could contribute to the underestimation of *S*-nitrosation occupancy.[10] To date, studies reveal that several determinants might contribute to the endogenous selectivity of SNO formation, yet no sequence motif or pK_a trend has been observed across these identified sites of *S*-nitrosation.[28-30]

2. Biological function of cysteine *S*-nitrosation

Cysteine *S*-nitrosation is often considered as functional PTM analogous to phosphorylation. The role of protein SNO in regulation of protein function and in cell signaling pathway are demonstrated by directly inhibiting catalytic cysteines, by affecting protein-protein interactions or by controlling regulatory cysteines.

In order to directly modulate enzyme function, active-site cysteine residues are often utilized as SNO targets. For example, Caspase-3, which is a cysteine protease and important in apoptotic cell death, is generated as the inactive zymogen, procaspase-3. Upon stimulation, Caspase-3 is cleaved to initiate the cell apoptosis pathway. Procaspase-3 is shown to be constitutively *S*-nitrosated at its active site Cys163, which results in functional inhibition. Stamler *et al*. identified that Trx1 can effectively denitrosate cytosolic SNO-Caspase-3 and control the cellular steady-state amount of Caspase-3. Moreover, upon cell death stimulation, mitochondrial specific Trx2 facilitates denitrosation of SNO-Caspase-3 to promote cell death.[31] The mechanism of denitrosation of SNO-Caspase-3 by Trx might be via an intermolecular disulfide formation between Trx-Cys32 and Caspase-3-Cys163 followed by attack of neighboring Trx-Cys35 to generate an intramolecular disulfide bond on Trx and free Caspase-3-Cys163. Another possibility is the direct transnitrosation of Trx-Cys32 by SNO-Caspase-3. Interestingly, Trx with a *S*-nitrosated Cys73, a non-active site cysteine, was reported to specifically transnitrosate Cys163 on Caspase-3, resulting in inactivation of that enzyme.[25, 32]

Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) presents another example of active-site cysteine *S*-nitrosation. Besides its important role in glycolysis, GAPDH is associated with the nuclear apoptotic signaling pathway. The inherited lacking of a nuclear localization signal (NLS) as well as its bulky 150 kDa homo-tetramer needed for reactivity in nucleus block its translocation from cytosol to nucleus where it mediates cell apoptosis. Hara *et al*. found a cell death cascade initiated by iNOS induced *S*-nitrosation of a catalytic Cys150 on GAPDH. SNO modification of GAPDH increased its binding to Siah1, which is an E3 ubiquitin ligase and contains an NLS signal. Once bound, Siah1

facilitated GAPDH translocation to nucleus, where GAPDH in turn stabilized Siah1. Collected nuclear Siah1 triggered protein degradation and cell death. Thus, GAPDH reacted as a sensor of RNS to regulate cell death upon cellular stress.[33] Furthermore, Kornberg *et al*. showed that *S*-nitrosated GAPDH could transnitrosate nuclear proteins including histone deacetylase 2 (HDAC2), DNA-activated protein kinase (DNA-PK) and deacetylating enzyme sirtuin 1 (SIRT1). The inhibition of SIRT1 by transnitrosation from SNO-GAPDH resulted in decreased transcriptional activity of peroxisome proliferator-activated receptor-gamma coactivator PGC1α, suggesting a role of SNO-GAPDH on regulating PGC1α in metabolic pathway.[34]

The c-Jun N-terminal kinase (JNK) belongs to mitogen-activated protein kinases (MAPKs), a family of serine/threonine kinase. Park *et al*. demonstrated that via induction of iNOS by IFN *in vivo* or via treatment with NO donor *in vitro*, JNK-mediated phosphorylation of c-Jun was inhibited. Site-specific studies showed that JNK inhibition was regulated by a thiol-redox mechanism where a regulatory thiol Cys116 on JNK was *S*-nitrosated, consequently suppressing the JNK-dependent trans-activating function of c-Jun. This cysteine SNO mediated protein interaction serves as evidence of the ability of *S*-nitrosation to regulate gene transcription.[35, 36]

3. Strategies to detect cysteine *S*-nitrosation

Despite the significant progress in studying the structural consequences and related biological importance of *S*-nitrosation, the low abundance and labile property of endogenous cysteine *S*-nitrosation adducts have challenged the direct detection and enrichment of these modified species.[23] From a methodology standpoint, methods for SNO detection need to address the following: (1) high accuracy and selectivity for

cysteine *S*-nitrosation sites; (2) chemical tagging and enrichment approaches; (3) quantitative analysis at the proteomic level; and (4) in-depth *S*-nitrosation sensitivity profiling.[37] The following content is a brief overview of the chemical strategies to investigate cysteine *S*-nitrosation in a biological context, emphasizing proteomic methods that can identify *S*-nitrosation sites within the context of a complex proteome.

3. 1. Detection of NO-related products

The inherent instability of protein SNO lies on the weak bond strength of S-N and its sensitivity to trace metal ion catalyzed decomposition.[10] The lability of the S-N bond, though making SNO detection difficult, has been used widely to develop methods for detection of liberated NO products after homolytic or heterolytic S-N cleavage.

Chemiluminescence-based assays are widely used for its relatively easy and fast selective detection of SNOs in a complex biological system. This reductive method measures NO released using the intensity of generated chemiluminescence during the ozone-dependent oxidation of NO to NO_2^* followed by relaxing to ground state (NO_2). Briefly, light induces homolytic cleavage of SNO by irradiation with a 200W mercury vapor lamp. Released NO gas is purged into the ozonator chamber following condensation of impurities (liquid and organic traces) in cold traps.[38, 39] Tri-iodide (I_3^-) is quantitatively used to reduce SNO to NO. The contribution of iron nitrosyls and nitrosamines to the chemiluminescent signals can be diminished by treating the sample with 10% of 100 mM sulfanilamide/ HCl solution.[40]

Copper-based detection methods utilize copper salt ($CuCl_2$), cysteine and CO gas to transnitrosate RSNO to Cys-SNO, which is then reduced to Cys-SH and NO by Cu (I). Samples are treated with or without $HgCl_2$ at neutral pH and the difference of peak areas

are converted to RSNO concentration. The CO gas serves to prevent auto-capture of NO by heme, making it suitable in blood sample detection. However, the pre-purification of CO gas is needed while special safety protection is required. Besides, this method is modified by pretreatment of sample with nitrite stabilization solution (K_3FeCN_6/ NEM/DTPA) to oxidize heme to ferric heme and to block free thiols.[38, 41, 42]

While chemiluminescence methods provide an accurate means to detect global SNO in a biological system, these methods are limited in the inability to assign the SNO modification to a particular protein.[38] Moreover, these methods do not provide any information on the specific cysteine residue that is modified, therefore failing to differentiate SNO sites of specific protein as well as identify novel SNO proteins.[30]

3. 2. Biotin-switch technique and its improvements

The biotin-switch technique (BST) is the most widely used method to detect protein *S*-nitrosation. It was initially presented in 2001 by Jaffrey *et al*. and was applied extensively in different biological systems. BST includes three basic steps (Figure 1-4): (1) block free cysteine thiols with a thiol-specific alkylating agent methyl methanethiosulfonate (MMTS); (2) selectively reduce SNOs to free thiols by decomposing S-N bond with ascorbate; and (3) label the nascent thiols with a biotinylating cysteine-reactive reagent N-[6-(biotinamido)hexyl]-3'-(2'-pyridyldithio)propionamide (biotin-HPDP). Biotinylated proteins can be detected by immunoblotting with a biotin-specific antibody, or subjected to avidin enrichment, trypsin digestion and analysis by mass spectrometry to further identify SNO proteins.[43, 44] Using this method, ~15 proteins were identified in rat cerebellum, including metabolic proteins (GAPDH), signaling proteins (heat-shock protein 72, Hsp72), ion channels (N-

methyl-D-aspartate receptor 1, NR1) and structural proteins (α- and β- tubulin). The advent of BST has enabled numerous biological studies that have illustrated the ubiquitous role of cysteine *S*-nitrosation in cellular function. A recent study utilized BST in red blood cells (RBCs) to show that NO generated by NOS is critical to maintain deformability in RBCs.[45] The cellular targets of NO in RBCs included several cytoskeleton proteins, such as α- and β-spectrins. *S*-nitrosation of these cytoskeletal proteins was shown to be important to maintaining RBC deformation. Similarly, BST was critical for identifying proteins that mediate the NO-induced resistance of melanoma cells to anticancer agents such as cisplatin.[46] Several nitrosated proteins were identified, including Caspase-3 and prolyl-hydroxylase-2, which are both inhibited by *S*-nitrosation. *S*-nitrosation of these and other proteins is thought to be directly involved in generating resistance to cisplatin.

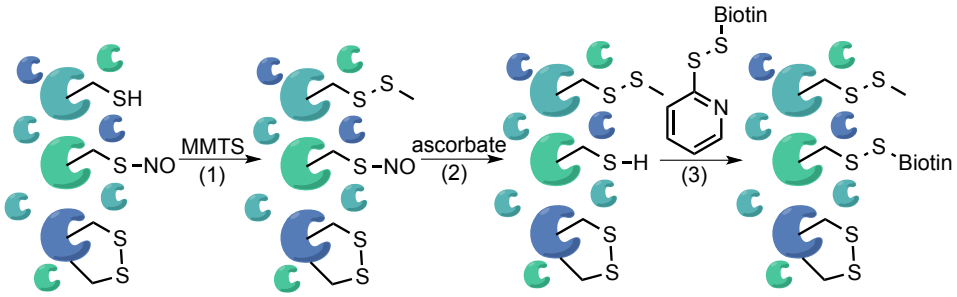


Figure 1-4. The biotin-switch technique (BST) involves capping of reduced thiols with MMTS, followed by selective reduction of *S*-nitrosated cysteines with ascorbate. The resulting newly-formed thiols are then capped with biotin-HPDP for enrichment of *S*-nitrosated proteins.

BST has been applied extensively in different biological systems since its invention, however several drawbacks exist. BST necessitates complete blocking of free

thiols in the initial alkylation step; incomplete alkylation will result in false positives. Furthermore, the sample preparation includes several processing steps, increasing the time lengthy so as the likelihood of SNO decomposition and scrambling of sites of *S*-nitrosation through disulfide exchange, thus affecting the assay accuracy. For the cleavage of the S-N bond, BST relies on the selective and complete reduction of S-NO to SH with ascorbate. However, the selectivity of ascorbate for reducing SNO cysteines relies on a mechanism postulated as an indirect reduction, whereby ascorbate does not directly donate electrons to the nitrosothiol, but instead undergoes a transnitrosation reaction.[47] This selectivity for SNO has been brought into question by the observation of artifacts that are generated due to reduction of sulfenic acid and disulfide bridges of low molecular weight disulfides like DTNB and glutathione disulfide with ascorbate in BST, which is accelerated by indirect sunlight.[48, 49] Huang *et al*. found that BST method gave false-positive signals of SNO even on pre-reduced bovine serium albumin (BSA), upon ascorbate treatment.[49] In response to the observed non-specificity reported for BST, Stamler *et al*. showed that the ascorbate-mediated reduction was highly specific, and inadvertent exposure to sunlight was the cause of false positives. It was suggested that analysis of a sample in which all SNO species were photolyzed prior to processing could act as an additional control to reduce false positives in BST experiments.[50]

Given the low abundance of cysteine *S*-nitrosation modification, this low level of inaccuracy would affect the sensitivity of detection methods dramatically and remains a challenge for its development. To improve the accuracy and sensitivity of SNO detection, various optimization of BST have been made. These improvements have facilitated the generation of increasing information related to different SNO functions.

MMTS, used in BST as the free thiol-blocking reagent, is a reversible alkylating agent. It was replaced with N-ethylmaleimide (NEM) and iodoacetamide (IA), which could react with free thiols irreversibly to form a thioether bond instead of a disulfide bond.[38, 51] In another study, Wang *et al*. found that the 1 mM ascorbate used in the original BST was not sufficiently fast at reducing RSNO and modified the assay by introducing copper "contaminants". This ascorbate/copper system was shown to be able to accelerate S-NO reduction while keeping endogenous disulfides untouched, thus improving assay specificity.[52]

Tagging the nascent thiol is critical to sample purification and RSNO identification. Forrester *et al*. modified BST by replacing thiol-reactive biotin with a thiol-reactive resin, termed *S*-nitrosation using resin-assisted capture (SNO-RAC). After MMTS blocking of free thiol and ascorbate reduction, nascent thiols were labeled with resin-bound disulfides. Newly generated disulfides were eluted by reducing reagent for further gel-based analysis, or by trypsin digestion on resin and subjected to isotopic/isobaric MS analysis on a peptide level. Using this method, novel SNO proteins like peroxiredoxin-1 (Prdx1) were identified. Compared to BST, SNO-RAC has higher sensitivity for high mass (>100 kDa) proteins and also has fewer steps to its workflow.[53] Alternatively, Camerini *et al*. set up a modified method termed His-tag switch by replacing thiol-reactive biotin with a synthetic His-tag that irreversibly bound to a cysteine thiol. Free thiols were initially irreversibly alkylated by NEM followed by ascorbate reduction of SNO cysteine residues. The second alkylation by synthetic peptide ($I\text{-}CH_2\text{-}CO\text{-}Gly\text{-}AArg\text{-}Ala\text{-}His_6$) on the nascent thiol groups facilitated purification on a Ni column. After trypsin digestion, eluted peptides were subjected to MS analysis with a

final mass shift of 271.12 Da. Using this method, 19 proteins from rat cerebral cortex, including 28 precise SNO modified peptides, were identified by MALDI-TOF or by nanoLC-MS/MS.[54] To further overcome the interference from intermolecular disulfide bonds, which lead to false detection of SNO protein by BST, Huang *et al*. developed an irreversible biotinylation procedure (IBP) by using a non-disulfide-based biotin reagent (biotin-maleimide or biotin-PEO-maleimide) and by adding a new step of selective reduction of intermolecular disulfide bonds with dithiothreitol (DTT) before avidin purification. This strategy eliminated false positive identifications from intermolecular disulfide bound proteins, and was able to detect SNO protein as well as specific SNO cysteine residues.[55]

Coupled with two-dimensional gel electrophoresis (2-DE), modified BST was applied to the selective detection of protein *S*-nitrosation. In a "fluorescent switch" method, after NEM blocking and ascorbate reduction, *S*-nitrosated targets were labeled by fluorescent maleimide and resolved in a 2-DE gel. It allowed easier identification of SNO proteins using a limited amount of protein extract, therefore increasing sensitivity. Using this method, 11 SNO proteins were identified in RAW264.7 cells, including novel targets like 26S proteasome non-ATPase regulatory subunit 2 (Psmd2).[56] Similar to "fluorescent switch", another combination of BST with 2-DE is SNO-DIGE (*S*-nitrosothiol difference in gel electrophoresis) method. The mitochondrial *S*-nitrosothiols (MitoSNO) were specifically reduced by copper (II) and ascorbate following NEM blocking. Control and MitoSNO proteomes were then incubated with two thiol-reactive Cy-dye systems (Cy3 and Cy5), which allowed differential fluorescence detection of SNO proteins by 2-DE. As a result, 13 novel mitochondrial SNO proteins were identified,

the majority of which are enzymes involved in mitochondrial metabolism. SNO-DIGE overcomes the non-specific reduction conditions by using copper (II) and ascorbate, improving detection sensitivity in access to low-abundance SNO proteins.[57] Similarly, in another study, Santhanam *et al*. described a modified BST named Selective Fluorescent Labeling Of *S*-nitrosothiols (S-FLOS). After blocking and reduction steps identical to BST, Cy-maleimide dye adduction was performed with the nascent thiol at pH 7. By bypassing immunoblotting or avidin enrichment steps, direct comparison of the fluorescent intensities between labeled proteins on the same 2D gel or in the same 1D gel lane was achieved by two Cy-dye systems (Cy3 and Cy5), allowing the detection of relative changes in SNO level of individual protein and quantification of SNO proteins. This detection method has low background and high signal to noise and sensitivity to allow for direct visualization of SNO content.[58]

3. 3. Direct detection of SNO by phosphine

Due to the limitations and artifacts associated with BST analysis, significant efforts have been invested in developing chemical probes with selectivity for *S*-nitrosothiols over other cysteine oxoforms (Figure 1-5). Analogous to the Staudinger ligation,[59] where phosphines react selectively with azides to generate aza-ylides, *S*-nitrosothiols can directly react with triarylphosphines to form thiol-aza-ylides.[60] This reaction inspired investigation of a series of phosphine-based molecules to probe SNO residues. Structural changes by introducing different electrophilic groups on the phosphine induced the thiol-aza-ylide to undergo an intramolecular reaction and generate stable products. Wang *et al*. developed a reductive ligation by the use of a phosphine ester in place of phosphine, resulting in rearrangement of the aza-ylide intermediate to form a stable sulfenamide.[60]

This "one-step" conversion of SNO to stable conjugates was compatible with biological systems. However, excess phosphine was considered as a source of reductive fragmentation to cleave ligation products. Further engineering by Zhang *et al*. resulted in a "traceless" version of reductive SNO ligation with the use of phosphine ester or thioester derivatives.[61] Specifically, if a tertiary RSNO was treated with phosphine thioester to undergo an intramolecular aza-Witting reaction, a stable thioimidate product was generated and the original S-N bond was maintained, while treatment of the relatively unstable but biologically relevant primary RSNO with a thioester thioester generated the stable disulfide iminophosphorane. A bis-ligation mechanism was proposed including initial thio-aza-ylide formation, followed by intramolecular acyl transfer from the thioester to the nitrogen on the thio-aza-ylide, and spontaneous intermolecular phenylthiolate nucleophilic attack onto the pseudo-sulfonamide to break the original S-N

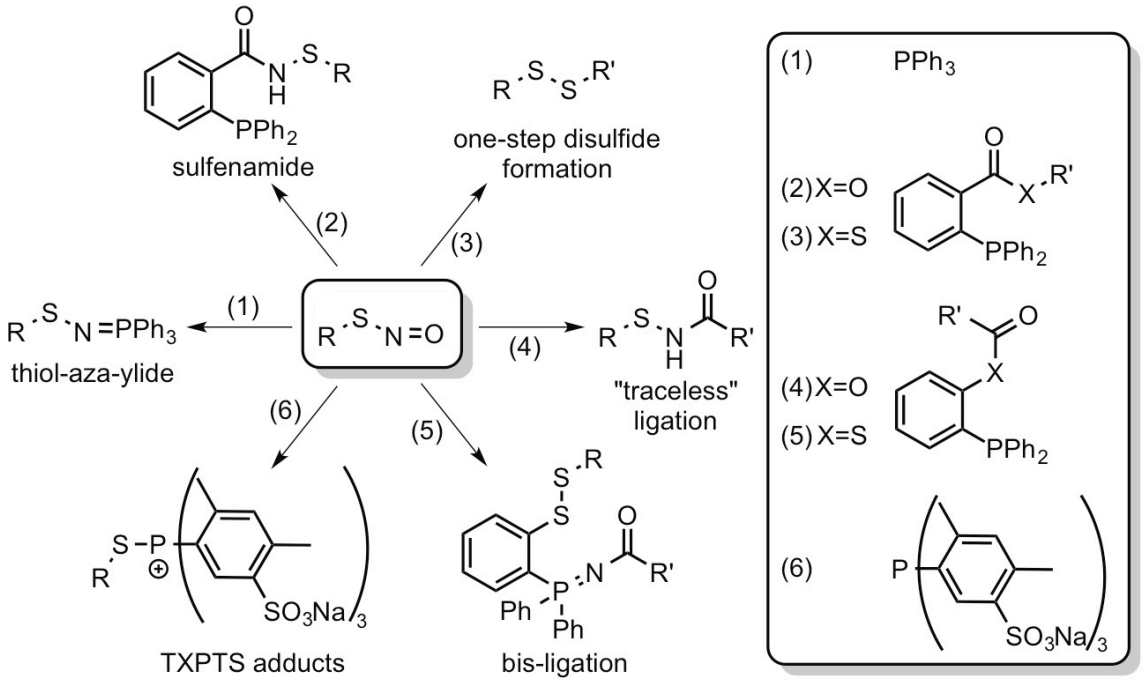


Figure 1-5. Chemical probes for *S*-nitrosation rely on the use of phosphine esters to form:

(1) thio-aza-ylides; (2) sulfenamides; (3) traceless disulfides; (4) traceless sulfonamides; (5) bis-ligation products and (6) adducts with water-soluble TXPTS.

bond, producing phosphine oxide and a relative simple and more stable disulfide.[61, 62] Without bulky phosphine adducts, the disulfide products were more suitable for biological systems and downstream analytical platforms. Together with a biotin-linked phosphine probe and western blot, this modification was successfully applied in the identification of SNO proteins from Cys-SNO treated COS-7 cells.[63]

To circumvent the poor water solubility of the phosphine reagents, tris(4,6-dimethyl-3-sulfonatophenyl)phosphine trisodium salt hydrate (TXPTS) was reported by Bechtold *et al*. as the first water-soluble triarylphosphine that specifically and directly reacted with *S*-nitrosothiols to form the corresponding azo-ylide. The proposed mechanisms included the formation of *S*-substituted aza-ylide followed by reaction with another equivalent of phosphine, and the direct nucleophilic attack of TXPTS on the SNO sulfur to displace the HNO from RSNO. TXPTS reacts with alkyl hydroperoxide reductase C (AhpC-SNO), which contains an *S*-nitrosation sensitive active site Cys46 with high efficiency. The resulting covalent *S*-alkylphosphonium product was detectable by ESI-TOF MS, and was stable under denaturing conditions at room temperature over several days.[64] To further improve the aqueous compatibility and robustness of these reactions, Tannenbaum and coworkers developed a panel of derivatized triphenylphosphines with sulfonate esters and tertiary amines to facilitate water solubility and MS ionization.[65] These modified probes were utilized to measure cellular GSNO levels using multiple reactions monitoring (MRM)-MS in malignant cancer cells and macrophages. These studies were the first to demonstrate the successful application of

phosphine probes for *S*-nitrosothiols within a complex biological sample. The limitations, however, remain that only low molecular-weight thiols were analyzed, and there are no reports on the application of phosphine probes for the enrichment of protein SNO from a complex proteome. With continued effort, the rates of reaction, water solubility of the phosphine reagent, stability of the resulting adducts and chemo-selectivity of the phosphine-nitrosothiol reaction will likely improve and enable the application of these probes to complex biological samples.

3. 4. Direct detection by organomercury-based method

An alternative approach to directly detect SNO was designed by Doulias et al. by developing a novel organomecury-based labeling and enrichment method. This method exploits the reaction of phenylmercury with SNO to form stable thiol-mercury conjugates by applying a synthetic phenylmercury compound coupled to either agarose (organomercury-conjugated resin, MRC) or biotin (phenylmercury-polyethyleneglycol-biotin, mPEGb) for subsequent MRC or avidin enrichment. Free cysteine thiols within the sample are blocked with MMTS, and *S*-nitrosated proteins are selectively captured and enriched on the MRC resin or mPEGb and subsequently released using performic acid or β–mercaptoethanol which concurrently oxidizes newly released thiols to sulfonic acids. The eluted peptides are then analyzed by LC-MS/MS, where the unique mass shift of the sulfonic acid modification (+48 Da) enables identification of SNO proteins and the exact site of *S*-nitrosation. Using this method, 328 endogenous modified SNO peptides from 192 proteins were identified with a large range of molecular weights (13-272 kDa) and wide cellular distribution in mouse liver.[29] Further systematic analysis of various mouse tissues using MRC uncovered 1011 SNO sites in 647 proteins across mouse liver,

brain, heart, kidney and lung. These identified *S*-nitrosated proteins participate in diverse metabolic processes including glycolysis, gluconeogenesis, oxidative phosphorylation, amino-acid metabolism and the tricarboxylic acid cycle. For example, about 70% of the SNO sites from heart tissue were annotated as mitochondrial proteins. In particular, *S*-nitrosation of Cys238 in very long chain acyl-coenzyme A dehydrogenase (VLCAD) was shown to activate the enzyme, thereby illustrating the role of *S*-nitrosation in regulating fatty-acid beta oxidation. This method demonstrated a high level of sensitivity and accurcy due to its direct capture of SNO sites by bypassing ascorbate reduction and its conversion of SNO to a sulfonic acid with a unique MS shift for proteomic annotation.[66] With data larger subset of SNO sites identified, the biochemical, biophysical and structural properties of cysteine SNO modification can be further analyzed .

Recently, Lee et al. developed an approach combining BST and MRC in a protein microarray platform. BST analysis was sequentially performed on a GSNO pretreated high-density protein microarray chip containing 16,368 unique GST-tagged full-length human proteins. *S*-nitrosated sites were biotinylated by BST, following by detection and quantification by immunobloting with an anti-biotin antibody coupled with a fluorescent Cy5 secondary antibody. Of the 834 SNO proteins identified, a subset was recombinantly expressed, purified with GST-tag, subject to organomercury MRC enrichment and subsequent MS analysis to identify the sites of *S*-nitrosation, including 113 novel SNO cysteine sites.[67] The combining of orthogonal methods like BST and MRC to identify *S*-nitrosation provides increased confidence in the identified targets and serves to mitigate the limitations associated with each of the methods.

3. 5. Quantitative mass-spectrometry methods

Two-dimensional gel electrophoresis (2DE) method has been extensively used for protein separation and comparisons of protein abundance. However, drawbacks of 2DE are existed, such as poor reproducibility, low resolution and accuracy, incompatibility with hydrophobic proteins, incapability of analyzing low abundant protein/PTMs and time and labor-consuming, greatly limit its analytical application on biological samples.[68] From the ground-breaking development in sample preparation, peptide fragmentation, accuracy and sensitivity of instrumentation and bioinformatics pipeline, the most common quantitative proteomic analysis on protein and its PTMs has shifted from 2DE-based methods to Mass Spectrometry-based technology, especially isotopic labeling-derived quantitative shotgun proteomics. Importantly, these MS improvements greatly facilitate quantitative measurement of protein *S*-nitrosation, allowing the analysis of the modification occupancy and dynamics, the characterization of specific modified cysteine residues, and the exploration of deeper cellular relationship.

Stable isotope labeling by amino acid in cell culture (SILAC) is an MS1-based isotopic labeling method and is used for relative protein quantification widely.[30] Benhar *et al*. applied BST coupled SILAC to identify a specific subset proteins. Two identical Jurkat cell populations were cultured in SILAC medium containing either light amino acid (Arg^0 ($^{12}C_6{}^{14}N_4$) and Lys^0 ($^{12}C_6{}^{14}N_2$)) or heavy amino acid ($Arg1^0$ ($^{13}C_6{}^{15}N_4$) and Lys^8 ($^{13}C_6{}^{15}N_2$)). After cytosolic extraction and nitrosation, the light cultured cell lysate underwent denitrosation by Trx system (Trx/TrxR/NADPH) and heavy cultured remained untreated as a control. Then the endogenously nitrosated proteins were detected by BST and LC-MS. Proteomic annotation showed that 145 proteins out of a total of ~280 SNO proteins were identified in both heavy and light samples. Out of these 145 SNO proteins,

46 were lower in terms of Light to Heavy ratio (≤0.65) than control after denitrosation, and thus were considered as substrates of Trx1. Detailed study showed that these proteins participate in a broad range of cellular processes like metabolism, signal transduction and protein folding.[69]

Instead of metabolic labeling by isotopes as in SILAC, a chemical labeling method, termed isotope-coded affinity tags (ICAT) was developed. This method, utilizing the ICAT reagent including a thiol reactive group, a biotin affinity tag and a heavy or light isotopic linker, expands upon a shotgun proteomic strategy and directly interface differential cysteine labeling with MS. [70] Cysteine containing proteins selectively captured by light or heavy ICAT reagents are enriched on streptavidin affinity beads to purify ICAT-coded proteins, which are subject to trypsin digestion, mixing and analysis by quantitative MS, whereby the tagged cysteine-containing peptides can be identified and the relative abundance between the light- and heavy-labeled samples can be quantified.[71] When coupled with ICAT, Sinha *et al*. developed a "d-switch" method by adapting BST to identify SNO targets and quantify the percentage of SNO level. The free thiol was block by d-NEM instead of MMTS. After ascorbate/Cu(I) reduction, newly-formed free thiols were labeled by d_5-NEM. Subsequent in-gel tryptic digestion and MS analysis identified SNO proteins. Quantification of relative amount of peptides from isotopic d-NEM/d_5-NEM labeling related to peptide-SH vesus peptide-SNO. Using this method, investigation of GST-P1 SNO by five classes of NO donors showed different SNO sensitivities.[72]

Isobaric tags are commonly used for multiplexed peptide quantification and include three functional parts: an amine-reactive group, a unique mass reporter group and

a cleavable linker as a mass balancer. Digested peptides from different biological samples are labeled with a set of multiplex isobaric tags by the reaction of the amine-reactive group on the tag with the peptide N-terminus or lysine residues of the peptides. Using a balancer moiety to compensate for the mass shift, all sets of multiplex isobaric tags are identical in total molecular weights but contain different reporter weights. These isobaric tags enable co-elution of peptides during LC as well as co-isolation for fragmentation of the linker during MS2, resulting in release of the reporter group. Importantly, the intensity of the reporter group serves as signature ions on MS spectra and represents the relative abundance of the original peptide, the feature used to quantify protein modification/expression levels.[30] This MS2 (MS/MS)-dependent isobaric labeling is able to analyze multiple peptide pools in a single analysis, using 8-plex iTRAQ (isobaric tags for relative and absolute quantification) and 6-plex TMT (tandem mass tags).[68] Instead of traditional iTRAQ assays where proteins were first digested to peptides and then labeled, Murray *et al*. developed a new isotope coded cysteine thiol-reactive multiplex reagent (cysTMT^6), coupled with BST to detect SNO proteins and quantify specific cysteine SNO reactivity. Similar to iTRAQ, the cysTMT^6 includes a mass reporter (126-131 Da), a cysteine pyridyldithiol reactive group and a mass normalizer. Once blocked by NEM and reduced by ascorbate/copper, samples were labeled by cysTMT^6 (cysTMT$^{126\text{-}131}$) and subjected to SDS-PAGE or trypsin digestion. TMT labeled peptides were enriched on TMT affinity resin and eluted with acid under low pH to be further analyzed by LC/MS/MS. The MS/MS fragmentation of reporter groups allowed analysis of up to six samples at the same time, thus study of the extent of SNO at each cysteine residue and the SNO site occupancy could be achieved.[73-75]

Recently, an isotopic tandem orthogonal proteolysis-activity-base protein profiling (isoTOP-ABPP) proteomic method was developed by Cravatt *et al*. to globally quantify cysteine reactivity and characterize cysteine functionality. This method included a cysteine reactive probe, idoacetamide-alkyne (IA-alkyne) that covalently labels free cysteine thiol, and an azide-functionalized TEV-protease recognition peptide with a biotin tag for streptavidin enrichment. IA-alkyne-captured proteins were conjugated to the biotin tag through a bioorthogonal "click-chemistry" reaction between the alkyne handle and azide. After enrichment, on-bead trypsin digestion and TEV protease cleavage, peptides were released and analyzed by LC-MS/MS, allowing the identification of the cysteine containing proteins and the specific probe-labeled cysteine residue. The isotopically labeled valine containing tags further facilitated quantitative measurement of cysteine reactivity.[76] A comparative analysis of IA-alkyne-reactive cysteines and SNO cysteines in WT mouse heart revealed that 38 out of 119 proteins were both SNO reactive and IA reactive, including 32 cysteine residues both sensitive to SNO and IA. This 15% coverage (32 of 211 cysteine SNO residue) suggested the selective reactivity to different modification on the same cysteine.[10] Therefore, the isoTOP-ABPP method bypassing free thiol blocking and SNO conversion procedures in BST, would serve as a potential quantitative identification strategy of cysteine *S*-nitrosation.

Conclusion

Despite being one of the least abundant amino acids on proteins, cysteine is frequently identified as a highly conserved functional site within the proteome. The unique characteristics of the cysteine thiol or thiolate group (nucleophilicity, high-affinity

to several metal/metal clusters and disulfide bond formation/exchange) that are commonly influenced by the intrinsic properties of the sulfur pK_a, redox potential and the local microenvironment, largely contribute to its catalytic, metal binding, structural as well as redox-dependent regulatory roles.[9] Cysteine could undergo a diverse set of posttranslational modifications, and often it is the cysteine PTMs that exert a significant impact on its proteomic functions.

Cysteine *S*-nitrosation, a covalent addiction of a NO moiety on the cysteine thiol, is emerging as an important PTM in regulation of protein function, translocation, degradation and signaling pathways. The low abundance, high dynamic and labile nature of cysteine SNO complicates the identification of SNO protein and specific SNO cysteine residues. Detection methods, from the chemiluminescence and chemical reduction assays, to the Biotin Switch Technique and its improvements, alongside phosphine and organomercury-based direct detection methods have been intensively used to identify and characterize SNO protein and cysteines. With advances in mass spectrometry-based proteomic technology, featured by metabolic or chemical isotopic coding, quantitative proteomic analysis on both the protein expression level and amino acid PTM level have been achieved.

With respect to cysteine SNO, this thesis is focused on the development of a MS-based platform to explore the extent of modification at individual cysteine residues (Chapter 2) in order to facilitate the identification of novel cysteine sites that regulate protein function (Chapter 3). A parallel comparison of cysteine sensitivity to different transnitrosating reagents reveals specific sets of SNO modification targets correlated with each transnitrosation donor (Chapter 4). Upon the successful application of this platform

to identify novel regulatory cysteines, we aimed to identify small molecule modifiers for these and other characterized regulatory cysteines. , Screening a small-molecule library against these cysteine-containing proteins enabled the discovery of cysteine-reactive irreversible inhibitors, which allow for pharmacological modulation of proteins containing regulatory cysteines (Chapter 5).

References

1. Go YM, Chandler JD and Jones DP. The cysteine proteome. *Free Radic Biol Med*. 2015;84:227-45.

2. Poole LB. The basics of thiols and cysteines in redox biology and chemistry. *Free Radic Biol Med*. 2015;80:148-57.

3. Cannan RK and Knight B. Dissociation Constants of Cystine, Cysteine, Thioglycollic Acid and α-Thiolactic Acid. *Biochem J*. 1927;21:1384-90.

4. Couvertier SM, Zhou Y and Weerapana E. Chemical-proteomic strategies to investigate cysteine posttranslational modifications. *Biochim Biophys Acta*. 2014;1844:2315-2330.

5. Yang YF and Wells WW. Identification and characterization of the functional amino acids at the active center of pig liver thioltransferase by site-directed mutagenesis. *J Biol Chem*. 1991;266:12759-65.

6. Gan ZR and Wells WW. Identification and reactivity of the catalytic site of pig liver thioltransferase. *J Biol Chem*. 1987;262:6704-7.

7. Lo Conte M and Carroll KS. The redox biochemistry of protein sulfenylation and sulfinylation. *J Biol Chem*. 2013;288:26480-8.

8. Pace NJ and Weerapana E. Diverse functional roles of reactive cysteines. *ACS chemical biology*. 2013;8:283-96.

9. Gould NS, Evans P, Martinez-Acedo P, Marino SM, Gladyshev VN, Carroll KS and Ischiropoulos H. Site-Specific Proteomic Mapping Identifies Selectively Modified Regulatory Cysteine Residues in Functionally Distinct Protein Networks. *Chemistry & biology*. 2015;22:965-75.

10. Gould N, Doulias PT, Tenopoulou M, Raju K and Ischiropoulos H. Regulation of protein function and signaling by reversible cysteine *S*-nitrosylation. *J Biol Chem*. 2013;288:26473-9.

11. Kabil O, Motl N and Banerjee R. H2S and its role in redox signaling. *Biochim Biophys Acta*. 2014;1844:1355-66.

12. Grek CL, Zhang J, Manevich Y, Townsend DM and Tew KD. Causes and consequences of cysteine *S*-glutathionylation. *J Biol Chem*. 2013;288:26497-504.

13. Gueraud F, Atalay M, Bresgen N, Cipak A, Eckl PM, Huc L, Jouanin I, Siems W and Uchida K. Chemistry and biochemistry of lipid peroxidation products. *Free radical research*. 2010;44:1098-124.

14. Shannon DA and Weerapana E. Orphan PTMs: Rare, yet functionally important modifications of cysteine. *Biopolymers*. 2014;101:156-64.

15. Zhang FL and Casey PJ. Protein prenylation: molecular mechanisms and functional consequences. *Annual review of biochemistry*. 1996;65:241-69.

16. Tom CT and Martin BR. Fat chance! Getting a grip on a slippery modification. *ACS chemical biology*. 2013;8:46-57.

17. Garcia-Garcia A, Zavala-Flores L, Rodriguez-Rocha H and Franco R. Thiol-Redox Signaling, Dopaminergic Cell Death, and Parkinson's Disease *Antioxid Redox Signal*; 2012(17): 1764-84.

18. Cysteine/cystine redox signaling in cardiovascular disease. 2011;50:495–509.

19. Resh MD. Targeting protein lipidation in disease. *Trends in molecular medicine*. 2012;18:206-14.

20. Lee T-Y, Chen Y-J, Lu C-T, Ching W-C, Teng Y-C, Huang H-D and Chen Y-J. dbSNO: a database of cysteine *S*-nitrosylation. 2012.

21. Lee TY, Chen YJ, Lu CT, Ching WC, Teng YC and Huang HD. dbSNO: a database of cysteine *S*-nitrosylation. *Bioinformatics*. 2012;28:2293-5.

22. Bogdan C. Nitric oxide and the immune response. *Nature Immunology*. 2001;2:907-916.

23. Majmudar JD and Martin BR. Strategies for profiling native *S*-nitrosylation. *Biopolymers*. 2014;101:173-9.

24. Smith BC and Marletta MA. Mechanisms of *S*-nitrosothiol formation and selectivity in nitric oxide signaling. *Curr Opin Chem Biol*. 2012;16:498-506.

25. Wu C, Liu T, Chen W, Oka S, Fu C, Jain MR, Parrott AM, Baykal AT, Sadoshima J and Li H. Redox regulatory mechanism of transnitrosylation by thioredoxin. *Mol Cell Proteomics*. 2010;9:2262-75.

26. Devarie-Baez NO, Zhang D, Li S, Whorton AR and Xian M. Direct methods for detection of protein *S*-nitrosylation. *Methods*. 2013;62:171-6.

27. Kohr MJ, Aponte A, Sun J, Gucek M, Steenbergen C and Murphy E. Measurement of *S*-nitrosylation occupancy in the myocardium with cysteine-reactive tandem mass tags: short communication. *Circ Res*. 2012;111:1308-1312.

28. Marino SM and Gladyshev VN. Structural analysis of cysteine *S*-nitrosylation: a modified acid-based motif and the emerging role of trans-nitrosylation. *J Mol Biol*. 2010;395:844-59.

29. Doulias PT, Greene JL, Greco TM, Tenopoulou M, Seeholzer SH, Dunbrack RL and Ischiropoulos H. Structural profiling of endogenous *S*-nitrosocysteine residues reveals unique features that accommodate diverse mechanisms for protein *S*-nitrosylation *Proceedings of the National Academy of Sciences of the United States of America*; 2010(107): 16958-63.

30. Chen YJ, Ching WC, Lin YP and Chen YJ. Methods for detection and characterization of protein *S*-nitrosylation. *Methods*. 2013;62:138-50.

31. Benhar M, Forrester MT, Hess DT and Stamler JS. Regulated protein denitrosylation by cytosolic and mitochondrial thioredoxins. *Science*. 2008;320:1050-4.

32. Mitchell DA, Morton SU, Fernhoff NB and Marletta MA. Thioredoxin is required for *S*-nitrosation of procaspase-3 and the inhibition of apoptosis in Jurkat cells. *Proceedings of the National Academy of Sciences of the United States of America*. 2007;104:11609-14.

33. Hara MR, Agrawal N, Kim SF, Cascio MB, Fujimuro M, Ozeki Y, Takahashi M, Cheah JH, Tankou SK, Hester LD, Ferris CD, Hayward SD, Snyder SH and Sawa A. *S*-nitrosylated GAPDH initiates apoptotic cell death by nuclear translocation following Siah1 binding. *Nat Cell Biol*. 2005;7:665-74.

34. Kornberg MD, Sen N, Hara MR, Juluri KR, Nguyen JV, Snowman AM, Law L, Hester LD and Snyder SH. GAPDH mediates nitrosylation of nuclear proteins. *Nat Cell Biol*. 2010;12:1094-100.

35. Hess DT, Matsumoto A, Kim SO, Marshall HE and Stamler JS. Protein *S*-nitrosylation: purview and parameters. *Nat Rev Mol Cell Biol*. 2005;6:150-66.

36. Park HS, Huh SH, Kim MS, Lee SH and Choi EJ. Nitric oxide negatively regulates c-Jun N-terminal kinase/stress-activated protein kinase by means of *S*-nitrosylation. *Proceedings of the National Academy of Sciences of the United States of America*. 2000;97:14382-7.

37. Bechtold E and King SB. Chemical Methods for the Direct Detection and Labeling of *S*-Nitrosothiols *Antioxid Redox Signal*; 2012(17): 981-91.

38. Diers AR, Keszler A and Hogg N. Detection of *S*-nitrosothiols. *Biochim Biophys Acta*. 2014;1840:892-900.

39. Stamler JS, Jaraki O, Osborne J, Simon DI, Keaney J, Vita J, Singel D, Valeri CR and Loscalzo J. Nitric oxide circulates in mammalian plasma primarily as an *S*-nitroso adduct of serum albumin. *Proceedings of the National Academy of Sciences of the United States of America*. 1992;89:7674-7.

40. Samouilov A and Zweier JL. Development of chemiluminescence-based methods for specific quantitation of nitrosylated thiols. *Anal Biochem*. 1998;258:322-30.

41. Wang X, Bryan NS, MacArthur PH, Rodriguez J, Gladwin MT and Feelisch M. Measurement of nitric oxide levels in the red cell: validation of tri-iodide-based chemiluminescence with acid-sulfanilamide pretreatment. *J Biol Chem*. 2006;281:26994-7002.

42. Rogers SC, Gibbons LB, Griffin S and Doctor A. Analysis of *S*-nitrosothiols via copper cysteine (2C) and copper cysteine-carbon monoxide (3C) methods. *Methods*. 2013;62:123-9.

43. Jaffrey SR, Erdjument-Bromage H, Ferris CD, Tempst P and Snyder SH. Protein *S*-nitrosylation: a physiological signal for neuronal nitric oxide. *Nat Cell Biol*. 2001;3:193-7.

44. Jaffrey SR and Snyder SH. The biotin switch method for the detection of *S*-nitrosylated proteins. *Science's STKE : signal transduction knowledge environment*. 2001;2001:pl1.

45. Grau M, Pauly S, Ali J, Walpurgis K, Thevis M, Bloch W and Suhr F. RBC-NOS-dependent *S*-nitrosylation of cytoskeletal proteins improves RBC deformability. *PloS one*. 2013;8:e56759.

46. Godoy LC, Anderson CT, Chowdhury R, Trudel LJ and Wogan GN. Endogenously produced nitric oxide mitigates sensitivity of melanoma cells to cisplatin. *Proceedings of the National Academy of Sciences of the United States of America*. 2012;109:20373-8.

47. Holmes AJ and Williams DLH. Reaction of ascorbic acid with *S*-nitrosothiols: clear evidence for two distinct reaction pathways. *J Chem Soc, Perkin Trans*. 2000;2:1639-1644.

48. Giustarini D, Dalle-Donne I, Colombo R, Milzani A and Rossi R. Is ascorbate able to reduce disulfide bridges? A cautionary note. *Nitric Oxide*. 2008;19:252-8.

49. Huang B and Chen C. An ascorbate-dependent artifact that interferes with the interpretation of the biotin switch assay. *Free Radic Biol Med*. 2006;41:562-7.

50. Forrester MT, Foster MW and Stamler JS. Assessment and application of the biotin switch technique for examining protein *S*-nitrosylation under conditions of pharmacologically induced oxidative stress. *J Biol Chem*. 2007;282:13977-83.

51. Chen YJ, Ku WC, Lin PY, Chou HC and Khoo KH. *S*-alkylating labeling strategy for site-specific identification of the *S*-nitrosoproteome. *Journal of proteome research*. 2010;9:6417-39.

52. Wang X, Kettenhofen NJ, Shiva S, Hogg N and Gladwin MT. Copper dependence of the biotin switch assay: modified assay for measuring cellular and blood nitrosated proteins. *Free Radic Biol Med*. 2008;44:1362-72.

53. Forrester MT, Thompson JW, Foster MW, Nogueira L, Moseley MA and Stamler JS. Proteomic analysis of *S*-nitrosylation and denitrosylation by resin-assisted capture. *Nat Biotechnol*. 2009;27:557-9.

54. Camerini S, Polci ML, Restuccia U, Usuelli V, Malgaroli A and Bachi A. A novel approach to identify proteins modified by nitric oxide: the HIS-TAG switch method. *Journal of proteome research*. 2007;6:3224-31.

55. Huang B and Chen C. Detection of protein *S*-nitrosation using irreversible biotinylation procedures (IBP). *Free Radic Biol Med*. 2010;49:447-56.

56. Tello D, Tarin C, Ahicart P, Breton-Romero R, Lamas S and Martinez-Ruiz A. A "fluorescence switch" technique increases the sensitivity of proteomic detection and identification of *S*-nitrosylated proteins. *Proteomics*. 2009;9:5359-70.

57. Chouchani ET, Hurd TR, Nadtochiy SM, Brookes PS, Fearnley IM, Lilley KS, Smith RA and Murphy MP. Identification of *S*-nitrosated mitochondrial proteins by *S*-nitrosothiol difference in gel electrophoresis (SNO-DIGE): implications for the

regulation of mitochondrial function by reversible *S*-nitrosation. *Biochem J*. 2010;430:49-59.

58. Santhanam L, Gucek M, Brown TR, Mansharamani M, Ryoo S, Lemmon CA, Romer L, Shoukas AA, Berkowitz DE and Cole RN. Selective fluorescent labeling of *S*-nitrosothiols (S-FLOS): a novel method for studying *S*-nitrosation. *Nitric Oxide*. 2008;19:295-302.

59. Saxon E. Cell Surface Engineering by a Modified Staudinger Reaction. *Science*. 2000;287:2007-2010.

60. Wang H and Xian M. Fast reductive ligation of *S*-nitrosothiols. *Angew Chem Int Ed Engl*. 2008;47:6598-601.

61. Zhang J, Wang H and Xian M. Exploration of the "traceless" reductive ligation of *S*-nitrosothiols. *Organic letters*. 2009;11:477-80.

62. Zhang J, Wang H and Xian M. An unexpected Bis-ligation of *S*-nitrosothiols. *Journal of the American Chemical Society*. 2009;131:3854-5.

63. Zhang J, Li S, Zhang D, Wang H, Whorton AR and Xian M. Reductive ligation mediated one-step disulfide formation of *S*-nitrosothiols. *Organic letters*. 2010;12:4208-11.

64. Bechtold E, Reisz JA, Klomsiri C, Tsang AW, Wright MW, Poole LB, Furdui CM and King SB. Water-soluble triarylphosphines as biomarkers for protein *S*-nitrosation. *ACS chemical biology*. 2010;5:405-14.

65. Seneviratne U, Godoy LC, Wishnok JS, Wogan GN and Tannenbaum SR. Mechanism-based triarylphosphine-ester probes for capture of endogenous RSNOs. *Journal of the American Chemical Society*. 2013;135:7693-704.

66. Doulias PT, Tenopoulou M, Greene JL, Raju K and Ischiropoulos H. Nitric oxide regulates mitochondrial fatty acid metabolism through reversible protein *S*-nitrosylation. *Sci Signal*. 2013;6:rs1.

67. Lee YI, Giovinazzo D, Kang HC, Lee Y, Jeong JS, Doulias PT, Xie Z, Hu J, Ghasemi M, Ischiropoulos H, Qian J, Zhu H, Blackshaw S, Dawson VL and Dawson TM. Protein microarray characterization of the *S*-nitrosoproteome. *Mol Cell Proteomics*. 2014;13:63-72.

68. Zhang Y, Fonslow BR, Shan B, Baek MC and Yates JR, 3rd. Protein analysis by shotgun/bottom-up proteomics. *Chem Rev*. 2013;113:2343-94.

69. Benhar M, Thompson JW, Moseley MA and Stamler JS. Identification of *S*-nitrosylated targets of thioredoxin using a quantitative proteomic approach. *Biochemistry*. 2010;49:6963-9.

70. Gygi SP, Rist B, Gerber SA, Turecek F, Gelb MH and Aebersold R. Quantitative analysis of complex protein mixtures using isotope-coded affinity tags. *Nat Biotechnol*. 1999;17:994-9.

71. Murray CI and Van Eyk JE. Chasing cysteine oxidative modifications: proteomic tools for characterizing cysteine redox status. *Circ Cardiovasc Genet*. 2012;5:591.

72. Sinha V, Wijewickrama GT, Chandrasena RE, Xu H, Edirisinghe PD, Schiefer IT and Thatcher GR. Proteomic and mass spectroscopic quantitation of protein *S*-nitrosation differentiates NO-donors. *ACS chemical biology*. 2010;5:667-80.

73. Murray CI, Chung HS, Uhrigshardt H and Van Eyk JE. Quantification of mitochondrial *S*-nitrosylation by CysTMT(6) switch assay. *Methods in molecular biology (Clifton, NJ)*. 2013;1005:169-79.

74. Murray CI, Uhrigshardt H, O'Meally RN, Cole RN and Van Eyk JE. Identification and quantification of *S*-nitrosylation by cysteine reactive tandem mass tag switch assay. *Mol Cell Proteomics*. 2012;11:M111 013441.

75. Murray CI and Van Eyk JE. A twist on quantification: measuring the site occupancy of *S*-nitrosylation. *Circ Res*. 2012;111:1253-5.

76. Weerapana E, Wang C, Simon GM, Richter F, Khare S, Dillon MB, Bachovchin DA, Mowen K, Baker D and Cravatt BF. Quantitative reactivity profiling predicts functional cysteines in proteomes. *Nature*. 2010;468:790-5.

Chapter 2

A chemical-proteomic platform to monitor cysteine sensitivity to transnitrosation by *S*-nitrosoglutathione

A significant portion of the work described in this chapter has been published in:

Yani Zhou, Sarah L. Wynia-Smith, Shalise M. Couvertier, Kelsey S. Kalous, Michael A. Marletta, Brian C. Smith, Eranthie Weerapana, A chemical-proteomic platform to monitor cysteine sensitivity to transnitrosation by *S*-nitrosoglutathione. *Cell Chem. Biol.*. Manuscript in press.

Introduction

Nitric oxide (NO) plays critical roles in mammalian physiology. In the immune response, cytotoxic NO concentrations are generated by inducible NOS (iNOS) at infection sites.[1] In cardiovascular and neuronal signaling, endothelial nitric oxide synthase (eNOS) and neuronal NOS (nNOS)[1] produce local bursts of NO that activate soluble guanylate cyclase[2] and mediate intercellular communication. Recently, an alternate NO signaling pathway has emerged involving modification of cysteine residues to form *S*-nitrosothiols (*S*-nitrosation)[3, 4]. The majority of cellular *S*-nitrosothiols are formed via a transnitrosation mechanism, whereby *S*-nitrosothiols are transferred through formation of specific protein-small molecule or protein-protein interactions and subsequent nucleophilic attack of a thiolate at the nitrogen of the *S*-nitrosothiol.[5, 6] Cellular transnitrosation is predominately mediated by abundant thiol containing small molecules or proteins, such as glutathione (GSH) and thioredoxin (Trx), which form the corresponding *S*-nitrosated species, GSNO and Trx-SNO, respectively.[4, 7] GSNO is the primary small molecule *S*-nitrosothiol in eukaryotes, and cellular GSNO concentrations range from high nanomolar in cells with basal NOS activity to micromolar in cells where NOS has been activated.[8]

Over 3000 sites of protein *S*-nitrosation have been identified including cysteine residues within two NOS isoforms (eNOS and iNOS), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), and Caspase-3 (Casp3).[9-13] In many cases, *S*-nitrosation alters subcellular localization or enzymatic activity, underscoring the importance of this posttranslational modification in the regulation of protein activity. Transnitrosation of the active-site cysteine of Casp3 by Trx-SNO inhibits protease activity and directly governs

the initiation of apoptosis.[14] Similarly, *S*-nitrosation of GAPDH at Cys152 triggers GAPDH translocation to the nucleus and subsequent transnitrosation of nuclear proteins and initiation of apoptosis.[15, 16] Dysregulation of *S*-nitrosation is implicated in a variety of diseases including cystic fibrosis, asthma, hypertension, cancer, and neurodegeneration.[17] Importantly, small-molecule inhibitors of GSNO reductase, the primary enzyme that catalyzes the cellular degradation of GSNO, are currently in clinical development for treatment of cystic fibrosis, asthma, and other diseases that exhibit decreased endogenous *S*-nitrosothiol levels.[18]

Although the endogenous regulation of protein function through *S*-nitrosation is well established, the properties of an individual cysteine residue that govern sensitivity to *S*-nitrosation are poorly characterized.[12, 19-21] The lack of a sequence or structural motif that dictates the substrate selectivity of each transnitrosation donor necessitates experimental methods for quantitative assessment of the sensitivity of cellular cysteine residues to undergo transnitrosation by donors such as GSNO.

The most widely utilized platform for identifying *S*-nitrosated proteins in complex proteomes is the Biotin-Switch Technique (BST), [22] which is comprised of three main steps: (1) blocking free cysteine residues with a thiol-reactive agent such as iodoacetamide, *N*-ethylmaleimide, or methyl methanethiosulfonate; (2) selective reduction of *S*-nitrosothiols with ascorbate; and (3) labeling the newly reduced cysteine residues with a biotinylated thiol-reactive agent. Since the initial development of the BST, several modifications to this platform have been developed. These include the SNO-RAC and d-Switch methodologies, which introduce resin-assisted capture and isotopic labeling to identify and quantify *S*-nitrosated species from proteomes. [23-25]

Similarly, enrichment of *S*-nitrosothiols with mercury resin has enabled the identification of *S*-nitrosated species from cells.[12, 13] More recently, chemical probes selective for *S*-nitrosothiols have been developed, including a variety of phosphine reagents that undergo a Staudinger-type reaction with *S*-nitrosothiols [26-28] and biotinylated sulfinic acids that form stable thiosulfonates upon reaction with *S*-nitrosothiols[29].

A significant limitation of existing methods to monitor *S*-nitrosation is the inability to quantitatively determine the extent of *S*-nitrosation for each individual cysteine residue, and thereby evaluate the sensitivity of a particular cysteine to a given transnitrosation donor. In this study, this limitation is addressed by implementing a competitive cysteine-labeling strategy to concurrently and quantitatively monitor the sensitivity to transnitrosation of hundreds of cysteine residues within the human proteome. Specifically, 609 cysteine residues in the human proteome were screened in parallel to determine the stoichiometry of *S*-nitrosation upon treatment with GSNO. From this data, a subset of cysteine residues with high sensitivity to GSNO-mediated transnitrosation was identified. To evaluate the functional consequences of *S*-nitrosation, two proteins that demonstrated high sensitivity to GSNO transnitrosation, 3-Hydroxyacyl-CoA dehydrogenase type-2 (HADH2) and Cathepsin D (CTSD), were selected for further biochemical evaluation. In both cases, *S*-nitrosation regulates protein function through a unique mechanism, thereby revealing previously uncharacterized functional roles for these cysteines.

Results

Visualization of protein sensitivity to transitrosation by in-gel fluorescence

In order to visualize protein sensitivity to transnitrosation, we took the advantage of in-gel fluorescence as well as a multifunctional cysteine-reactive probe. This iodoacetamide alkyne (IA) probe is composed of an iodoacetamide electrophile to covalently modify reactive cysteine residues, and a terminal alkyne that can be further functionalized through click chemistry. (Figure 2-1, C) The widely used click chemistry reaction is the bioorthogonal copper (I)-catalyzed azide alkyne cycloaddition (CuAAC) reaction to generate a 1,4-disubstituted 1,2,3-triazole.[30, 31] The CuAAC reaction, derived from the Huisgen 1,3-dipolar cycloaddition, is ideal for biological applications due to the high stability of azides to water, ambient oxygen and a wide-variety of synthetic transformations. Moreover, the synthetic ease of incorporating azides and alkynes into biological probes, coupled with the minimal steric disruption caused by these functionalities, has further promoted its application in probing expanded enzyme classes, enabling cellular and in vivo studies, and providing technological platforms to quantitatively monitor protein activities in complex biological systems.[32]

MCF7 breast cancer-cell lysates were transitrosated by increasing concentrations of GSNO (50, 100, 200 and 500 μM) at 37°C for 1 hr. Cysteine reactivity was probed by IA, and CuAAC was performed with rhodamine-azide (Rh-N_3) as a fluorescent reporter group. The resulting fluorescence-tagged lysates were subjected to SDS-PAGE separation and imaged by in-gel fluorescence. (Figure 2-1, A) Comparing untreated to GSNO-treated lysates identified a subset of cysteines that showed a loss in reactivity

upon GSNO treatment. Similarly, monitoring cysteine reactivity upon increasing the GSNO concentration showed that proteins can have variable sensitivities to GSNO. Some labeling number of protein bands showed no detectable changes in cysteine reactivity with increasing GSNO, whereas other bands showed significant changes in reactivity upon increasing GSNO concentrations.

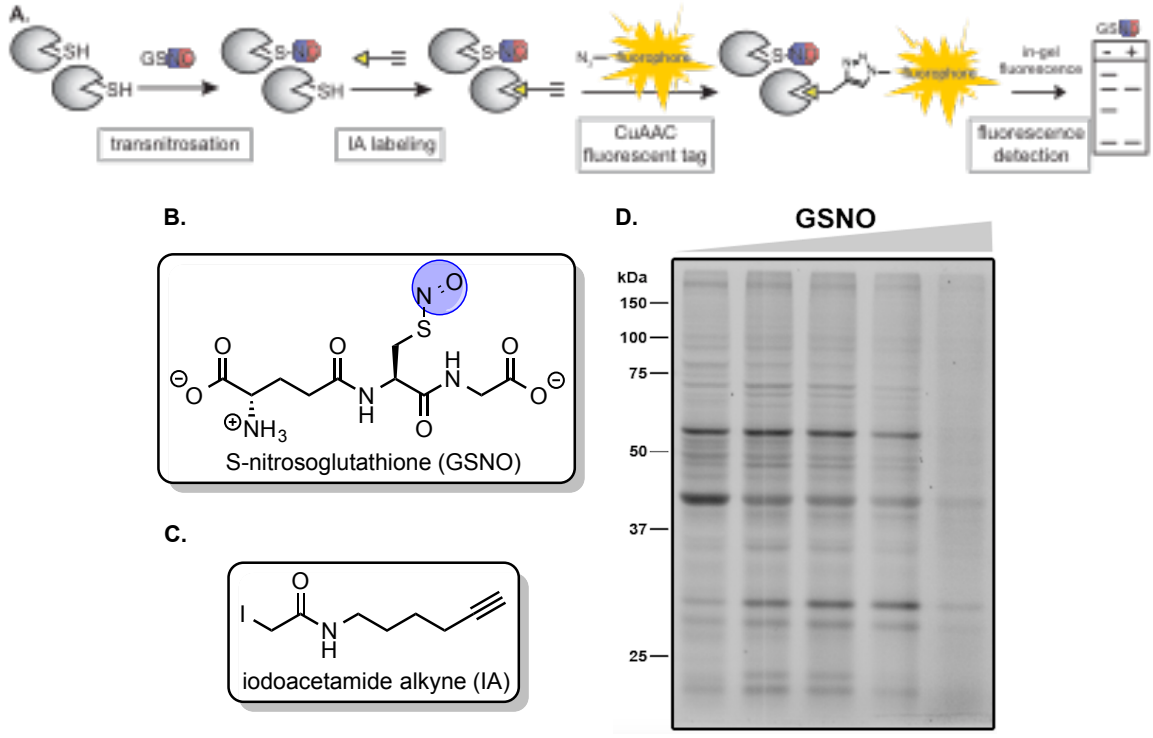


Figure 2-1. In-gel fluorescence to visualize protein sensitivity to transnitrosation. (**A**) 1 mg/mL MCF7 cell lysates were treated either with buffer or GSNO (50, 100, 200 and 500 µM) at 37°C for 1 hr, then labeled by 1 µM IA and conjugated to rhodamine azide using CuAAC. Samples were separated by SDS-PAGE and visualized by in-gel fluorescence. (**B**) Structure of GSNO. (**C**) Structure of the iodoacetamide alkyne probe. (**D**) Fluorescent gel of A.

A competitive cysteine-labeling strategy to quantitatively measure cysteine sensitivity to GSNO

The extent of cysteine *S*-nitrosation was quantitatively monitored using a mass spectrometry (MS)-based proteomic platform that exploits the characteristic loss in nucleophilicity of a cysteine thiol upon conversion to a *S*-nitrosothiol, which is reflected in decreased reactivity with the IA probe. This platform is derived from the previously reported isotopic tandem orthogonal proteolysis-ABPP (isoTOP-ABPP) method,[31, 33] which reliably and quantitatively monitors the intrinsic reactivity of 500-1000 cysteine residues concurrently within cell and tissue proteomes generated without protein denaturation. To date, the isoTOP-ABPP method and derivatives thereof have been successfully applied to quantitatively measure the loss in cysteine reactivity upon oxidation,[34] reaction with lipid-derived electrophiles,[35] and metal binding.[36] These studies identified cysteine residues that are highly sensitive to these cysteine-modifying agents, resulting in the discovery of functional cysteine residues that regulate protein activity. Therefore, the isoTOP-ABPP platform and its derivatives are ideally suited to quantify the extent of modification by transnitrosation donors (e.g. GSNO) for hundreds of cysteine residues concurrently within a cell proteome. In this approach (Figure 2-2), a cell lysate is exposed to GSNO or a buffer control. Both proteomes are then treated with a cysteine-reactive IA probe, which covalently modifies hundreds of reactive and functional cysteine residues within the proteome. Following alkylation by the iodoacetamide of the IA probe, the terminal alkyne of the IA probe can be further functionalized through (CuAAC) reactions.[30, 31] The IA probe-labeled proteins are covalently linked to light (GSNO-treated sample) or heavy (buffer treated sample) biotin-

azide tags (Azo-L and Azo-H) that contain an azobenzene linker for reductive cleavage by sodium dithionite[33] (Figure 2-2. A). The light and heavy samples are then combined and subjected to streptavidin enrichment, on-bead trypsin digestion, and sodium dithionite cleavage to afford a mixture of light and heavy-labeled peptides for MS analysis. These cysteine-containing isotopically labeled peptides are identified using the fragmentation (MS/MS or MS2) spectra and the relative abundance between the GSNO and control samples is measured by the heavy:light ratio (R) that reflects the intensity of these species in the parent ion (MS1) spectra. An R-value of ~1 signifies a cysteine residue that was unaffected by GSNO treatment, whereas R-values greater than one indicate modification of that cysteine residue by GSNO. A larger R-value reflects a greater percentage of cysteine modification.

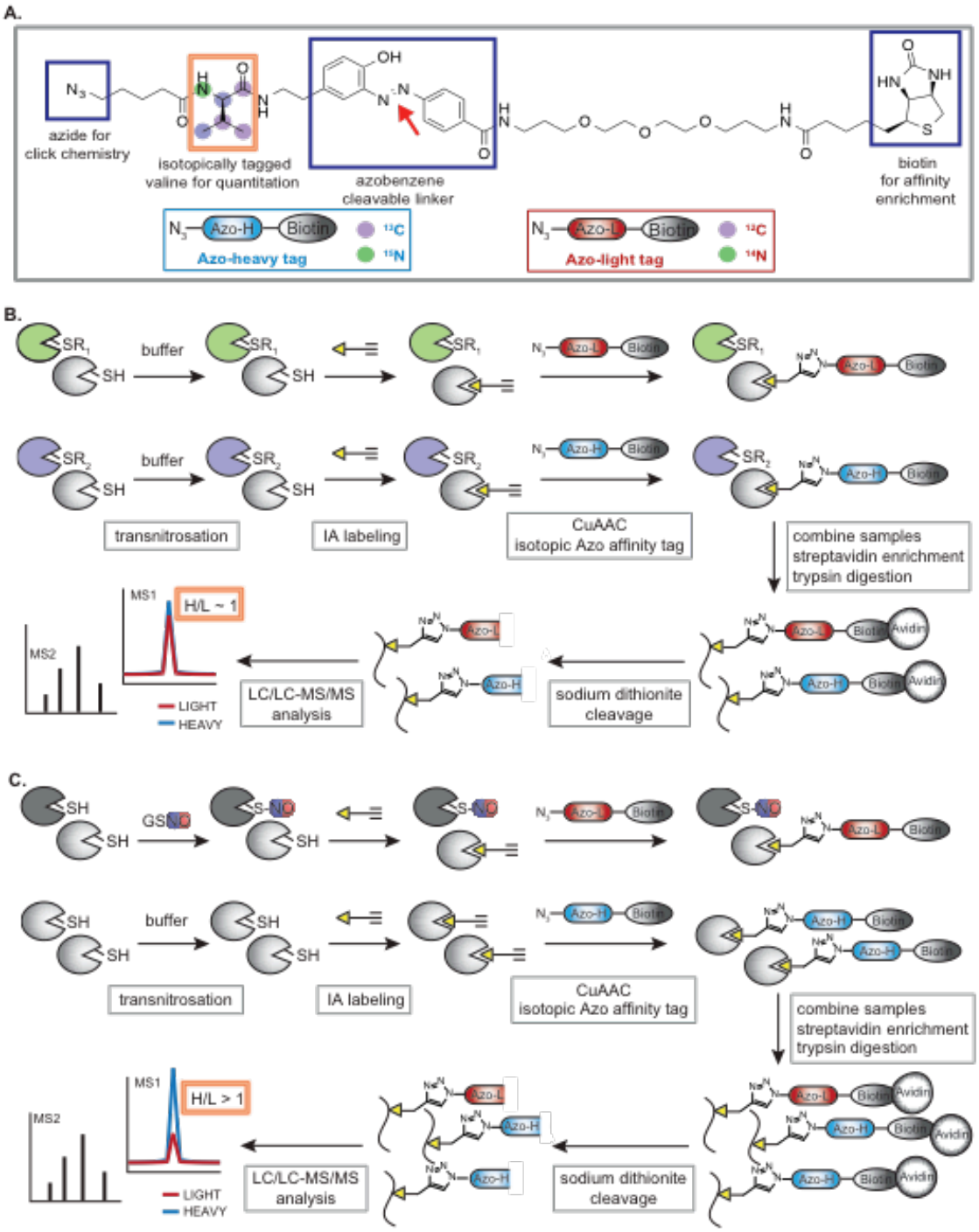


Figure 2-2. A competitive cysteine-profiling strategy to quantify sensitivity to transnitrosation. (**A**) Structure of the Azo-L/Azo-H tags. The atoms ^{12}C and ^{14}N on the valine residue of Azo-L indicated are replaced by ^{13}C and ^{15}N in Azo-H, providing a mass difference of 6 Da between the Azo-L and Azo-H tags. (**B**) and (**C**), Schematic

showing the application of the Azo-L and Azo-H tags for quantitative proteomics. Cell lysates are either treated with only buffer (B), or treated with a transnitrosation donor (*e.g.* GSNO) or a buffer control (C), labeled with the IA probe, and subjected to CuAAC to append either the Azo-L (buffer (B), GSNO (C)) or Azo-H (buffer (B and C)) biotin-azide tags. The resulting isotopically tagged proteomes are mixed together and subjected to streptavidin enrichment and on-bead trypsin digestion. The probe-labeled peptides are eluted by reductive cleavage of the azobenzene with sodium dithionite and analyzed by high resolution LC/LC-MS/MS to identify (MS2) and quantify (MS1) the IA-probe reacted cysteine residues within each sample. A loss in cysteine reactivity is indicative of transnitrosation donor-mediated *S*-nitrosation or other cysteine modification.

Quantitatively measuring cysteine sensitivity to GSNO

MCF-7 breast cancer-cell lysate proteomes were subjected to the following treatments; (1) 500 μM GSNO (light) versus no GSNO added (heavy) as the experimental sample (n=5) (Figure 2-2, C); and (2) both the light and heavy samples left untreated by GSNO as a control (n=2) to verify the quantitative accuracy of the MS approach (Figure 2-2, B). In total, 609 cysteine residues were identified with accurate heavy:light ratios in all of the experimental and control samples (Figures 2-3, A and B). The full dataset is presented in Appendix I as Table 2A-1. As expected, the control samples showed a limited distribution of R-values, closely centered on R = 1. In contrast, the experimental samples showed a wider distribution of R-values, where the majority of cysteine residues exhibited R-values > 1 (Figure 2-3, C). These higher R values are reflective of a loss in reactivity for cysteine residues in the GSNO-treated (light) sample. The majority of

cysteines (583 out of 609; 96%) were minimally affected by GSNO treatment with R-values < 3. However, a small subset of cysteines (27 out of 609) showed high sensitivity (R > 3) to GSNO treatment. P values (Appendix I, Table 2A-1, 2-way ANOVA analysis) indicate the high confidence in the observed decrease in cysteine reactivity for those with ratios >3, which is the cut-off we placed for cysteines that are highly sensitive to GSNO. The proteins containing these GSNO-sensitive cysteines serve diverse cellular functions, and are found in all subcellular compartments (cytoplasm, nucleus, ER, mitochondria, etc.), with the majority located on enzymes or structural proteins according to gene ontology (GO) analysis (Figure 2-4).

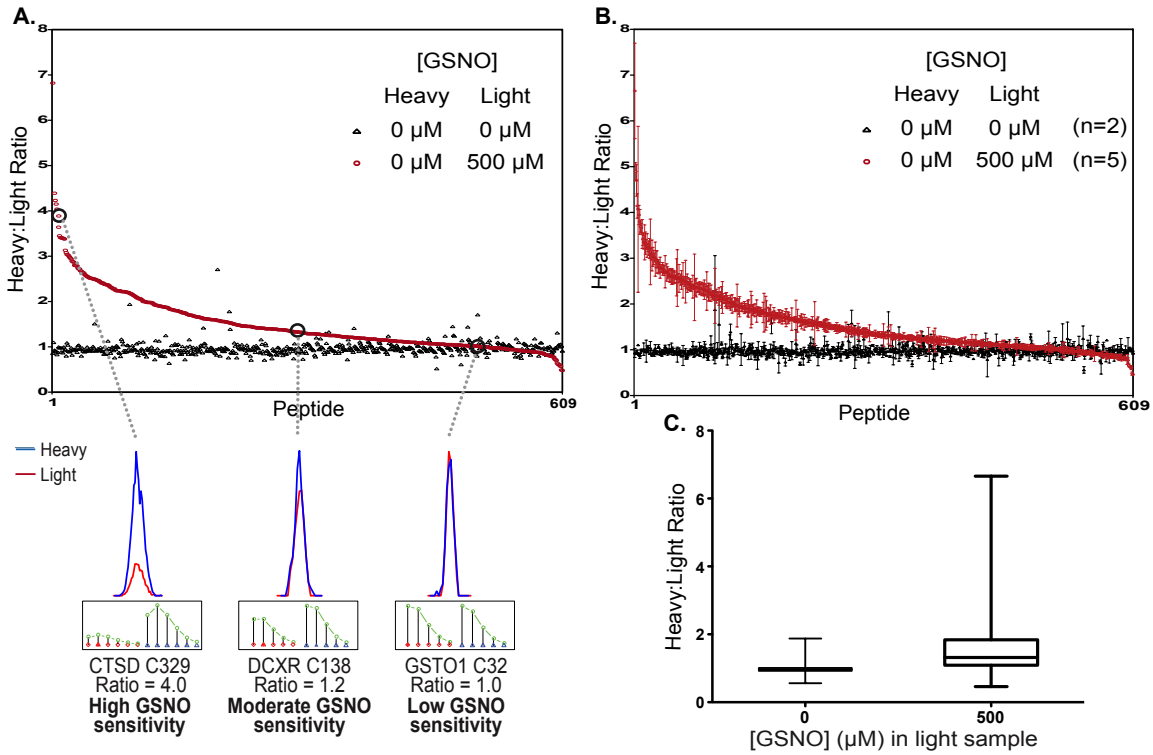


Figure 2-3. Identifying cysteines sensitive to modification by GSNO. (**A**) Heavy:light ratios (R) are shown for 609 cysteine residues identified in GSNO-treated (in red; light: 500 µM GSNO; heavy: buffer;) and control (in black; light: buffer; heavy: buffer) MS analyses (Appendix I, Table 2A-1). R-values from the control sample are centered around

R~1, whereas R-values from the experimental sample show a large proportion of cysteine residues with R>>1, indicating a loss in the free reduced form of individual cysteine residues upon GSNO treatment. A greater R-value is indicative of a higher extent of cysteine modification. Representative extracted ion chromatograms and isotopic envelopes (light: red; heavy: blue) are shown for three cysteine residues with high, moderate, and low sensitivity to GSNO. Ratio values are averaged across the different charge states identified, but displayed chromatograms are for a single representative charge state. The data shown here are for a representative dataset of GSNO and control proteomes. (**B**) Quantitative MS analysis of GSNO-treated cell lysates. Average heavy:light ratios (R) are shown for 609 cysteine residues identified in 5 GSNO-treated (in red; light: 500 μM GSNO; heavy: buffer;) and 2 control (in black; light: buffer; heavy: buffer) MS analyses. Error bars represent standard deviation from the mean across the replicate analyses. A complete list of all identified cysteines are displayed in Appendix I as Table 2A-1 and gene ontology (GO) analyses for cysteine residues sensitive and insensitive to GSNO are shown in Figure 2-4. (**C**) Distribution of R-values for the control and GSNO-treated (500 μM) samples.

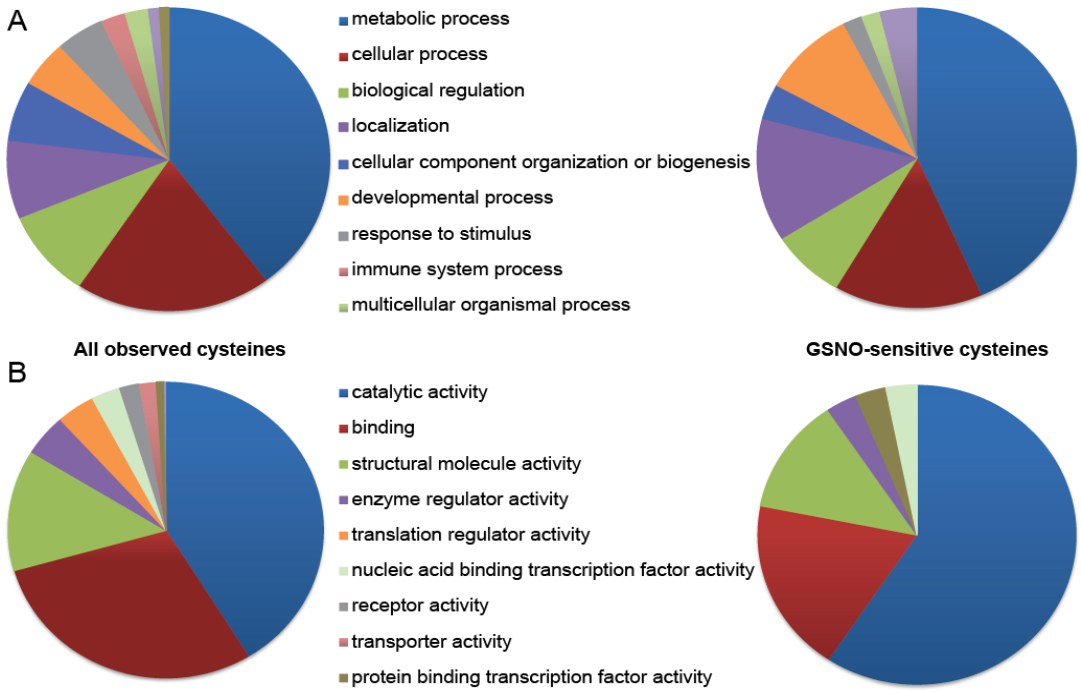


Figure 2-4. Gene ontology (GO) analysis (From data in Appendix I, Table 2A-1). Biological process (**A**) and molecular function (**B**) are shown for all proteins (left) and proteins containing the 27 cysteines with greatest GSNO sensitivity (right) (R >3) from the cysteine-reactivity profiling analyses. GO analysis was performed using PANTHER (www.pantherdb.org).

To evaluate the data obtained here within the context of previously identified sites of *S*-nitrosation, a comparison to the dbSNO database[37] was performed, which integrates data from 219 research articles to generate a list of >3000 S-nitrosation sites obtained through global proteomic analyses. Of the 27 cysteine residues observed to be highly sensitive to GSNO transnitrosation, 14 were previously identified sites of *S*-nitrosation according to the dbSNO database (Appendix I, Table 2A-2). This comparison highlights the ability of this cysteine-profiling platform to identify both known and previously

uncharacterized putative *S*-nitrosation sites. Furthermore, since this platform monitors a loss in cysteine reactivity, it enables the identification of other cysteine modifications (e.g. *S*-glutathionylation) beyond *S*-nitrosation triggered by GSNO treatment.

To evaluate the data obtained here within the context of cysteine functionality, the function of each cysteine residue (active site, metal-binding, redox-active, etc) and its conservation in six different species were denoted as annotated in the UniProt database (Appendix I, Table 2A-1). Several of the cysteines that were highly sensitive to *S*-nitrosation (e.g. AKT1, CTSD, DLD) were annotated as part of a redox-active disulfide according to the UniProt , but there was no significant enrichment in functional cysteines within the subset of residues we identified to be highly susceptible to GSNO-mediated transnitrosation. Moreover, no correlation between cysteine conservation and sensitivity to *S*-nitrosation was observed. Furthermore, in a previous study, it was demonstrated that ratios obtained in such comparative analyses of cysteine reactivity are independent of protein abundance.[31] Because we were comparing the population of unmodified reactive cysteines across two samples and were not looking at absolute amounts of modified protein, the relative abundance of the protein did not contribute to the ratio value obtained.

Importantly, since this platform measures the extent of modification at the level of individual cysteine residues, the sensitivity of multiple cysteine residues within the same protein can be measured in a single experiment. For example, Cys194 in the poly(rC)-binding protein 1 (PCBP1), is highly sensitive to GSNO (R = 3.4) whereas three other observed cysteines, Cys54 (R = 1.2), Cys109 (R = 1.2), and Cys158 (R = 1.0), are insensitive to GSNO (Figure 2-6). In contrast, the three cysteine residues observed for the

chloride intracellular channel protein 1 (CLIC1), Cys24 (R = 1.1), Cys178 (R = 0.8), and Cys223 (R = 1.0), are all insensitive to GSNO (Figure 2-5).

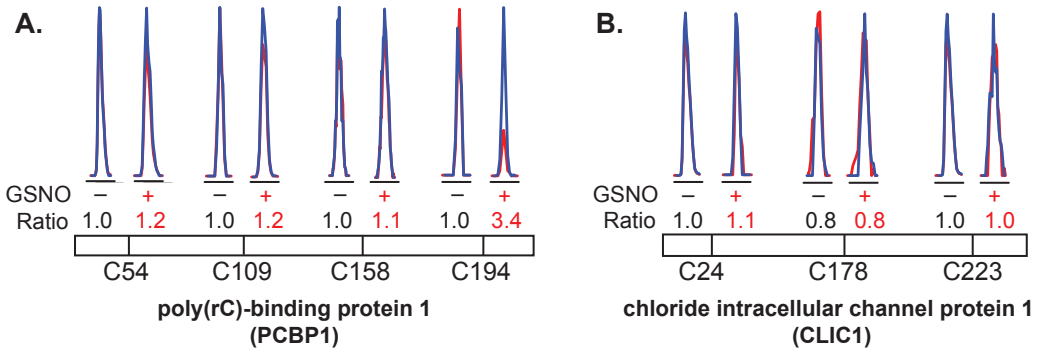


Figure 2-5. Measurement of transnitrosation sensitivity at the level of individual cysteine residues within the same protein. (**A**) Of the four cysteine residues identified in PCBP1, Cys194 demonstrated high sensitivity to GSNO transnitrosation (R=3.4), whereas Cys54, Cys109, and Cys158 were insensitive (R~1). (**B**) All three cysteine residues identified in CLIC1 were insensitive to GSNO transnitrosation compared to the control (0 µM GSNO) sample (R~1).

Of the GSNO-sensitive cysteines, one of the highest R-values of 4.9 was observed for the active-site cysteine, Cys152, in GAPDH, which is indicative of ~80% *S*-nitrosation of this cysteine residue when exposed to 500 µM GSNO. Cys152 is the active-site nucleophile of GAPDH and a well-characterized biologically relevant site of *S*-nitrosation,[15, 16] thereby validating the ability of this platform to detect functionally important sites of *S*-nitrosation. Since the active-site cysteine containing peptide of GAPDH contains two cysteine residues (IISNASC(152)TTNCLAPLAK), we assigned the exact site of modification to a single cysteine residue using our MS/MS fragmentation

data (Figure 2-6, A). We did not find any MS2 spectra that contain the modification at the second cysteine on this peptide.

To alleviate concerns that the TCEP used in the CuAAC reaction could reduce *S*-nitrosated cysteines, which could subsequently react with residual IA remaining in solution, we sought to demonstrate that the IA probe is a limiting reagent and no free IA remains after the initial 1 hr incubation step. It is important to note that we performed all labeling at 100 μM IA probe, which was significantly less than the ~5-10 mM iodoacetamide required to alkylate all cysteines within a proteome in typical proteomic analyses. To confirm that IA is limiting, we performed an experiment (Figure 2-6, B) where we added a purified reactive-cysteine containing protein, protein disulfide isomerase A1 (PDIA1), to a lysate before (lane 3) or after (lane 2) IA labeling. As shown in the fluorescence gel image, negligible PDIA1 labeling was observed when PDIA1 was added after the 1 hour IA incubation step, indicating there was no free IA probe remaining after the 1 hour incubation time. Therefore, it was unlikely that any IA probe is remaining after the addition of the click chemistry reagents to label any newly reduced thiol groups.

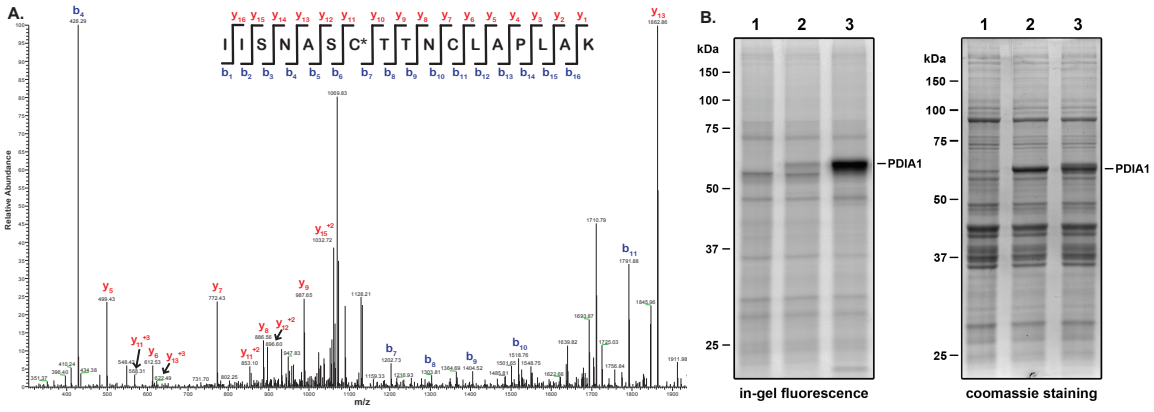


Figure 2-6. (**A**) Manual interrogation of the MS2 fragmentation data assigned the exact site of modification for peptides with two or more cysteines. MS2 fragmentation of peptide IISNASCTTNCLAPLAK of GAPDH was interpreted to assign the b and y ions, with Cys152 as the modified residue. (**B**) IA probe was completely consumed before click chemistry in our analysis platform. Purified PDIA1 was added to a lysate before (lane 3) or after (lane 2) IA labeling, or not added (lane 1), then clicked on Rh-N_3 and resolved in SDS-PAGE. As shown in the fluorescence gel image (left), negligible PDIA1 labeling was observed when PDIA1 was added after the 1 hour IA incubation step, indicating there was no free IA probe remaining after the 1 hour incubation time. Coomassie stain (right) showed the total proteome loaded on the gel.

To further quantify cysteine sensitivity to GSNO, proteomes were treated with varying GSNO concentrations (0, 50, 100, 200, 500 μM) followed by labeling with the IA probe and Azo tags and subsequent MS analysis. R values were quantified at each GSNO concentration for 576 cysteine residues. The full dataset is presented in Appendix I as Table 2A-3. 2-way ANOVA analysis (for P value) was not performed for these data, but since there are five concentrations analyzed, we focus on those cysteines that show

the expected concentration-dependent increases in ratio. Cysteine residues that were highly sensitive to transnitrosation at 500 μM GSNO, such as Cys329 in cathepsin D (CTSD) and Cys58 in HADH2, showed a concentration-dependent increase in modification at increasing GSNO concentrations (Figure 2-7, A). In contrast, Cys32 in glutathione-S-transferase omega 1 (GSTO1) showed a R-value of ~1 at all GSNO concentrations (Figure 2-7, A), confirming GSNO insensitivity. A wide array of GSNO transnitrosation sensitivities were observed as exemplified by plotting the R values at increasing GSNO concentrations for cysteine residues from six different proteins (GAPDH, CTSD, HADH2, L-xylulose reductase (DCXR), GSTO1 and chloride intracellular channel protein 4 (CLIC4)) (Figure 2-7, B).

Two proteins from the list, one highly sensitive to GSNO (CTSD) and one completely insensitive to GSNO (GSTO1), were selected for verification using a secondary detection method. According to the MS data (Appendix I, Table 2A-1 and 2), both CTSD and GSTO1 were selectively labeled by the IA probe at a single cysteine residue. For secondary verification, CTSD and GSTO1 were overexpressed by transient transfection in HEK293T cells with a C-terminal Myc/His tag. The CTSD and GSTO1 overexpressing cells were lysed and the resulting proteomes were split into five aliquots and treated with four GSNO concentrations or left untreated. These samples were then treated with the IA probe followed by CuAAC and enrichment steps identical to that used for the MS analysis. After the streptavidin enrichment, proteins were eluted from the streptavidin beads with sodium dithionite, separated by SDS-PAGE, and analyzed by immunoblotting with an anti-Myc antibody. Protein cysteine modification is expected to decrease IA-probe labeling, reflected by reduced protein detection in the immunoblot. In

agreement with the MS data, GSTO1 enrichment was not affected by GSNO treatment (Figure 2-7, C), confirming the insensitivity of GSTO1 to GSNO. In contrast, CTSD enrichment showed a concentration-dependent decrease upon GSNO treatment, mirroring the increasing R values observed in the MS studies for CTSD Cys329 at increasing GSNO concentrations (Figure 2-7, C). These immunoblotting studies, therefore, provide a secondary verification of the quantitative MS platform.

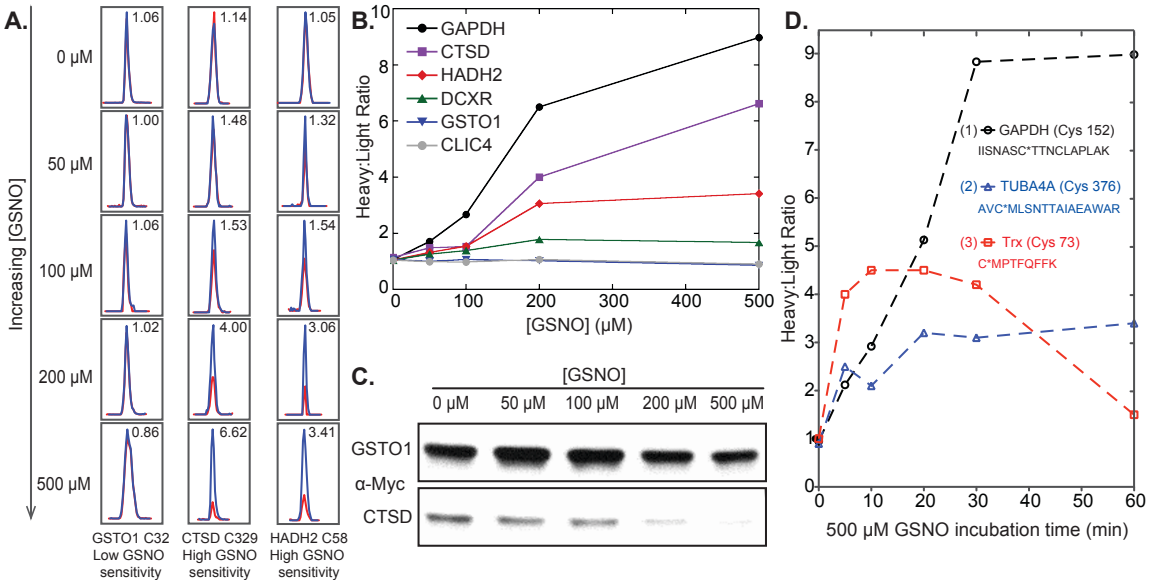


Figure 2-7. Systematic analysis of cysteine-reactivity upon GSNO treatment. **(A)** Concentration-dependent analysis. The light-tagged proteomes were treated with 0, 50, 100, 200, or 500 μM GSNO and compared to a buffer-treated heavy-tagged sample. Heavy:light ratio values (R) were obtained for each identified cysteine residue at every GSNO concentration (Appendix I, Table 2A-3). Representative extracted ion chromatograms (light:red; heavy:blue) are shown for a cysteine residue that is insensitive to GSNO (GSTO1) and two cysteine residues with high GSNO sensitivity (CTSD and HADH2). Cysteine residues with high sensitivity to GSNO show a clear concentration-dependent increase in R values. **(B)** R values are plotted with increasing GSNO

concentration for six cysteine residues (from CLIC4, GSTO1, DCXR, HADH2, CTSD, and GAPDH) with varying sensitivity to GSNO transnitrosation. The quantitative nature of the analysis allows ranking of cysteine residues by their sensitivity to GSNO transnitrosation. **(C)** Corroboration of the MS-based identification of cysteine sensitivity and insensitivity using a gel-based assay for two proteins. Myc/His-tagged GSTO1 or CTSD overexpressing cell lysates were treated with varying GSNO concentrations, followed by IA labeling. IA-labeled proteins were tagged with biotin using CuAAC and subjected to streptavidin enrichment, SDS-PAGE analysis, and immunoblotting with an anti-Myc antibody. A decrease in CTSD enrichment was observed at increasing GSNO concentrations, indicative of decreased cysteine reactivity and therefore IA labeling upon GSNO treatment. In contrast, no change in IA labeling and GSTO1 enrichment was observed at increasing GSNO concentrations, indicating insensitivity of the GSTO1 cysteine residues to GSNO. **(D)** Time-dependent analysis. R values are plotted with increasing 500 μM GSNO incubation time for three cysteine residues (from GAPDH Cys152, TUBA4A Cys376 and Trx Cys73) representative of cysteines that are characterized by a variety of kinetic patterns of GSNO transnitrosation and lifetime of the *S*-nitrosated species.

In addition to the concentration-dependent labeling experiment, a time-dependent analysis was performed to explore how the abundance of the various *S*-nitrosated species changes within a 60-min incubation period with GSNO (Appendix I, Table 2A-4). In this analysis, 191 cysteine-containing peptides were identified with ratios at 5 different time points (5, 10, 20, 30 and 60 mins). These cysteines could be categorized into three classes

that indicate the kinetics of *S*-nitrosation and the lifetime of each species within cell lysates: (1) a gradual increase in cysteine modification with time; (2) an initial increase in modification that stays constant with time; and (3) an increase in modification at a short time point that then decreases with time (Figure 2-7, D). The active-site cysteine in GAPDH falls into the first category, whereby a steady increase in modification is observed over time. Interestingly, Cys73 of thioredoxin (Trx) falls into the third category, where maximal modification is observed at 10 mins (R = 4.5) followed by a decrease in modification at 60 mins (R = 1.6). This observation suggests that *S*-nitrosated Cys73 in thioredoxin has a short lifetime in cell lysates relative to the other *S*-nitrosated species we identify, and agrees well with the previously characterized role of Cys73 *S*-nitrosated thioredoxin as a transnitrosating agent that is able to *S*-nitrosate a variety of cellular proteins.[10]

Functional characterization of Cys58 in HADH2

To identify previously uncharacterized cysteine residues on enzymes within the human proteome that are posttranslationally regulated by *S*-nitrosation, the GSNO proteomics data was searched for cysteine residues that satisfied the following criteria: (1) demonstrated high sensitivity and clear concentration-dependence to GSNO transnitrosation (R > 1.3 at 50 μM GSNO, R > 1.5 at 100 μM GSNO, and R > 3 at 200 μM GSNO); (2) were not known active-site or regulatory cysteine residues; (3) were located distal to the active site of the enzyme; and (4) were found on enzymes implicated in human disease. Only two cysteine residues satisfied these four criteria–HADH2 Cys58 and CTSD Cys329–and were characterized further.

HADH2 (a.k.a. HSD17B10, HCD2, ERAB, MRPP2, SCHAD, and XH98G2), encoded by the *HSD17B10* gene, is a mitochondrial multifunctional protein. Due to the flexible accommodation of its active site to diverse substrates, HADH2 is involved in a variety of metabolic pathways, catalyzing the oxidation of several neuroactive steroids (e.g. 17β-oestradiol, 3α-androstanediol and oestrone)[38], sex hormones such as androgens and estrogens[39], isoleucine and xenobiotics[40]. Importantly, it is characterized as a short-chain L-Hydroxyacyl-CoA dehydrogenase (SCHAD) to catalyze the third step in fatty acid beta-oxidation (Figure 2-8, A).[39, 41] HADH2 also has several non-catalytic functions, including forming a complex with mitochondrial ribonuclease P and amyloid-beta.[42, 43] Studies showed that missense mutations of HADH2 led to aberrant enzyme activity, abolishing the catalytic function in the degradation of isoleucine, affecting the homeostasis of neuroactive steroid metabolism and biogenesis of brain cells. The abnormality caused by HADH2 dysfunction is implicated in altered mitochondrial structure and functions,[38] attributing to the cause of neurological disorders such as Alzheimer's disease and Parkinson's disease.[42-44] Furthermore, inherited HADH2 mutations lead to 2-methyl-3-hydroxybutyryl-CoA dehydrogenase deficiency, which is characterized by neurological abnormalities.[45]

Since the cysteine-profiling platform indirectly measures *S*-nitrosation through loss in cysteine reactivity, and since GSNO can result in both *S*-nitrosation or glutathionylation, the ability of GSNO to *S*-nitrosate and glutathionylate HADH2 were directly compared. Recombinantly expressed and purified HADH2 (Figure 2-8, D) was treated *in vitro* with increasing GSNO concentrations and split into two samples for analysis of glutathionylation and *S*-nitrosation. While HADH2 glutathionylation was not

observed under these conditions, a clear concentration-dependent increase in HADH2 *S*-nitrosation was observed by the BST (Figure 2-8, C) indicating that GSNO treatment of HADH2 selectively results in *S*-nitrosation. To ascertain the relative sensitivity of HADH2 cysteine residues towards GSNO, NO (released from DEA NONOate), and the alternative transnitrosating agent *S*-nitrosocysteine (Cys-SNO) was determined. Purified HADH2 protein (Figure 2-8, D) was treated *in vitro* with increasing concentrations of GSNO, DEA NONOate, or Cys-SNO and then monitored for *S*-nitrosation by the BST. HADH2 showed increasing levels of *S*-nitrosation up to 30 μM GSNO without further increases in *S*-nitrosation at up to 100 μM GSNO (Figure 2-8, C and E). Conversely, DEA NONOate treatment did not result in low levels of *S*-nitrosation near the detection limit of the BST (Figure 2-8, F), indicating HADH2 is uniquely sensitive to GSNO transnitrosation compared to NO-derived reactive nitrogen species. The observed HADH2 *S*-nitrosation signal was ascorbate-dependent, further confirming GSNO treatment results in *S*-nitrosation (Figure 2-8, E and F). To determine if HADH2 possesses a GSNO binding site that is necessary for transnitrosation, *S*-methylglutathione (MeGSH) was used as a competitive inhibitor. Increasing *S*-methylglutathione concentrations partially diminished GSNO transition of HADH2 consistent with GSNO transnitrosation of HADH2 preceding through a GSNO-binding step (Figure 2-8, G). The inability of *S*-methylglutathione to fully compete against GSNO transnitrosation even at concentrations up to 3 mM may be due to the irreversibility of *S*-nitrosation under these conditions.

Although HADH2 contains four cysteine residues, the concentration-dependent cysteine-profiling studies identified Cys58 as the only cysteine residue in HADH2

sensitive to increasing GSNO concentrations (Appendix I, Table 2A-3). Cys58 is located distal to the HADH2 active site within a hydrophobic pocket flanked by two leucine residues (Leu39 and Leu54) (Figure Figure 2-8, B). To investigate the functional consequences of Cys58 modification, this cysteine was first confirmed to be a target of *S*-nitrosation both in vitro and in cells. HADH2 transnitrosation by GSNO was dependent on the presence of Cys58 (Figure 2-8, F and H), confirming that GSNO selectively modifies HADH2 at only one cysteine residue, Cys58. To confirm HADH2 is selectively *S*-nitrosated at Cys58 in the context of a proteome, HEK293T cell lysates overexpressing HADH2 with a C-terminal Myc/His tag were treated with GSNO, and as seen with recombinant HADH2, HADH2 WT but not HADH2 C58S was *S*-nitrosated under these conditions (Figure 2-8, I). Overexpressed Myc/His tagged HADH2 exhibited immunofluorescence staining consistent with the mitochondrial localization of endogenous HADH2 (Figure 2-8, J). As HADH2 contains four cysteine residues, the BST data both confirms that HADH2 is transnitrosated at low micromolar GSNO concentrations and that GSNO selectively modifies only one cysteine residue, Cys58, which was identified in the concentration-dependent cysteine-profiling studies as the only cysteine residue in HADH2 sensitive to increasing GSNO concentrations (Appendix I, Table 2A-3).

To determine if HADH2 is selectively *S*-nitrosated in intact cells and if this *S*-nitrosation requires endogenous nitric oxide synthase (NOS) activity, HEK293T cells overexpressing HADH2 WT or C58S were treated with a pan-NOS inhibitor (L-N-nitroarginine methyl ester; L-NAME), an iNOS specific inhibitor (1400W), or left untreated, and HADH2 *S*-nitrosation was monitored using the BST. *S*-nitrosation of

HADH2 WT but not HADH2 C58S was observed in cells without exogenous NO or *S*-nitrosothiol addition (Figure 2-8, K). Although the exact cellular GSNO concentrations are unknown, previous studies showed that endogenous levels of GSNO in a variety of cell lines ranges from ~1-4 μM, and macrophages activation results in a ~2-fold increase in cellular GSNO concentrations.[8] Furthermore, NOS inhibition resulted in decreased HADH2 WT *S*-nitrosation for the pan-NOS inhibitor (L-NAME) but not the iNOS specific inhibitor (1400W) (Figure 2-8, K), indicating that HADH2 is endogenously *S*-nitrosated at Cys58 by eNOS or nNOS activity and that either iNOS activity does not lead to HADH2 *S*-nitrosation or iNOS is not expressed under these conditions. Gene expression profiling studies show the presence of both eNOS and nNOS transcript in HEK293T cells, but the relative protein levels of eNOS and nNOS are unknown. To determine if HADH2 is *S*-nitrosated by NO endogenously generated by iNOS, HADH2 *S*-nitrosation was monitored in A549 cells, a human adenocarcinoma line in which iNOS can be induced with cytokines. A549 cells overexpressing HADH2 WT or C58A were treated with cytokines (IFNγ, TNF-α and IL-1β) with and without the pan-NOS inhibitor L-NAME, and HADH2 *S*-nitrosation was monitored using the BST. Cytokine-treated HADH2 WT was *S*-nitrosated under these conditions; *S*-nitrosation was diminished in the presence of L-NAME, in the absence of cytokines, by omitting ascorbate in the BST in cells transfected with HADH2 WT, and by removal of Cys58 in the HADH2 C58A mutant (Figure 2-8, F). These results in A549 cells are consistent with the results in HEK293T cells, where HADH2 is selectively *S*-nitrosated at Cys58 by endogenous NOS activity. Furthermore, these results suggest that NO synthesized by NOS, while not

capable of directly *S*-nitrosating HADH2 (Figure 2-8, E), generates transnitrosating agents (e.g. GSNO) that then transnitrosate HADH2.

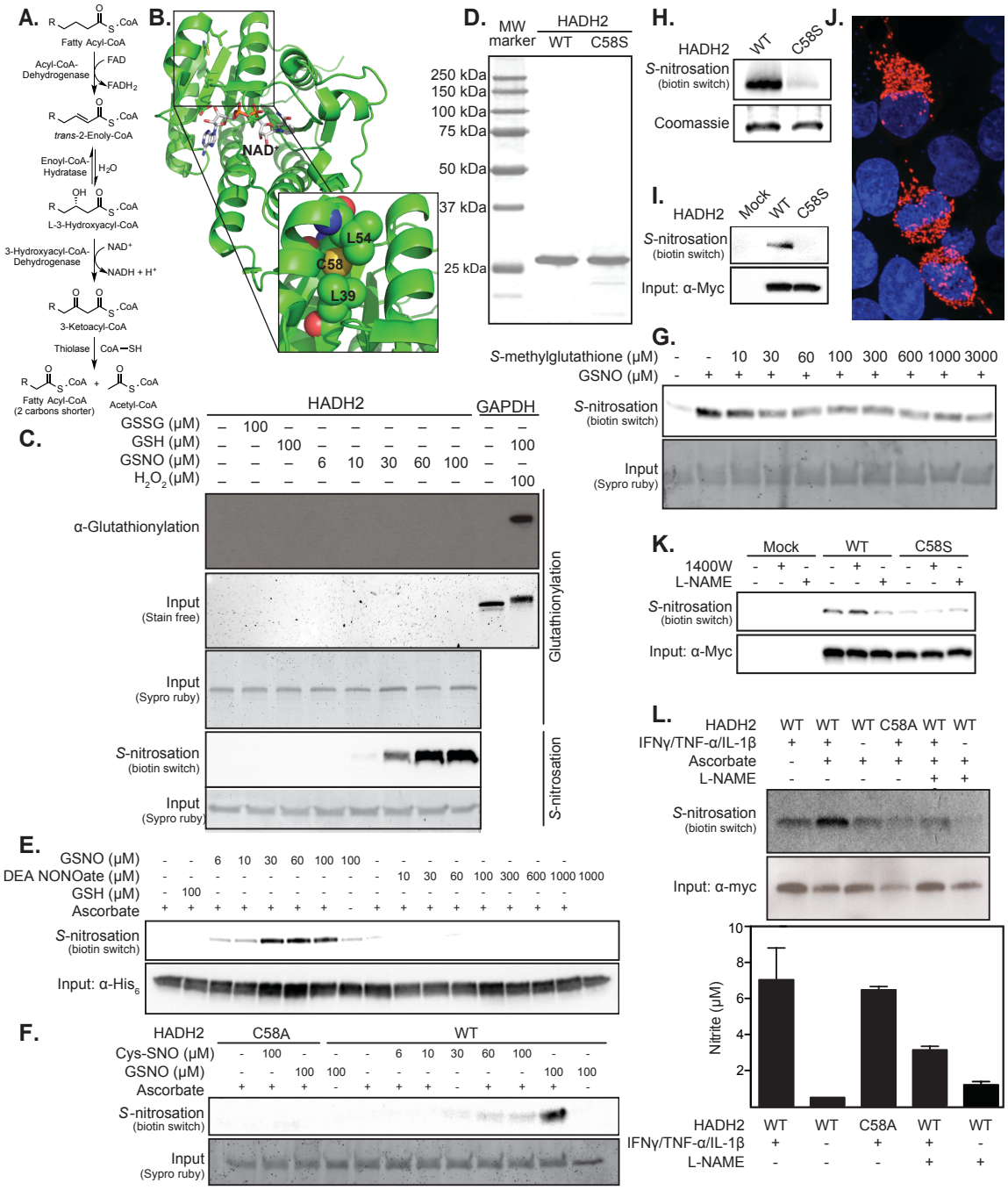


Figure 2-8. HADH2 is selectively *S*-nitrosated at Cys58. (**A**) Pathway of β–oxidation of fatty acids. It starts with the oxidation of C_a-C_b bond of fatty Acyl-CoA to a double bond,

which undergoes a hydration reaction to make a Hydroacyl-CoA. The second oxidation, catalyzed by HADH2, is then taken place to oxidize the hydroxyl group at the beta position to a Ketoacyl-CoA. The pathway is terminated by thiolase to cleave the beta Ketoacyl-CoA and produce an acetyl-CoA and a fatty acid that is shortened by two carbons. (**B**) Structure of HADH2 (PDB: 2O23) with NAD^+ bound in the active site. The GSNO transnitrosation-sensitive cysteine, Cys58, is located distal to the active site within a hydrophobic pocket flanked by Leu39 and Leu54 (inset). (**C**) HADH2 is not glutathionylated when treated with 100 μM GSSG, 100 μM GSH, or 6-100 μM GSNO. GAPDH treated with 100 μM GSH and 100 μM H_2O_2 is used as a positive control for glutathionylation. In contrast, the same HADH2 samples analyzed by the BSM show increasing *S*-nitrosation at increasing concentrations of GSNO. SYPRO Ruby stained gels are shown to control for protein loading. (**D**) Purified HADH2 WT and C58S mutant. Silver-stained gel shows HADH2 that was recombinantly expressed and purified as described in Experimental Procedures. (**E**) *S*-nitrosation of recombinantly expressed and purified HADH2 WT treated with varying concentrations of GSNO or DEA NONOate. Silver-stained gel of purified HADH2 WT and C58S is shown in **D**. (**F**) *S*-nitrosation of recombinantly expressed and purified HADH2 WT and C58A treated with varying concentrations of GSNO or Cys-SNO. (**G**) *S*-nitrosation of recombinantly expressed and purified HADH2 WT pretreated with GSNO and then treated with increasing concentration of *S*-methylglutathione. (**H**) *S*-nitrosation of recombinantly expressed and purified HADH2 WT and C58S treated with 100 μM GSNO. (**I**) HADH2 *S*-nitrosation in lysates from HEK293T cells overexpressing mock (empty vector), HADH2 WT, or HADH2 C58S treated with 100 μM GSNO. (**J**) Immunofluorescence

staining of the mitochondrial localization of endogenous HADH2 and overexpressed Myc/His tagged HADH2. (**K**) HADH2 *S*-nitrosation in HEK293T cells overexpressing mock (empty vector), HADH2 WT, or HADH2 C58S were treated with DMSO (control), L-NAME (pan-NOS inhibitor), or 1400W (iNOS-selective inhibitor). (**L**) HADH2 *S*-nitrosation in A549 cells overexpressing HADH2 WT or HADH2 C58A were treated with cytokines (IFNγ, TNF-α, IL-1β) and/or L-NAME. In panels **B**-**L**, *S*-nitrosation was monitored using the biotin-switch technique as detailed under Experimental Procedures.

Upon confirming that Cys58 in HADH2 is targeted by *S*-nitrosation, the effect of *S*-nitrosation on HADH2 enzymatic activity was investigated (Figure 2-9, A). Initially, the activities of recombinant HADH2 WT and C58A (Figure 2-9, B) were compared. The catalytic efficiency (k_{cat}/K_M) at varying acetoacetyl-CoA concentrations for HADH2 C58A (923 ± 90 $M^{-1}s^{-1}$) was indistinguishable from that of HADH2 WT (888 ± 37 $M^{-1}s^{-1}$). Treatment with GSNO led to a significant ~50% decrease ($p = 0.005$) in catalytic efficiency for the HADH2 WT protein (456 ± 27 $M^{-1}s^{-1}$), whereas HADH2 C58A activity was unaffected by GSNO treatment (906 ± 149 $M^{-1}s^{-1}$). Further kinetic analysis at sub-saturating substrate concentrations demonstrated clear GSNO concentration-dependent inhibition of HADH2 WT (Figure 2-9, C). Therefore, HADH2 *S*-nitrosation affects the ability of acetoacetyl-CoA to bind or form a catalytically productive complex, likely through long-range structural perturbations that disrupt active-site recognition or positioning of the acetoacetyl-CoA substrate for catalysis. Interestingly, a ~75% decrease in catalytic efficiency (k_{cat}/K_M) at varying acetoacetyl-CoA concentrations was observed for HADH2 C58S (196 ± 41 $M^{-1}s^{-1}$) relative to HADH2 WT, even in the absence of

GSNO (Figure 4-9, D). Replacement of Cys58 by the more polar serine likely disrupts the hydrophobic pocket defined by Leu39 and Leu54, in which Cys58 is located (Figure 2-8, B). *S*-nitrosated Cys58 is likely similarly poorly accommodated within this hydrophobic pocket, resulting in structural alterations that are transmitted to the active site. To determine if HADH2 activity is uniquely sensitive to GSNO compared to other cysteine-oxidizing agents, HADH2 WT was treated with varying concentrations of GSNO, NO (released from DEA NONOate), peroxynitrite (released from SIN-1), oxidized glutathione (GSSG), and hydrogen peroxide. Kinetic analyses at sub-saturating acetoacetyl-CoA concentrations demonstrated clear concentration-dependent inhibition of HADH2 WT by GSNO, but inhibition was not observed for HADH2 WT treated with the other oxidants or HADH2 C58A treated with GSNO (Figure 2-9, E). Taken together, these studies identify a previously uncharacterized site of GSNO transnitrosation and demonstrate that HADH2 activity is allosterically regulated through this posttranslational modification.

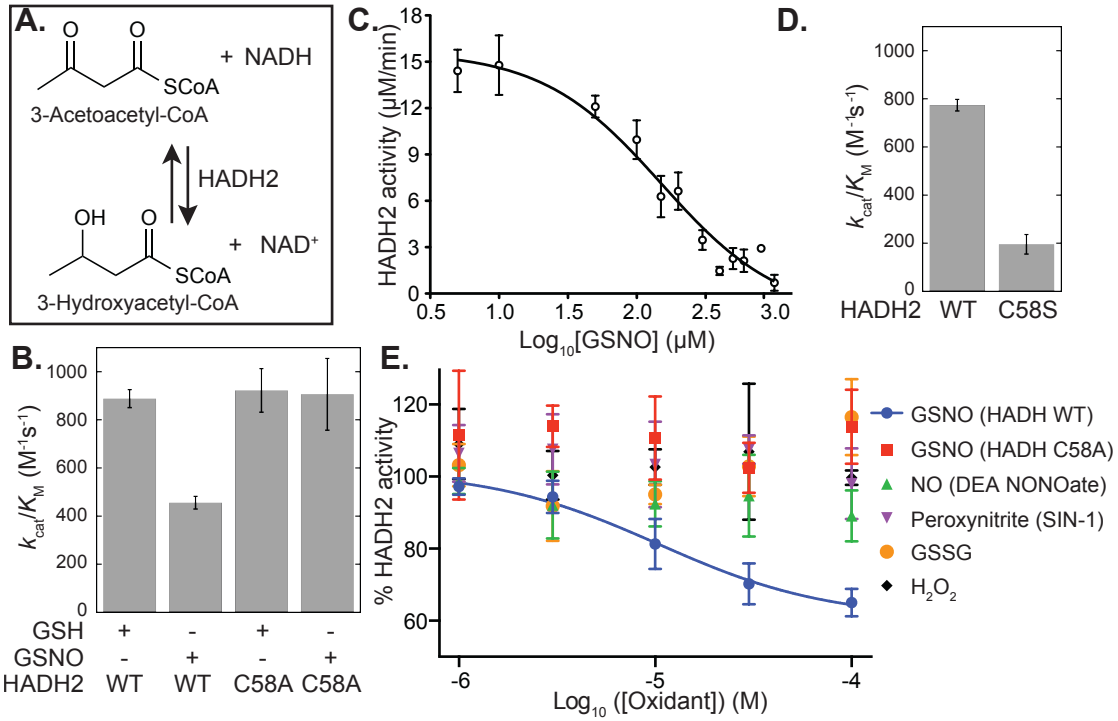


Figure 2-9. Functional characterization of Cys58 of HADH2. (**A**) HADH2-catalyzed reduction of acetoacetyl-CoA by NADH monitored *in vitro* by a decrease in absorbance at 340 nm. (**B**) Catalytic efficiency (k_{cat}/K_M) for WT and C58A-mutant HADH2 with varying acetoacetyl-CoA concentrations in the presence of 100 μM GSNO or GSH. (**C**) Effect of GSNO on WT HADH2 activity**.** HADH2 WT activity was monitored as described in Methods in the presence of increasing concentrations of GSNO. Error bars represent standard deviation from the mean. (**D**) Catalytic efficiency (k_{cat}/K_M) for WT and C58S mutant HADH2 with varying acetoacetyl-CoA concentrations. (**E**) Effect of cysteine oxidants on HADH2 activity. HADH2 WT and C58A activity was monitored as described in Experimental Procedures in the presence of increasing concentrations of GSNO, DEA NONOate, SIN-1, GSSG, or H_2O_2. Error bars represent standard error from the mean.

Conclusion

With the advent of proteomic methods to study *S*-nitrosation within complex proteomes ~3,000 cysteine residues targeted by *S*-nitrosation have been identified, which testifies to the ubiquity of this modification as a potential redox-regulatory signaling mechanism. However, the majority of these proteomic methods are qualitative and unable to differentiate between an abundant protein with a low percentage of *S*-nitrosation and a low-abundance protein with a high percentage of *S*-nitrosation. To discover functionally relevant *S*-nitrosation sites, a competitive cysteine-profiling strategy was utilized to concurrently and quantitatively rank 609 cysteine residues by their sensitivity to GSNO (Figure 2-3). In validation of this approach, one of the most sensitive cysteine residues to GSNO was the active-site cysteine of GAPDH, which is a well-established site of *S*-nitrosation that leads to GAPDH nuclear translocation, transnitrosation of nuclear proteins, and induction of apoptosis.[11, 15, 16] The cysteine-profiling platform described herein affords several advantages over the BST, primarily the ability to quantify the extent of modification of individual cysteine residues. However, several limitations currently exist that may be improved in subsequent iterations of this platform. The platform is optimized for analysis of cell lysates treated with exogenous GSNO at largely physiological concentrations. The data obtained provide important insight into the sensitivity of hundreds of cysteines to GSNO treatment, and for HADH2 in particular, the *in vitro* data correlated with cellular data (Figure 2-8 and 2-9). However, some targets may not be *S*-nitrosated to the extent predicted by the cysteine profiling platform either due to lower cellular GSNO levels or different reducing environments in distinct cellular compartments that could reduce the resulting *S*-nitrosothiol. Furthermore, the sensitivity

of the current platform does not allow accurate quantification where the stoichiometry of modification is less than 5%.

This cysteine-profiling platform enabled identification and functional annotation of an uncharacterized mode of regulation through *S*-nitrosation. The dehydrogenase HADH2 was shown to be *S*-nitrosated at Cys58 and *S*-nitrosation of this distal cysteine allosterically inhibited HADH2 enzymatic activity. *S*-nitrosation of Cys58 is hypothesized to disrupt the hydrophobic interactions surrounding this cysteine residue (Figure 2-8, B) resulting in long-range structural perturbations that reduce the ability of the acetoacetyl-CoA substrate to bind or form a productive catalytic complex in the HADH2 active site. Further studies are needed to determine if increased HADH2 *S*-nitrosation contributes to Alzheimer's disease and other neurological disorders[42-44] that exhibit decreased HADH2 activity. Importantly, even though the initial proteomic studies that indicated HADH2 is highly sensitive to GSNO were performed at supraphysiological GSNO concentrations, follow-up characterization demonstrated Cys58 of HADH2 is *S*-nitrosated under physiologically relevant and endogenously generated nitrosative stress. This observation further underscores the promise of translating GSNO sensitivity data acquired through cysteine-reactivity profiling in cell lysates to (patho)physiologically relevant sites of *S*-nitrosation.

In conclusion, the application of a competitive cysteine reactivity profiling strategy to investigate transnitrosation unearthed two previously uncharacterized and mechanistically distinct modes of allosteric protein regulation through *S*-nitrosation. Future studies will focus on further functional characterization of unannotated *S*-

nitrosation-sensitive cysteine residues identified in these global MS studies, as well as expansion of this platform to other biologically relevant transnitrosation donors.

Acknowledgement

I would like to acknowledge Dr. Shalise Couvertier for her study on functional characterization of cysteine 329 in CTSD (not included in this thesis). I would also like to thank Dr. Michael A. Marletta and Dr. Sarah L. Wynia-Smith, Dr. Kelsey S. Kalous and Dr. Brian C. Smith from Marletta lab for their investigation of cysteine function in HADH2 and CTSD using Biotin Switch Method. I thank Megan C. Harwig for assistance with immunofluorescence staining. Special thanks to Lisa Crawford for her help on analyzing MS spectrums. I would also like to acknowledge Dr. Alex Shannon, Dr. Dan Bark and Tyler Bechtel for their continued help maintaining the Orbitrap mass spectrometer and also for their assistance in data analysis.

Experimental Procedures

Reagents and general procedures.

All materials were purchased from Sigma Aldrich (Milwaukee, WI) unless otherwise noted. RPMI 1640 medium, DMEM/High glucose medium, phosphate buffered saline (PBS), 2% Trypsin-EDTA and penicillin/streptomycin (Pen/Strep) were purchased from Fisher Scientific (Pittsburgh, PA). Rabbit-anti-Myc (2278S), rabbit-anti-CTSD

(2284S), and goat-anti-rabbit HRP-conjugated IgG (7074S) were purchased from Cell Signaling (Danvers, MA). Rabbit anti-Myc (MA5-15125) and goat anti-rabbit HRP-conjugated IgG (31463), goat anti-mouse HRP-conjugated IgG (31439) were purchased from Pierce/ThermoFisher Scientific (Grand Island, NY). Mouse-anti-His6 antibody (AM1010A) was purchased from ABgent (San Diego, CA). Cathepsin D Activity Assay Kit was purchased from BioVision (Mountain View, CA). X-tremeGENE 9 DNA transfection reagent was purchased from Roche (Indianapolis, IN). Polyethylenimine MW25K (PEI) transfection reagent was purchased from Polyscience, Inc (Warrington, PA). Protein concentrations were determined using a Bio-Rad DC protein assay or Bradford Protein Concentration assay from Bio-Rad Life Science (Hercules, CA) or a bicinchoninic acid (BCA) assay from Pierce. Streptavidin-agarose beads, Ni-NTA beads and SuperSignal West Pico Chemiluminescent Substrate were purchased from Thermo Scientific (Armarillo, TX). QuikChange Site-Directed Mutagenesis Kit was purchased from Agilent Technologies (Santa Clara, CA). Illustra Nap-5 Columns were purchased from GE Healthcare Bio-Sciences (Piscataway, NJ). Micro BioSpin-6 desalting columns were purchased from Bio-Rad Life Science (Hercules, CA). Ni-NTA Magnetic Agarose Beads were purchased from QIAGEN (Valencia, CA). GSNO, DEA NONOate, and L-NAME were purchased from Cayman Chemicals (Ann Arbor, MI).

Cell Culture.

MCF7 and HEK293T cells were maintained in RPMI1640 medium and DMEM medium (with 2 mM glutamine), respectively. Media was supplemented with 10% fetal

bovine serum (FBS) and 1% Pen/Strep. Cells were grown at 37 °C under an atmosphere of 5% CO_2.

Preparation of MCF7 cell lysates.

Cells were grown to 100% confluency and harvested by scraping. The cells were washed three times with PBS, resuspended in an appropriate volume of PBS and sonicated to obtain whole-cell lysates. The lysates were then separated by ultracentrifugation at 45,000 rpm at 4 °C under high vacuum for 45 min. The resulting supernatant was collected as the soluble proteome. Protein concentrations were determined using the Bradford Protein Concentration Assay.

Mass-spectrometry analysis of GSNO-treated MCF7 lysates.

S-nitrosoglutathione (GSNO) was dissolved in freshly-made HEN buffer (125 mM HEPES pH 7.7, 1 mM EDTA, 0.1 mM neocuproine). The GSNO concentration was determined by measuring the UV absorbance at 336 nm based on an extinction coefficient of 0.9 $mM^{-1}cm^{-1}$. MCF7 cell lysates (4 mg total protein/mL) were aliquoted to 500 µL and incubated with 5 µL HEN buffer or 5 µL of GSNO (50 µM, 100 µM, 200 µM, or 500 µM final concentration) in HEN buffer at 37 °C for 1 hr. Excess GSNO was then removed by filtration through a Nap-5 column. Proteins were eluted with 1 mL PBS and aliquoted to produce two 500 µL samples.

Each 500 µL sample was treated with 100 µM IA probe using 5 µL of a 10 mM stock in DMSO. The labeling reactions were incubated at room temperature for 1 hr. Click chemistry was performed by the addition of either Azo-L or Azo-H (100 µM, 5

mM stock in DMSO), tris(2-carboxyethyl)phosphine hydrochloride (TCEP) (1 mM, fresh 50 mM stock in water), tris[(1-benzyl-1H-1,2,3-triazol-4-yl)methyl]amine (TBTA ligand) (100 μM, 17× stock in DMSO:t-Butanol 1:4) and $CuSO_4$ (1 mM, 50 mM stock in water). Samples were allowed to react at room temperature for 1 hr. The Azo-L and Azo-H samples were mixed together immediately following click chemistry. Precipitated proteins were pelleted by centrifugation at 6500 × g (10 min, 4 °C). The pellets were washed twice by resuspending the pellet in cold methanol, after which the pellets were solubilized in PBS containing 1.2% w/v SDS via sonication and heating (5 min, 80 °C).

The SDS-solubilized, probe-labeled proteome samples were diluted with PBS to a final SDS concentration of 0.2% w/v. The solutions were incubated with 100 μL streptavidin-agarose beads at 4 °C for 16 hr, followed by incubation at room temperature for 2.5 hr. The beads were washed sequentially with 0.2% w/v SDS/PBS, PBS, and water, and pelleted by centrifugation (1300 × g, 2 min) between washes.

The washed beads were suspended in 500 μL 6 M urea/PBS and 10 mM dithiothreitol (DTT, from 200 mM stock in water) and placed in a 65 °C heat block for 15 min. 20 mM iodoacetamide (from 1 M stock in water) was then added and incubated at 37 °C for 30 min. Following reduction and alkylation the beads were pelleted by centrifugation (1300 × g, 2 min), re-suspended in 200 μL of 2 M urea/PBS, 1 mM $CaCl_2$ (100 mM stock in water) and trypsin (2 μg), and digested overnight at 37 °C. The digest was washed with PBS and water. The azobenzene linker was cleaved with 50 mL of fresh 25 mM sodium dithionite/PBS for 30 min at room temperature on a rotator, followed by centrifugation to collect supernatant. The sodium dithionite cleavage was repeated twice and then the beads were washed with water (2 × 75 μL). All supernatants and washes

were combined and acidified with 15 µL formic acid. The samples were stored at -20 °C until mass spectrometry analysis.

LC/LC-MS/MS analysis was performed on an Agilent 1200 series HPLC coupled to an LTQ-Orbitrap Discovery mass spectrometer (ThermoFisher). Peptide digests were pressure loaded onto a 250 µm fused silica desalting column packed with 4 cm of Aqua C18 reverse-phase resin (Phenomenex). The peptides were eluted onto a biphasic column (100 µm fused silica with a 5 µm tip, packed with 10 cm Aqua C18 reverse-phase resin (Phenomenex) and 3 cm Partisphere strong-cation-exchange resin (SCX, Whatman) using a gradient 5-100% Buffer B in Buffer A (Buffer A: 95% water, 5% acetonitrile, 0.1% formic acid; Buffer B: 20% water, 80% acetonitrile, 0.1% formic acid). The peptides were then eluted from the SCX onto the C18 resin and into the mass spectrometer using four salt steps as previously described [31, 58]. The flow rate through the column was set to ~0.25 mL/min and the spray voltage was set to 2.75 kV. One full MS scan (FTMS) (400-1800 m/z) was followed by 18 data dependent scans (ITMS) of the n^{th} most intense ions with dynamic exclusion enabled.

Mass-spectrometry analysis of time-dependent GSNO-treated MCF7 lysates.

GSNO was dissolved in freshly-made HEN buffer and the concentration was determined as described above. MCF7 cell lysates (4 mg/mL) were aliquoted to 500 µL and incubated with 5 µL HEN buffer at 37 °C for 1 hr, or 5 µL of GSNO (500 µM final concentration) in HEN buffer at 37 °C for 5 mins, 10 mins, 20 mins, 30 mins and 1 hr, respectively. Excess GSNO was then removed by filtration through a Nap-5 column.

Proteins were eluted with 1 mL PBS and aliquoted to produce two 500 µL samples. The IA probing and rest mass-spectrometry preparation steps were as described above.

Mass-spectrometry data analyses.

The generated tandem MS data were searched using the SEQUEST algorithm against the human IPI database. A static modification of +57.02146 on cysteine was specified to account for iodoacetamide alkylation and differential modifications of +456.2849 (Azo-L modification) and +462.2987 (Azo-H modification) were specified on cysteine to account for probe modifications. SEQUEST output files were filtered using DTASelect 2.0. Quantification of heavy:light ratios (R) was performed using the CIMAGE quantification package as previously described [31].

Gel-based analysis of GSTO1 and CTSD.

The cDNA constructs for GSTO1 and CTSD were purchased as full-length expressed sequence tags (Open Biosystems) and subcloned into a pcDNA3.1-Myc/His mammalian-expression vector using the primers indicated for PCR amplification (Appendix I. Table 2A-5). All constructs were verified by DNA sequencing (Genewiz, Cambridge, MA). HEK293T cells were transfected with GSTO1 or CTSD using the X-tremeGENE DNA transfection reagent. The cells were incubated at 37 °C for 48 hr after transfection, harvested and then lysed in PBS. The concentrations of soluble proteins were normalized. Protein overexpression was then analyzed by immunoblot using an anti-Myc antibody (2278S).

HADH2 and PDIA1 subcloning.

The cDNA for HADH2 PDIA1 were subcloned into a pET23a-T7/His bacterial expression vector. Site-directed mutagenesis was performed to obtain cysteine to serine or cysteine to alanine mutants using the Quikchange procedure (Agilent, Santa Clara, CA) with the appropriate primers (Appendix I. Table 2A-5). All constructs were verified by DNA sequencing (Genewiz, Cambridge, MA or La Jolla, CA).

HADH2 expression and purification.

HADH2 (WT, C58S, or C58A) was expressed in *Escherichia coli* BL21 (DE3) cells. Cells were inoculated in 5 mL LB medium containing 100 μM ampicillin at 37 °C overnight. The overnight culture was added to 500 mL LB or 1 L 2×YT medium containing 100 μM ampicillin and allowed to grow at 37 °C until OD_{600} ~ 0.6-0.8. Expression was then induced by the addition of 1 mM IPTG for 4 hr at 30 °C. Cells were harvested and lysed in PBS or 20 mM Tris pH 8.0 at 4 °C with 200 mM NaCl. The expressed fusion protein was purified using a Ni-NTA packed chromatography column. After loading the cell lysate onto the column, the Ni-NTA resin was washed with 50 mM imidazole in PBS or 10 mM imidazole in 20 mM Tris pH 8.0 at 4 °C with 200 mM NaCl and HADH2 was eluted with 500 mM imidazole in PBS or 300 mM imidazole in 20 mM Tris pH 8.0 at 4 °C with 200 mM NaCl. Protein purity was then assessed by 10% SDS-PAGE and Silver staining. Excess imidazole was then removed by use of a Nap-5 column and eluting the purified protein with 20 mM potassium phosphate, pH 7.4, with 5% v/v glycerol and 5 mM β-mercaptoethanol, and stored at -80 °C [59]. Alternatively, the purified

protein was dialyzed against 20 mM Tris pH 8.0 at 4 °C with 200 mM NaCl, 10% v/v glycerol, and 1 mM TCEP.

PDIA1 expression and purification.

PDIA1 was expressed in *Escherichia coli* BL21 (DE3) cells. Cells were inoculated in 5 mL LB medium containing 100 μM ampicillin at 37 °C overnight. The overnight culture was added to 250 mL LB containing 100 μM ampicillin and allowed to grow at 37 °C until OD_{600} ~ 0.6-0.8. Expression was then induced by the addition of 0.3 mM IPTG for ~ 18 hrs at 30 °C. Cells were harvested and lysed in PBS. The expressed fusion protein was purified using a Ni-NTA packed chromatography column. After loading the cell lysate onto the column, the Ni-NTA resin was washed with 25 mM imidazole in PBS PDIA1 was eluted with 500 mM imidazole in PBS. Protein purity was then assessed by 10% SDS-PAGE and silver staining. Excess imidazole was removed by use of a Nap-5 column and the purified protein was stored at 4 °C.

Gel-based analysis of IA probe consumption before performing click chemistry.

Purified concentrated PDIA1 (3.25 mg/mL) in PBS or equal amount of PBS were added to MCF7 cell lysates with a final concentration of 2 mg total protein/mL MCF7 cell lysate and 0.1 mg/mL PDIA1. The mixture was aliquoted to 50 μL. Each aliquot was treated with 10 μM IA probe using 1 μL of a 500 μM stock in DMSO. The labeling reactions were incubated at room temperature for 1 hr. Then same concentrated PDIA1 was added to none-PDIA1-containing aliquot to a final concentration of 0.1 mg/mL and equal amount of PBS was added to PDIA1-containg aliquot or none-PDIA1-containg

aliquot as a control. Click chemistry was performed by the addition of 20 μM rhodamine azide (Rh-N_3), TCEP (1 mM, fresh 50 mM stock in water), TBTA ligand (100 μM, 17× stock in DMSO:t-Butanol 1:4) and $CuSO_4$ (1 mM, 50 mM stock in water). Samples were allowed to react at room temperature for 1 hr followed by adding 50 μL 2X SDS-PAGE loading buffer (reducing). 12.5 μL of each of this mixture solutions was separated by 10% SDS-PAGE under 100 volts for 2 hrs. Gel was visualized on a Hitachi FMBIO II multiview flatbed laser- induced fluorescent scanner. After analysis, gel underwent a typical procedure for Coomassie staining and destaining. Stained gel was visualized on a ChemiDoc MP Imaging System (BioRad).

***In vitro* biotin switch assay of purified HADH2**.

All biotin switch assays were conducted similar to previously described[60] with modifications as detailed below. Briefly, *S*-nitrosated purified protein or cell lysates were alkylated with iodoacetamide, proteins were precipitated with acetone, and the resulting pellets resuspended into label buffer (PBS containing SDS, ascorbate, and biotin iodoacetamide). Labeling reactions were quenched with DTT and analyzed by immunoblotting for biotin.

All biotin switch assays were conducted under low ambient light conditions. Purified HADH2 WT or C58S proteins (50 μM) were incubated with 100 μM TCEP for 15 min at room temperature and then desalted with a Micro BioSpin-6 column (Bio-Rad, Hercules, CA). Desalted HADH2 WT or C58S (5 μM) was incubated with 6-100 μM GSNO, 100 μM GSH, or the molar equivalent of DEA NONOate for 60 min at 37ºC in HEN buffer (250 mM HEPES pH 7.7, 1 mM EDTA, 0.1 mM neocuproine) in 100 μL

total volume. Free thiols were alkylated with an equal volume of blocking buffer (HEN buffer with 1% w/v SDS and 200 mM iodoacetamide) for 1 hr at 37ºC. Proteins were precipitated with 1.2 mL ice-cold high-purity acetone and incubated at -80ºC for 15 minutes. Precipitated protein was pelleted at >12,000 × g at 4ºC and the supernatant was discarded. Pellets were washed once more with acetone, pelleted by centrifugation, and the supernatant removed. Pellets were air dried for 15 min at room temperature and then resuspended into label buffer (PBS containing 1% w/v SDS, 30 mM ascorbate, 200 μM EZ-link biotin iodoacetamide). Controls were run as detailed above except ascorbate was omitted from the nitrosothiol reduction and labeling step. After 1 hr at 37ºC, the reactions were quenched with 6× Laemmli Sample Buffer (LSB) containing 100 mM DTT and 30 μL of each sample was loaded onto a Bio-Rad (Hercules, CA) TGX AnyKD Stain-Free gel. Equal protein loading was verified by imaging under UV light on a ChemiDoc MP gel imager (Bio-Rad, Hercules, CA). Proteins were transferred to a nitrocellulose membrane using a TransBlot Turbo semi-dry transfer system (Bio-Rad, Hercules, CA). The membrane was blocked for 1 hr at room temperature in PBS containing 1% v/v TWEEN-20 (PBS-T) and 2.5% w/v dry milk. The membrane was washed 3 × 5 min with PBS-T. Biotin-labeled proteins were then rocked for one hour at room temperature with the VectaStain ABC kit (Vector Laboratories, Burlingame, CA) where reagents A and B were diluted into 15 mL PBS-T. The membrane was again washed 3 × 5 min in PBST. The membrane was then imaged using 2 mL of Luminata Classico HRP Substrate (EMD Millipore, Billerica, MA) and the chemiluminescence settings on a ChemiDoc MP gel imager (Bio-Rad, Hercules, CA). Protein loading controls for GSNO and DEA NONOate titrations were obtained by stripping the nitrocellulose membrane in mild strip buffer

(200 mM glycine, 1 % v/v TWEEN-20, 0.1 % w/v SDS), re-blocking in PBS-T with 2.5% w/v milk, and re-probing with anti-His_6 antibody (1:1000 dilution in PBS-T with 2.5% w/v milk) for 2 hours at room temperature. The membrane was washed with PBS-T 3× for 10 minutes and incubated in goat anti-mouse-HRP secondary antibody (1:5000 dilution in PBS-T with 2.5% w/v milk) for 2 hours at room temperature. Blot was washed with PBS-T 3× for 10 minutes and imaged with chemiluminescent substrate. Protein loading controls for HADH2 WT and C58S were obtained by running an accompanying gel with the same protein amounts and staining with Coomassie blue.

HADH2 cellular lysate biotin switch.

HEK293T cells were plated onto 60 mm dishes at 10^6 cells. Upon reaching ~80% confluency, cells were transfected with 2 μg of Myc-tagged pcDNA3.1(+) HADH2 (WT or C58S) in the presence of 800 ng of PEI dissolved in serum-free DMEM. After 8 hr, cells were harvested by scraping and lysed via sonication into 200 μL PBS supplemented with 100 μM GSNO. Insoluble cellular debris was pelleted at maximum speed in a microcentrifuge. The supernatant was transferred to a fresh tube and incubated at 37ºC for 1 hr. Blocking conditions, acetone precipitation, and labeling steps were the same as described above for purified HADH2 biotin switch, except for the following modifications. Biotin-HPDP (200 μM, Pierce) was used in place of EZ-link biotin iodoacetamide and a second acetone precipitation was performed after biotin-HPDP labeling as described above to remove labeling buffer components. Following 15 min of air drying, the pellets were resuspended in 100 μL of PBS with 1% w/v SDS and protein concentrations were normalized between samples using a BCA assay. A small aliquot of

each sample was set aside to run a protein loading control gel. The remainder was diluted to yield a final SDS concentration of 0.1% w/v. Biotin-labeled proteins were pulled down by addition of 50 µL of a 50% slurry of streptavidin-conjugated agarose beads pre-equilibrated with PBS. The samples were rocked 16 hr at 4ºC. Beads containing bound biotin-labeled proteins were spun down for 5 min at 2500 × g and washed with 3 × 1 mL of PBS. Biotin-labeled proteins were eluted from beads by addition of 50 µL of 2× LSB containing DTT. Beads were heated at 95ºC for 5 min and spun for 1 min at ≥12,000 × g before loading the supernatant on a TGX AnyKD Stain Free gel followed by transfer to a nitrocellulose membrane, blocking, and washing as described above for HADH2 purified protein biotin switch. Membranes were probed with rabbit anti-Myc antibody (Pierce, MA5-15125) for 16 hr at 4ºC diluted 1:1000 in PBS-T with 2.5% w/v milk. Membranes were washed 3× with PBS-T, then probed with goat anti-rabbit antibody (Pierce, #31463) diluted 1:5000 in PBS-T with 2.5% w/v milk for 1 hr at room temperature. Blots were washed 3× with PBS-T and imaged by chemiluminescence as described above.

HADH2 endogenous *S*-nitrosation biotin switch.

HEK293T cells were plated and transfected as described for cellular lysate biotin switch. 8 hours post-transfection, Cys-SNO was added to each dish to a final concentration of 100 µM. Cys-SNO was prepared by incubating 10 mM L-cysteine in 10 mM $NaNO_3$, 10 mM HCl, and 1 mM EDTA for 1 hr in the dark. Cys-SNO concentration was determined using UV absorption at 336 nm and an extinction coefficient of 0.9 $mM^{-1}cm^{-1}$. The remainder of the biotin switch procedure was completed as described above for cellular lysate biotin switch.

HADH2 cellular biotin switch with NOS inhibitors.

HEK293T cells were plated and transfected with HADH2 WT or HADH2 C58S in the Myc-tagged pcDNA3.1(+) vector as described above. After 8 hr, cells were treated with 100 μM L-NAME, 100 μM 1400W, or DMSO vehicle control and incubated for 16 hr at 37 °C. Cells were washed 3× with PBS, collected, and lysed by sonication in block buffer. The biotin switch procedure was carried out as described above for cellular lysate biotin switch.

HADH2 cellular switch with cytokine-mediated iNOS induction.

A549 cells (8.5 x 10^6 cells) were plated on 150 mm dishes. The following day, cells were transfected with 16 μg of Myc-tagged pcDNA3.1(+) HADH2 (WT or C58S) in the presence of 32 μg PEI. After 24 hours, the media was changed and cytokine mix was added (human IFNγ, 2000 U/mL; human TNF-α, 10 ng/mL; human IL-1β, 25 ng/mL). L-NAME was added to 100 μM from a freshly made stock. Cells were incubated for 48 hr at 37 °C prior to harvest. Due to risks of degradation of L-NAME during the 48 hr cytokine/L-NAME treatment, the media was replaced after 24 hr with fresh media containing 100 μM L-NAME. Production of nitric oxide was assessed via the Griess Assay for nitrite detection in the media [61]. Briefly, in triplicate, aliquots were taken from each dish, mixed in equal volume with freshly-prepared Griess buffer (0.6% w/v sulfanilamide, 30% v/v acetic acid, 0.05% w/v *N*-1-naphthyl-ethylenediamine-HCl) and an absorbance taken at 540 nm. Nitrite concentrations were deduced by comparison with

a freshly-prepared sodium nitrite standard curve. Cells were then harvested and processed using the BST as described above for HEK293T cells.

HADH2 activity assays.

The purified HADH2 enzyme was assayed as described previously [62], where HADH2 activity was measured spectrophotometrically using the decrease in absorbance at 340 nm due to NADH oxidation. Purified HADH2 (WT or C58S) in 20 mM potassium phosphate, pH 7.4, with 5% v/v glycerol and 5 mM β-mercaptoethanol, was pre-incubated in a mixture of 100 mM potassium phosphate (pH 7) and 100 μM NADH at room temperature for 30 min. The kinetic assay was initiated by adding varying acetoacetyl-CoA concentrations up to 100 μM. The reaction was carried out at 30 °C and the absorbance at 340 nm was measured using a Molecular Devices Spectramax M5 plate reader. Relative activity was determined as the slope of the absorbance vs. time curve within the linear range.

To evaluate the concentration dependence of GSNO on enzyme activity, HADH2 WT (0.5 μM) was pre-incubated with varying GSNO concentrations in HEN buffer (pH 7.7) at room temperature for 30 minutes. HADH2 was added to the kinetic assay to a final concentration of 0.1 μM. Kinetic assays were carried out at 30 °C in 100 mM sodium phosphate buffer pH 7.0 and were initiated by addition of 100 μM NADH and acetoacetyl-CoA. Rates were monitored at 340 nm for 10 minutes.

The assay was initiated by addition of 100 μM acetoacetyl-CoA. To determine the effect of GSNO treatment on the catalytic efficiency (k_{cat}/K_M), HADH2 WT and C58A (100 μL of 25 μM HADH2 in HEN buffer) was reduced with 100 μL of a 50% slurry of

TCEP immobilized reducing resin (Pierce) for 20-25 min at room temperature. The TCEP resin was removed by centrifugation (1000 × g for 1 min). The reduced HADH2 supernatant was diluted to 2.5 μM and incubated with 100 μM GSNO or GSH in HEN buffer at room temperature. After 30 min, HADH2 activity (0.5 μM final concentration) was assayed by monitoring the absorbance at 340 nm as described above in 150 μL reactions containing 400 μM NADH, 100 mM sodium phosphate pH 7.5, and varying acetoacetyl-CoA concentrations from 50 μM to 1 mM.

Reference

1. Forstermann U and Sessa WC. Nitric oxide synthases: regulation and function. *Eur Heart J*. 2012;33:829-37, 837a-837d.

2. Derbyshire ER and Marletta MA. Structure and regulation of soluble guanylate cyclase. *Annual review of biochemistry*. 2012;81:533-59.

3. Broniowska KA and Hogg N. The chemical biology of *S*-nitrosothiols. *Antioxid Redox Signal*. 2012;17:969-80.

4. Smith BC and Marletta MA. Mechanisms of *S*-nitrosothiol formation and selectivity in nitric oxide signaling. *Curr Opin Chem Biol*. 2012;16:498-506.

5. Perissinotti LL, Turjanski AG, Estrin DA and Doctorovich F. Transnitrosation of nitrosothiols: characterization of an elusive intermediate. *Journal of the American Chemical Society*. 2005;127:486-7.

6. Wang K, Wen Z, Zhang W, Xian M, Cheng JP and Wang PG. Equilibrium and kinetics studies of transnitrosation between *S*-nitrosothiols and thiols. *Bioorg Med Chem Lett*. 2001;11:433-6.

7. Broniowska KA, Diers AR and Hogg N. *S*-nitrosoglutathione. *Biochim Biophys Acta*. 2013;1830:3173-81.

8. Seneviratne U, Godoy LC, Wishnok JS, Wogan GN and Tannenbaum SR. Mechanism-based triarylphosphine-ester probes for capture of endogenous RSNOs. *Journal of the American Chemical Society*. 2013;135:7693-7704.

9. Erwin PA, Mitchell DA, Sartoretto J, Marletta MA and Michel T. Subcellular targeting and differential *S*-nitrosylation of endothelial nitric-oxide synthase. *J Biol Chem*. 2006;281:151-7.

10. Mitchell DA and Marletta MA. Thioredoxin catalyzes the *S*-nitrosation of the caspase-3 active site cysteine. *Nat Chem Biol*. 2005;1:154-8.

11. Tristan C, Shahani N, Sedlak TW and Sawa A. The diverse functions of GAPDH: views from different subcellular compartments. *Cell Signal*. 2011;23:317-23.

12. Gould NS, Evans P, Martinez-Acedo P, Marino SM, Gladyshev VN, Carroll KS and Ischiropoulos H. Site-Specific Proteomic Mapping Identifies Selectively Modified Regulatory Cysteine Residues in Functionally Distinct Protein Networks. *Chemistry & biology*. 2015;22:965-975.

13. Doulias PT, Tenopoulou M, Greene JL, Raju K and Ischiropoulos H. Nitric oxide regulates mitochondrial fatty acid metabolism through reversible protein *S*-nitrosylation. *Sci Signal*. 2013;6:rs1.

14. Mitchell DA, Morton SU, Fernhoff NB and Marletta MA. Thioredoxin is required for *S*-nitrosation of procaspase-3 and the inhibition of apoptosis in Jurkat cells. *Proceedings of the National Academy of Sciences of the United States of America*. 2007;104:11609-14.

15. Hara MR, Agrawal N, Kim SF, Cascio MB, Fujimuro M, Ozeki Y, Takahashi M, Cheah JH, Tankou SK, Hester LD, Ferris CD, Hayward SD, Snyder SH and Sawa A. *S*-nitrosylated GAPDH initiates apoptotic cell death by nuclear translocation following Siah1 binding. *Nat Cell Biol*. 2005;7:665-74.

16. Kornberg MD, Sen N, Hara MR, Juluri KR, Nguyen JV, Snowman AM, Law L, Hester LD and Snyder SH. GAPDH mediates nitrosylation of nuclear proteins. *Nat Cell Biol*. 2010;12:1094-1100.

17. Anand P and Stamler JS. Enzymatic mechanisms regulating protein S-nitrosylation: implications in health and disease. *J Mol Med (Berl)*. 2012;90:233-44.

18. Green LS, Chun LE, Patton AK, Sun X, Rosenthal GJ and Richards JP. Mechanism of inhibition for N6022, a first-in-class drug targeting *S*-nitrosoglutathione reductase. *Biochemistry*. 2012;51:2157-68.

19. Doulias PT, Greene JL, Greco TM, Tenopoulou M, Seeholzer SH, Dunbrack RL and Ischiropoulos H. Structural profiling of endogenous *S*-nitrosocysteine residues reveals unique features that accommodate diverse mechanisms for protein *S*-nitrosylation. *Proceedings of the National Academy of Sciences of the United States of America*. 2010;107:16958-63.

20. Greco TM, Hodara R, Parastatidis I, Heijnen HF, Dennehy MK, Liebler DC and Ischiropoulos H. Identification of *S*-nitrosylation motifs by site-specific mapping of the *S*-nitrosocysteine proteome in human vascular smooth muscle cells. *Proceedings of the National Academy of Sciences of the United States of America*. 2006;103:7420-5.

21. Marino SM and Gladyshev VN. Structural analysis of cysteine *S*-nitrosylation: a modified acid-based motif and the emerging role of trans-nitrosylation. *J Mol Biol*. 2010;395:844-59.

22. Jaffrey SR and Snyder SH. The biotin switch method for the detection of *S*-nitrosylated proteins. *Sci STKE*. 2001;2001:pl1.

23. Sinha V, Wijewickrama GT, Chandrasena RE, Xu H, Edirisinghe PD, Schiefer IT and Thatcher GR. Proteomic and mass spectroscopic quantitation of protein *S*-nitrosation differentiates NO-donors. *ACS Chem Biol*. 2010;5:667-80.

24. Forrester MT, Thompson JW, Foster MW, Nogueira L, Moseley MA and Stamler JS. Proteomic analysis of *S*-nitrosylation and denitrosylation by resin-assisted capture. *Nat Biotechnol*. 2009;27:557-9.

25. Fares A, Nespoulous C, Rossignol M and Peltier JB. Simultaneous identification and quantification of nitrosylation sites by combination of biotin switch and ICAT labeling. *Methods Mol Biol*. 2014;1072:609-20.

26. Bechtold E, Reisz JA, Klomsiri C, Tsang AW, Wright MW, Poole LB, Furdui CM and King SB. Water-soluble triarylphosphines as biomarkers for protein *S*-nitrosation. *ACS Chem Biol*. 2010;5:405-14.

27. Seneviratne U, Godoy LC, Wishnok JS, Wogan GN and Tannenbaum SR. Mechanism-based triarylphosphine-ester probes for capture of endogenous RSNOs. *Journal of the American Chemical Society*. 2013;135:7693-704.

28. Wang H and Xian M. Fast reductive ligation of *S*-nitrosothiols. *Angew Chem Int Ed Engl*. 2008;47:6598-601.

29. Majmudar JD, Konopko AM, Labby KJ, Tom CT, Crellin JE, Prakash A and Martin BR. Harnessing Redox Cross-Reactivity To Profile Distinct Cysteine Modifications. *Journal of the American Chemical Society*. 2016;138:1852-1859.

30. Rostovtsev VV, Green LG, Fokin VV and Sharpless KB. A stepwise huisgen cycloaddition process: copper(I)-catalyzed regioselective "ligation" of azides and terminal alkynes. *Angew Chem Int Ed Engl*. 2002;41:2596-9.

31. Weerapana E, Wang C, Simon GM, Richter F, Khare S, Dillon MB, Bachovchin DA, Mowen K, Baker D and Cravatt BF. Quantitative reactivity profiling predicts functional cysteines in proteomes. *Nature*. 2010;468:790-5.

32. Martell J and Weerapana E. Applications of copper-catalyzed click chemistry in activity-based protein profiling. *Molecules*. 2014;19:1378-93.

33. Qian Y, Martell J, Pace NJ, Ballard TE, Johnson DS and Weerapana E. An isotopically tagged azobenzene-based cleavable linker for quantitative proteomics. *Chembiochem*. 2013;14:1410-4.

34. Deng X, Weerapana E, Ulanovskaya O, Sun F, Liang H, Ji Q, Ye Y, Fu Y, Zhou L, Li J, Zhang H, Wang C, Alvarez S, Hicks LM, Lan L, Wu M, Cravatt BF and He C. Proteome-wide quantification and characterization of oxidation-sensitive cysteines in pathogenic bacteria. *Cell Host Microbe*. 2013;13:358-70.

35. Wang C, Weerapana E, Blewett MM and Cravatt BF. A chemoproteomic platform to quantitatively map targets of lipid-derived electrophiles. *Nat Methods*. 2014;11:79-85.

36. Pace NJ and Weerapana E. A competitive chemical-proteomic platform to identify zinc-binding cysteines. *ACS chemical biology*. 2014;9:258-65.

37. Lee TY, Chen YJ, Lu CT, Ching WC, Teng YC and Huang HD. dbSNO: a database of cysteine *S*-nitrosylation. *Bioinformatics*. 2012;28:2293-5.

38. Porcu P, Barron AM, Frye CA, Walf AA, Yang SY, He XY, Morrow AL, Panzica GC and Melcangi RC. Neurosteroidogenesis Today: Novel Targets for Neuroactive Steroid Synthesis and Action and Their Relevance for Translational Research. *Journal of neuroendocrinology*. 2016;28.

39. Shafqat N, Marschall HU, Filling C, Nordling E, Wu XQ, Bjork L, Thyberg J, Martensson E, Salim S, Jornvall H and Oppermann U. Expanded substrate screenings of human and Drosophila type 10 17beta-hydroxysteroid dehydrogenases (HSDs) reveal multiple specificities in bile acid and steroid hormone metabolism: characterization of multifunctional 3alpha/7alpha/7beta/17beta/20beta/21-HSD. *Biochem J*. 2003;376:49-60.

40. Froemming MK and Sames D. Harnessing functional plasticity of enzymes: a fluorogenic probe for imaging 17beta-HSD10 dehydrogenase, an enzyme involved in Alzheimer's and Parkinson's diseases. *Journal of the American Chemical Society*. 2007;129:14518-14522.

41. Pu X and Yang K. Guinea pig 11beta-hydroxysteroid dehydrogenase type 1: primary structure and catalytic properties. *Steroids*. 2000;65:148-56.

42. Yan SD, Fu J, Soto C, Chen X, Zhu H, Al-Mohanna F, Collison K, Zhu A, Stern E, Saido T, Tohyama M, Ogawa S, Roher A and Stern D. An intracellular protein that binds amyloid-beta peptide and mediates neurotoxicity in Alzheimer's disease. *Nature*. 1997;389:689-95.

43. Holzmann J, Frank P, Loffler E, Bennett KL, Gerner C and Rossmanith W. RNase P without RNA: identification and functional reconstitution of the human mitochondrial tRNA processing enzyme. *Cell*. 2008;135:462-74.

44. Yang SY, He XY and Miller D. Hydroxysteroid (17beta) dehydrogenase X in human health and disease. *Mol Cell Endocrinol*. 2011;343:1-6.

45. Ofman R, Ruiter JP, Feenstra M, Duran M, Poll-The BT, Zschocke J, Ensenauer R, Lehnert W, Sass JO, Sperl W and Wanders RJ. 2-Methyl-3-hydroxybutyryl-CoA dehydrogenase deficiency is caused by mutations in the HADH2 gene. *Am J Hum Genet*. 2003;72:1300-7.

46. Kohr MJ, Aponte A, Sun J, Gucek M, Steenbergen C and Murphy E. Measurement of *S*-nitrosylation occupancy in the myocardium with cysteine-reactive tandem mass tags: short communication. *Circ Res*. 2012;111:1308-1312.

47. Joyce JA, Baruch A, Chehade K, Meyer-Morse N, Giraudo E, Tsai FY, Greenbaum DC, Hager JH, Bogyo M and Hanahan D. Cathepsin cysteine proteases are effectors of invasive growth and angiogenesis during multistage tumorigenesis. *Cancer Cell*. 2004;5:443-53.

48. Liaudet-Coopman E, Beaujouin M, Derocq D, Garcia M, Glondu-Lassis M, Laurent-Matha V, Prebois C, Rochefort H and Vignon F. Cathepsin D: newly discovered functions of a long-standing aspartic protease in cancer and apoptosis. *Cancer Lett*. 2006;237:167-79.

49. Masson O, Bach AS, Derocq D, Prebois C, Laurent-Matha V, Pattingre S and Liaudet-Coopman E. Pathophysiological functions of Cathepsin D: Targeting its catalytic activity versus its protein binding activity? *Biochimie*. 2010;92:1635-43.

50. Zaidi N, Maurer A, Nieke S and Kalbacher H. Cathepsin D: a cellular roadmap. *Biochem Biophys Res Commun*. 2008;376:5-9.

51. Masa M, Maresova L, Vondrasek J, Horn M, Jezek J and Mares M. Cathepsin D propeptide: mechanism and regulation of its interaction with the catalytic core. *Biochemistry*. 2006;45:15474-82.

52. Broniowska KA, Zhang Y and Hogg N. Requirement of transmembrane transport for *S*-nitrosocysteine-dependent modification of intracellular thiols. *J Biol Chem*. 2006;281:33835-41.

53. Zhang Y and Hogg N. The mechanism of transmembrane *S*-nitrosothiol transport. *Proceedings of the National Academy of Sciences of the United States of America*. 2004;101:7891-6.

54. Wang X, Kettenhofen NJ, Shiva S, Hogg N and Gladwin MT. Copper dependence of the biotin switch assay: modified assay for measuring cellular and blood nitrosated proteins. *Free Radic Biol Med*. 2008;44:1362-72.

55. Fusek M and Vetvicka V. Dual role of Cathepsin D: ligand and protease. *Biomed Pap Med Fac Univ Palacky Olomouc Czech Repub*. 2005;149:43-50.

56. Glondu M, Coopman P, Laurent-Matha V, Garcia M, Rochefort H and Liaudet-Coopman E. A mutated Cathepsin-D devoid of its catalytic activity stimulates the growth of cancer cells. *Oncogene*. 2001;20:6920-9.

57. Glynn SA, Boersma BJ, Dorsey TH, Yi M, Yfantis HG, Ridnour LA, Martin DN, Switzer CH, Hudson RS, Wink DA, Lee DH, Stephens RM and Ambs S. Increased NOS2 predicts poor survival in estrogen receptor-negative breast cancer patients. *J Clin Invest*. 2010;120:3843-54.

58. Weerapana E, Speers AE and Cravatt BF. Tandem orthogonal proteolysis-activity-based protein profiling (TOP-ABPP)--a general method for mapping sites of probe modification in proteomes. *Nat Protoc*. 2007;2:1414-25.

59. Liu X, Chu X, Yu W, Li P and Li D. Expression and purification of His-tagged rat mitochondrial short-chain 3-hydroxyacyl-CoA dehydrogenase wild-type and Ser137 mutant proteins. *Protein Expr Purif*. 2004;37:344-51.

60. Forrester MT, Foster MW, Benhar M and Stamler JS. Detection of protein *S*-nitrosylation with the biotin-switch technique. *Free Radic Biol Med*. 2009;46:119-26.

61. Hevel JM and Marletta MA. Nitric-oxide synthase assays. *Methods Enzymol*. 1994;233:250-8.

62. Binstock JF and Schulz H. Fatty acid oxidation complex from Escherichia coli. *Methods Enzymol*. 1981;71 Pt C:403-11.

Chapter 3

Global proteomic analysis of cysteine sensitivity to transnitrosation

Introduction

Nitric oxide (NO) plays critical roles in mammalian physiology by participating in cell signaling pathways that regulate broad aspects of cellular function. These effects are achieved by activation of guanylate cyclase to form cGMP as a secondary messenger molecule, or alternately by *S*-nitrosation of regulatory cysteines within proteins.[1-3] Three isoforms of nitric oxide synthases (NOSs) have been identified, constitutively active eNOS and nNOS, and iNOS, which is cytokine-inducible.[4, 5] NO generated from NOS diffuses and efficiently *S*-nitrosates nearby proteins near the diffusion-controlled limit.[6] Once formed, *S*-nitrosothiols can be transferred through formation of specific protein-small molecule or protein-protein interactions and subsequent nucleophilic attack of the thiolate at the *S*-nitrosothiol nitrogen atom.[7-9] (Figure 3-1) In particular, abundant thiol containing small molecules or proteins, such as glutathione (GSH), thioredoxin (Trx) and Coezyme A (CoA), form the corresponding *S*-nitrosated species, GSNO, Trx-SNO and CoA-SNO, which can transnitrosate a variety of protein cysteine residues. (Figure 3-2) [2, 10, 11] This transnitrosation between proteins and between proteins and small molecules appears to be an important cellular mechanism of *S*-nitrosation and thus protein-SNO production, imparting the necessary selectivity for protein *S*-nitrosation to be a viable cellular signaling mechanism.[2] Moreover, the significant impact of transnitrosation on cellular functions has been intensively studied. In many cases, *S*-nitrosation causes significant changes in protein activity or subcellular localization.

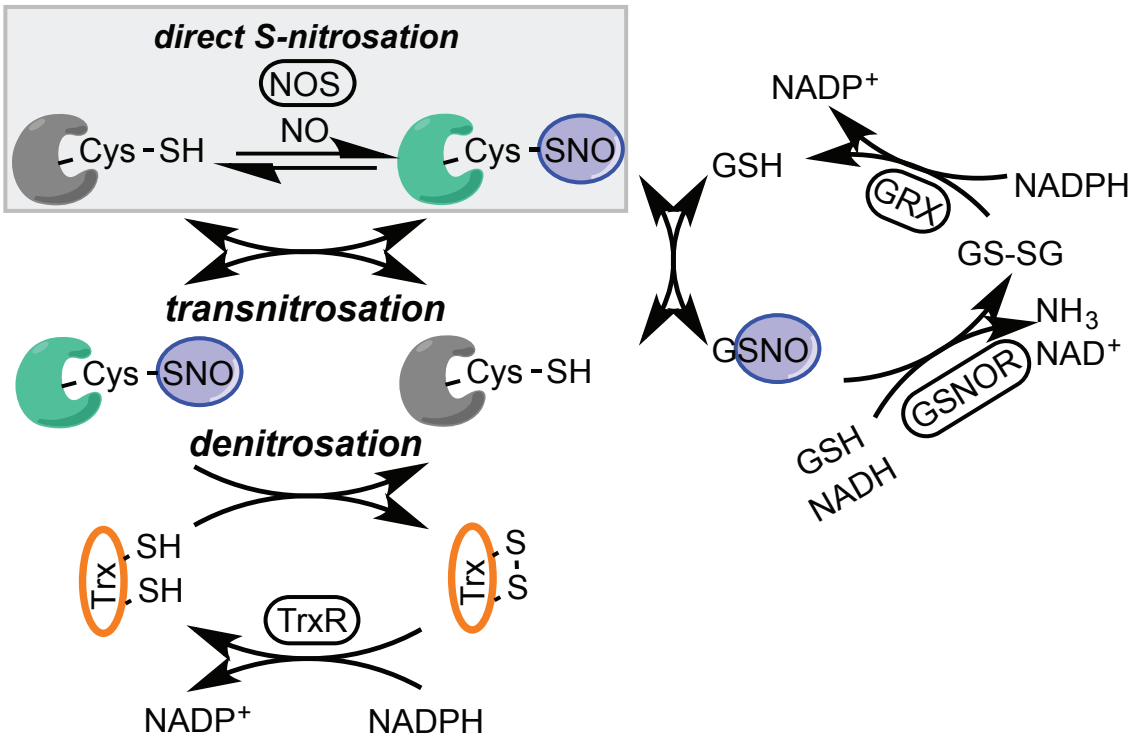


Figure 3-1. Protein *S*-nitrosation, transnitrosation and denitrosation systems. *S*-nitrosothiols can be formed upon the direct interaction with NO or could rely on the reaction between a thiolate and low molecular weight NO donor (*e.g.* GSNO). Due to the reversibility of the process, GSNO also similarly promotes *S*-nitrosation reactions, generating a delicate equilibrium between the redox couples GSH/GSNO and protein-SH/protein-SNO that are strictly maintained by GSNO reductase (GSNOR) activity. GSNOR converts GSNO to glutathione disulfide (GSSG), thereby deeply affecting *S*-nitrosothiol concentrations. The concerted activity of glutaredoxin (GRX), by reducing GSSG back to GSH, contributes to the maintenance of the system. The NO moiety can also be transferred directly among proteins (transnitrosation). Nitrosothiol homeostasis also relies on the activity of the thioredoxin/thioredoxin reductase (Trx/TrxR) system. NADPH-dependent Trx-mediated reduction of protein-SNO to thiols directs NO release and tunes many NO-mediated signaling pathways.

Glutathione (GSH), present at millimolar concentrations in mammalian cells, is a major cellular antioxidant, and plays an important role in maintaining a reduced intracellular environment. It is involved in a number of cellular functions such as defending against oxidative stress, redox signaling, and modulating immune functions, cell proliferation and apoptosis.[12, 13] GSNO, found both intra- and extracellularly, is the most abundant cellular low-molecular-weight SNO with a concentration range of 1-5 μM.[14] GSNO is formed by the direct *S*-nitrosation on GSH, or through GSH-mediated denitrosation of cellular SNOs. Once formed, GSNO can react as a transnitrosation reagent to modify specific cysteine thiols, or undergo reduction by GSNO Reductase (GSNOR) using NADH as an electron donor. GSNOR is widely expressed in both prokaryotic and eukaryotic organisms. The GSH/GSNOR system plays a central role in maintaining the equilibrium of cellular GSNO with other SNOs.[9, 15]

Trx is a 12 kDa cytosolic protein with five cysteine residues: two redox-active cysteines (32 and 35) and three non-active-site cysteines (62, 69 and 73). The conserved CGPC active site of Trx functions as a protein disulfide oxidoreductase, and the functional disulfide formation and reduction between active site cysteine 32 and 35 is NADPH-dependent. In parallel with GSH/GSNOR, Trx, coupled with Trx reductase (Trx/TrxR), is also considered an evolutionarily conserved mechanism to regulate protein SNOs. It regulates multiple cellular processes and plays a key role in protection from oxidative stress. For example, Caspase-3, a cysteine protease that is important for cell apoptotic death, is found constitutively *S*-nitrosated on active site cysteine 163, thus inhibiting its enzyme activity. However, in unstressed conditions, Trx is able to

selectively denitrosate SNO-Cys163 on Caspase-3, revealing the active site cysteine in order to regulate protein function.[16] Similarly, Trx/TrxR1 was found to denitrosate eNOS, as well as protein Tyr phosphatase 1b and GAPDH under resting conditions. [17, 18] Besides the involvement of Trx/TrxR in protein denitrosation, Trx is also identified as a target of *S*-nitrosation, and nitrosated Trx is able to transnitrosate specific cysteine residues, thus expanding its functional roles in regulating protein *S*-nitrosation. Though all five cysteines on Trx have been reported as *S*-nitrosation targets, a detailed kinetic analysis on the SNO selectivity under physiologically relevant concentration suggested that reduced Trx was *S*-nitrosated primarily and rapidly on cysteine 62 by GSNO, whereas cysteine 73 was the only SNO target of oxidized Trx. Trx cysteine 73 is located on opposite face of Trx from cysteine 62, and is the most surface accessible cysteine on Trx. This specificity of nitrosation for Trx was thought to be controlled by protein conformational changes while binding GSNO, or by the different local dynamics of the two redox states.[14] Interestingly, once nitrosated, Trx-Cys73-SNO possesses transnitrosation activity to many protein targets, including the active site of Caspase-3 cysteine 163. Trx-Cys73-SNO was showed to reversibly transnitrosate Caspase-3 120-fold faster than GSNO, inactivating Caspase-3 and directly governing the initiation of apoptosis. Loss of cysteine 73 or of nearby residues prevents binding to Caspase-3 and results in decreased Caspase-3 SNO levels, highlighting the regulatory role of Cys73-SNO transnitrosation events.[19, 20]

Coenzyme A (CoA) is another small-molecular-weight thiol and plays a central role in cellular metabolism.[21] CoA is found to be nitrosated to form *S*-nitroso-CoA (CoA-SNO). In yeast, CoA-SNO regulates metabolism by transnitrosation of a subset of proteins. The levels of CoA-SNO is regulated by a CoA-SNO reductase, Ad6.[22] Thus,

CoA-SNO could serve as a targeted source of transnitrosation to regulate specific protein *S*-nitrosation events.

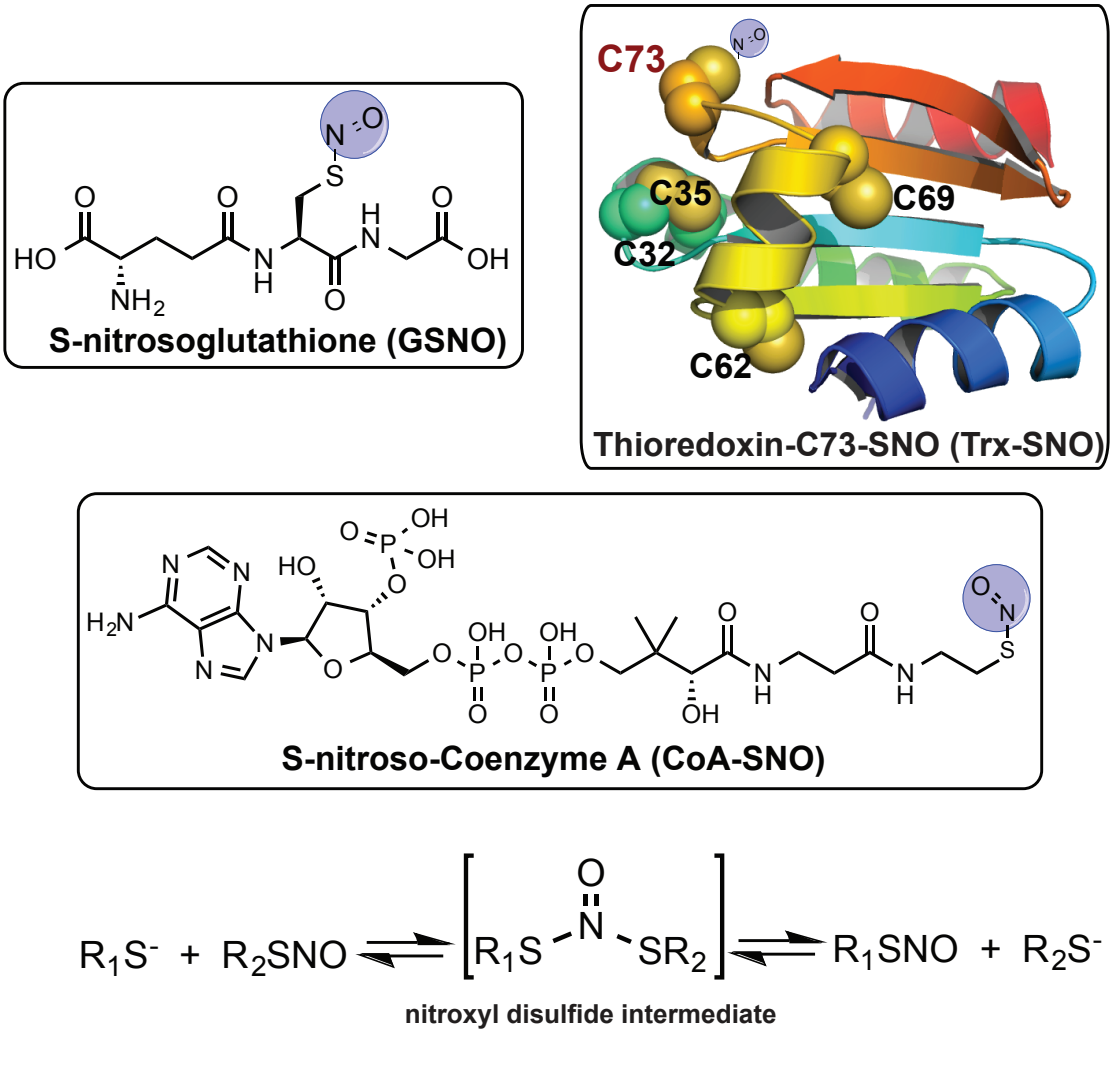


Figure 3-2. Structure of transnitrosation donors: (**A**) *S*-nitrosoglutathione (GSNO), (**B**) Thioredoxin-C73-SNO (Trx-SNO), and (**C**) *S*-nitroso-Coenzyme A (CoA-SNO). (**D**) Transnitrosation reaction proceeding through a nitroxyl disulfide intermediate.

Although the endogenous regulation of protein function through *S*-nitrosation is well established, only a small subset of reactive cysteines were showed to be modified *in vivo* despite the promiscuous reactivity between NO and a thiol moiety. The properties of

an individual cysteine residue that govern its sensitivity to *S*-nitrosation are poorly characterized. Potential contributors to *S*-nitrosation selectivity include primary sequence, cysteine pK_a, cysteine reactivity, direct interaction with NOS or other transnitrosation donors, local concentrations of transnitrosation donors, and the potential to be denitrosated by GSH or Trx. While it is established that selectivity for the vast majority of *S*-nitrosated cysteine residues is not governed by the surrounding primary sequence[23], a transnitrosase complex comprised of iNOS, S100A8, and S100A9 was recently shown to specifically nitrosate cysteine residues within a I/L-X-C-X-D/E consensus sequence[24]. However, the subset of known *S*-nitrosation sites containing this sequence is small, suggesting the majority of *S*-nitrosated proteins are not generated via this complex. Factors such as pK_a and proximal protein environment that can dictate cysteine reactivity *in vitro* do not correlate with the *S*-nitrosation selectivity observed *in vivo* [25]. One defining characteristic of known *S*-nitrosated cysteines is the presence of charged residues within 6-8 Å[26]; however, these charged residues are positioned too distant to directly activate cysteines toward *S*-nitrosation. Instead, cysteines near charged residues are more likely to be surface exposed and therefore provide hotspots for transnitrosation reactions.

Despite the advent of chemical and proteomic methods to study *S*-nitrosation, the subset of cellular cysteine residues that show uniquely high reactivity to endogenous transnitrosation donors is poorly characterized. To further these existing global studies, in chapter 2, a competitive cysteine-reactivity profiling strategy was implemented to quantitatively measure the sensitivity of >600 cysteine residues to transnitrosation by GSNO. These proteomic studies revealed several previously uncharacterized sites of *S*-

nitrosation with high propensity for GSNO-mediated transnitrosation. Here, by applying the same proteomic platform, the selectivity determinants for GSNO, CoA-SNO and Trx-SNO transnitrosation will be explored in detail *via* systematic evaluation of the corresponding cysteine targets.

Results

A competitive cysteine-labeling strategy to quantitatively measure sensitivity to transnitrosating agents

The extent of cysteine *S*-nitrosation was quantitatively monitored using a mass spectrometry (MS)-based proteomic platform derived from the previously reported isotopic tandem orthogonal proteolysis-ABPP (isoTOP-ABPP) method.[27, 28] This platform exploits the characteristic loss in nucleophilicity of a cysteine thiol upon conversion to a *S*-nitrosothiol, which is reflected in blocked reactivity with a cysteine-reactive chemical probe. In this approach (Figure 3-3), a cell lysate is exposed to one of three different transnitrosation donors (GSNO, CoA-SNO or Trx-Cys73-SNO) or a buffer control. Both proteomes are then treated with a cysteine-reactive IA probe, which covalently modifies hundreds of reactive and functional cysteine residues within the proteome. Following alkylation by the iodoacetamide of the IA probe, the terminal alkyne of the IA probe can be further functionalized through (CuAAC) reactions.[28, 29] The IA probe-labeled proteins are covalently linked to light (SNO-treated sample) or heavy (buffer treated control sample) biotin-azide tags (Azo-L and Azo-H) that contains an azobenzene linker for reductive cleavage by sodium dithionite.[27] The light and heavy

samples are then combined and subjected to streptavidin enrichment, on-bead trypsin digestion, and sodium dithionite cleavage to afford a mixture of light- and heavy-labeled peptides for MS analysis. These cysteine-containing isotopically labeled peptides are identified using the fragmentation (MS/MS or MS2) spectra and the relative abundance between the SNO and control samples is measured by the heavy:light ratio (R) that reflects the intensity of these species in the parent ion (MS1) spectra. An R-value of ~1 signifies a cysteine residue that was unaffected by SNO treatment, whereas R-values greater than one indicate modification of that cysteine residue by the transnitrosating agent. A larger R-value reflects a greater percentage of cysteine modification.

Quantitatively measuring cysteine sensitivity to different transnitrosation donors

MCF-7 breast cancer-cell proteomes were initially evaluated using either GSNO, CoA-SNO and Trx-SNO as the transnitrosation donors. To ensure selective *S*-nitrosation of Cys73 in these experiments, a Trx C62/69S double mutant was transnitrosated by GSNO and desalted to remove excess GSNO and GSH. Furthermore, the active-site cysteines of Trx (Cys32 and Cys35) were oxidized to ensure that any observed effects were not due to reactivity with these thiols.[31] This Trx-C73-SNO (Trx-SNO) was then used as a transnitrosation donor. Similarly, fresh CoA-SNO was generated by addition of sodium nitrite to equal amount of CoA in acidic solution.

Initially, MCF-7 breast cancer-cell lysate proteomes were subjected to the following treatments: (1) 500 μM GSNO (light) versus no GSNO added (heavy) as GSNO transnitrosation sample (n=5), (2) 500 μM CoA-SNO (light) versus no CoA-SNO added (heavy) as CoA-SNO transnitrosation sample (n=5), (3) 90 μM Trx-SNO (light)

versus no Trx-SNO added (heavy) as Trx-SNO transnitrosation sample (n=5); and (2) for each transnitrosation experiment above, both the light and heavy samples left untreated by SNO as a control for the quantitative capacity of the MS approach (n=2). In total, 610 (GSNO treated), 477 (CoA-SNO treated) and 379 (Trx-SNO treated) cysteine residues were identified with accurate heavy:light ratios in at least three of all five experimental samples. The full datasets are listed in Appendix I as Table 3A-1 (GSNO), 2 (CoA-SNO) and 3 (Trx-SNO), respectively. As expected, the control sample showed a limited distribution of R-values, closely centered on R = 1. In contrast, the experimental sample showed a wider distribution of R-values, where the majority of cysteine residues exhibited R-values >>1. These high R values are reflective of a loss in reactivity for cysteine residues subject to transnitrosation in the SNO-treated (light) sample, where P values (Appendix I, Table 3A-1, 2 and 3, 2-way ANOVA analysis) indicate the high

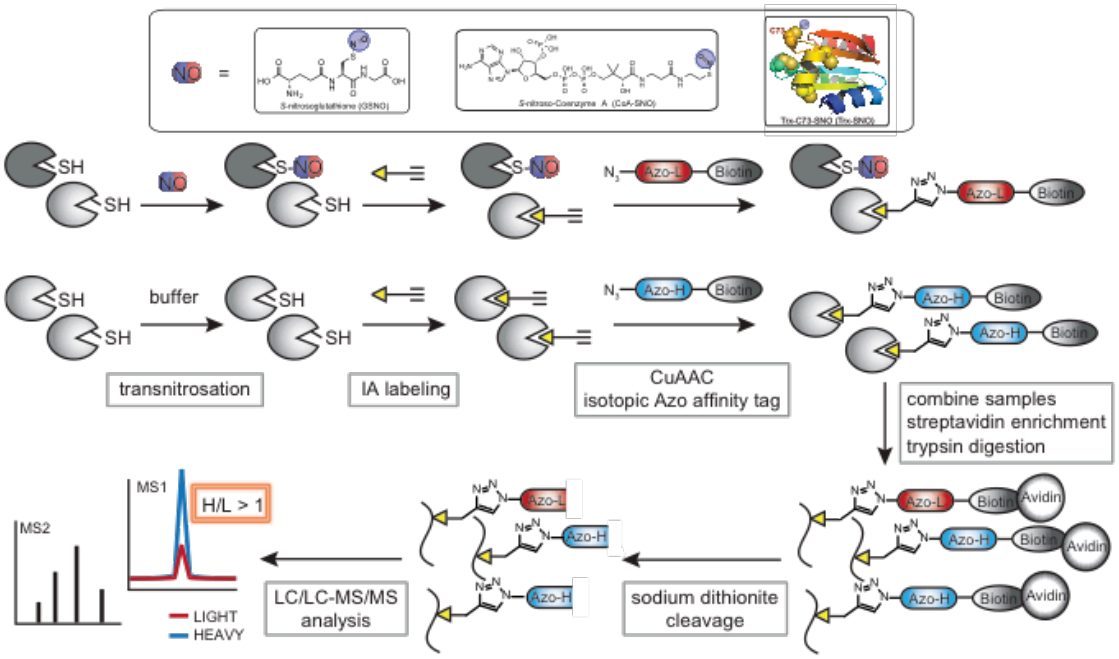


Figure 3-3. A competitive cysteine-profiling strategy to quantify sensitivity to transnitrosation. Cell lysates are treated with a transnitrosation donor (inset, GSNO, CoA-

SNO and Trx-SNO) or a buffer control, labeled with the IA probe and subjected to CuAAC to append either the Azo-L (SNO) or Azo-H (buffer) biotin-azide tags. The resulting isotopically tagged proteomes are mixed together and subjected to streptavidin enrichment and on-bead trypsin digestion. The probe-labeled peptides are eluted by reductive cleavage of the azobenzene with sodium dithionite and analyzed by high resolution LC/LC-MS/MS to identify (MS2) and quantify (MS1) the IA-probe labeled cysteine residues within each sample. A loss in cysteine reactivity is indicative of transnitrosation donor-mediated *S*-nitrosation.

To facilitate further parallel analysis, these three sets of transitrosated cysteines were compared in parallel, resulting in an overlapping peptide list of 756 cysteine residues (Figures 3-4, A, B and C; Appendix I, Table 3A-4). This overlapping peptide list is featured by individual cysteine with specific heavy:light ratios towards three transnitrosation donors, highlighting the different degree of a single cysteine to undergo transnitrosation by distinct transnitrosation donors. The R values for each donor, however, distribute widely to different degree, with GSNO showing R smaller than 5 and Trx-SNO distributing most widely up to R~20. (Figure 3-4, D). The top 50 sensitive cysteine residues have R ratios > 2.6 (GSNO), 5.1 (CoA-SNO) and 7.5 (Trx-SNO). P values (Appendix I, Table 3A-1, 2 and 3, 2-way ANOVA analysis) indicate the high confidence in the observed decrease in cysteine reactivity for these ratios, which are the cut-off we placed for cysteines that are highly sensitive to transnitrosation. The proteins containing these transnitrosation-sensitive cysteines serve diverse cellular functions, and are found in all subcellular compartments (cytoplasm, nucleus, ER, mitochondria, etc.),

with the majority located on enzymes, binding or structural proteins, and concentrated in the metabolic and cellular process according to gene ontology (GO) analysis (Figure 3-5).

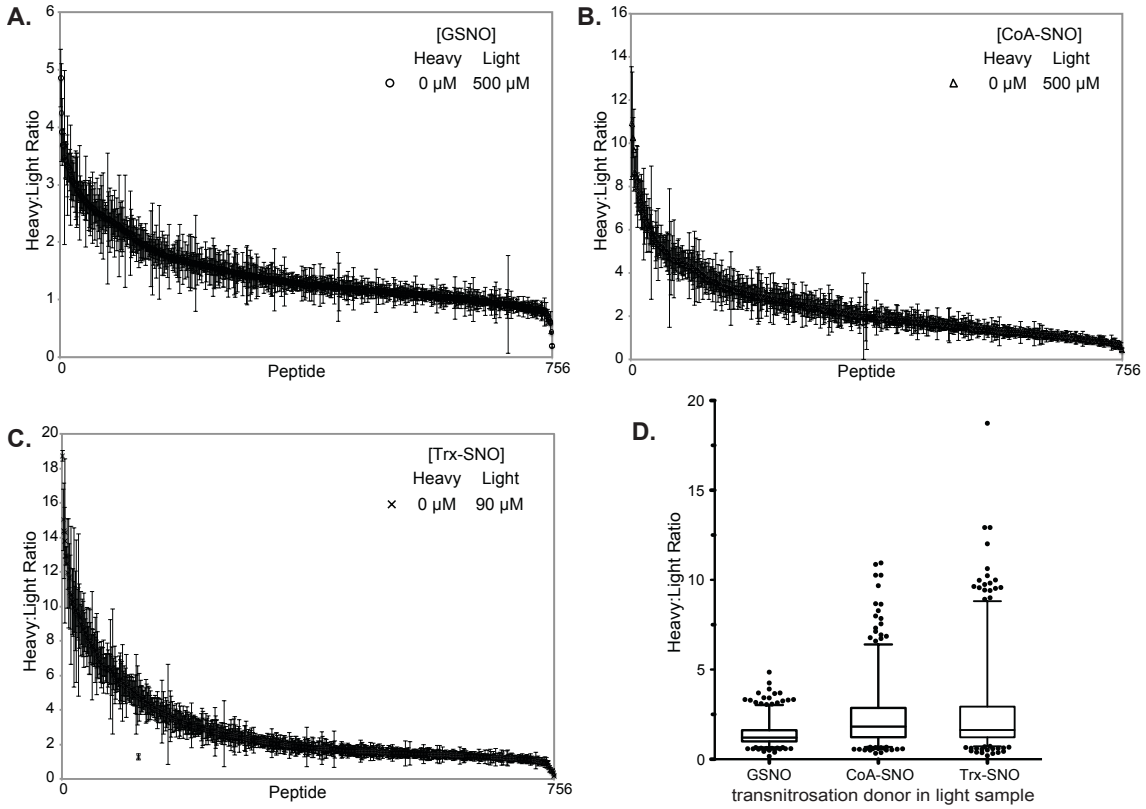


Figure 3-4. Identifying cysteines sensitive to transnitrosation by GSNO, CoA-SNO and Trx-SNO. Quantitative MS analysis of GSNO (**A**), CoA-SNO (**B**), and Trx-SNO (**C**) -treated cell lysates. Average heavy:light ratios (R) are shown for 756 cysteine residues identified in all three transnitrosation donor-treated (light: SNO; heavy: buffer;) MS analyses (Appendix I, Table 3A-4). Error bars represent standard deviation from the mean across the replicate analyses. (**D**) Distribution of R-values for the GSNO, CoA-SNO and Trx-SNOtreated samples.

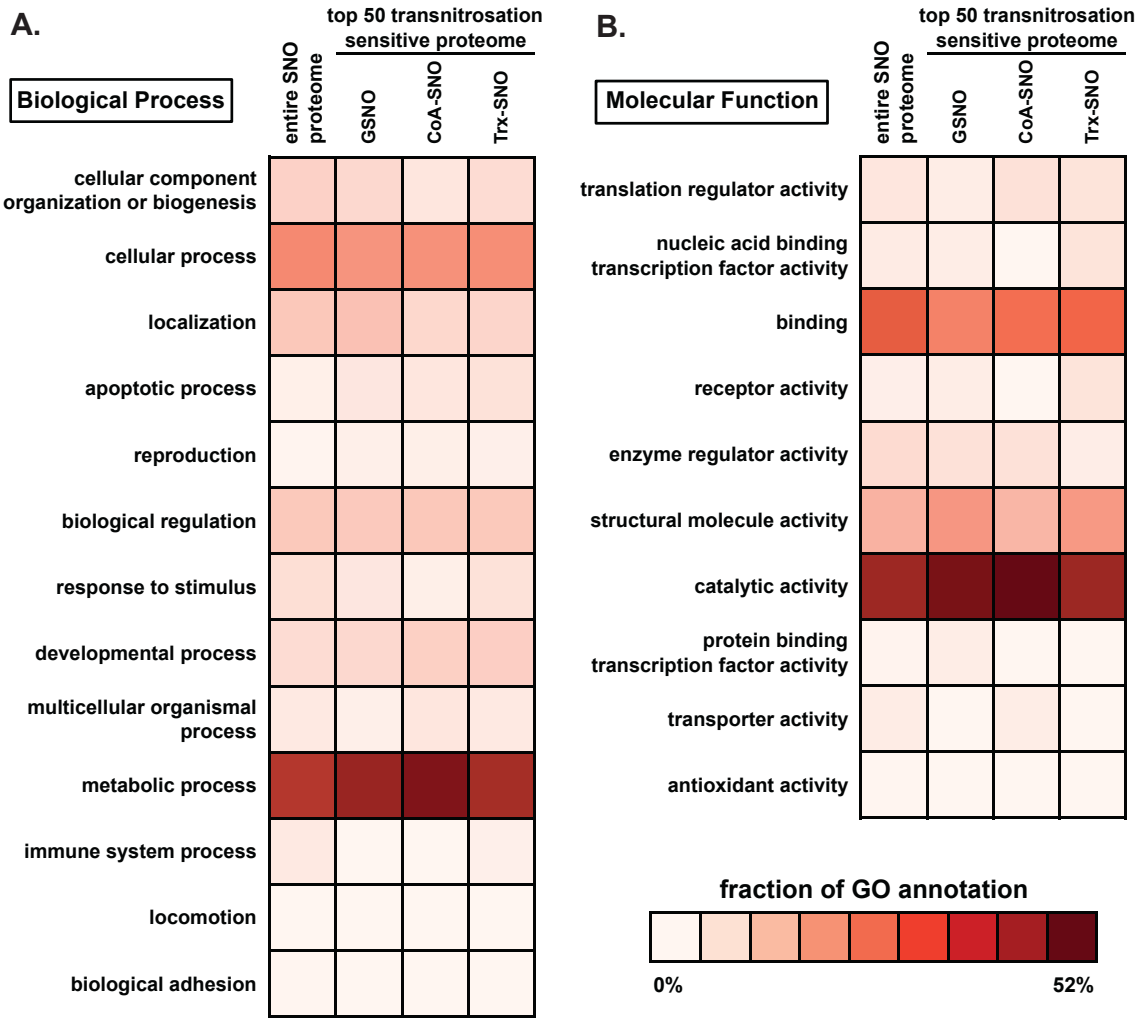


Figure 3-5. Biological process (**A**) and molecular function (**B**) are shown for all proteins and proteins containing the 50 cysteines with most or least transnitrosation sensitivity from the cysteine-reactivity profiling analyses (Appendix I, Table 3A-4). GO analysis was performed using PANTHER (www.pantherdb.org).

Identifying factors that dictate cysteine sensitivity to transnitrosation

To identify factors that unify the subset of cysteine residues highly sensitive to transnitrosation, the importance of primary sequence, cysteine pK_a, surface exposure, cysteine reactivity, and the identity of the transnitrosation donor was evaluated.

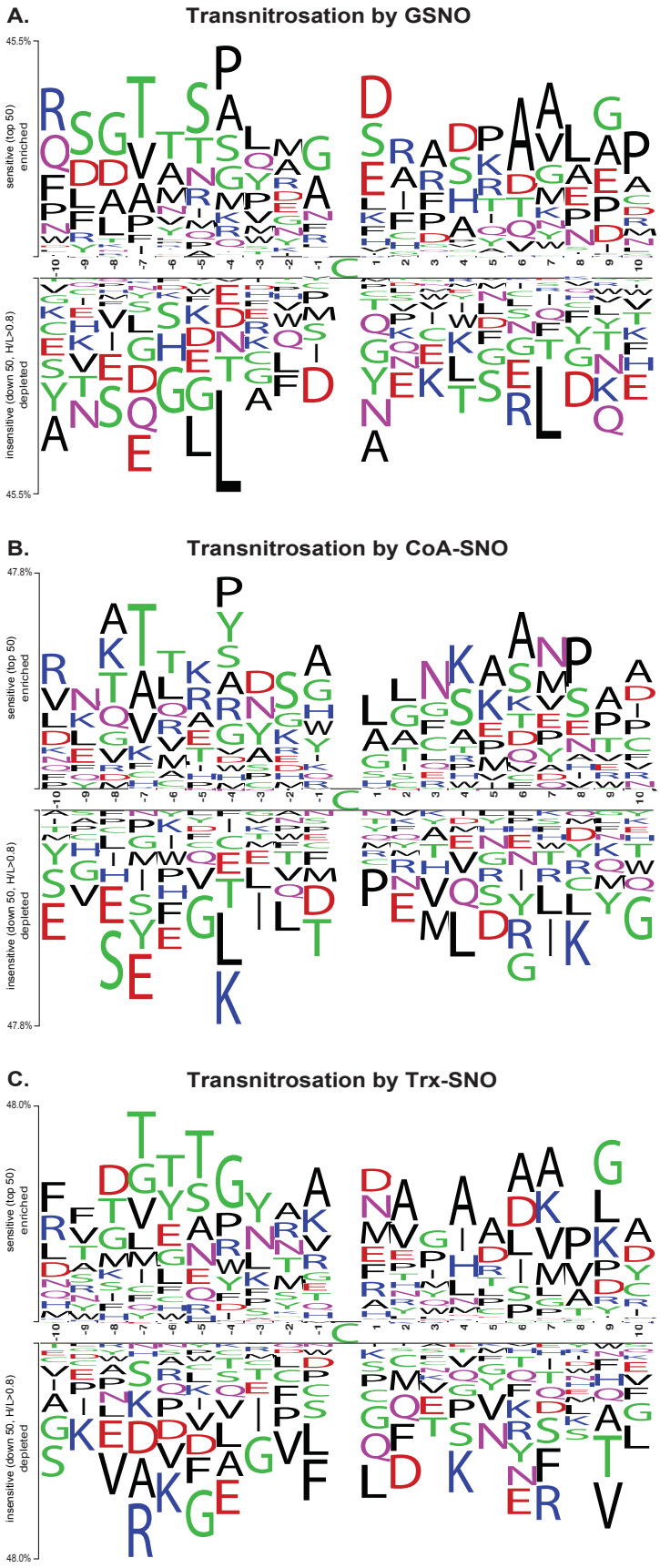

A.
Transnitrosation by GSNO
45.5%
sensitive (top 50)
enriched
insensitive (down 50, H/L>0.8)
depleted
45.5%
B.
Transnitrosation by CoA-SNO
47.8%
sensitive (top 50)
enriched
insensitive (down 50, H/L>0.8)
depleted
47.8%
C.
Transnitrosation by Trx-SNO
48.0%
sensitive (top 50)
enriched
insensitive (down 50, H/L>0.8)
depleted
48.0%

Figure 3-6. Sequence conservation flanking sites of cysteine transnitrosation**.** The ten amino-acids *N*- and *C*-terminal to the observed cysteine were aligned to identify primary sequence motifs for the 50 cysteines most (top) and least (down) sensitive to GSNO (**A**), CoA-SNO (**B**) and Trx-SNO (**C**) transnitrosation. Sequence alignments and plots generated using Two Sample Logo software (http://www.twosamplelogo.org/index.html) using default settings and the following tailored parameters: First position number: -10; Logo Range: -10, 10; Show residue if p-value < 1.[30]

First, the 50 most sensitive and the 50 least GSNO, CoA-SNO and Trx-SNO sensitive cysteine residues were analyzed for primary sequence motifs. Alignment of the ten N- and C-terminal residues to the transnitrosated cysteine did not reveal a consensus sequence that dictates transnitrosation sensitivity (Figure 3-6). The lack of a clear primary sequence motif is in agreement with previous analyses of *S*-nitrosation sites from a conglomerate of proteomic studies[23, 26], and suggests that transnitrosation by GSNO, CoA-SNO and Trx-SNO is not driven by a primary sequence motif in contrast to proteins *S*-nitrosated by the iNOS-S100A8/A9 complex[24].

Furthermore, analysis of surface exposure (solvent-accessible surface area, SASA) and pK_a distribution indicate that no trends in cysteine pK_a and surface exposure were identified across cysteines sensitive and insensitive to GSNO, CoA-SNO and Trx-SNO transnitrosation (Figure 3-7; Appendix I, Table 3A-5).

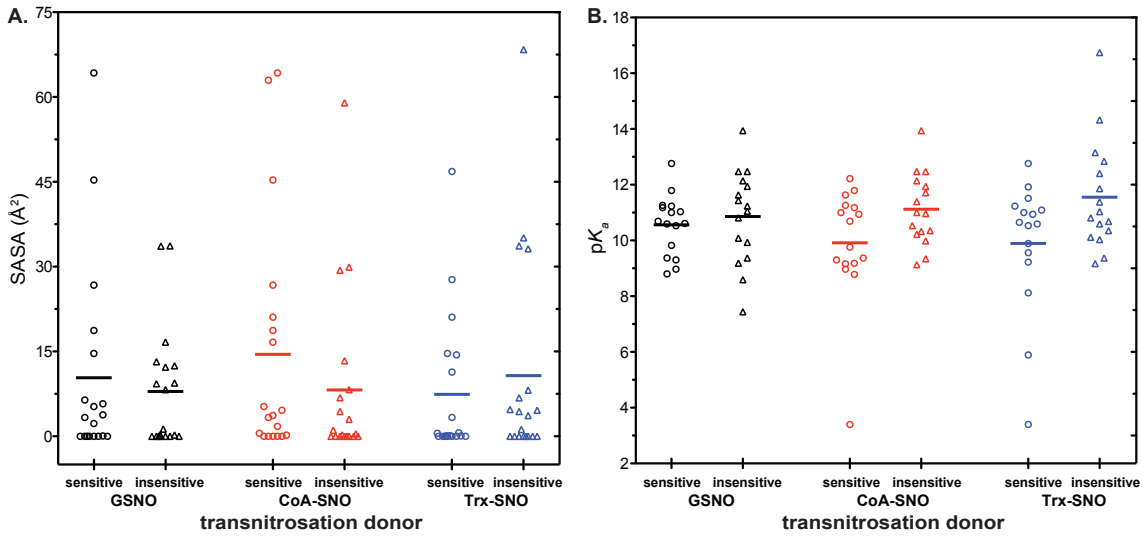


Figure 3-7. Surface-exposure (**A**) and pK_a (**B**) analysis of cysteines that were identified as sensitive and insensitive to transnitrosation**.** PDB files were obtained for 19 cysteine residues with high and low sensitivity to transnitrosation (Appendix I, Table 3A-5). Prediction of pK_a values for each cysteine residue was performed by VegaZZ implemented with PropKa (version 3.0.5.12, http://nova.disfarm.unimi.it/cms/index.php) using default settings. Solvent accessible surface area (SASA) calculations were performed using Naccess (Hubbard,S.J. & Thornton, J.M. (1993), 'NACCESS', Computer Program, Department of Biochemistry and Molecular Biology, University College London.). Naccess calculates atomic accessible surface areas using a previously reported method (Lee & Richards 1971, J. Mol. Biol., 55, 379-400) in which a spherical probe is rolled over the entire Van der Waal's surface of the macromolecule. The accessible surface area is then calculated from the path traced out from the center of the spherical probe, usually using the radius of water, which is 1.4 Å. The SASA of individual atoms is achieved through using thin slices of the molecular volume and these slices are used to calculate an approximation of the accessibility of each individual atom to the accessible surface area.

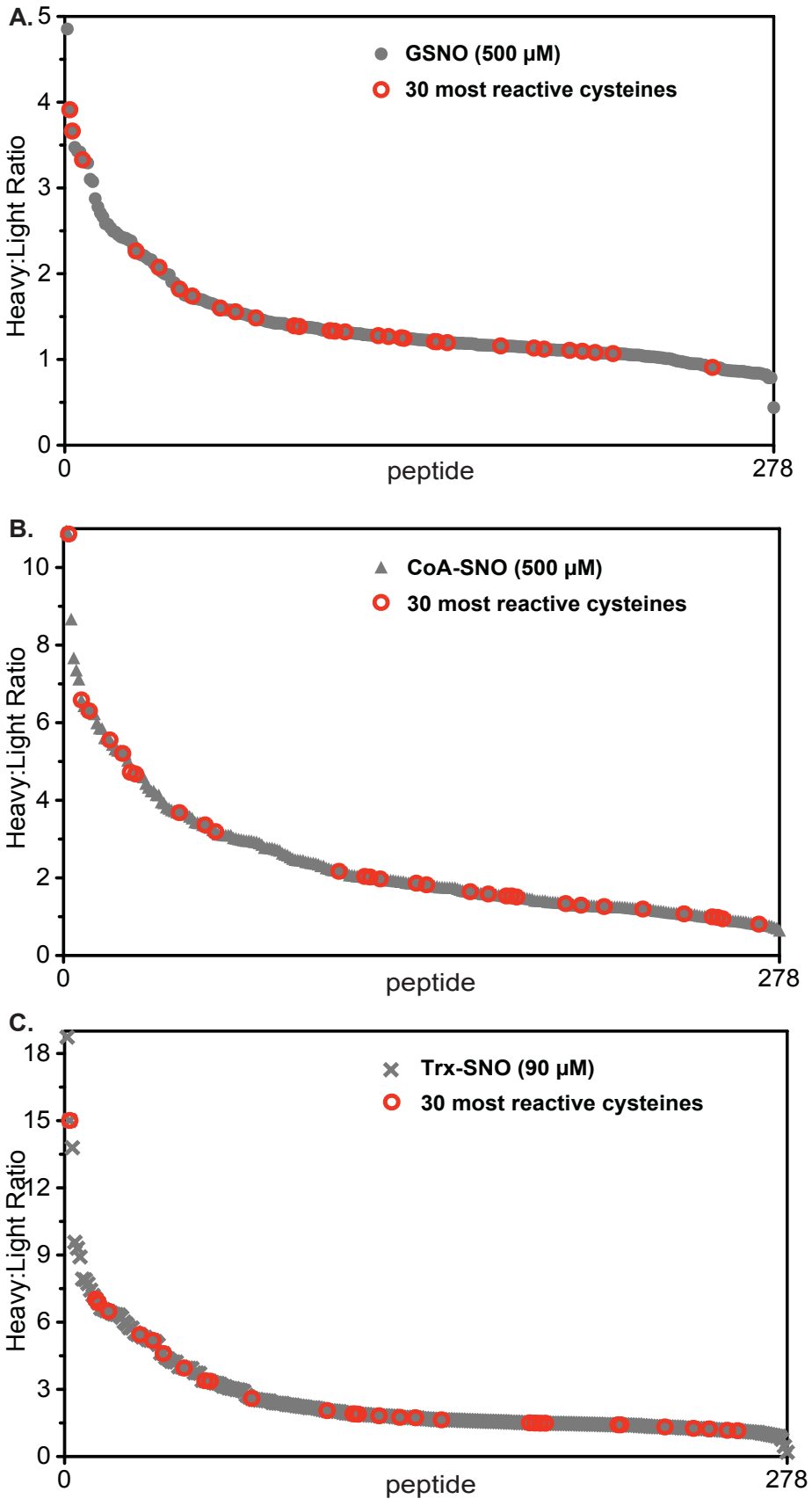

A.
GSNO (500 µM)
30 most reactive cysteines
Heavy:Light Ratio
peptide
0
278
B.
CoA-SNO (500 µM)
30 most reactive cysteines
Heavy:Light Ratio
peptide
0
278
C.
Trx-SNO (90 µM)
30 most reactive cysteines
Heavy:Light Ratio
peptide
0
278

Figure 3-8. Correlation of cysteine reactivity with transnitrosation sensitivity. To correlate sensitivity to GSNO transnitrosation with cysteine reactivity, the 30 most reactive cysteine residues[28] are highlighted (in red) across the range of R-values measured for GSNO (**A**), CoA-SNO (**B**) and Trx-SNO (**C**) sensitivity (Appendix I, Table 3A-6).

The role of inherent cysteine reactivity in directing transnitrosation donor towards particular cysteine residues was also evaluated. Previously, the IA probe was used in a global proteomic study to rank cysteine residues by reactivity, as reflected by the extent of IA-probe modification measured using both time and concentration-dependent analysis[28]. This reactivity data was correlated with the transnitrosation data (Appendix I, Table 3A-6) to determine if the cysteine residues most sensitive to transnitrosation are also highly reactive. Cysteine reactivity did not correlate with transnitrosation sensitivity. Indeed, for each transnitrosation donor, the top 30 most reactive cysteine residues from this previous study span the entire spectrum of transnitrosation sensitivity (Figure 3-8), suggesting that transnitrosation is not primarily driven by cysteine reactivity. However, it is important to note that this measure of reactivity is potentially biased toward cysteine residues that preferentially react with the IA probe, since different electrophiles target diverse subsets of cysteine residues[31].

Global analysis of binding interaction effects on cysteine sensitivity to transnitrosation

A potential determinant of the cysteine selective sensitivity to transnitrosation, is the specific binding interaction between the target protein and the transnitrosation donor, directing *S*-nitrosation to cysteine residues within the binding interface. To interrogate this possibility, a direct analysis across three subsets of proteins carrying the 50 most sensitive cysteines to GSNO, CoA-SNO and Trx-SNO transnitrosation were directly compared, demonstrating clear relationships between these protein subsets. (Figure 3-9). 14 proteins are common to all three subsets, indicative of their high sensitivity and promiscuity toward all three transnitrosation donors. Importantly, each subset contains 10-15 proteins that are exclusive from the other subsets, indicating their inherent selectivity to a specific transnitrosation donor. Next, to evaluate the selectivity at the amino acid level, the relative sensitivity across all 756 cysteines or the 50 most sensitive cysteines ranked by GSNO transnitrosation were compared to the other two transnitrosation donors. Importantly, sensitivity to either CoA-SNO or Trx-SNO transnitrosation did not correlate with sensitivity to GSNO transnitrosation. Specifically, the top 50 CoA-SNO-sensitive cysteine residues spanned the entire range of observed GSNO sensitivities (Figure 3-10; Appendix I, Table 3A-4). Similarly, the top 50 Trx-SNO-sensitive cysteine residues demonstrated variable GSNO sensitivity (Figure 3-10). Taken together, these results suggest that specific interactions between the protein target and the transnitrosation donor or specific properties of the transnitrosation donor itself are important determinants of *S*-nitrosation selectivity.

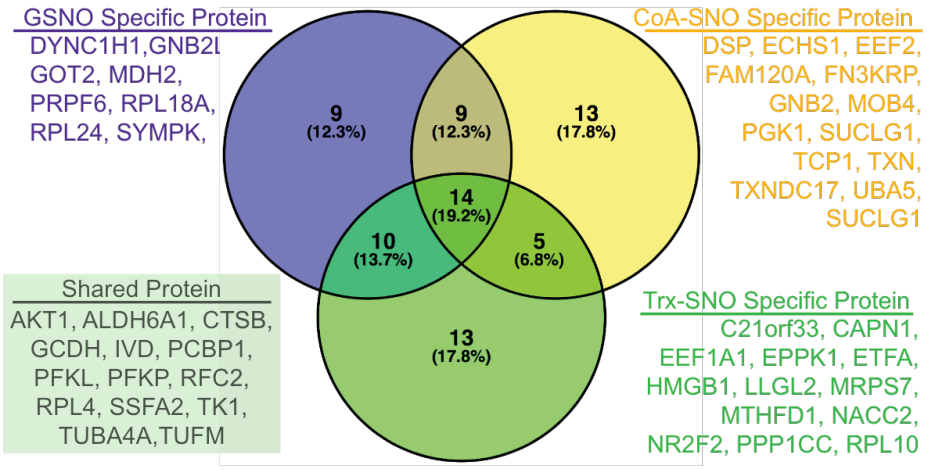


Figure 3-9. Venn diagram of the proteins carrying 50 most sensitive transnitrosation cysteines to GSNO, CoA-SNO and Trx-SNO. Proteins in the specific subsets are listed using the same color mode. Purple: only highly sensitive to GSNO; yellow, only highly sensitive to CoA-SNO; green: only highly sensitive to Trx-SNO; black: highly sensitive to all three donors.

To globally investigate the potential role of binding interactions on cysteine transnitrosation selectivity and sensitivity, we revised the quantitative proteomic strategy and performed a competitive cysteine transnitrosation analysis. We hypothesized that if the binding interaction between the target protein and the transnitrosation donor dictates selective transnitrosation of a specific cysteine residue, that cysteine would show an altered sensitivity toward the transnitrosation donor upon pretreatment with small molecules that are either structurally similar to the transnitrosation donor, or serves as a protein binding substrate. Interestingly, indeed, among the 20 most CoA-SNO sensitive cysteines, most are within proteins that use ATP as a binding substrate (Table 3-1). ATP shares the same adenine and ribose ring structures with CoA-SNO (Figure 3-12, A),

which serves as a good binding competitor of CoA-SNO. *S*-methyl-glutathione (MeGSH), a glutathione (GSH) derivative with a methylated cysteine thiol (Figure 3-11, A), was found to be released upon hypoxia and depolarization in extracellular space of the brain.[32] MeGSH, is incapable of conversion to GSNO and is therefore an ideal competitor for investigating binding effect on GSNO transnitrosation.

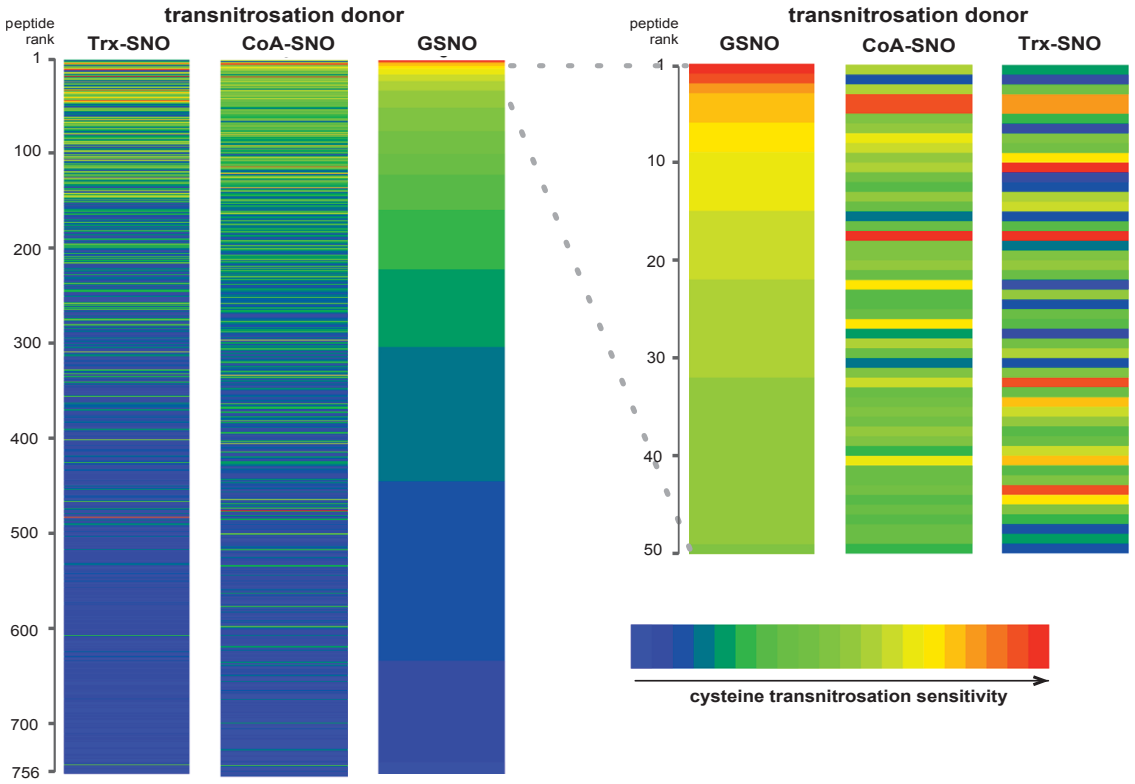


Figure 3-10. Heatmap of relative sensitivity across all 756 cysteines (left) or the 50 most sensitive cysteines (right) ranked by GSNO transnitrosation. Each line represents a single cysteine residue (Appendix I, Table 3A-4) with its relative sensitivity to CoA-SNO and Trx-SNO lined up in parallel. Sensitivity to either CoA-SNO or Trx-SNO transnitrosation did not correlate with sensitivity to GSNO transnitrosation.

cysteine sensitivity rank #	protein	description	cofactor/substrate/ binding partner
1	AKT1	RAC-alpha serine/threonine-protein kinase	ATP
2	TXNDC17	Thioredoxin domain-containing protein 17	TrxR with NADPH
3	PFKP	6-phosphofructokinase type C	ATP
4	GCDH	Glutaryl-CoA dehydrogenase, mitochondrial	Fatty-acyl-CoA
5	FAM120A	Constitutive coactivator of PPAR-gamma-like protein 1	RNA
6	RPL30	60S ribosomal protein L30	RNA, poly-A
7	ECHS1	Enoyl-CoA hydratase, mitochondrial	3-hydroxyacyl-CoA
8	PGK1	Phosphoglycerate kinase 1	ATP
9	RPS12	40S ribosomal protein S12	RNA, poly-A
10	PREX1	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein	phospholipids
11	TK1	Thymidine kinase, cytosolic	ATP
12	UBA5	Ubiquitin-like modifier-activating enzyme 5	ATP
13	ALDH18A1	Delta-1-pyrroline-5-carboxylate synthase	ATP, RNA
14	DSP	DSP Desmoplakin	RNA
15	PCBP1	Poly(rC)-binding protein 1	RNA, poly-A
17	HADH2	3-hydroxyacyl-CoA dehydrogenase type-2	NADH, NADPH, poly-A
18	PFKL	6-phosphofructokinase, liver type	ATP
19	MOB4	MOB-like protein phocein	Zn
20	DSP	Desmoplakin	RNA
21	EEF2	EEF2 Elongation factor 2	RNA, GTP

Table 3-1. The 20 most CoA-SNO sensitive cysteine containing proteins that were also detected in a 1 mM ATP pre-treatment mass spectrometry experiment (mass spectrometry data in Appendix I, Table 3A-4 and 3A-8) with their annotated cofactors, substrates or binding partners. The data were sorted by ratio (R) in 500 μM CoA-SNO (light) treated cell lysate. Gray-colored proteins contain CoA-SNO transnitrosated cysteines whose sensitivity to CoA-SNO decreased upon 1 mM ATP pre-treatment.

In detail, MCF7 cell lysates were pre-treated with 1 mM small molecule competitor (light, MeGSH for GSNO sample or ATP for CoA-SNO sample), or left untreated as a control (heavy). Both samples were then transnitrosated by 500 μM GSNO or CoA-SNO and taken through the quantitative mass spectrometry workflow mentioned

above. In total, 554 (GSNO treated) and 848 (CoA-SNO treated) cysteine residues were identified with accurate heavy:light ratios (R) in both control and experimental samples (Appendix I, Table 3A-7 and 8). For each cysteine residue, a shifted R ratio between control and experimental conditions reflected the subtle change of cysteine transnitrosation sensitivity upon small molecule/substrate binding. Specifically, a decreased ratio (R) upon competitor treatment indicated that binding interaction between protein and the small molecule de-sensitized cysteine to undergo transnitrosation, therefore more cysteines became available for subsequent probe labeling in the experimental sample, while an increased ratio (R) signified that small molecule/substrate binding facilitated cysteine transnitrosation. A subset of cysteine residues showed decreased ratios, impling that the innate sensitivity of these cysteines toward transnitrosation donors is governed at some level by specific interactions between the protein target and the transnitrosation donor, which can be perturbed by competitive small molecules or substrates.

Previous proteomic study on *S*-nitrosation sensitivity indicated that cysteine 58 of HADH2 is highly sensitive to GSNO transnitrosation. Cysteine 58 is located distal to the HADH2 active site and NADH binding site, within a hydrophobic pocket flanked by two leucine residues (Leu39 and Leu54) (Figure 3-11, B). Transnitrosation of cysteine 58 by GSNO led to a high ratio of 3.03. However, this ratio was partially quenched by MeGSH pre-treatment, resulting in a ratio of 2.35 (Figure 3-11, C). This partial loss in the sensitivity of cysteine 58 was well correlated with a gel-based study, where MeGSH was used as a competitive inhibitor and partially outcompeted GSNO binding to cysteine 58

in a concentration-dependent manner. Both of these studies indicate that GSNO transnitrosation of HADH2 proceeds through a GSNO-binding step.

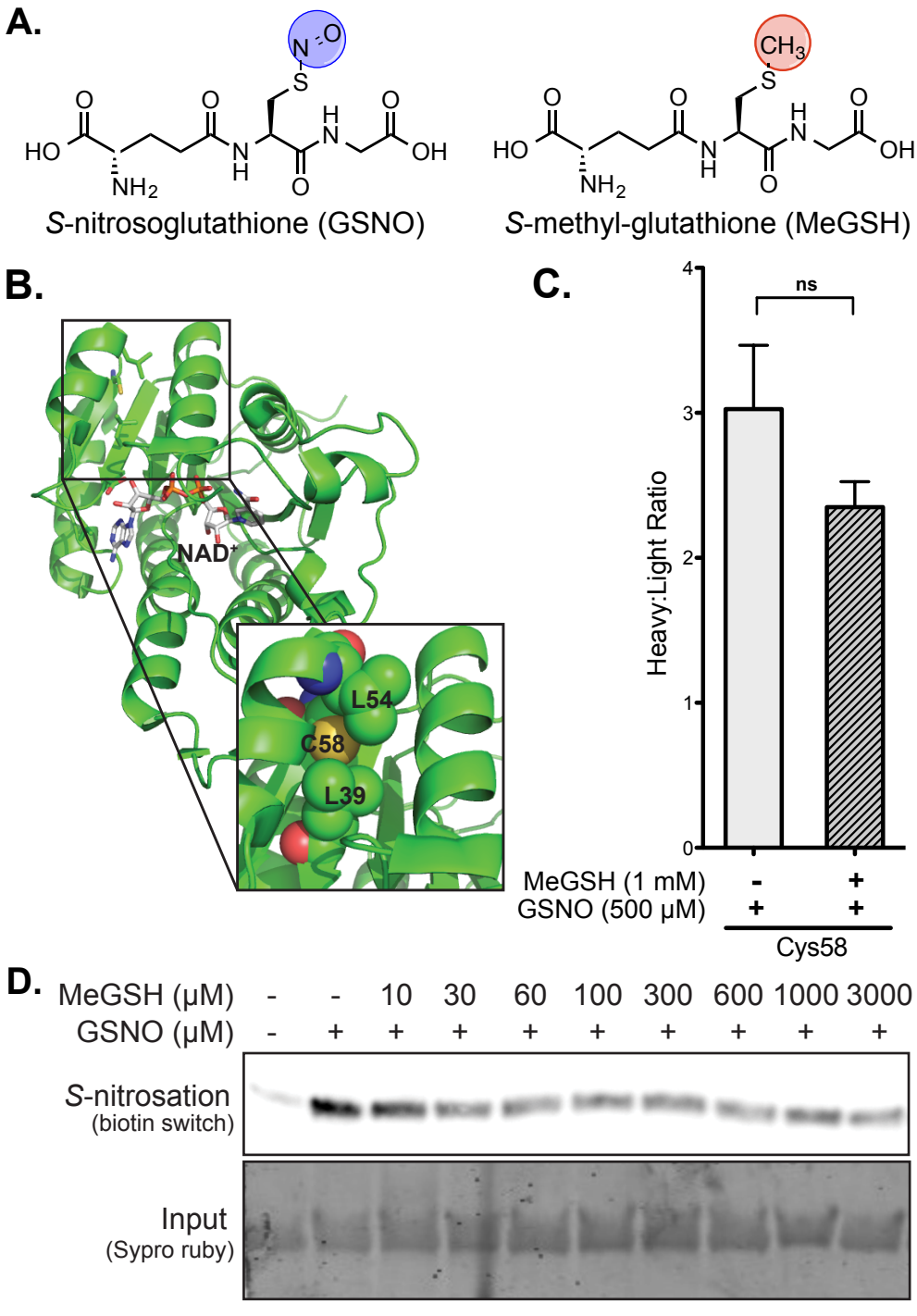


Figure 3-11. MeGSH pre-treatment desensitizes GSNO transnitrosation on cysteine 58 of HADH2. (**A**). Structures of GSNO (left) and MeGSH (right). (**B**) Structure of HADH2 (PDB: 2O23) with NAD^+ bound in the active site. The GSNO transnitrosation-sensitive cysteine, Cys58, is located distal to the active site within a hydrophobic pocket flanked by Leu39 and Leu54 (inset). (**C**) MCF7 cell lysate were pre-treated with 1 mM MeGSH (light, n=3), or left untreated as a control (heavy, n=5). Both samples were then transnitrosated by 500 μM GSNO and taken through the quantitative mass spectrometry workflow. R ratios of cysteine 58 of HADH2 in both control and MeGSH-treated sample are plotted. Data were presented as s.d. with $^{ns}p > 0.05$ by 2-way ANOVA. (**D**) *S*-nitrosation of recombinantly expressed and purified HADH2 WT pretreated with GSNO and then treated with increasing concentration of MeGSH. *S*-nitrosation was monitored using the biotin-switch technique as detailed under Experimental Procedures in chapter 2.

Another strong indication of the role of binding interaction perturbations are cysteines 360 and 641 on ATP-dependent 6-phosphofructokinase, platelet type (PFKP). PFKP is involved in the first committed step of glycolysis, catalyzing the Mg-ATP dependent phosphorylation of D-fructose-6-phosphate to fructose-1,6-bisphosphate in prokaryotic and eukaryotic cells. It acts as the "gatekeeper", the main control point of flux through glycolysis.[33, 34] Cysteine 360 and 641 on PFKP both showed high sensitivity to CoA-SNO transnitrosation (R>7) (Appendix I, Table 3A-8). However, ATP binding to PFKP quenched this high sensitivity to a large, though different extent, on both cysteines. ATP pre-treatment diminished sensitivity of cysteine 360 by 50%, leading to a ratio decrease from 9.7 to 5.0. However, the same treatment resulted in a smaller diminishment

in (~25%) sensitivity for cysteine 641 with a decrease in ratio from 6.8 to 5.1 (Figure 3-12, B). Interestingly, both cysteines are located in neither the direct substrate binding site, nor the allosteric activator region of PFKP. Crystal structure analysis demonstrated that cysteine 360 is located at an alpha helix adjacent to the ATP binding pocket (GDGS, position 127~130), whereas cysteine 641 is on a loop region, relatively distal to ATP binding site (Figure 3-12, C). As a result, binding of ATP would affect cysteine 360 more significantly than cysteine 641, hindering direct contact of NO moiety to cysteine thiol, making it much less sensitive to CoA-SNO transnitrosation. This conformational effect on cysteine sensitivity to transnitrosation suggests that direct binding interaction between cysteine residue and transnitrosation donor play an important role in governing its selectivity and extent of transnitrosation.

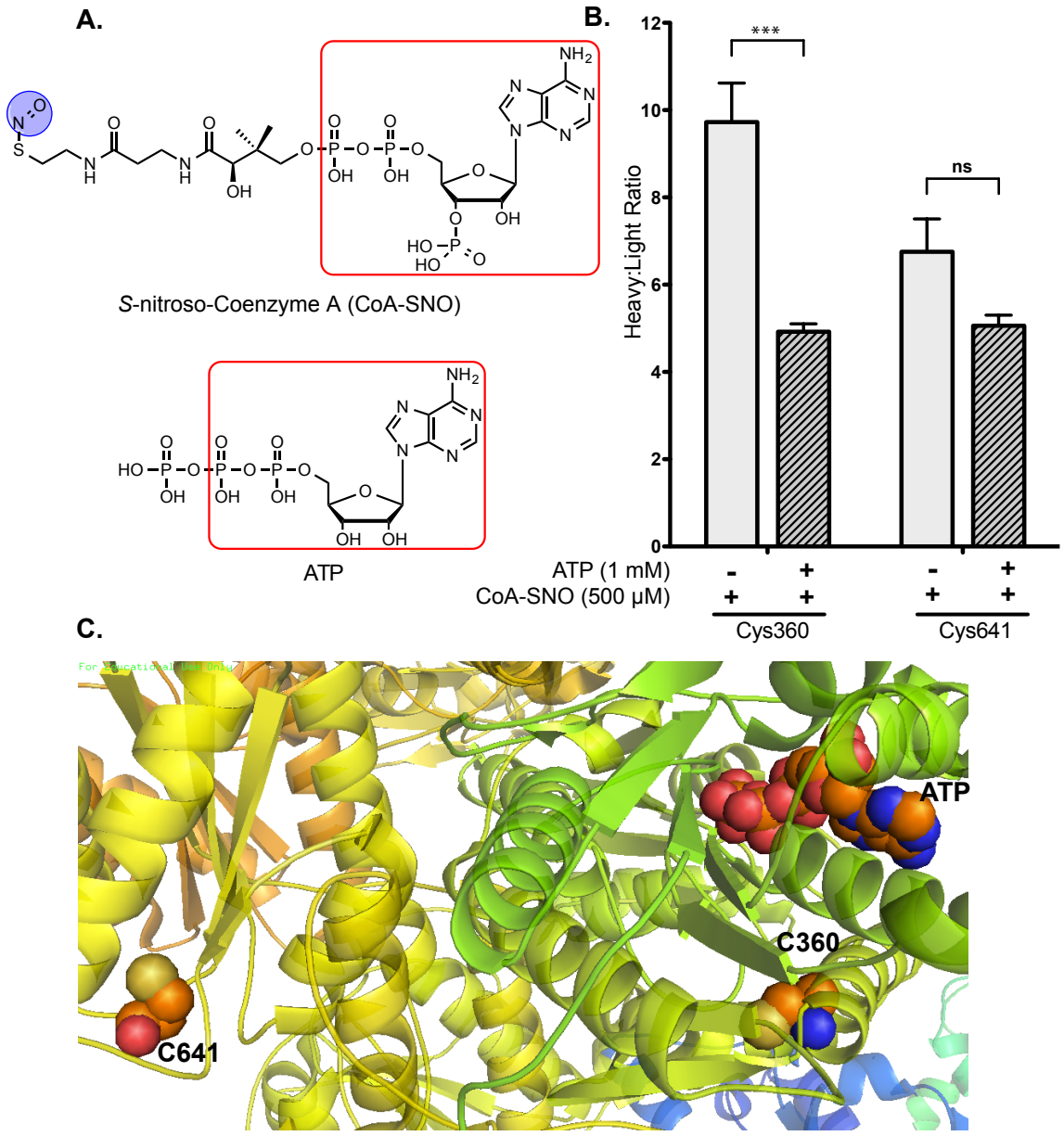


Figure 3-12. ATP pre-treatment desensitizes CoA-SNO transnitrosation on cysteine 360 and 641 of PFKP. (**A**). Structures of CoA-SNO (top) and ATP (bottom). Structural similarity in these two molecules is boxed in red. (**B**) MCF7 cell lysate were pre-treated with 1 mM ATP (light, n=2), or left untreated as a control (heavy, n=5). Both samples were then transnitrosated by 500 µM CoA-SNO and taken through the quantitative mass spectrometry workflow. R ratios of cysteine 360 and 641 of PFKP in both control and

MeGSH-treated sample are plotted. Data were presented as s.d. with $^{***}p < 0.001$ by 2-way ANOVA. (**C**) Structure of PFKP binding with ATP (PDB: 4xyj). Cysteine 360 is located close to the ATP binding pocket, while cysteine 641 is relatively distal to the ATP binding region.

Conclusion

In summary, we report a competitive cysteine-profiling strategy to globally and quantitatively rank 609, 477 and 379 cysteine residues by their transnitrosation sensitivity to GSNO, CoA-SNO and Trx-SNO respectively (Appendix I, Table 3A-1, 2 and 3). This platform relies on monitoring a loss in cysteine reactivity induced by direct transnitrosation of the thiol group. The data obtained provide important insight into the sensitivity of hundreds of cysteines to different transnitrosation donors. Direct comparison of the data resulted in a list of 756 cysteine-containing peptides that were transnitrosated by all three donors (Appendix I, Table 3A-4). This overlapping peptide list features individual cysteine residues with specific heavy:light ratios (R) for all three transnitrosation donors, highlighting the different degree of transnitrosation that a single cysteine undergoes by distinct transnitrosation donors. Interestingly, different transnitrosation donors targeted distinct subsets of cysteine residues (Figure 3-5, 3-9), consistent with the hypothesis that each transnitrosation donor specifically interacts with its protein targets, and this interaction is a key component governing selective transnitrosation of a specific cysteine residue.

The difference in redox potential between two interacting cysteine residues is often considered as the major determinant for protein transnitrosation.[5] Specifically, the

cysteine with the higher redox potential tends to acquire an electron to be reduced. Thus, when it interacts with a free thiol with a lower redox potential within an appropriate microenvironment for transnitrosation, transfer of the NO moiety will occur. Here, we investigated more determinants that could facilitate NO transfer and unify the subset of cysteine residues highly sensitive to transnitrosation. A primary sequence motif, surface-exposure, or pK_a trend dictating transnitrosation by GSNO, CoA-SNO and Trx-SNO was not identified. Importantly, sensitivity to transnitrosation by all three transnitrosation donors is not solely determined by the reactivity of a cysteine residue.

A potential determinant of cysteine selective sensitivity is specific binding interactions between the target protein and the transnitrosation donor that directs *S*-nitrosation to cysteine residues within the binding interface. To investigate this possibility, we performed a global proteomic analysis, where the transnitrosation reaction was performed after pre-treatment with a small molecule competitor, either structurally related to the transnitrosation donor such as MeGSH for GSNO, or protein binding partner such as ATP for CoA-SNO. This competitive binding effect resulted in a broad range of ratio shifts with regard to non-pretreated samples, indicating that binding interactions globally affect cysteine transnitrosation. In particular, cysteine 58 on HADH2, which was shown to be highly sensitivity to GSNO, was desensitized by MeGSH binding, leading to a ratio decrease of ~0.7. This ratio shift was consistent with the partially diminished band intensity of HADH2 transnitrosation after MeGSH competitive pre-treatment, indicating that GSNO transnitrosation of HADH2 precedes through a GSNO-binding step. Similarly, cysteine 360 and 641 on PFKP, both highly sensitive to CoA-SNO, were desensitized by ATP binding to a large, though different

degree. Compared to ~25% decrease of cysteine 641, a significant reduction (50%) of cysteine 360 sensitivity to CoA-SNO was observed upon ATP pre-treatment. Structural analysis revealed that cysteine 360 is located adjacent to the ATP binding pocket while cysteine 641 is relatively distal to this binding region. Thus ATP binding could potentially interrupt the accurate positioning of transnitrosation donor to cysteine thiol, resulting in decreased transnitrosation.

The two examples above demonstrated that the donor-protein binding interactions play an important role in transnitrosation selectivity. Moreover, direct association of the SNO donor and its target is also thought to alter protein conformation, affecting the microenvironment of specific cysteine residues and activating their ability to undergo transnitrosation. As a result, only a specific subset of proteins are transnitrosated, resulting in selective activation/inhibition of particular signaling pathways. This finding further supports the regulatory role of *S*-nitrosation modification in cell signaling and other cellular functions.

Taken together, the cysteine-profiling platform described here was used to interrogate the driving forces that dictate the selectivity of transnitrosation within proteomes, by allowing for a direct and quantitative comparison of the effects of distinct transnitrosation donors on their respective targets. These global studies enable a deeper understanding of the factors that dictate cysteine sensitivity to transnitrosation, consistent with the hypothesis that each transnitrosation donor specifically interacts with its protein targets, and this interaction is a key component governing selective transnitrosation of a specific cysteine residue.

Acknowledgement

I would like to acknowledge Kyle Cole for his calculation of pK_a and surface exposure area. Special thanks to Dr. Alex Shannon, Dr. Dan Bak and Tyler Bechtel for their continued help maintaining the Orbitrap mass spectrometer and also for their assistance in data analysis.

Experimental Procedures

Reagents and general procedures.

All materials were purchased from Sigma Aldrich (Milwaukee, WI) unless otherwise noted. RPMI 1640 medium, phosphate buffered saline (PBS), 2% Trypsin-EDTA and penicillin/streptomycin (Pen/Strep) were purchased from Fisher Scientific (Pittsburgh, PA). Protein concentrations were determined by Bradford Protein Concentration assay from Bio-Rad Life Science (Hercules, CA). Streptavidin-agarose beads and Ni-NTA beads were purchased from Thermo Scientific (Armarillo, TX). Nap-5 Columns were purchased from GE Healthcare Bio-Sciences (Piscataway, NJ). Micro BioSpin-6 desalting columns were purchased from Bio-Rad Life Science (Hercules, CA). Ni-NTA Magnetic Agarose Beads were purchased from QIAGEN (Valencia, CA). GSNO were purchased from Cayman Chemicals (Ann Arbor, MI).

MCF7 cell culture and lysate preparation.

MCF7 cells were maintained in RPMI1640 medium. Media was supplemented with 10% fetal bovine serum (FBS) and 1% Pen/Strep. Cells were grown at 37 °C under an atmosphere of 5% CO_2.

Cells were grown to 100% confluency and harvested by scraping. The cells were washed three times with PBS, resuspended in an appropriate volume of PBS and sonicated to obtain whole-cell lysates. The lysates were then separated by ultracentrifugation at 45,000 rpm at 4 °C under high vacuum for 45 min. The resulting supernatant was collected as the soluble proteome. Protein concentrations were determined using the Bradford Protein Concentration Assay.

MCF7 lysates transnitrosation and mass-spectrometry analysis.

GSNO was dissolved in freshly-made HEN buffer (125 mM HEPES pH 7.7, 1 mM EDTA, 0.1 mM neocuproine). The GSNO concentration was determined by measuring the UV absorbance at 336 nm (extinction coefficient: 0.9 $mM^{-1}cm^{-1}$.).

To generate Thioredoxin-SNO (Trx-C73-SNO), human Trx C62S/C69S was expressed and purified as previously described[35]. Trx C62S/C69S was reduced with 2.5 mM TCEP at room temperature for 15 min. A small excess of bovine insulin (1.2 equivalents) was then added to the mixture at room temperature for 30 min in order to oxidize the active-site cysteines of Trx (Cys32 and Cys35) to a disulfide. Finally Cys73 of Trx was *S*-nitrosated with two equivalents of GSNO at 37°C for 30 min. At the end of each step, Trx was desalted by Micro Bio-Spin Columns P-6 to remove extra reagent, and eluted with PBS. The concentration of Trx-C73-SNO was determined by measuring the UV absorbance at 336 nm, using an extinction coefficient of 0.9 $mM^{-1}cm^{-1}$. For protein

transnitrosation by Trx-C73-SNO, 250 μL aliquots of MCF7 lysate (4 mg/mL) were incubated with 250 μL PBS or 250 μL Trx-C73-SNO at 30°C for 30 min. Excess Trx-C73-SNO was then captured by Ni-NTA Magnetic Agarose Beads at room temperature for 30 min due to the presence of the His_{10}-tag on Trx-C73-SNO. The beads were separated using a QIAGEN 12-Tube Magnet. The supernatant was prepared for MS analysis as described above.

To generate fresh CoA-SNO, 0.1 M CoA in 1 M HCl was mixed with 0.1 M sodium nitrite (NaNO2) in buffer (100uM EDTA and 100 uM DTPA (pH 8~9.5)) on ice. The CoA-SNO concentration was determined by measuring the UV absorbance at 340 nm based on an extinction coefficient of 0.92 $mM^{-1}cm^{-1}$.

MCF7 cell lysates (4 mg/mL) were aliquoted to 500 μL and incubated with 5 μL buffer or 5 μL of NO donor (100X stock concentration: 50 mM GSNO, 50 mM CoA-SNO and 9 mM Trx-SNO) in buffer at 37 °C for 1 hr. Excess SNO was then removed by filtration through a Nap-5 column. Proteins were eluted with 1 mL PBS and aliquoted to produce two 500 μL samples.

Each 500 μL sample was treated with 100 μM IA probe using 5 μL of a 10 mM stock in DMSO. The labeling reactions were incubated at room temperature for 1 hr. Click chemistry was performed by the addition of either Azo-L or Azo-H (100 μM, 5 mM stock in DMSO), tris(2-carboxyethyl)phosphine hydrochloride (TCEP) (1 mM, fresh 50 mM stock in water), tris[(1-benzyl-1H-1,2,3-triazol-4-yl)methyl]amine (TBTA ligand) (100 μM, 17× stock in DMSO:t-Butanol 1:4) and $CuSO_4$ (1 mM, 50 mM stock in water). Samples were allowed to react at room temperature for 1 hr. The Azo-L and Azo-H samples were mixed together immediately following click chemistry. Precipitated

proteins were pelleted by centrifugation at 6500 × g (10 min, 4 °C). The pellets were washed twice by resuspending the pellet in cold methanol, after which the pellets were solubilized in PBS containing 1.2% w/v SDS via sonication and heating (5 min, 80 °C).

The SDS-solubilized, probe-labeled proteome samples were diluted with PBS to a final SDS concentration of 0.2% w/v. The solutions were incubated with 100 µL streptavidin-agarose beads at 4 °C for 16 hr, followed by incubation at room temperature for 2.5 hr. The beads were washed sequentially with 0.2% w/v SDS/PBS, PBS, and water, and pelleted by centrifugation (1300 × g, 2 min) between washes.

The washed beads were suspended in 500 µL 6 M urea/PBS and 10 mM dithiothreitol (DTT, from 200 mM stock in water) and placed in a 65 °C heat block for 15 min. 20 mM iodoacetamide (from 1 M stock in water) was then added and incubated at 37 °C for 30 min. Following reduction and alkylation the beads were pelleted by centrifugation (1300 × g, 2 min), re-suspended in 200 µL of 2 M urea/PBS, 1 mM $CaCl_2$ (100 mM stock in water) and trypsin (2 µg), and digested overnight at 37 °C. The digest was washed with PBS and water. The azobenzene linker was cleaved with 50 mL of fresh 25 mM sodium dithionite/PBS for 30 min at room temperature on a rotator, followed by centrifugation to collect supernatant. The sodium dithionite cleavage was repeated twice and then the beads were washed with water (2 × 75 µL). All supernatants and washes were combined and acidified with 15 µL formic acid. The samples were stored at -20 °C until mass spectrometry analysis.

LC/LC-MS/MS analysis was performed on an Agilent 1200 series HPLC coupled to an LTQ-Orbitrap Discovery mass spectrometer (ThermoFisher). Peptide digests were pressure loaded onto a 250 µm fused silica desalting column packed with 4 cm of Aqua

C18 reverse-phase resin (Phenomenex). The peptides were eluted onto a biphasic column (100 μm fused silica with a 5 μm tip, packed with 10 cm Aqua C18 reverse-phase resin (Phenomenex) and 3 cm Partisphere strong-cation-exchange resin (SCX, Whatman) using a gradient 5-100% Buffer B in Buffer A (Buffer A: 95% water, 5% acetonitrile, 0.1% formic acid; Buffer B: 20% water, 80% acetonitrile, 0.1% formic acid). The peptides were then eluted from the SCX onto the C18 resin and into the mass spectrometer using four salt steps as previously described [28, 36]. The flow rate through the column was set to ~0.25 mL/min and the spray voltage was set to 2.75 kV. One full MS scan (FTMS) (400-1800 m/z) was followed by 18 data dependent scans (ITMS) of the n^{th} most intense ions with dynamic exclusion enabled.

Mass-spectrometry analysis of small molecule binding effect on transnitrosation

GSNO and CoA-SNO was freshly-made as described above. MCF7 cell lysates (4 mg/mL) were aliquoted to 500 μL and incubated with 5 μL water at 37 °C for 1 hr (control), or 5 μL of small molecule (100X stock: 100 mM MeGSH or 100 mM ATP, 1 mM final concentration) in water at 37 °C for 1 hr (sample), respectively. Each sample was then incubated with 5 μL of NO donor (100X stock concentration: 50 mM GSNO or 50 mM CoA-SNO, final concentration: 500 μM) in buffer at 37 °C for 1 hr. Then Excess NO donor was then removed by filtration through a Nap-5 column. Proteins were eluted with 1 mL PBS and aliquoted to produce two 500 μL samples. The IA probing and rest mass-spectrometry preparation steps were as described above.

Mass-spectrometry data analyses.

The generated tandem MS data was searched using the SEQUEST algorithm against the human IPI database. A static modification of +57.02146 on cysteine was specified to account for iodoacetamide alkylation and differential modifications of +456.2849 (Azo-L modification) and +462.2987 (Azo-H modification) were specified on cysteine to account for probe modifications. SEQUEST output files were filtered using DTASelect 2.0. Quantification of heavy:light ratios (R) was performed using the CIMAGE quantification package as previously described [28].

References

1. Nakamura T and Lipton SA. Emerging role of protein-protein transnitrosylation in cell signaling pathways. *Antioxid Redox Signal*. 2013;18:239-249.

2. Smith BC and Marletta MA. Mechanisms of S-nitrosothiol formation and selectivity in nitric oxide signaling. *Curr Opin Chem Biol*. 2012;16:498-506.

3. Broniowska KA and Hogg N. The chemical biology of S-nitrosothiols. *Antioxid Redox Signal*. 2012;17:969-80.

4. Forstermann U and Sessa WC. Nitric oxide synthases: regulation and function. *Eur Heart J*. 2012;33:829-37, 837a-837d.

5. Montagna C, Rizza S, Maiani E, Piredda L, Filomeni G and Cecconi F. To eat, or NOt to eat: S-nitrosylation signaling in autophagy. *The FEBS journal*. 2016.

6. Madej E, Folkes LK, Wardman P, Czapski G and Goldstein S. Thiyl radicals react with nitric oxide to form S-nitrosothiols with rate constants near the diffusion-controlled limit. *Free Radic Biol Med*. 2008;44:2013-2018.

7. Perissinotti LL, Turjanski AG, Estrin DA and Doctorovich F. Transnitrosation of nitrosothiols: characterization of an elusive intermediate. *Journal of the American Chemical Society*. 2005;127:486-7.

8. Wang K, Wen Z, Zhang W, Xian M, Cheng JP and Wang PG. Equilibrium and kinetics studies of transnitrosation between S-nitrosothiols and thiols. *Bioorg Med Chem Lett*. 2001;11:433-6.

9. Benhar M, Forrester MT and Stamler JS. Protein denitrosylation: enzymatic mechanisms and cellular functions. *Nat Rev Mol Cell Biol*. 2009;10:721-732.

10. Broniowska KA, Diers AR and Hogg N. S-nitrosoglutathione. *Biochim Biophys Acta*. 2013;1830:3173-81.

11. Roediger WE, Hems R, Wiggins D and Gibbons GF. Inhibition of hepatocyte lipogenesis by nitric oxide donor: could nitric oxide regulate lipid synthesis? *IUBMB life*. 2004;56:35-40.

12. Lu SC. Glutathione synthesis. *Biochim Biophys Acta*. 2013;1830:3143-3153.

13. Ramsay EE and Dilda PJ. Glutathione S-conjugates as prodrugs to target drug-resistant tumors. *Frontiers in pharmacology*. 2014;5:1-16.

14. Barglow KT, Knutson CG, Wishnok JS, Tannenbaum SR and Marletta MA. Site-specific and redox-controlled S-nitrosation of thioredoxin. *Proceedings of the National Academy of Sciences of the United States of America*. 2011;108:E600-E606.

15. Hess DT, Matsumoto A, Kim SO, Marshall HE and Stamler JS. Protein S-nitrosylation: purview and parameters. *Nat Rev Mol Cell Biol*. 2005;6:150-66.

16. Benhar M, Forrester MT, Hess DT and Stamler JS. Regulated protein denitrosylation by cytosolic and mitochondrial thioredoxins. *Science*. 2008;320:1050-1054.

17. Erwin PA, Lin AJ, Golan DE and Michel T. Receptor-regulated dynamic S-nitrosylation of endothelial nitric-oxide synthase in vascular endothelial cells. *J Biol Chem*. 2005;280:19888-19894.

18. Ravi K, Brennan LA, Levic S, Ross PA and Black SM. S-nitrosylation of endothelial nitric oxide synthase is associated with monomerization and decreased enzyme activity. *Proceedings of the National Academy of Sciences of the United States of America*. 2004;101:2619-2624.

19. Mitchell DA and Marletta MA. Thioredoxin catalyzes the S-nitrosation of the caspase-3 active site cysteine. *Nat Chem Biol*. 2005;1:154-158.

20. Mitchell DA, Morton SU, Fernhoff NB and Marletta MA. Thioredoxin is required for S-nitrosation of procaspase-3 and the inhibition of apoptosis in Jurkat cells. *Proceedings of the National Academy of Sciences of the United States of America*. 2007;104:11609-11614.

21. Leonardi R, Zhang YM, Rock CO and Jackowski S. Coenzyme A: back in action. *Progress in lipid research*. 2005;44:125-153.

22. Anand P, Hausladen A, Wang YJ, Zhang GF, Stomberski C, Brunengraber H, Hess DT and Stamler JS. Identification of S-nitroso-CoA reductases that regulate protein S-nitrosylation. *Proceedings of the National Academy of Sciences of the United States of America*. 2014;111:18572-18577.

23. Greco TM, Hodara R, Parastatidis I, Heijnen HF, Dennehy MK, Liebler DC and Ischiropoulos H. Identification of S-nitrosylation motifs by site-specific mapping of the S-nitrosocysteine proteome in human vascular smooth muscle cells. *Proceedings of the National Academy of Sciences of the United States of America*. 2006;103:7420-5.

24. Jia J, Arif A, Terenzi F, Willard B, Plow EF, Hazen SL and Fox PL. Target-selective protein S-nitrosylation by sequence motif recognition. *Cell*. 2014;159:623-634.

25. Doulias PT, Greene JL, Greco TM, Tenopoulou M, Seeholzer SH, Dunbrack RL and Ischiropoulos H. Structural profiling of endogenous S-nitrosocysteine residues reveals unique features that accommodate diverse mechanisms for protein S-nitrosylation. *Proc Natl Acad Sci U S A*. 2010;107:16958-63.

26. Marino SM and Gladyshev VN. Structural analysis of cysteine S-nitrosylation: a modified acid-based motif and the emerging role of trans-nitrosylation. *J Mol Biol*. 2010;395:844-59.

27. Qian Y, Martell J, Pace NJ, Ballard TE, Johnson DS and Weerapana E. An isotopically tagged azobenzene-based cleavable linker for quantitative proteomics. *Chembiochem*. 2013;14:1410-4.

28. Weerapana E, Wang C, Simon GM, Richter F, Khare S, Dillon MB, Bachovchin DA, Mowen K, Baker D and Cravatt BF. Quantitative reactivity profiling predicts functional cysteines in proteomes. *Nature*. 2010;468:790-5.

29. Rostovtsev VV, Green LG, Fokin VV and Sharpless KB. A stepwise huisgen cycloaddition process: copper(I)-catalyzed regioselective "ligation" of azides and terminal alkynes. *Angew Chem Int Ed Engl*. 2002;41:2596-9.

30. Vacic V, Iakoucheva LM and Radivojac P. Two Sample Logo: a graphical representation of the differences between two sets of sequence alignments. *Bioinformatics*. 2006;22:1536-1537.

31. Wong HL and Liebler DC. Mitochondrial protein targets of thiol-reactive electrophiles. *Chem Res Toxicol*. 2008;21:796-804.

32. Yamane H, Tomonaga S, Suenaga R, Denbow DM and Furuse M. Intracerebroventricular injection of glutathione and its derivative induces sedative and hypnotic effects under an acute stress in neonatal chicks. *Neuroscience letters*. 2007;418:87-91.

33. Kloos M, Bruser A, Kirchberger J, Schoneberg T and Strater N. Crystal structure of human platelet phosphofructokinase-1 locked in an activated conformation. *Biochem J*. 2015;469:421-432.

34. Webb BA, Forouhar F, Szu FE, Seetharaman J, Tong L and Barber DL. Structures of human phosphofructokinase-1 and atomic basis of cancer-associated mutations. *Nature*. 2015;523:111-114.

35. Barglow KT, Knutson CG, Wishnok JS, Tannenbaum SR and Marletta MA. Site-specific and redox-controlled S-nitrosation of thioredoxin. *Proc Natl Acad Sci U S A*. 2011;108:E600-6.

36. Weerapana E, Speers AE and Cravatt BF. Tandem orthogonal proteolysis-activity-based protein profiling (TOP-ABPP)--a general method for mapping sites of probe modification in proteomes. *Nat Protoc*. 2007;2:1414-25.

Chapter 4

Proteomic mass spectrometry analysis of protein glutathionylation in response to glucose metabolism

A significant portion of the work described in this chapter has been published in:

Kusal T. G. Samarasinghe, Dhanushka N. P. Munkanatta Godage, Yani Zhou, Fidelis T. Ndombera, Eranthie Weerapana, Young-Hoon Ahn, Clickable Glutathione Approach for Identification of Protein Glutathionylation in Response to Glucose Metabolism. *Mol. Biosyst.*. Manuscript in press.

.

I performed the on-bead tryptic digestion for proteomic mass spectrometry as well as the mass spectrometry experiments and analysis.

Introduction

Regulation of cellular redox environment is important for normal cellular physiology, and its alteration is known to induce different biological states of cells, including proliferation, differentiation, and apoptosis. The reactive oxygen and nitrogen species (ROS and RNS) generated from various sources, including the normal activity of mitochondrial enzymes, act as signaling molecules in redox signaling, and are sensed by cysteine residues, which undergo various types of oxidative modifications, such as *S*-nitrosation, *S*-glutathionylation, and disulfide bond formation. These oxidative cysteine modifications profoundly influence physiological functions of many proteins, serving as regulatory switches for many cellular processes. Consequently, its aberrant regulation often correlates with many disease conditions.

Among the various oxoforms, *S*-glutathionylation is the disulfide formation of a protein cysteine residue with glutathione.[1] Glutathione (GSH), an abundant tripeptide made of γGlu-Cys-Gly (L-γ-glutamyl-L-cysteinylglycine) is primarily found in the cytosol in both a reduced (GSH) and oxidized form (GSSG) (Figure 3A).[2, 3] GSH is biosynthesized by two ATP-dependent enzymes, γ-glutamylcysteine ligase (GCL) and glutathione synthetase (GS). GCL, the rate limiting step of GSH formation, ligates Glu and Cys to generate γGlu-Cys. Subsequently, GS catalyzes the coupling of γGlu-Cys to Gly to form glutathione.

The formation of *S*-glutathionylated proteins is dependent on the cellular GSH/GSSG ratio and involves a thiol/disulfide exchange between a protein thiol and GSSG and can also result from the reaction of *S*-nitrosated cysteines or sulfenic acids

with glutathione.[4] This process is highly reversible and the removal of glutathionylated adducts is driven by thiol/disulfide exchange with free GSH, or enzymatically by glutaredoxin. Several important cellular pathways are regulated through glutathionylation. These include the NF-κB survival pathway, whereby *S*-glutathionylation of a critical DNA-binding cysteine on NF-κB inhibits DNA binding and downstream transcriptional activation.[5] Other key proteins in this pathway such as IκB kinase (IKK) are also known to be glutathionylated,[6] rendering the NF-κB response system highly sensitive to oxidative stress and changes in cellular GSH/GSSG ratios. [7] Numerous studies have demonstrated that glutathionylation serves as an important regulatory switch of protein function in response to ROS in physiological redox signaling and pathological diseases.[1]

Mitochondria are the central organelle for cellular metabolism and their metabolic activity directly correlates with cellular fate, such as growth, differentiation, and apoptosis.[1,2] Glucose, a major nutrient for mitochondrial metabolism is converted via glycolysis to pyruvate for production of ATP, which is accompanied by a large consumption of oxygen and production of mitochondrial ROS (mROS).[4] However, when cells are subjected to glucose starvation, mitochondrial respiration and redox homeostasis is disturbed, including an increase of mROS, a decrease in NADPH levels, and an increased ratio of oxidized over reduced glutathione in cells.[6,7] Glucose starvation decreases the production of NADPH due to the decreased flux of glucose to the pentose phosphate pathway.[6] NADPH is an essential cofactor for both removing ROS and maintaining the normal redox environment. This redox disturbance by glucose starvation induces various other cellular processes such as apoptosis when metabolic stress is

severe.[8] Importantly, many of these cellular pathways are partially regulated by mechanisms involving mROS-mediated redox regulation.[8, 9]

Despite the fact that glucose starvation induces redox disturbances of various cellular processes mediated by mROS, [6,7] the role of dynamic protein glutathionylation in response to glucose metabolism remains unknown. Recently, Ahn *et al.* reported a chemical approach for chemoselective detection of protein glutathionylation using a glutathione synthetase mutant (GS M4). [10] GS M4 catalyzes the condensation of azido-Ala with γGlu-Cys in place of Gly, which produces clickable azido-glutathione (γGlu-Cys-azido-Ala) *in situ* in cells upon transfection of GS M4 and incubation with azido-Ala (Figure 4-1).[10] In response to ROS, glutathionylation of proteins by azido-glutathione, and subsequent click chemistry allows for effective enrichment and identification of glutathionylated proteins (Figure 1).[10] This small versatile azide handle can conjugate with biotin for purification in proteomics, or click with fluorophores for imaging applications. Thus, here we sought to use clickable glutathione approach for detection and identification of protein glutathionylation in response to glucose starvation.

Results

Clickable glutathione is catalyzed by enzymes implicated in glutathionylation

In order to analyze the cellular reversible change of protein glutathionylation in response to glucose metabolism, the ability of clickable glutathione to detect the reversible change of glutathionylation was determined. Several major enzymes are known to be involved in the processes of cellular glutathionylation. Glutathione-*S*-transferase pi (GSTP) catalyzes the transfer of glutathione to proteins, while glutaredoxin

1 (Grx1), glutathione reductase (GSNOR), together with Glutathione-S-transferase Omega 1(GSTO1) catalyze the deglutathionylation (removal of *S*-glutathione adducts) of proteins. To determine whether azido-glutathione can be accepted as a substrate for these enzymes involved in glutathionylation events, the catalytic efficiency of these enzymes was compared using substrates containing either endogenous glutathione (GSH) or azido-glutathione (^{N3}GSH). Similar K_M and k_{cat} values confirmed that the small size of the azide-group on ^{N3}GSH could be tolerated by these enzymes involved in cellular glutathionylation.

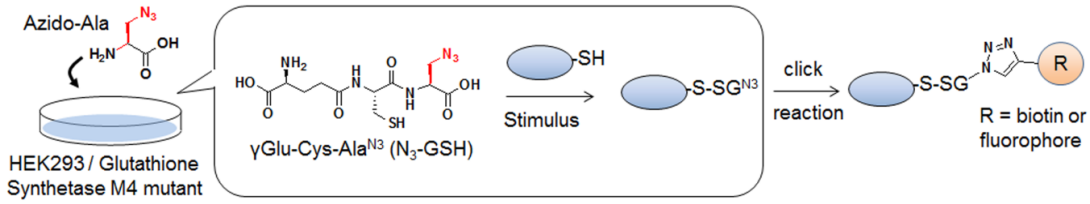


Figure 1. A workflow using a clickable azido-glutathione approach for detecting protein glutathionylation. Incubation of azido-Ala forms azido-glutathione (γGlu-Cys-azido-Ala) *in situ* in HEK293 cells stably expressing GS M4, which uses azido-Ala in place of Gly. In response to stimulus, proteins are oxidized by azido-glutathione instead of GSH. Subsequent click chemistry allows for identifying these glutathionylated proteins.

Cellular studies demonstrated that glucose starvation alone was not able to induce glutathionylation (Figure 4-2). However, in the presence of electron transport chain blocker (e.g. antimycin A and rotenone), glucose starvation readily induces a high level of global glutathionylation in a time- and concentration-dependent manner, (Figure 4-2, A, B) which was restored back to low level by addition of glucose or pyruvate in cells (Figure 4-3). Both antimycin A and rotenone stimulated mitochondrial dysfunction and

increased mROS by inhibiting complex III and I, respectively. Likewise, antimycin A or rotenone alone was not capable of inducing global glutathionylation. (Figure 4-2, C, D) This result was in agreement with previous reports that glucose starvation in combination with electron transport blockers induces the higher mROS and lower cell viability.

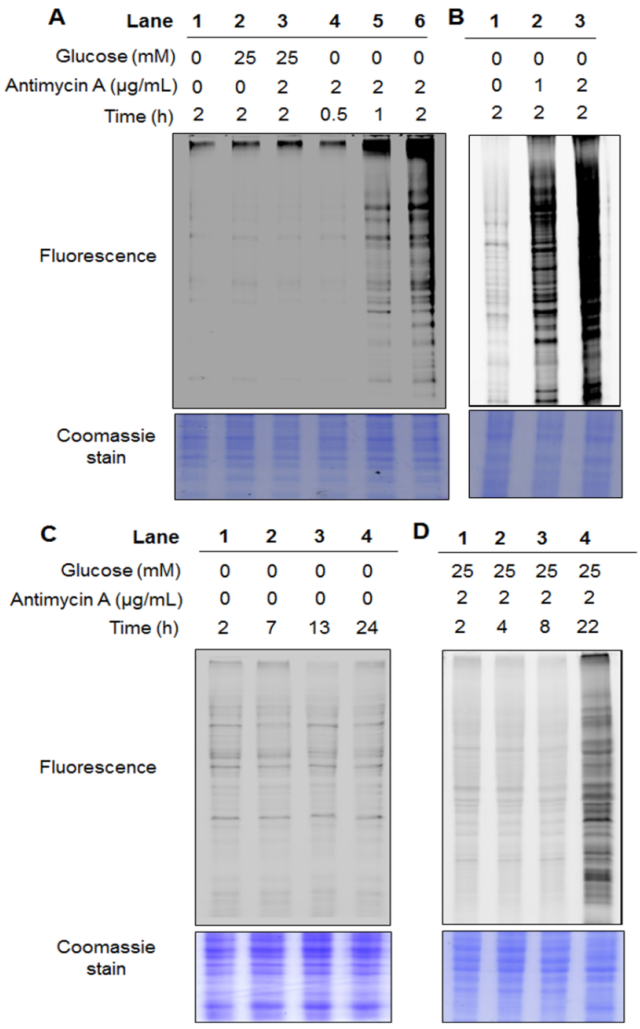


Figure 4-2. Glucose starvation readily induces global glutathionylation in the presence of an electron transport chain blocker. After incubation of azido-Ala to HEK293/GS M4 cells for 20 h, cells were subjected to the following stimulus: glucose starvation with treatment of antimycin A in time- (**A**) and dose- (**B**) dependent manners, glucose

starvation alone (**C**), and antimycin A alone (**D**). After stimulus, cell lysates were subjected to click chemsitry with rhodamine-alkyne, and analyzed for fluorescence and Coomassie stain. Here, a proteomic mass spectrometry platform was utilized to identify gutathionylated protein targets induced by glucose starvation in combination with antimycin A or rotenone treatment.

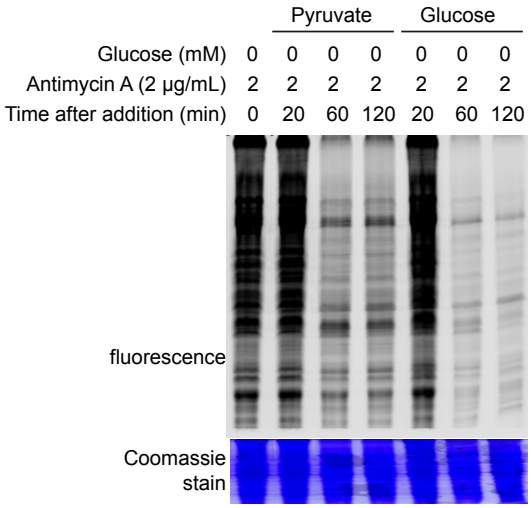


Figure 4-3. Glutathionylation is reversed by re-addition of glucose. After incubation of azido-Ala to HEK293/GS M4 cells for 20 h, glutathionylation was induced by glucose starvation with treatment of antimycin A for 2 h. Subsequently, glucose (5 mM) or pyruvate (5 mM) was added to the cells for the indicated time period. Cell lysates were subjected to click reaction with rhodamine-alkyne, and analyzed for fluorescence and Coomassie stain.

Identification of glutathionylated proteins in response to glucose starvation with mROS production.

The strong signals induced by glucose starvation with treatment of antimycin A indicate that a significant number of proteins are glutathionylated. To determine the identity of these glutathionylated proteins, a gel-based separation was performed, followed by click chemistry with biotin-alkyne, to enrich glutathionylated on streptavidin-beads. Labeled proteins were eluted, run on a gel, and detected by silver staining (Figure 4-4). Strong signals, indicative of glutathionylation, were observed under glucose starvation with antimycin A treatment (Figure 4-4, B lane 4). In control samples, relatively weak band intensity was observed with glucose, glucose starvation, or antimycin A alone (Figure 4-4, B lane 1-3). For proteins in lane 1 (negative) and 4 (positive) in Figure 4-4 B, an on-bead trypsin digestion was performed, followed by a standard LC/LC-MS/MS workflow (Figure 4-4, A). Mass spectrometry analysis identified 278 and 1493 potential protein glutathionylation candidates from lane 1 (negative) and 4 (positive), respectively (Figure 4-5, A). The full dataset was listed in Appendix I as Table 4A-1. Importantly, 1383 out of 1493 identified proteins (92.6%) had at least a two-fold increase in spectral counts (defined as the total number of fragmentation (MS2) spectra identified for a protein, average spectral count of at least 3 replicates)[11] in the positive versus negative control (Figure 4-6, A and Appendix I, Table 4A-1), which likely corresponds to an over 2-fold enrichment of proteins in the positive versus negative control. Of the 1493 proteins identified in the positive samples, ~156 proteins afforded spectral counts above 10, indicating a significant level of enrichment (Figure 4-6, B). 1383 proteins that showed at least a two-fold spectral count increase in positive versus negative control were categorized by DAVID software[12] for cellular localization, molecular function, and cellular processes (Figure 4-5, B-D).

Glutathionylated proteins are found in all major cellular compartments, and they are implicated in various cellular processes, including RNA processing, cell cycle, proteolysis, translation, stress response, glucose metabolism, and apoptosis (in the order of a decreasing P value, EASE score[13]) (Figure 4-5, B-D).

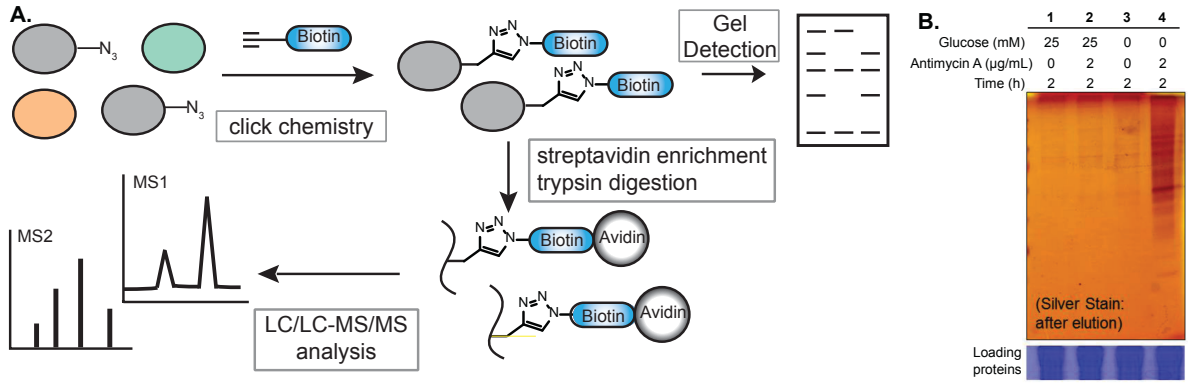


Figure 4-4. Proteomic analysis of glutathionylated proteins. (**A**) Approach for pull-down and mass analysis: after click chemistry with biotin-alkyne, glutathionylated proteins enriched by streptavidin-agarose were eluted for silver staining or directly digested on-bead for LC-MS/MS analysis. (**B**) Analysis of enriched proteins in indicated conditions.

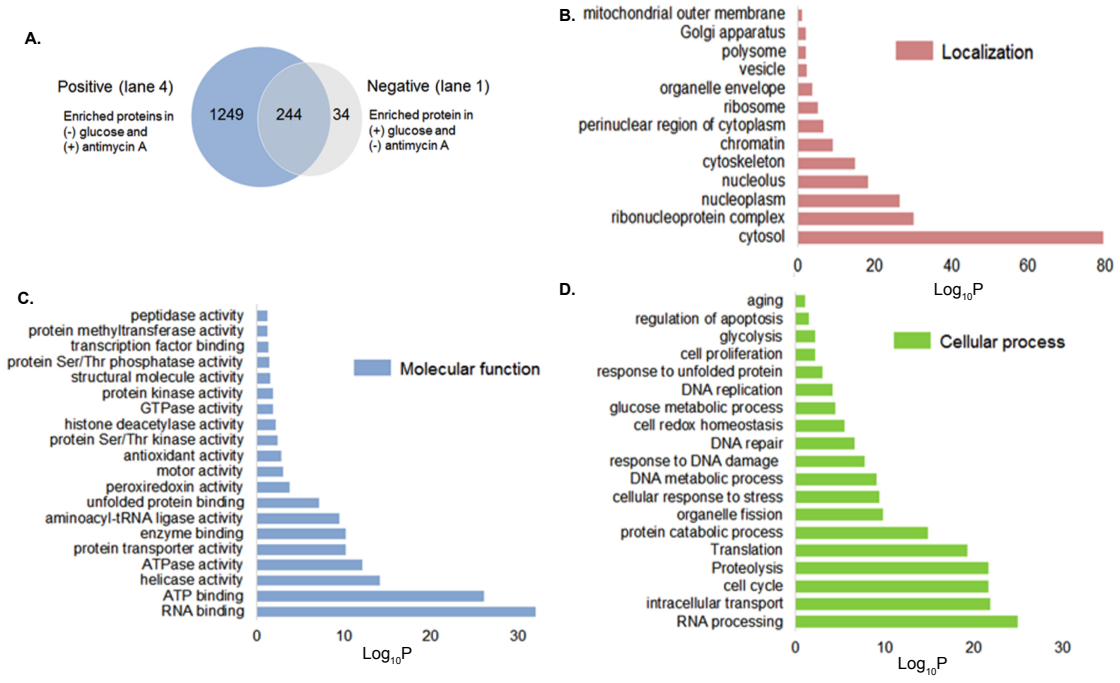


Figure 4-5. Systematic analysis of identified glutahionylated protein**.** (**A**) The number of glutathionylated proteins in indicated conditions by LC-MS/MS. (**B-D**) Gene ontology analysis of identified glutathionylated proteome.

A

A ratio of spectral count in positive vs. negative			# of protein
10 ≤	ratio		1291
5 ≤	ratio	< 10	28
2 ≤	ratio	< 5	64
0 ≤	ratio	< 2	145

B

Range of spectral count			# of protein
10 ≤	spectral count		156
5 ≤	spectral count	< 10	172
3 ≤	spectral count	< 5	180
2 ≤	spectral count	< 3	99
1 ≤	spectral count	< 2	397
0 ≤	spectral count	< 1	524

Figure 4-6. Proteomic data analysis of glutathionylated proteins. (**A**) Identified proteins in glucose starvation with antimycin A for 2-h (positive) or in the presence of glucose

without antimycin A (negative) were compared for the ratio of spectral counts in positive versus negative sample. (**B**) The range of spectral count for all proteins identified in LC-MS/MS. All spectral counts are the average of at least triplicate experiments of identical conditions.

Confirming the identity and reversibility of individual protein glutathionylation events.

In order to validate the mass spectrometry data, a further confirmation of the identity of several glutathionylated proteins was assayed by pull-down and western blot analysis. Glutathionylated proteins were enrichment on streptavidin-agarose beads, and probed with various antibodies. A time-dependent increase of glutathionylation was observed for a number of individual proteins (Figure 4-7, A). Glutathionylation of heat shock protein 90 (Hsp90), actin, catalase, and SMYD2 was clearly observed within 1 h. On the other hand, glutathionylation became obvious within 2 h for protein tyrosine phosphatase 1B (PTP1B), Src-homology phosphatase 2 (SHP2), AMP-activated kinase (AMPK), and protein phosphatase 2cα (PP2cα) (Figure 4-7, B). This time-dependent glutathionylation may result from different protein abundances or redox-sensitivity of individual protein cysteine residues. Analysis of the reversibility of glutathionylation for several selected proteins was demonstrated upon addition of pyruvate to the cell media. Deglutathionylation of PTP1B, AMPK, PP2Cα, and catalase was readily observed within 1 h, while actin glutathionylation was less significantly reduced under identical condition (Figure 4-7, B). This data confirmed not only glutathionylated proteins identified by mass

spectrometry analysis, as well as the time-dependent reversibility of glutathionylation for individual proteins in response to redox disturbance or glucose metabolism.

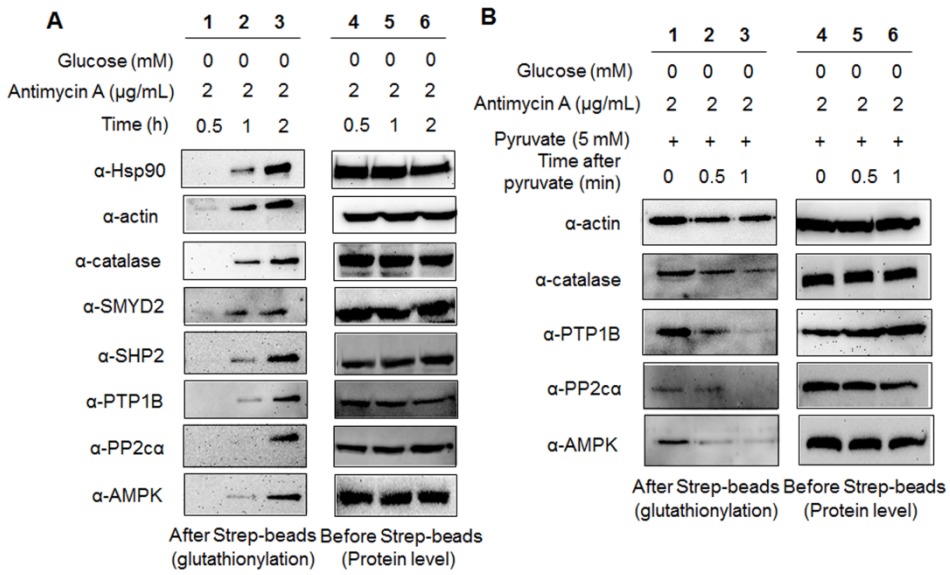


Figure 4-7. Determination of glutathionylated proteins by pull-down and Western blotting. After incubation of azido-Ala to HEK293/GS M4 cells for 20 h, cells were subjected to glucose starvation with antimycin A in a time-dependent manner (**A**), or pyruvate was added to cells after glucose starvation with antimycin A for 2 h (**B**). After click chemistry with biotin-alkyne, the individual proteins were probed by specific antibodies before and after pull-down by streptavidin-agarose.

Conclusion

Glutathione is a major cellular thiol for redox homeostasis. Protein glutathionylation is thought to increase during cellular redox disturbances, and is considered a marker of oxidative stress. However, global and individual protein glutathionylation in response to glucose metabolism and mitochondrial ROS level has not been examined previously. A clickable glutathione approach demonstrates that protein

glutathionylation is readily induced in response to glucose starvation when mitochondrial reactive oxygen species (mROS) are elevated in cells.

This work demonstrates the use of a proteomic mass spectrometry platform to determining the identity and reversibility of glutathionylated proteins in response to glucose metabolism. Proteomic analysis identified over 1,300 glutathionylated proteins including SMYD2, PP2Cα, and catalase. These proteins are involved in various cellular processes (Figure 4-5). Further analysis showed that many of identified proteins overlappped with proteins previously reported to be glutathionylated, and additionally overlapped with known sulfenylation events induced by addition of exogenous hydrogen peroxide, suggesting the fundamental redox-sensitivity for proteins under different stimulus. Confirmation of glutathionylation for selected proteins by in gel analysis further validated the mass spectrometry results, and highlights the dynamic change of glutathionylation on an individual protein level. Our findings highlight the ability of the proteomic mass spectrometry approaches to dissect complex cellular glutathionylation and suggest that application of this approach could yield important insights into the underlying mechanism of cysteine posttranslational modification in cellular function.

Acknowledgement

I would like to acknowledge Professor Young-Hoon Ahn (Wayne State University) and his lab group members for the gel-based study and kinetic measurement. Special thanks to Dr. Alex Shannon and Dr. Dan Bak for their continued help maintaining the Orbitrap mass spectrometer and also for their assistance in data analysis.

Experimental Procedures

Reagents and general procedures.

All materials were purchased from Sigma Aldrich (Milwaukee, WI) unless otherwise noted. Streptavidin-agarose beads were purchased from Thermo Scientific (Armarillo, TX). QuikChange.

LC/LC-MS/MS analysis of glutathionylated protein

After protein enrichment on streptavidin-agarose beads, the beads were pelleted and washed twice in DPBS. After resuspending in 50 µL 6 M urea/PBS, the beads were incubated at room temperature for 1 hr. 100 µL DPBS was then added to dilute the urea to a final concentration of 2 M. On-bead trypsin digestion was performed overnight at 37 °C with sequencing-grade trypsin (2 µg; Promega) and 1 mM $CaCl_2$ (100 mM stock in water). The peptide digests were centrifuged and the supernatant collected. The beads were washed twice with water (2 × 75 µL). All supernatants and washes were combined and acidified with 15 µL formic acid. The samples were stored at -20 °C until mass spectrometry analysis.

LC/LC-MS/MS analysis was performed on an Agilent 1200 series HPLC coupled to an LTQ-Orbitrap Discovery mass spectrometer (ThermoFisher). Peptide digests were pressure loaded onto a 250 µm fused silica desalting column packed with 4 cm of Aqua C18 reverse-phase resin (Phenomenex). The peptides were eluted onto a biphasic column (100 µm fused silica with a 5 µm tip, packed with 10 cm Aqua C18 reverse-phase resin (Phenomenex) and 3 cm Partisphere strong-cation-exchange resin (SCX, Whatman) using

a gradient 5-100% Buffer B in Buffer A (Buffer A: 95% water, 5% acetonitrile, 0.1% formic acid; Buffer B: 20% water, 80% acetonitrile, 0.1% formic acid). The peptides were then eluted from the SCX onto the C18 resin and into the mass spectrometer using four salt steps as previously described [14, 15]. The flow rate through the column was set to ~0.25 μL/min and the spray voltage was set to 2.75 kV. One full MS scan (FTMS) (400-1800 m/z) was followed by 8 data dependent scans (ITMS) of the n^{th} most intense ions with dynamic exclusion enabled.

Mass-spectrometry data analyses.

The generated tandem MS data was searched using the SEQUEST algorithm against the human UniProt database. A static modification of +57.02146 on cysteine was specified to account for iodoacetamide alkylation. SEQUEST output files were filtered using DTASelect 2.0. [15].

References

1. Samarasinghe KTG and Ahn Y-H. Synthesizing Clickable Glutathione by Glutathione Synthetase Mutant for Detecting Protein Glutathionylation. *Synlett*. 2015;26:285-293.

2. Mieyal JJ, Gallogly MM, Qanungo S, Sabens EA and Shelton MD. Molecular mechanisms and clinical implications of reversible protein S-glutathionylation. *Antioxid Redox Signal*. 2008;10:1941-88.

3. Pastore A and Piemonte F. S-Glutathionylation signaling in cell biology: progress and prospects. *Eur J Pharm Sci*. 2012;46:279-92.

4. Gan ZR and Wells WW. Identification and reactivity of the catalytic site of pig liver thioltransferase. *J Biol Chem*. 1987;262:6704-7.

5. Pineda-Molina E, Klatt P, Vazquez J, Marina A, Garcia de Lacoba M, Perez-Sala D and Lamas S. Glutathionylation of the p50 subunit of NF-kappaB: a mechanism for redox-induced inhibition of DNA binding. *Biochemistry*. 2001;40:14134-42.

6. Reynaert NL, van der Vliet A, Guala AS, McGovern T, Hristova M, Pantano C, Heintz NH, Heim J, Ho YS, Matthews DE, Wouters EF and Janssen-Heininger YM. Dynamic redox control of NF-kappaB through glutaredoxin-regulated S-glutathionylation of inhibitory kappaB kinase beta. *Proceedings of the National Academy of Sciences of the United States of America*. 2006;103:13086-91.

7. Couvertier SM, Zhou Y and Weerapana E. Chemical-proteomic strategies to investigate cysteine posttranslational modifications. *Biochim Biophys Acta*. 2014;1844:2315-2330.

8. Spitz DR, Sim JE, Ridnour LA, Galoforo SS and Lee YJ. Glucose deprivation-induced oxidative stress in human tumor cells. A fundamental defect in metabolism? *Annals of the New York Academy of Sciences*. 2000;899:349-362.

9. Graham NA, Tahmasian M, Kohli B, Komisopoulou E, Zhu M, Vivanco I, Teitell MA, Wu H, Ribas A, Lo RS, Mellinghoff IK, Mischel PS and Graeber TG. Glucose deprivation activates a metabolic and signaling amplification loop leading to cell death. *Molecular systems biology*. 2012;8:589.

10. Samarasinghe KT, Munkanatta Godage DN, VanHecke GC and Ahn YH. Metabolic synthesis of clickable glutathione for chemoselective detection of glutathionylation. *Journal of the American Chemical Society*. 2014;136:11566-11569.

11. Lundgren DH, Hwang SI, Wu L and Han DK. Role of spectral counting in quantitative proteomics. *Expert review of proteomics*. 2010;7:39-53.

12. Huang da W, Sherman BT and Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. *Nat Protoc*. 2009;4:44-57.

13. Huang DW, Sherman BT, Tan Q, Collins JR, Alvord WG, Roayaei J, Stephens R, Baseler MW, Lane HC and Lempicki RA. The DAVID Gene Functional Classification Tool: a novel biological module-centric algorithm to functionally analyze large gene lists. *Genome biology*. 2007;8:R183.

14. Weerapana E, Speers AE and Cravatt BF. Tandem orthogonal proteolysis-activity-based protein profiling (TOP-ABPP)--a general method for mapping sites of probe modification in proteomes. *Nat Protoc*. 2007;2:1414-25.

15. Weerapana E, Wang C, Simon GM, Richter F, Khare S, Dillon MB, Bachovchin DA, Mowen K, Baker D and Cravatt BF. Quantitative reactivity profiling predicts functional cysteines in proteomes. *Nature*. 2010;468:790-5.

Chapter 5

Identification of covalent chemical probes to investigate cysteine-mediated protein activities

Introduction

Highly conserved within proteins (typically above 90%), the chemical and physical properties of cysteine make it one of the most functionally versatile amino acids. Functional cysteines can be found on a diverse array of protein families, ranging from oxidoreductases, to proteases and protein kinases. Functional cysteine residues tend to be located in protein microenvironments that perturbs their pK_a and makes them somewhat more nucleophilic then surface-exposed non-functional cysteines within the proteome.[1] This increased nucleophilicity of the thiol side chain can be exploited in the development of covalent inhibitors.[2] This is particularly useful in the field of protein kinases, a large number of which contain a reactive cysteine residue within the ATP-binding pocket. These cysteine residues serve important regulatory roles in a variety of cellular functions,[3] and its reactivity has be explored by the pharmaceutical industry, resulting in the development of several clinically relevant drugs. In particular, covalent cysteine-reactive inhibitors of the protein kinase EGFR are currently in clinical trials (HKI-272, CI-1033, EKB-569, and PF-00299804) for the treatment of lung and colon cancer. Additionally, Afatinib has been approved in the U.S. as a first-line treatment for metastatic non-small cell lung carcinoma.[4, 5] These inhibitors are distinguished by the presence of electrophilic Michael acceptors within their scaffold, covalently reacting with the cysteine residue of the target kinase through an irreversible inhibition mechanism.

In order to expand on the understanding of the functional role of the cysteine residues in biological systems, our lab has developed libraries of covalent small molecule probes to target diverse cysteine-mediated protein activities. Unlike small molecule libraries screened by typical chemical genetic approaches, all of our small molecules

were specifically designed to react covalently with functional cysteine residues. Downstream target identification was facilitated by incorporation of a small bio-orthogonal alkyne handle within the small molecule probe to be used for copper-catalyzed azide-alkyne cycloaddition (CuAAC), [6, 7] to incorporate reporter tags.

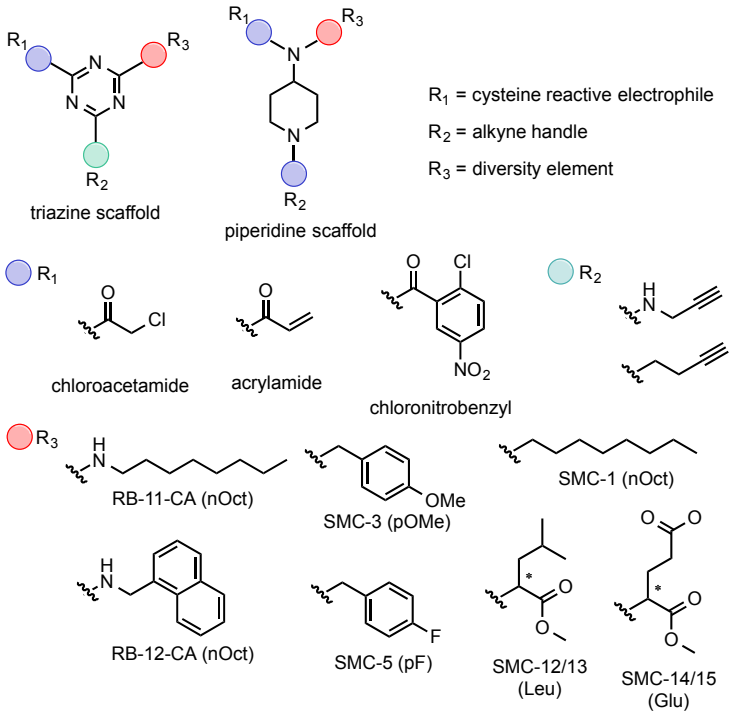


Figure 5-1. 1,3,5-triazines and 4-aminopiperidine scaffolds were utilized to generate cysteine-reactive small-molecule libraries. Each scaffold was functionalized with a cysteine-reactive electrophile (R_1), an alkyne handle (R_2) and a diversity element (R_3). Structures of R_1, R_2 and R_3 groups for a number of the compounds evaluated in this study are shown.

A library of small molecule probes based on 1,3,5-triazine as the central scaffold allows the incorporation of three different functionalities around the triazine ring (Figure 5-1).[8] These three elements include a cysteine-reactive electrophile (eg. chloroacetamide

(CA), chloronitrobenzyl (CNB) or acrylamide (Acr) reactive groups) to covalently modify a target cysteine residue, a terminal bio-orthogonal alkyne handle for CuAAC in order to append different reporter groups for downstream analysis, and a diversity element to help direct the small molecule probe towards different subsets of the proteome. Importantly, modification of either the diversity element or the electrophile in the triazine scaffold can modulate the protein targets of this small-molecule library. Gel-based screening[9] of this panel of compounds, combined with Multi-dimensional Protein Identification Technology (MudPIT) mass-spectrometry workflow,[10] allowed for the identification of diverse protein targets, including highly selective covalent modifiers for cysteine 239 of β–tublin and cysteine 53 of protein disulfide isomerase (PDI) respectively. To circumvent the rigidity of the triazine scaffold, development of a second covalent probe library utilizing a 4-aminopiperidine scaffold allowed for increased conformational flexibility (Figure 5-1).[11] Evaluation of this panel of compounds identified activity-dependent small-molecule probes for Glutathione *S*-transferase Omega 1 (GSTO1) and the protein kinase Akt1. The successful application of cysteine-reactive covalent modifier libraries along with their target identification highlights their promising use in the development of site-selective small molecule probes for diverse proteins.

First, we aimed to target 3-hydroxyacyl-CoA dehydrogenase (HADH2), a mitochondrial multifunctional protein involved in fatty acid synthesis and the oxidation of several neuroactive steroids and sex hormones.[12-14] Previously we identified cysteine 58 of HADH2, an uncharacterized cysteine residue located distal to the active site, as highly sensitivity to GSNO transnitrosation. *In vitro* studies demonstrated that

transnitrosation of this cysteine residue inhibited HADH2 dehydrogenation activity, highlighting the functional role of cysteine 58 as an allosteric regulator of HADH2. To further investigate the role of HADH2 cysteine 58, we sought to identify a selective covalent probe for this cysteine by screening our small-molecule libraries.

The second protein we were interested in is ASK1, as it is involved in the mitogen-activated protein kinase (MAPK) pathway. The MAPK pathway is an intracellular signaling system, regulating various cellular functions including cell survival, proliferation, differentiation, apoptosis, and response to cellular stress. The MAPK pathway consists of a kinase cascade of three classes of protein kinases: MAPK kinase kinase (MAP3K), MAPK kinase (MAP2K), and MAPK. MAP2K is phosphorylated and activated by MAP3K, and in turn phosphorylates and activates MAPK. These MAPKs are the most extensively studied kinases.[15] Specifically, MAP3Ks control the activation status of the signaling pathway, and thus are important for the regulation of downstream cellular responses. Apoptosis signal-regulating kinase 1 (ASK1), a MAP3K, is activated in response to various types of physiological and pathological stimuli, including growth factors, pro-inflammatory cytokines, and ER and oxidative stress (ROS).[16-18] As a result, downstream MAPKs, like stress-activated kinases p38 and c-Jun N-terminal kinase (JNK), responds to cellular stress by regulating apoptosis, inflammation, and proliferation through the phosphorylation of various targets. Thus, the dysregulation and excessive activation of ASK1 are closely related to various disease states such as cancer, diabetes, cardiovascular and neurodegenerative diseases.[19-21]

ASK1 homooligomerizes through its C-terminal coiled-coil domain and forms a high molecular mass complex called the signalosome (154.5 kDa). It includes a redox-sensitive protein, Thioredoxin 1 (Trx1), whose reduced form binds to the N-terminal domain of ASK1 and inhibits its kinase activity. Oxidative stimuli, like H_2O_2, activate ASK1 by oxidizing Trx1, and promoting its dissociation from the ASK1 signalosome. This allows ASK1 to tightly oligomerize through its N-terminal coiled-coil domain, leading to autophosphorylation of threonine 854 and full activation. Studies showed that an oligomerization step after treatment is crucial to ASK activation[22]. This was supported by a more recent study demonstrating that a H_2O_2-induced intermolecular disulfide bond between two cysteines in ASK1 molecules was involved in ASK1 oligomerization. This oxidation step was independent of ASK1 autophosphorylation, both of which were required for signal transaction.[23] Moreover, a detailed study revealed that in unstressed cells, Trx1 covalently binds to cysteine 250 on ASK1. Stimulation by H_2O_2 induces the active ASK1 sigalosome formation by autophosphorylation and simultaneously Trx1 dissociation from cysteine 250 as well as increased covalent interaction between Trx1 and cysteine 22 and 30 on ASK1. This study also suggested two different thiol reductase activities of Trx1 on ASK1, by transient reduction of the ASK1 intermolecular disulfide and by reduction of cysteine 22, 30 and 250 on ASK1.[24] These studies highlight the role of ASK1, besides its kinase activity, as an effective Trx oxidation sensor. The cysteine-dependent regulation of ASK1 renders it a possible cysteine-reactive small molecule target in order to modulate its function. Mace *et al*. has recombinantly purified and crystalized ASK1-28 (amino acid sequence from 88 to 658), a truncated version of ASK1 containing the N-terminal region where the Trx1-binding/redox active center is located.

In this study, we screened purified ASK1-28 against our cysteine-selective small molecule libraries to identify possible cysteine-reactive probes to functionally regulate ASK1.

The last protein we explored is Peroxiredoxin1 (Prdx1). In cells, H_2O_2 can be efficiently scavenged by peroxiredoxins. Existing as a dimer, a typical 2-cys Prdx has two critical cysteine residues per monomer; the peroxidatic cysteine and the resolving cysteine. Upon interaction with H_2O_2, the peroxidatic cysteine is oxidized to a sulfenic acid derivative, followed by the formation of an intermolecular disulfide with the resolving cysteine of the other monomer to release hydroxide. This disulfide bond is reduced by the thioredoxin–thioredoxin reductase (Trx/TrxR) system using electrons from NADPH.[25] In contrast, Prdx1 is an atypical 1-cys Prdx in that it conserves only the peroxidatic cysteine but not the resolving cysteine. Prdx1 is a small protein (22 kDa) with four total cysteine residues (52, 71, 83 and 173). Cysteine 52 is the redox-active site. Its cysteine sulfenic acid, generated on reaction with H_2O_2, is presumably reduced by a thiol-containing electron donor, the identity of which is still unknown.[26] Nevertheless, recent studies on role of Prdx1 in regulating the ASK1/p38 pathway revealed that upon treatment, oxidized Prdx1 could activate ASK1 via a transient formation of an intermolecular disulfide intermediate between Prdx1 and ASK1, followed by resolving and transferring the disulfide to an ASK1 protein substrate. This resulted in activation of downstream p38 phosphorylation. Oxidized ASK1 is subsequently reduced by the Trx/TrxR system.[27] The presence of Prdx1 in a disulfide bond transferring cascade expands the regulatory role of the Prdx1 cysteine in redox-signaling systems.

Result

Identification of a cysteine-reactive chemical probe for ASK1-28, Prdx1, and HADH2

To identify cysteine reactive probes that covalently bind to ASK1-28, Prdx1 and HADH2, we initially screened 1,3,5-trizine-based and 4-aminopiperidine-based probe libraries against purified ASK1-28 and Prdx1 protein obtained from Mace lab (University of Otago), and recombinantly overexpressed and purified HADH2 wild type (WT) and C58S mutant. Protein samples were treated with each of the probes from the library, followed by CuAAC to append a fluorescent Rhodamine-azide (Rh–N_3) tag for subsequent visualization by in-gel fluorescence (Figure 5-2). Using iodoacetamide alkyne (IA probe, Figure 5-4, C) as a control, ten probes from our library showed covalent modification of each of the proteins (Figure 5-1, R_3 groups). Analysis of gel band intensity indicated that, relative to iodoacetamide alkyne, RB-11-CA and SMC-1, both of which contain an n-octyl diversity element, showed the greatest selectivity and potency to ASK1 and Prdx1 respectively (Figure 5-3).

RB-21-CA (adamantine R_3 diversity element) demonstrated a concentration-dependent labeling of HADH2 WT across the small-molecule probe library (Figure 5-4 A, C). Kinetic studies of RB-21-CA on HADH WT activity indicated an IC_{50} of ~ 20.5 μM (Figure 5-4, B). However, a C58S mutant, which diminished the covalent interaction between the cysteine and RB-21-CA, showed no labeling, confirming that covalent modification of HADH2 by RB-21-CA occurs at cysteine 58. Interestingly, an IA labeled C58A mutant showed a concentration-dependent increase in labeling greater than that of the C58S mutant (Figure 5-4, D) This change in labeling pattern is possibly the result of

the cysteine to alanine mutation inducing a larger conformational change then that of cysteine to serine mutation, which could result in alternate cysteine residues available to interact with the IA probe.

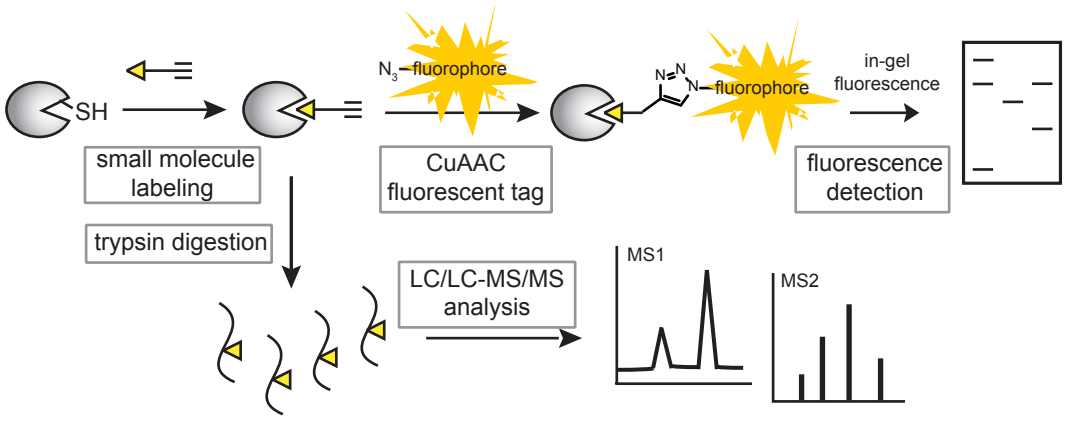


Figure 5-2. In-gel fluorescence and MS proteomic analysis for target identification of Prdx1 and ASK1-28. Small molecule treated proteins were appended to a fluorescent Rh–N_3 tag by click chemistry and subsequently visualized by in-gel fluorescence. Alternatively, Small molecule treated proteins were digested by trypsin and labeled peptides were identified by LC/LC-MS/MS.

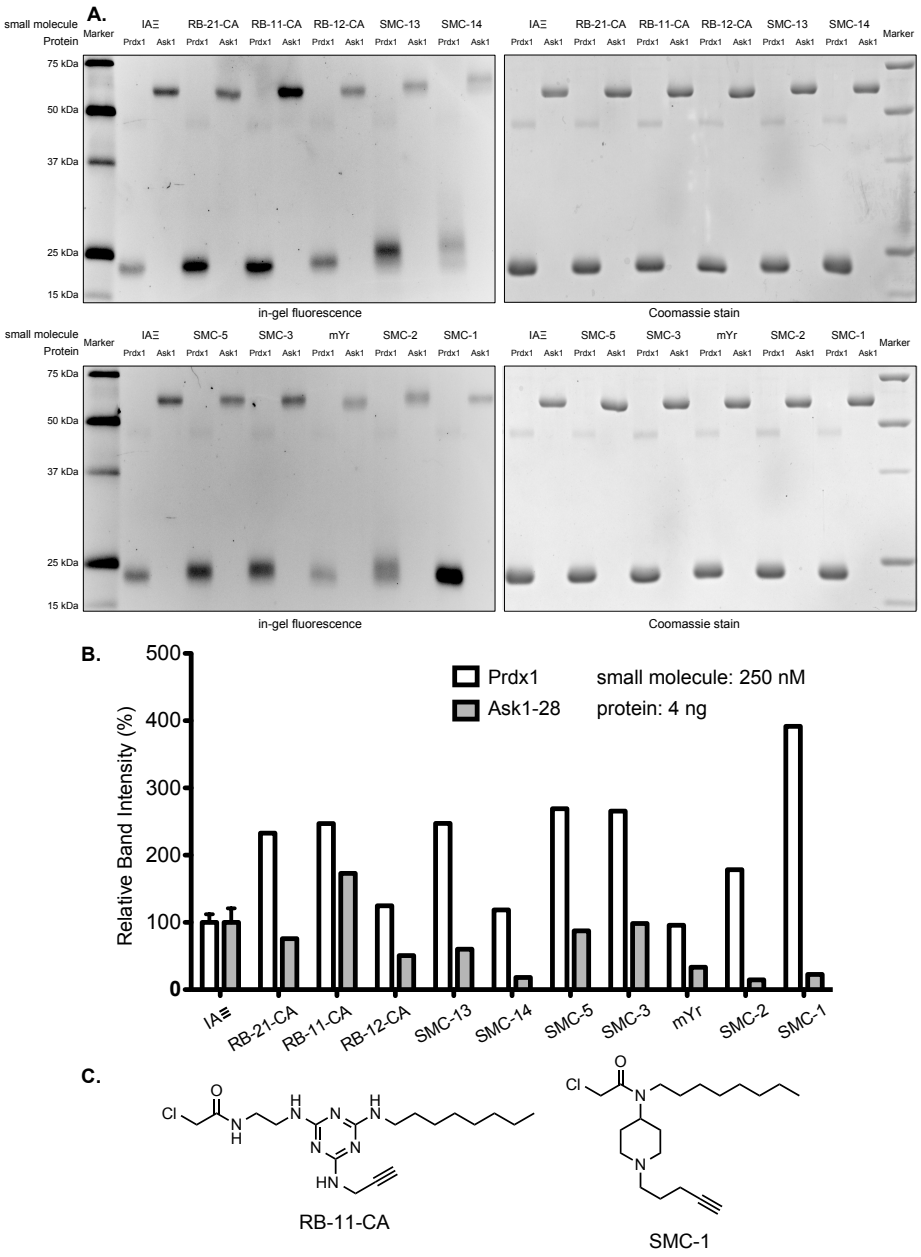


Figure 5-3. In-gel fluorescence analysis of small molecule labeling of ASK1-28 and Prdx1. (**A**) Prdx1 and ASK1 treated by small molecules were resolved by fluorescent gel using IA probe as labeling control. (**B**) Band intensity relative to IA probe treatment was calculated. (**C**) Structure of RB-11-CA and SMC-1 that demonstrated greatest labeling for ASK1-28 and Prdx1, respectively.

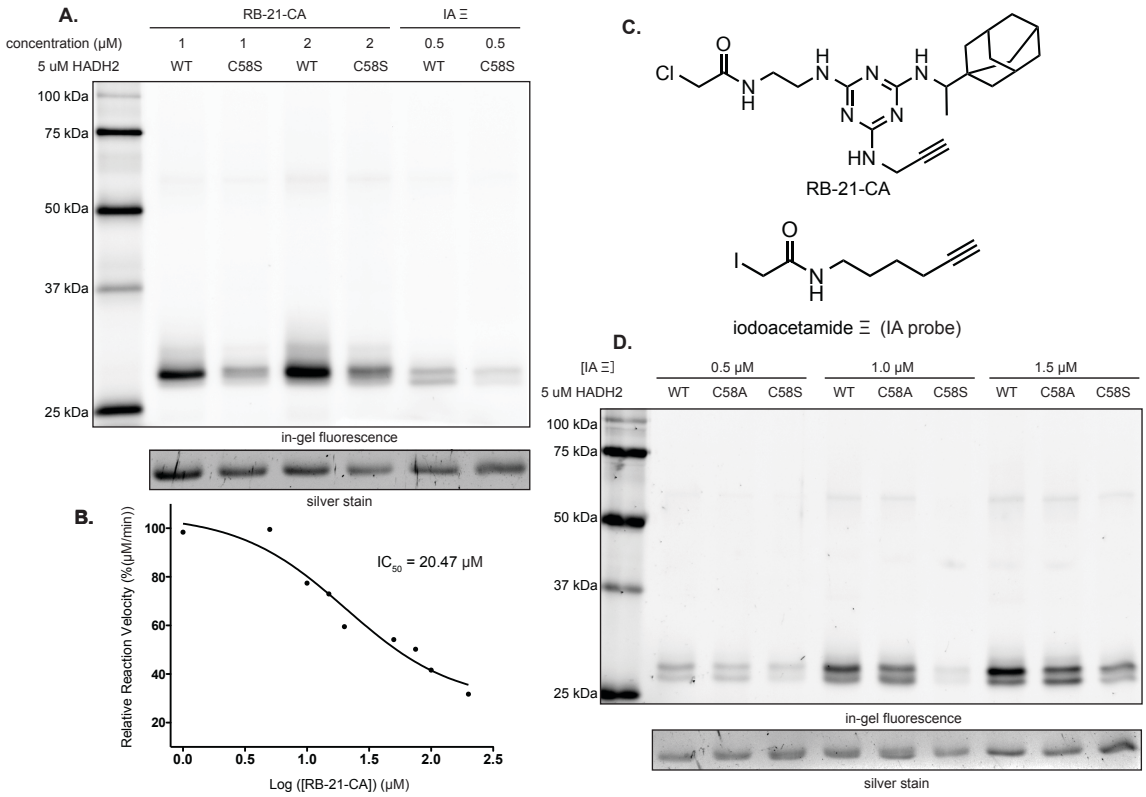


Figure 5-4. Modification of HADH2 cysteine 58 by RB-21-CA and IA probe. (**A**) RB-21-CA labeled HADH WT in a concentration-dependent manner. This labeling diminished for the C58S mutant. (**B**) Kinetic study of RB-21-CA on HADH2 WT with IC_{50} of 20.47 μM. (**C**) Structure of RB-21-CA and IA probe. (**D**) IA probe labeling events were increased in HADH2 C58A mutant than that of C58S mutant in a concentration-dependent manner.

A. **Prdx1 (cysteine 173)**

SMC-1 (modstat)	
Sequence	Spectrum #
K.HGEVC*PAGWKPGSDTIKPDVQK.S	7
SMC-1 (trypstat)	
Sequence	Spectrum #
R.SVDETLRLVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQK.S	1
R.LVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQK.S	31
F.TDKHGEVC*PAGWKPGSDTIKPDVQK.S	1
K.HGEVCPAGWK.P	1
K.HGEVCPAGWKPGSD.T	1
K.HGEVCPAGWKPGSDTIKPDVQ.K	1
K.HGEVCPAGWKPGSDTIKPDVQK.S	72
K.HGEVC*PAGWKPGSDTIKPDVQK.S	7
DMSO (trypstat)	
Sequence	Spectrum #
R.LVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQK.S	27
K.HGEVCPAGWK.P	3
K.HGEVCPAGWKPGSDTIKPDVQK.S	42

B. **ASK1-28 (cysteine 225)**

RB-11-CA (modstat)	
Sequence	Spectrum #
K.VYC*CDSSFMK.G	2
RB-11-CA (trypstat)	
Sequence	Spectrum #
H.NKVYCCDSSFMK.G	1
N.KVYCCDSSFMK.G	1
K.VYCCDSSFMK.G	28
K.VYC*CDSSFMK.G	3
V.YCCDSSFMK.G	1
Y.CCDSSFMK.G	1
Y.C*CDSSFMK.G	1
DMSO (trypstat)	
Sequence	Spectrum #
K.VYCCDSSFMK.G	1
K.VYCCDSSFMK.G	17

Table 5-1. LC-MS/MS identification of small molecule cysteine targets. (**A**) Cysteine 173 of Prdx1 is the target of SMC-1. (**B**) Cysteine 225 of ASK1-28 is the target of RB-11-CA. Spectral counts of the small molecule treated sample is significantly higher than that of DMSO control.

LC-MS/MS analysis to identify the cysteine targets on ASK1-28 and Prdx1

To identify the sites of probe labeling, RB-11-CA-labeled ASK1-28 and SMC-1-labeled Prdx1 were precipitated and concentrated by standard trichloroacetic acid precipitation (TCA) and digested to peptides by trypsin. LC–MS/MS analysis was then performed using a targeted mass list generated by prediction of the entire potential cysteine-containing tryptic peptides of each of these two proteins.[28] Proteins identified in

the small molecule treated samples were compared to DMSO treated control by mass spectrometry. This analysis enabled us to identify cysteine 173 of Prdx1 as the target of SMC-1 and cysteine 225 of ASK1-28 as the target of RB-11-CA, because high spectral counts were observed in probe treated samples (Spectral counts: the total number of fragmentation spectra found to correspond to peptides from a protein), while low spectral counts were seen in the DMSO-treated samples (Table 5-1). This confirms that RB-11-CA and SMC-1 demonstrate cysteine-specific labeling of ASK1-28 and SMC-1, respectively.

Conclusion

Here we screened purified ASK1-28, Prdx1 and HADH2 against 1,3,5-triazine and 4-aminopiperidine scaffold based cysteine reactive small molecule libraries. In-gel fluorescence revealed that RB-11-CA and SMC-1, both of which contain an n-octyl group as a diversity element, showed greatest selectivity and potency to ASK1 and Prdx1, respectively. LC-MS/MS analysis further identified cysteine 225 of ASK1-28 and cysteine 173 of Prdx1 as the sites of covalent probe modification. Another small molecule, RB-21-CA with an adamantine moiety as a diversity element, demonstrated extensive concentration-dependent labeling on HADH2 WT with an $IC_{50} \sim 20.5$ μM. However, a C58S mutant diminished this labeling to a large extent, further confirming that covalent modification of HADH2 by RB-21-CA occurs at cysteine 58. Interestingly, a HADH2 C58A mutant showed a concentration-dependent increase in labeling compared to the C58S mutant when labeled with an IA probe, which demonstrates the intrinsic similarity of serine and cysteine residues.

Further LC-MS/MS analysis is needed to confirm that RB-21-CA is targeting cysteine 58 of HADH2. Systematic analysis of RB-21-CA inhibition on HADH2 by kinetic studies would facilitate revealing the effect of RB-21-CA on protein function and its relation to the regulation of protein function by *S*-nitrosation. Furthermore, cysteine 225 of ASK1-28 is close to cysteine 250, which forms a disulfide bond with Trx1 in its inactive state[23]. Investigation of RB-21-CA modulation of cysteine 225 would shed light on the regulatory role of this cysteine residue on ASK1-28 function. Prdx1 activates ASK1 and its downstream target p38 by forming an inter-molecular disulfide intermediate with ASK1-28. A detailed study of SMC-1 on cysteine 173 of Prdx1 would reveal the role of cysteine 173 on the protein function and its relation to the ASK1 and Trx1 system, facilitating deeper understanding of the cellular redox-signaling pathways of Prdx1.

Acknowledgement

I would like to acknowledge Professor Peter Mace (University of Otago, New Zealand) for providing purified ASK1-28 and Prdx1 proteins. Special thanks to Dr. Alex Shannon and Dr. Dan Bak for their continued help maintaining the Orbitrap mass spectrometer and also for their assistance in data analysis.

Experimental Procedures

Reagents and general procedures.

All materials were purchased from Sigma Aldrich (Milwaukee, WI) unless otherwise noted. Protein concentrations were determined using a Bio-Rad DC protein assay or Bradford Protein Concentration assay from Bio-Rad Life Science (Hercules, CA) or a bicinchoninic acid (BCA) assay from Pierce. QuikChange Site-Directed Mutagenesis Kit was purchased from Agilent Technologies (Santa Clara, CA).

HADH2 subcloning.

HADH2 cDNA were subcloned into a pET23a-T7/His bacterial expression vector. Site-directed mutagenesis was performed to obtain cysteine to serine or cysteine to alanine mutants using the Quikchange procedure (Agilent, Santa Clara, CA) with the appropriate primers (Appendix I, Table 2A-4). All constructs were verified by DNA sequencing (Genewiz, Cambridge, MA or La Jolla, CA).

HADH2 expression and purification.

HADH2 (WT, C58S, or C58A) was expressed in *Escherichia coli* BL21 (DE3) cells. Cells were inoculated in 5 mL LB medium containing 100 μM Ampicillin at 37 °C overnight. The overnight culture was added to 500 mL LB or 1 L 2×YT medium containing 100 μM ampicillin and allowed to grow at 37 °C until OD_{600} ~ 0.6-0.8. Expression was then induced by the addition of 1 mM IPTG for 4 hr at 30 °C. Cells were harvested and lysed in PBS (for gel analysis) or 20 mM Tris pH 8.0 at 4 °C with 200 mM NaCl (for kinetic analysis). The expressed fusion protein was purified using a Ni-NTA packed chromatography column. After loading the cell lysate onto the column, the Ni-NTA resin was washed with 50 mM imidazole in PBS or 10 mM imidazole in 20 mM

Tris pH 8.0 at 4 °C with 200 mM NaCl and HADH2 was eluted with 500 mM imidazole in PBS or 300 mM imidazole in 20 mM Tris pH 8.0 at 4 °C with 200 mM NaCl. Protein purity was then assessed on a silver stained 10% SDS-PAGE gel. Excess imidazole was removed by use of a Nap-5 column and the purified protein was eluted in 20 mM potassium phosphate, pH 7.4, with 5% v/v glycerol and 5 mM β-mercaptoethanol, and stored at -80 °C [29]. Alternatively, the purified protein was dialyzed against 20 mM Tris pH 8.0 at 4 °C with 200 mM NaCl, 10% v/v glycerol, and 1 mM TCEP.

Small molecule screening of cysteine reactive probes

Purified Prdx1 or Ask1-28 was aliquoted to 4 ng /25 μL in DPBS. Each sample was treated with 0.5 μL of a 12.5 μM stock of cysteine reactive probe (50X stock in DMSO, 250 nM as final concentration) for 1 hr at room temperature. Purified HADH2 (WT, C58A and C58S) was was aliquoted to 5 μM /50 μL in DPBS. Each sample was treated with 1 μL a 12.5 μM stock of cysteine reactive probe (50X stock in DMSO) for 1 hr at room temperature. Click chemistry was then performed with the addition of Rhodamine-azide (25 μM, 1.25 mM stock in DMSO), tris(2-carboxyethyl)phosphine hydrochloride (TCEP) (1 mM, fresh 50 mM stock in water), tris[(1-benzyl-1H-1,2,3-triazol-4-yl)methyl]amine (TBTA ligand) (100 μM, 17× stock in DMSO:t-Butanol 1:4) and $CuSO_4$ (1 mM, 50 mM stock in water). Samples were allowed to react at room temperature for 1 hr. SDS-PAGE loading buffer 2x (reducing, 25 μL) was added to the samples and 25 μL of labeled protein sample was separated by 10% SDS-PAGE under 100 volts for 2 hrs. Gels were visualized on a Hitachi FMBIO II multiview flatbed laser-

induced fluorescent scanner. After analysis, gels were Coomassie or silver stained. Stained gel was visualized on a ChemiDoc MP Imaging System (BioRad).

HADH2 activity assays.

The purified HADH2 enzyme was assayed as described previously [30], where HADH2 activity was measured spectrophotometrically by monitoring the decrease in absorbance at 340 nm due to NADH oxidation. Purified HADH2 (WT C58A, or C58S) in 20 mM potassium phosphate, pH 7.4, with 5% v/v glycerol and 5 mM β-mercaptoethanol, was pre-incubated in a mixture of 100 mM potassium phosphate (pH 7), vary concentration of cysteine-reactive small molecule in DMSO and 100 μM NADH at room temperature for 30 min, using DMSO without small molecule as control reaction. The kinetic assay was initiated by the addition of varying concentrations of acetoacetyl-CoA (up to 100 μM). The reaction was carried out at 30 °C and the absorbance at 340 nm was measured using a Molecular Devices Spectramax M5 plate reader. Relative activity was determined as the slope of the absorbance vs. time curve within the linear range.

Mass-spectrometry analysis to identify small molecule targets

Peptide sample preparation

Purified Prdx1 or Ask1-28 was aliquoted to 33.5 μg /50 μL in DPBS. Each sample was treated with either 1 μL DMSO as a control, or 1 μL of 500 μM small molecule (50X stock in DMSO, 10 μM as final concentration) for 1 hr at room temperature. TCA protein precipitation of each small molecule labeled protein sample was performed in order to get proteins out of buffer and concentrate them. Specifically, 5

μL of freshly made 100% (w/v) trichloroacetic acid (TCA) was added to each protein sample, vortex and stored overnight, frozen at -80°C. Thawed samples were pelleted down by centrifuging for 10 minutes at top speed (15,000 rpm) at 4 °C. Supernatant was removed carefully in order not to disturb the pellet. Pellets were then washed by addition of 500 μL ice-cold acetone, re-suspended by sonication, centrifuging 10 minutes at top speed (15,000 rpm) at 4 °C and the supernatant carefully removed. The pellets were air dried and re-suspended in 30 μL of 8 M urea/DPBS by sonication. 70 μL of 100 mM ammonium bicarbonate was added to get a final volume of 100 μL. After addition of 1.5 μL 1M DTT, the mixture was incubated at 65 °C for 15 mins. Then 2.5 μL of 500 mM iodoacetamide was added and incubated at room temperature for 30 mins. After dilution with 120 μL of DPBS, the sample was trypsin digested with the addition of 4 μL of trypsin in buffer and 2.5 μL of 100mM $CaCl_2$, and incubated at 37 °C overnight. The trypsin was quenched with 10 μL of formic acid. Sample was pelleted by centrifugation at 15,000 rpm for 20 mins. After removing the supernatant, the samples were stored at -20 °C until mass spectrometry analysis.

Liquid chromatography-mass spectrometry (LC-MS/MS) analysis

LC-MS/MS mass spectrometry was performed using a Thermo LTQ Orbitrap Discovery mass spectrometer coupled to an Agilent 1200 series HPLC. Labeled peptide samples were pressure loaded onto 250 um fused silica desalting column packed with 4 cm of Aqua C18 reverse phase resin (Phenomenex). Peptides were eluted onto a 100 um fused silica biphasic column packed with 10 cm C18 resin and 4 cm Partisphere strong cation exchange resin (SCX, Whatman), using a five step multidimensional LC-MS

protocol (MudPIT) . Each of the five steps used a salt push (0%, 50%, 80%, 100%, and 100%), followed by a gradient of 5-100% buffer B in Buffer A (Buffer A: 95% water, 5% acetonitrile, 0.1% formic acid; Buffer B: 20% water, 80% acetonitrile, 0.1% formic acid). The flow rate through the column was ~0.25 uL/min, with a spray voltage of 2.75 kV. One full MS1 scan (400-1800 MW) was followed by 8 data dependent scans of the n^{th} most intense ion from the supplied mass list or if no more present, the n^{th} most intense ions otherwise. For each purified protein, a targeted mass list generated by prediction of the entire potential cysteine-containing tryptic peptides, was used. Dynamic exclusion was disabled, while monoisotopic precursor selection was enabled.

Mass-spectrometry data analyses.

The tandem MS data, generated from the 5 MudPIT runs, was analyzed by the SEQUEST algorithm. Static modification of cysteine residues (+57.0215 m/z, iodoacetamide alkylation) was assumed with no enzyme specificity. The precursor-ion mass tolerance was set at 50 ppm while the fragment-ion mass tolerance was set to 0 (default setting). Data was searched using a human reverse-concatenated non-redundant FASTA database. Datasets were independently searched with potential small molecule tagging parameter files; for these searches dynamic modifications on cysteine of +421.2764 (SMC-1 modification on Prdx1) or +462.27635 (RB-11-CA modification on ASK1-28) were used to account for small molecule modifications. MS2 spectra matches were assembled into protein identifications and filtered using DTASelect with the –trypstat (different statistical models for tryptic, half-tryptic, and non-tryptic peptides) and –modstat options applied. Redundant peptides identifications from multiple proteins were

allowed, but the database contained only a single consensus splice variant for each protein.

References

1. Couvertier SM, Zhou Y and Weerapana E. Chemical-proteomic strategies to investigate cysteine posttranslational modifications. *Biochim Biophys Acta*. 2014;1844:2315-2330.

2. Pace NJ and Weerapana E. Diverse Functional Roles of Reactive Cysteines. 2012.

3. Zhang J, Yang PL and Gray NS. Targeting cancer with small molecule kinase inhibitors. *Nature reviews Cancer*. 2009;9:28-39.

4. Minkovsky N and Berezov A. BIBW-2992, a dual receptor tyrosine kinase inhibitor for the treatment of solid tumors. *Current opinion in investigational drugs (London, England : 2000)*. 2008;9:1336-1346.

5. Singh J, Petter RC and Kluge AF. Targeted covalent drugs of the kinase family. *Curr Opin Chem Biol*. 2010;14:475-480.

6. Weerapana E, Wang C, Simon GM, Richter F, Khare S, Dillon MB, Bachovchin DA, Mowen K, Baker D and Cravatt BF. Quantitative reactivity profiling predicts functional cysteines in proteomes. *Nature*. 2010;468:790-5.

7. Rostovtsev VV, Green LG, Fokin VV and Sharpless KB. A stepwise huisgen cycloaddition process: copper(I)-catalyzed regioselective "ligation" of azides and terminal alkynes. *Angew Chem Int Ed Engl*. 2002;41:2596-2599.

8. Banerjee R, Pace NJ, Brown DR and Weerapana E. 1,3,5-Triazine as a modular scaffold for covalent inhibitors with streamlined target identification. *Journal of the American Chemical Society*. 2013;135:2497-2500.

9. Speers AE and Cravatt BF. Profiling enzyme activities in vivo using click chemistry methods. *Chemistry & biology*. 2004;11:535-546.

10. Speers AE and Cravatt BF. Activity-Based Protein Profiling (ABPP) and Click Chemistry (CC)-ABPP by MudPIT Mass Spectrometry. *Current protocols in chemical biology*. 2009;1:29-41.

11. Couvertier SM and Weerapana E. Cysteine-reactive chemical probes based on a modular 4-aminopiperidine scaffold. *Med Chem Commun*. 2013;5:358-362.

12. Porcu P, Barron AM, Frye CA, Walf AA, Yang SY, He XY, Morrow AL, Panzica GC and Melcangi RC. Neurosteroidogenesis Today: Novel Targets for Neuroactive Steroid Synthesis and Action and Their Relevance for Translational Research. *Journal of neuroendocrinology*. 2016;28.

13. Froemming MK and Sames D. Harnessing functional plasticity of enzymes: a fluorogenic probe for imaging 17beta-HSD10 dehydrogenase, an enzyme involved in Alzheimer's and Parkinson's diseases. *Journal of the American Chemical Society*. 2007;129:14518-14522.

14. Shafqat N, Marschall HU, Filling C, Nordling E, Wu XQ, Bjork L, Thyberg J, Martensson E, Salim S, Jornvall H and Oppermann U. Expanded substrate screenings of human and Drosophila type 10 17beta-hydroxysteroid dehydrogenases (HSDs) reveal multiple specificities in bile acid and steroid hormone metabolism: characterization of multifunctional 3alpha/7alpha/7beta/17beta/20beta/21-HSD. *Biochem J*. 2003;376:49-60.

15. Takeda K, Naguro I, Nishitoh H, Matsuzawa A and Ichijo H. Apoptosis signaling kinases: from stress response to health outcomes. *Antioxid Redox Signal*. 2011;15:719-761.

16. Liu H, Nishitoh H, Ichijo H and Kyriakis JM. Activation of Apoptosis Signal-Regulating Kinase 1 (ASK1) by Tumor Necrosis Factor Receptor-Associated Factor 2 Requires Prior Dissociation of the ASK1 Inhibitor Thioredoxin† *Mol Cell Biol*; 2000(20): 2198-2208.

17. Nishitoh H, Matsuzawa A, Tobiume K, Saegusa K, Takeda K, Inoue K, Hori S, Kakizuka A and Ichijo H. ASK1 is essential for endoplasmic reticulum stress-induced neuronal cell death triggered by expanded polyglutamine repeats. *Genes & development*. 2002;16:1345-1355.

18. Matsuzawa A, Saegusa K, Noguchi T, Sadamitsu C, Nishitoh H, Nagai S, Koyasu S, Matsumoto K, Takeda K and Ichijo H. ROS-dependent activation of the TRAF6-ASK1-p38 pathway is selectively required for TLR4-mediated innate immunity. *Nat Immunol*. 2005;6:587-592.

19. Ichijo H, Nishida E, Irie K, ten Dijke P, Saitoh M, Moriguchi T, Takagi M, Matsumoto K, Miyazono K and Gotoh Y. Induction of apoptosis by ASK1, a mammalian MAPKKK that activates SAPK/JNK and p38 signaling pathways. *Science*. 1997;275:90-94.

20. Nishitoh H, Saitoh M, Mochida Y, Takeda K, Nakano H, Rothe M, Miyazono K and Ichijo H. ASK1 is essential for JNK/SAPK activation by TRAF2. *Molecular cell*. 1998;2:389-395.

21. Hattori K, Naguro I, Runchel C and Ichijo H. The roles of ASK family proteins in stress responses and diseases. *Cell communication and signaling : CCS*. 2009;7:9.

22. Tobiume K, Saitoh M and Ichijo H. Activation of apoptosis signal-regulating kinase 1 by the stress-induced activating phosphorylation of pre-formed oligomer. *Journal of cellular physiology*. 2002;191:95-104.

23. Nadeau PJ, Charette SJ, Toledano MB and Landry J. Disulfide Bond-mediated Multimerization of Ask1 and Its Reduction by Thioredoxin-1 Regulate H2O2-induced c-Jun NH2-terminal Kinase Activation and Apoptosis *Molecular biology of the cell*; 2007(18): 3903-3913.

24. Nadeau PJ, Charette SJ and Landry J. REDOX reaction at ASK1-Cys250 is essential for activation of JNK and induction of apoptosis. *Molecular biology of the cell*. 2009;20:3628-3637.

25. Bak DW and Weerapana E. Cysteine-mediated redox signalling in the mitochondria. *Mol Biosyst*. 2015;11:678-97.

26. Wood ZA, Schroder E, Robin Harris J and Poole LB. Structure, mechanism and regulation of peroxiredoxins. *Trends in biochemical sciences*. 2003;28:32-40.

27. Jarvis RM, Hughes SM and Ledgerwood EC. Peroxiredoxin 1 functions as a signal peroxidase to receive, transduce, and transmit peroxide signals in mammalian cells. *Free Radic Biol Med*. 2012;53:1522-15230.

28. Weerapana E, Speers AE and Cravatt BF. Tandem orthogonal proteolysis-activity-based protein profiling (TOP-ABPP)--a general method for mapping sites of probe modification in proteomes. *Nat Protoc*. 2007;2:1414-25.

29. Liu X, Chu X, Yu W, Li P and Li D. Expression and purification of His-tagged rat mitochondrial short-chain 3-hydroxyacyl-CoA dehydrogenase wild-type and Ser137 mutant proteins. *Protein Expr Purif*. 2004;37:344-51.

30. Binstock JF and Schulz H. Fatty acid oxidation complex from Escherichia coli. *Methods Enzymol*. 1981;71 Pt C:403-11.

Appendix I

Mass spectrometry tables

All p values were calculated by 2-way ANOVA with *p < 0.5.

Table 2A-1. R-values from transnitrosation experiment at 500 μM GSNO**.** A list of all identified peptides (* denotes labeled cysteine) is presented together with calculated Heavy:Light Ratios (R-values) in untreated (0 μM) (n=2) versus GSNO-treated (500 μM) (n=5) MS analysis. Two replicates of control and five replicates of GSNO-treated experiments were performed. Date were sorted by their average R-values of GSNO-treated experiments and numbered as "Peptide #". P values, cysteine position, its conservation across six species and conservation ratio, and cellular location of protein that contains each cysteine are listed. Cysteines with high sensitivity to GSNO are highlighted in grey.

Peptide #	Uniprot #	Description	Symbol	Sequence	0 μM GSNO		
					1	2	average
1	Q99798	ACO2 Aconitate hydratase, mitochondrial	ACO2	VGLIGSC*TNSSYEDMGR	0.9	1.0	0.9
2	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	IISNASC*TTNCLAPLAK	0.9	0.9	0.9
3	P13674	P4HA1 Prolyl 4-hydroxylase subunit alpha-1	P4HA1	PC*TLSELE	0.9	1.0	1.0
4	P43034	PAFAH1B1 Platelet-activating factor acetylhydrolase IB subunit alpha	PAFAH1B1	PNQDGTLIASC*SNDQTVR	1.0	0.9	0.9
5	Q9H479	FN3K Fructosamine-3-kinase	FN3K	AFGGPGAGC*ISEGR	1.1	1.1	1.1
6	Q9BSD7	NTPCR Cancer-related nucleoside-triphosphatase	NTPCR	NADC*SSGPGQR	0.9	0.9	0.9
7	P07339	CTSD Cathepsin D	CTSD	AIGAVPLIQGEYMIPC*EK	0.8	0.9	0.9
8	Q01813	PFKP 6-phosphofructokinase type C	PFKP	LPLMEC*VQMTQDVQK	0.9	1.0	0.9
9	P07437	TUBB Tubulin beta chain	TUBB	LTTPTYGDLNHLVSATMSGVTTC*LR	1.0	1.0	1.0
10	Q06210	GFPT1 Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	C*QNALQQVVAR	1.0	1.0	1.0
11	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	VMTIPYQPMPASSPVIC*AGGQDR	1.0	1.0	1.0
12	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	IAC*LDFSLQK	0.9	1.1	1.0
13	Q04726	TLE3 Transducin-like enhancer protein 3	TLE3	SPISQLDC*LNR	1.0	1.0	1.0
14	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	ALDH6A1	C*MALSTAVLVGEAK	0.9	1.0	1.0
15	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	QC*PIMDPAWEAPEGVPIDAIIFGGR	0.8	1.1	1.0
16	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	VWNLANC*K	1.0	1.1	1.0
17	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	AYHEQLSVAEITNAC*FEPANQMVK	1.0	1.0	1.0
18	O00244	ATOX1 Copper transport protein ATOX1	ATOX1	VC*IESEHSMDTLLATLK	1.0	1.1	1.0
19	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	TSAPITC*ELLNK	0.9	0.9	0.9
20	P49207	RPL34 60S ribosomal protein L34	RPL34	AYGGSMC*AK	0.9	1.1	1.0
21	P31749	AKT1 RAC-alpha serine/threonine-protein kinase	AKT1	TFC*GTPEYLAPEVLEDNDYGR	1.0	1.0	1.0
22	P09622	DLD Dihydrolipoyl dehydrogenase, mitochondrial	DLD	NETLGGTC*LNVGC*IPSK	0.9	0.9	0.9
23	P04183	TK1 Thymidine kinase, cytosolic	TK1	NTMEALPAC*LLR	0.9	0.9	0.9
24	Q92947	GCDH Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	GYGC*AGVSSVAYGLLAR	0.9	1.0	0.9
25	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	AVC*MLSNTTAIAEAWAR	0.9	1.0	0.9
26	P62140	PPP1CB Serine/threonine-protein phosphatase PP1-beta catalytic subunit	PPP1CB	IC*GDIHGQYTDLLR	1.1	1.0	1.0
27	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	LGNNC*VFAPADVTSEK	0.9	1.0	0.9

Heavy : Light Ratio							Protein location	Cys position	Cysteine conservation across species						
500 μM GSNO						Significance			Species (cysteine is conserved: Yes/No/--)[1]						Conservation Ratio (%)[2]
1	2	3	4	5	average				Human	Mouse	Fly	Yeast	Mustard	Worms	
5.5	5.1	6.8	10.7	5.3	6.7	***	Mitochondrion {ECO	385	Yes	Yes	Yes	Yes	Yes	Yes	100.0
5.4	4.8	4.2	5.0	5.1	4.9	***	Cytoplasm, cytosol {ECO	152	Yes	Yes	Yes	Yes	Yes	Yes	100.0
5.0	4.0	4.4	5.9	4.2	4.7	***	Endoplasmic reticulum lumen.	528	Yes	Yes	Yes	--	--	Yes	100.0
4.9	4.4	3.4	3.8	4.2	4.1	***	Cytoplasm, cytoskeleton. Cytoplasm, cytoskeleton, microtubule organizing center, centrosome. Cytoplasm, cytoskeleton, spindle {ECO	252	Yes	Yes	Yes	No	No	No	50.0
10.8	1.4	5.0	1.8	1.3	4.1	***		24	Yes	Yes	--	--	Yes	--	100.0
3.6	3.5	3.9	4.7	4.1	3.9	***		101	Yes	No	No	--	No	--	25.0
3.4	3.2	4.0	4.7	3.7	3.8	***	Lysosome. Melanosome. Secreted, extracellular space.	329	Yes	Yes	Yes	Yes	--	Yes	100.0
3.9	3.5	3.4	4.0	3.7	3.7	***	Cytoplasm {ECO	360	Yes	Yes	Yes	No	--	Yes	80.0
3.8	3.5	3.5	4.0	3.6	3.7	***	Cytoplasm, cytoskeleton.	239	Yes	Yes	Yes	No	Yes	Yes	83.3
4.2	3.0	3.4	4.3	2.8	3.5	***		620	Yes	Yes	Yes	No	No	No	50.0
3.2	3.2	3.4	3.9	3.4	3.4	***	Nucleus. Cytoplasm.	194	Yes	Yes	No	No	No	--	40.0
3.8	2.9	3.4	3.5	3.2	3.4	***	Cytoplasm. Cytoplasm, cytoskeleton, microtubule organizing center, centrosome.	236	Yes	Yes	Yes	Yes	Yes	Yes	100.0
4.6	3.4	2.3	2.9	3.5	3.3	***	Nucleus.	528	Yes	Yes	Yes	--	No	Yes	80.0
3.0	3.2	2.8	4.2	3.4	3.3	***	Mitochondrion.	317	Yes	Yes	Yes	Yes	Yes	Yes	100.0
3.5	3.1	3.1	3.7	3.2	3.3	***	Mitochondrion.	431	Yes	Yes	Yes	--	--	Yes	100.0
3.0	4.1	2.6	3.3	3.5	3.3	***	Cell membrane {ECO	182	Yes	Yes	Yes	No	Yes	Yes	83.3
3.3	3.0	3.1	3.5	3.3	3.2	***	Cytoplasm, cytoskeleton.	295	Yes	Yes	Yes	Yes	No	Yes	83.3
2.8	3.1	3.6	3.1	3.5	3.2	***		41	Yes	Yes	No	No	No	No	33.3
3.8	3.3	2.4	3.3	3.3	3.2	***	Cytoplasm, cytoskeleton.	1999	Yes	Yes	No	No	--	No	40.0
2.5	2.3	2.5	6.0	2.3	3.1	***		83	Yes	Yes	Yes	Yes	No	No	66.7
3.6	2.9	2.9	3.2	2.9	3.1	***	Cytoplasm. Nucleus. Cell membrane. tracellular vesicles (PubMed	310	Yes	Yes	Yes	Yes	Yes	Yes	100.0
3.0	3.5	3.4	1.8	3.7	3.1	***	Mitochondrion matrix.	80	Yes	Yes	Yes	Yes	Yes	Yes	100.0
								85	Yes	Yes	Yes	Yes	Yes	Yes	100.0
3.0	2.4	3.0	3.7	3.1	3.0	***	Cytoplasm.	79	Yes	Yes	--	--	No	No	50.0
2.5	3.4	2.9	3.2	3.1	3.0	***	Mitochondrion matrix.	115	Yes	Yes	Yes	--	Yes	Yes	100.0
3.0	2.9	2.8	3.3	3.0	3.0	***	Cytoplasm, cytoskeleton.	376	Yes	Yes	Yes	Yes	Yes	Yes	100.0
3.2	1.5	3.0	3.6	3.5	3.0	***	Cytoplasm {ECO	61	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.9	2.6	3.0	3.7	2.8	3.0	***	Mitochondrion {ECO	58	Yes	Yes	No	No	No	No	33.3

28	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	GC*DVVVIPAGVPR	0.9	0.9	0.9
29	P04183	TK1 Thymidine kinase, cytosolic	TK1	YSSSFC*THDR	1.0	1.0	1.0
30	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	VDVAVNC*AGIAVASK	1.0	1.1	1.1
31	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	NMITGTAPLDGC*ILVVAA NDGPMPQTR	0.9	1.0	1.0
32	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	AEPPQC*TSLAWSADGQTL FAGYTDNLVR	1.0	0.9	0.9
33	P07437	TUBB Tubulin beta chain	TUBB	NMMAAC*DPR	0.9	1.0	0.9
34	Q09028	RBBP4 Histone-binding protein RBBP4	RBBP4	YMPQNPC*IIATK	1.0	0.9	0.9
35	P49327	FASN Fatty acid synthase	FASN	LGMLSPEGTC*K	0.9	1.0	1.0
36	P60709	ACTB Actin, cytoplasmic 1	ACTB	C*DVDIR	1.0	1.0	1.0
37	P62280	RPS11 40S ribosomal protein S11	RPS11	DVQIGDIVTVGEC*R	0.9	1.0	0.9
38	Q9Y5M8	SRPRB Signal recognition particle receptor subunit beta	SRPRB	NTPSFLIAC*NK	1.0	1.1	1.1
39	P07437	TUBB Tubulin beta chain	TUBB	VSDTVVEPYNATLSVHQLV ENTDETYC*IDNEALYDIC* FR	0.9	1.0	1.0
40	P51610	HCFC1 Host cell factor 1	HCFC1	VAGINAC*GR	1.0	1.0	1.0
41	P17858	PFKL 6-phosphofructokinase, liver type	PFKL	VFANAPDSAC*VIGLK	0.9	1.0	0.9
42	P07437	TUBB Tubulin beta chain	TUBB	TAVC*DIPPR	0.9	1.0	0.9
43	P29401	TKT Transketolase	TKT	QAFTDVATGSLGQGLGAA C*GMAYTGK	0.9	1.1	1.0
44	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta--like 1	GNB2L1	LWNTLGVC*K	1.0	1.0	1.0
45	P23396	RPS3 40S ribosomal protein S3	RPS3	GC*EVVVSGK	1.0	1.0	1.0
46	P83731	RPL24 60S ribosomal protein L24	RPL24	VELC*SFSGYK	0.9	1.1	1.0
47	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	ALC*QITDSTMLQAIER	1.0	1.0	1.0
48	P10644	PRKAR1A cAMP-dependent protein kinase type I-alpha regulatory subunit	PRKAR1A	EC*ELYVQK	0.9	1.0	1.0
49	Q01813	PFKP 6-phosphofructokinase type C	PFKP	NESC*SENYTTDFIYQLYSE EGK	1.0	1.0	1.0
50	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	SLLINAVEASC*IR	0.9	1.0	0.9
51	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	C*PTSGR	0.9	0.9	0.9
52	O95833	CLIC3 Chloride intracellular channel protein 3	CLIC3	ASEDGESVGHC*PSCQR	0.9	1.0	1.0
53	Q9BUF5	TUBB6 Tubulin beta-6 chain	TUBB6	EIVHIQAGQC*GNQIGTK	0.8	1.0	0.9
54	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	FSPNSSNPIIVSC*GWDK	0.9	1.0	0.9
55	P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	VEQLFQVMNGILAQDSAC *SQR	0.9	1.0	1.0
56	P42677	RPS27 40S ribosomal protein S27	RPS27	LTEGC*SFR	0.9	1.0	0.9
57	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	VVVVQAISALC*QK	0.9	1.0	0.9
58	Q92616	GCN1L1 Translational activator GCN1	GCN1L1	C*GLALALNK	0.9	0.9	0.9
59	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	SIQFVDWC*PTGFK	0.9	1.0	1.0
60	P11498	PC Pyruvate carboxylase, mitochondrial	PC	ADFAQAC*QDAGVR	1.0	0.7	0.9
61	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	C*MTNTPVVVR	1.0	1.0	1.0
62	P27635	RPL10 60S ribosomal protein L10	RPL10	MLSC*AGADR	0.9	1.0	0.9
63	P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	TFVSGAC*DASIK	0.8	1.0	0.9

3.3	2.5	3.0	3.6	2.2	2.9	***	Mitochondrion matrix.	93	Yes	Yes	No	No	No	No	33.3
2.8	2.6	2.8	3.0	3.1	2.9	***	Cytoplasm.	66	Yes	No	--	--	No	No	25.0
3.3	2.5	3.0	2.8	2.5	2.8	***	Mitochondrion {ECO	91	Yes	Yes	Yes	No	No	Yes	66.7
2.7	2.7	2.5	3.0	3.2	2.8	***	Mitochondrion.	147	Yes	Yes	No	No	No	No	33.3
2.4	2.1	2.9	3.4	3.2	2.8	***	Cell membrane {ECO	286	Yes	Yes	Yes	No	Yes	Yes	83.3
2.9	2.6	2.6	3.0	2.8	2.8	***	Cytoplasm, cytoskeleton.	303	Yes	Yes	Yes	No	No	Yes	66.7
2.5	2.9	2.6	3.0	2.9	2.8	***	Nucleus.	138	Yes	Yes	Yes	No	No	No	50.0
2.7	2.8	2.6	3.3	2.4	2.8	***	Cytoplasm {ECO	212	Yes	Yes	Yes	No	--	Yes	80.0
2.6	2.8	2.7	3.1	2.6	2.8	***	Cytoplasm, cytoskeleton {ECO	285	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.9	2.5	2.5	3.1	2.7	2.7	***		131	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.6	1.4	2.7	3.4	3.3	2.7	***	Endoplasmic reticulum membrane {ECO	179	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.7	2.7	2.6	2.7	2.7	2.7	***	Cytoplasm, cytoskeleton.	201	Yes	Yes	Yes	Yes	No	Yes	83.3
								211	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.5	2.2	2.8	3.4	2.5	2.7	***	Cytoplasm. Nucleus.	1872	Yes	Yes	--	--	--	--	100.0
3.0	2.5	2.6	3.0	2.4	2.7	***	Cytoplasm {ECO	708	Yes	Yes	No	No	--	No	40.0
2.6	2.6	2.5	2.9	2.7	2.7	***	Cytoplasm, cytoskeleton.	354	Yes	Yes	Yes	Yes	Yes	Yes	100.0
3.2	2.5	2.5	2.6	2.4	2.6	***		133	Yes	Yes	No	No	No	No	33.3
2.9	2.1	2.7	2.8	2.6	2.6	***	Cell membrane {ECO	138	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.3	3.1	2.5	2.5	2.7	2.6	***	Cytoplasm {ECO	134	Yes	Yes	Yes	Yes	Yes	No	83.3
2.6	2.5	2.1	2.6	3.2	2.6	***		6	Yes	Yes	Yes	No	Yes	Yes	83.3
2.8	2.7	2.1	3.1	2.4	2.6	***	Cytoplasm {ECO	129	Yes	Yes	Yes	No	Yes	Yes	83.3
2.2	3.1	2.4	2.5	2.8	2.6	***	Cell membrane {ECO	18	Yes	Yes	Yes	--	--	Yes	100.0
2.7	2.3	2.3	2.9	2.8	2.6	***	Cytoplasm {ECO	641	Yes	Yes	No	No	--	No	40.0
2.7	2.2	2.6	2.9	2.6	2.6	***	Mitochondrion {ECO	262	Yes	Yes	No	--	No	No	40.0
2.6	2.5	2.5	2.6	2.8	2.6	***	Cytoplasm {ECO	144	Yes	Yes	--	No	No	No	40.0
2.4	1.8	4.2	2.3	2.3	2.6	***	Nucleus. Membrane; Single-pass membrane protein. Cytoplasm.	22	Yes	Yes	Yes	--	Yes	--	100.0
3.1	1.7	2.0	4.7	1.3	2.6	***	Cytoplasm, cytoskeleton {ECO	12	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.8	2.3	2.6	2.8	2.4	2.6	***	Cell membrane {ECO	168	Yes	Yes	Yes	No	No	No	50.0
1.8	2.0	2.5	3.5	3.0	2.6	***	Nucleus {ECO	3781	Yes	Yes	No	Yes	No	No	50.0
2.5	2.5	2.4	2.8	2.5	2.5	***		77	Yes	Yes	Yes	No	Yes	Yes	83.3
2.6	2.6	2.2	2.9	2.4	2.5	***	Cytoplasm {ECO	387	Yes	Yes	Yes	No	Yes	Yes	83.3
3.2	2.0	2.4	2.8	2.4	2.5	***	Cytoplasm {ECO	1235	Yes	Yes	No	No	No	No	33.3
2.5	2.4	2.4	2.8	2.5	2.5	***	Cytoplasm, cytoskeleton.	347	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.6	1.7	2.7	3.7	2.9	2.5	***	Mitochondrion matrix.	131	Yes	Yes	No	No	Yes	Yes	66.7
2.7	2.4	2.5	2.7	2.3	2.5	***	Mitochondrion {ECO	120	Yes	Yes	No	No	No	No	33.3
2.4	2.2	2.5	2.9	2.5	2.5	***		105	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.8	3.0	1.7	4.1	1.9	2.5	***	Cytoplasm, perinuclear region {ECO	204	Yes	Yes	Yes	No	Yes	Yes	83.3

64	Q9BQ52	ELAC2 Zinc phosphodiesterase ELAC protein 2	ELAC2	C*VLSGPPQLEK	0.8	0.9	0.9
65	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	GANDFMC*DEMER	0.9	0.8	0.8
66	P35250	RFC2 Replication factor C subunit 2	RFC2	VC*DEPHPLLVK	1.0	0.9	0.9
67	Q71U36	TUBA1A Tubulin alpha-1A chain	TUBA1A	TIQFVDWC*PTGFK	0.9	1.0	0.9
68	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	YVAAAFPSAC*GK	1.0	0.9	0.9
69	P25398	RPS12 40S ribosomal protein S12	RPS12	LGEWVGLC*K	1.0	1.0	1.0
70	P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	AC*GDSTLTQITAGLDPVGR	1.0	0.9	0.9
71	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	YMAC*C*LLYR	0.9	1.0	1.0
72	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	SLHDALC*VVK	1.0	1.2	1.1
73	P50914	RPL14 60S ribosomal protein L14	RPL14	C*MQLTDFILK	0.9	1.0	0.9
74	Q16576	RBBP7 Histone-binding protein RBBP7	RBBP7	VHIPNDDAQFDASHC*DSDK	0.9	1.0	0.9
75	P49327	FASN Fatty acid synthase	FASN	AFDTAGNGYC*R	1.0	1.0	1.0
76	P53582	METAP1 Methionine aminopeptidase 1	METAP1	VCETDGC*SSEAK	0.9	1.1	1.0
77	P53597	SUCLG1 Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	IIC*QGFTGK	1.0	0.9	1.0
78	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	GYLGPEQLPDC*LK	0.9	0.9	0.9
79	O00567	NOP56 Nucleolar protein 56	NOP56	IINDNATYC*R	1.0	1.0	1.0
80	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	GNHEC*ASINR	0.9	1.1	1.0
81	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	LC*PNSTGAEIR	0.9	1.0	0.9
82	P31153	MAT2A S-adenosylmethionine synthase isoform type-2	MAT2A	TC*NVLVALEQQSPDIAQGVHLDR	1.1	1.1	1.1
83	P62280	RPS11 40S ribosomal protein S11	RPS11	C*PFTGNVSIR	1.0	1.0	1.0
84	P50914	RPL14 60S ribosomal protein L14	RPL14	ALVDGPC*TQVR	0.9	1.0	1.0
85	P40939	HADHA Trifunctional enzyme subunit alpha, mitochondrial	HADHA	C*LAPMMSEVIR	0.9	1.0	0.9
86	Q16555	DPYSL2 Dihydropyrimidinase-related protein 2	DPYSL2	FQLTDC*QIYEVLSVIR	1.1	0.9	1.0
87	P53384	NUBP1 Cytosolic Fe-S cluster assembly factor NUBP1	NUBP1	GASC*QGC*PNQR	1.0	1.1	1.0
88	E9PPU0	EPPK1 Epiplakin	EPPK1	LLDAQLATGGLVC*PAR	0.9	1.0	1.0
89	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	VGAFTMVC*K	0.9	1.0	1.0
90	P36578	RPL4 60S ribosomal protein L4	RPL4	SGQGAFGNMC*R	0.8	0.9	0.8
91	P11586	MTHFD1 C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	GC*LELIK	0.8	0.9	0.9
92	Q96I99	SUCLG2 Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	IDATQVEVNPFGETPEGQVVC*FDAK	1.0	1.0	1.0

2.6	2.1	2.4	2.4	2.9	2.5	***	Mitochondrion {ECO	136	Yes	Yes	No	No	No	No	33.3
2.8	2.0	2.0	2.8	2.8	2.5	***	Cytoplasm. Cytoplasm, cytoskeleton, microtubule organizing center, centrosome.	385	Yes	Yes	Yes	No	No	No	50.0
2.2	2.8	2.1	2.7	2.4	2.4	***	Nucleus {ECO	255	Yes	Yes	Yes	No	Yes	Yes	83.3
2.4	2.3	2.2	2.7	2.5	2.4	***	Cytoplasm, cytoskeleton.	347	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.8	2.1	2.3	2.6	2.4	2.4	***	Mitochondrion.	306	Yes	Yes	Yes	--	--	Yes	100.0
2.1	2.4	2.4	2.9	2.3	2.4	***	Cytoplasm.	92	Yes	Yes	Yes	No	Yes	Yes	83.3
2.6	2.2	2.2	2.7	2.3	2.4	***	Cytoplasm, perinuclear region {ECO	25	Yes	Yes	No	No	--	No	40.0
2.4	2.3	2.3	2.6	2.4	2.4	***	Cytoplasm, cytoskeleton.	315	Yes	Yes	Yes	No	Yes	No	66.7
								316	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.9	2.0	2.5	3.3	2.3	2.4	***	Cytoplasm. Cytoplasm, cytoskeleton, microtubule organizing center, centrosome.	397	Yes	Yes	Yes	No	Yes	Yes	83.3
2.5	2.3	2.2	2.5	2.4	2.4	***		54	Yes	Yes	No	No	No	No	33.3
1.7	1.6	1.4	1.9	5.3	2.4	***	Nucleus.	97	Yes	Yes	No	No	No	No	33.3
2.5	1.9	2.2	2.9	2.3	2.4	***	Cytoplasm {ECO	223	Yes	Yes	No	No	--	Yes	60.0
2.3	2.6	1.6	2.8	2.5	2.4	***	Cytoplasm {ECO	14	Yes	Yes	Yes	No	Yes	Yes	83.3
2.0	2.3	2.4	2.6	2.5	2.4	***	Mitochondrion.	60	Yes	Yes	Yes	No	Yes	No	66.7
2.2	2.1	2.3	2.8	2.4	2.4	***	Mitochondrion matrix.	89	Yes	Yes	No	No	No	No	33.3
2.3	2.2	2.4	2.6	2.2	2.4	***	Nucleus, nucleolus. Cytoplasm {ECO	211	Yes	Yes	No	No	No	No	33.3
2.8	2.0	2.2	2.5	2.2	2.3	***	Cytoplasm. Nucleus. Nucleus, nucleolus. Nucleus, nucleoplasm. Nucleus speckle. Chromosome, centromere, kinetochore. Cleavage furrow. Midbody. Mitochondrion. ow and midbody by telophase. {ECO	127	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.6	2.1	2.2	2.4	2.4	2.3	***	Cytoplasm. Nucleus. Cytoplasm, P-body {ECO	377	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.3	2.0	2.2	2.6	2.6	2.3	***		104	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.3	2.2	1.9	2.4	2.8	2.3	***		60	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.5	2.1	2.1	2.7	2.3	2.3	***		42	Yes	Yes	No	No	No	No	33.3
2.6	1.8	2.3	2.6	2.3	2.3	***	Mitochondrion.	550	Yes	Yes	No	--	No	Yes	60.0
3.0	2.5	1.9	2.3	1.9	2.3	***	Cytoplasm, cytosol {ECO	179	Yes	No	No	No	No	No	16.7
2.2	2.2	2.2	2.8	2.1	2.3	***	Cytoplasm {ECO	22/25	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.5	2.1	2.4	2.2	2.3	2.3	***		Bad ID	Error	Error	Error	Error	Error	Error	#DIV/0!
3.0	2.8	1.3	3.1	1.2	2.3	***	Mitochondrion matrix {ECO	295	Yes	Yes	Yes	No	Yes	No	66.7
1.9	2.1	2.2	2.6	2.5	2.3	***		96	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.9	1.8	2.7	2.8	2.1	2.3	***	Cytoplasm.	152	Yes	Yes	Yes	No	--	--	75.0
2.3	2.0	1.7	2.9	2.5	2.3	***	Mitochondrion.	255	Yes	Yes	No	Yes	No	Yes	66.7

93	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	GEETPVIVGSALC*ALEGR	1.0	0.9	1.0
94	P33992	MCM5 DNA replication licensing factor MCM5	MCM5	C*SVLAAANSVFGR	1.3	1.0	1.1
95	P60709	ACTB Actin, cytoplasmic 1	ACTB	LC*YVALDFEQEMATAASSSSLEK	0.9	1.0	1.0
96	P26440	IVD Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	GSNTC*ELIFEDC*K	1.0	0.9	1.0
97	P10589	NR2F1 COUP transcription factor 1	NR2F1	SQC*ALEEYVR	0.8	1.0	0.9
98	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	YNFFTGC*PK	0.9	1.1	1.0
99	P45984	MAPK9 Mitogen-activated protein kinase 9	MAPK9	TAC*TNFMMTPYVVTR	2.7	1.0	1.9
100	P07384	CAPN1 Calpain-1 catalytic subunit	CAPN1	C*LQSGTLFR	0.8	1.0	0.9
101	Q8N163	KIAA1967 DBIRD complex subunit KIAA1967	KIAA1967	VVTQNIC*QYR	0.9	0.8	0.9
102	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	C*EYPAAC*NALETLLIHR	0.9	1.1	1.0
103	P13804	ETFA Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	LGGEVSC*LVAGTK	0.9	1.0	0.9
104	P46734	MAP2K3 Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	FSPEFVDFTAQC*LR	1.9	1.2	1.6
105	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	ALNALC*DGLIDELNQALK	0.9	1.0	1.0
106	P13804	ETFA Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	TIYAGNALC*TVK	1.0	1.0	1.0
107	O43719	HTATSF1 HIV Tat-specific factor 1	HTATSF1	GFEGSC*SQK	1.1	1.2	1.1
108	Q9Y399	MRPS2 28S ribosomal protein S2, mitochondrial	MRPS2	DC*GEYAHTR	0.8	0.9	0.9
109	P42025	ACTR1B Beta-centractin	ACTR1B	AC*YLSINPQK	0.9	1.0	0.9
110	P62829	RPL23 60S ribosomal protein L23	RPL23	ISLGLPVGAVINC*ADNTGAK	0.9	1.0	1.0
111	P62249	RPS16 40S ribosomal protein S16	RPS16	TATAVAHC*K	1.0	1.0	1.0
112	Q9NZB2	FAM120A Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	VAAASGHC*GAFSGSDSSR	1.0	1.1	1.0
113	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	VGILDVDLC*GPSIPR	1.0	1.0	1.0
114	P53618	COPB1 Coatomer subunit beta	COPB1	ALSGYC*GFMAANLYAR	0.7	1.0	0.8
115	Q14152	EIF3A Eukaryotic translation initiation factor 3 subunit	EIF3A	NIC*QQVNIK	0.9	1.0	0.9
116	P62714	PPP2CB Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	PPP2CB	NVVTIFSAPNYC*YR	0.9	1.0	1.0
117	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	AC*ALQVLSAILEGSK	0.9	1.3	1.1
118	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	GQPC*SQNYR	1.5	1.3	1.4
119	P24468	NR2F2 COUP transcription factor 2	NR2F2	FGSQC*MQPNNIMGIENIC*ELAAR	1.2	1.0	1.1
120	P21333	FLNA Filamin-A	FLNA	LQVEPAVDTSGVQC*YGPGIEGQGVFR	1.0	1.1	1.1
121	P62888	RPL30 60S ribosomal protein L30	RPL30	VC*TLAIIDPGDSDIIR	0.9	0.9	0.9
122	P62753	RPS6 40S ribosomal protein S6	RPS6	LNISFPATGC*QK	0.9	0.9	0.9
123	P53384	NUBP1 Cytosolic Fe-S cluster assembly factor NUBP1	NUBP1	NC*DK	1.0	1.0	1.0
124	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	DLLVQQASQC*LSK	1.1	1.0	1.0

2.2	2.1	2.2	2.5	2.3	2.3	***	Mitochondrion.	222	Yes	Yes	Yes	Yes	No	Yes	83.3
2.2	2.8	1.9	2.5	1.9	2.2	**	Nucleus.	482	Yes	Yes	Yes	No	No	Yes	66.7
2.2	2.1	2.2	2.4	2.1	2.2	**	Cytoplasm, cytoskeleton {ECO	217	Yes	Yes	Yes	Yes	No	Yes	83.3
2.2	2.1	2.2	2.5	2.0	2.2	**	Mitochondrion matrix.	251	Yes	Yes	Yes	--	Yes	Yes	100.0
								258	Yes	Yes	No	--	Yes	Yes	80.0
2.1	2.0	2.1	2.5	2.4	2.2	***	Nucleus {ECO	350	Yes	Yes	Yes	--	--	No	75.0
2.2	2.0	2.1	2.6	2.1	2.2	**	Cytoplasm {ECO	364	Yes	Yes	Yes	Yes	Yes	Yes	100.0
4.6	1.4	1.6	1.6	1.7	2.2	ns	Cytoplasm {ECO	177	Yes	Yes	No	No	No	No	33.3
2.3	2.2	1.9	2.4	2.1	2.2	***	Cytoplasm {ECO	49	Yes	Yes	Yes	--	--	Yes	100.0
1.8	2.4	1.9	2.4	2.5	2.2	***	Nucleus {ECO	754	Yes	Yes	--	--	--	--	100.0
2.3	2.1	2.0	2.0	2.5	2.2	**	Mitochondrion inner membrane.	612	Yes	Yes	Yes	Yes	Yes	Yes	100.0
								606	Yes	Yes	Yes	No	No	Yes	66.7
2.3	1.9	2.2	2.4	2.0	2.2	**	Mitochondrion matrix.	53	Yes	Yes	No	No	No	No	33.3
1.7	2.0	2.2	2.8	2.2	2.2	ns		305	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.3	2.1	2.1	2.3	2.1	2.2	**	Mitochondrion matrix.	62	Yes	Yes	Yes	No	No	Yes	66.7
1.9	2.1	2.3	2.5	2.0	2.2	**	Mitochondrion matrix.	155	Yes	Yes	No	No	Yes	No	50.0
1.7	1.8	2.0	2.2	3.1	2.1	ns	Nucleus {ECO	480	Yes	No	--	--	--	--	50.0
1.0	1.7	2.9	2.7	2.4	2.1	***	Mitochondrion {ECO	162	Yes	Yes	No	No	No	No	33.3
2.3	2.1	1.9	2.5	1.9	2.1	**	Cytoplasm, cytoskeleton. Cytoplasm, cytoskeleton, microtubule organizing center, centrosome.	222	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.2	1.9	2.0	2.3	2.2	2.1	**		28	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.2	1.9	2.2	2.3	1.9	2.1	*		25	Yes	Yes	Yes	No	Yes	Yes	83.3
2.3	1.7	2.0	2.5	2.0	2.1	*	Cytoplasm {ECO	919	Yes	Yes	--	--	--	--	100.0
2.1	1.7	2.0	2.7	1.9	2.1	**	Nucleus {ECO	54	Yes	Yes	Yes	No	Yes	Yes	83.3
2.1	1.5	1.9	2.3	2.3	2.0	**	Cytoplasm. Golgi apparatus membrane {ECO	888	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.3	1.7	2.0	2.2	2.0	2.0	*	Cytoplasm {ECO	78	Yes	Yes	No	No	Yes	No	50.0
2.3	1.8	2.2	2.0	1.9	2.0	*	Cytoplasm {ECO	266	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.1	1.6	2.0	2.3	2.1	2.0	ns		476	Yes	Yes	No	--	--	--	66.7
1.7	1.7	2.5	2.1	2.2	2.0	ns	Mitochondrion {ECO	44	Yes	No	No	No	No	No	16.7
2.2	2.1	2.2	1.7	1.9	2.0	ns	Nucleus.	200/213	Yes	Yes	Yes	--	--	No	75.0
1.8	2.0	1.8	2.8	1.6	2.0	ns	Cytoplasm, cell cortex. Cytoplasm, cytoskeleton.	1260	Yes	Yes	No	--	--	No	50.0
2.1	1.9	1.8	2.2	2.0	2.0	*		92	Yes	Yes	Yes	No	No	Yes	66.7
2.0	1.9	1.9	2.2	2.0	2.0	*		12	Yes	Yes	Yes	No	Yes	No	66.7
2.0	2.1	1.6	2.5	1.7	2.0	ns	Cytoplasm {ECO	277	Yes	Yes	Yes	Yes	No	No	66.7
2.0	1.5	2.1	2.4	1.9	2.0	ns	Nucleus {ECO	518	Yes	Yes	No	--	--	No	50.0

125	Q14318	FKBP8 Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8	C*LNNLAASQLK	1.1	1.0	1.1
126	P11586	MTHFD1 C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	GDLNDC*FIPC*TPK	1.1	1.0	1.1
127	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	MLSAVSQQVQC*IQEALR	1.0	0.9	1.0
128	P15924	DSP Desmoplakin	DSP	YC*YLQNEVFGLFQK	1.0	1.0	1.0
129	Q9C0C9	UBE2O Ubiquitin-conjugating enzyme E2 O	UBE2O	NC*AQGEGSMAK	1.0	1.0	1.0
130	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	C*FIVGADNVGSK	0.9	1.0	1.0
131	Q92616	GCN1L1 Translational activator GCN1	GCN1L1	YLLDSC*APLLR	0.8	1.3	1.0
132	Q07020	RPL18 60S ribosomal protein L18	RPL18	GC*GTVLLSGPR	0.9	1.0	1.0
133	P13639	EEF2 Elongation factor 2	EEF2	DLEEDHAC*IPIK	0.9	1.0	1.0
134	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	EMQNLSFQDC*YSSK	0.9	0.9	0.9
135	Q8TC07	TBC1D15 TBC1 domain family member 15	TBC1D15	TLLVNC*QNK	1.1	1.0	1.1
136	P62701	RPS4X 40S ribosomal protein S4, X isoform	RPS4X	FDTGNLC*MVTGGANLGR	0.9	0.9	0.9
137	P46776	RPL27A 60S ribosomal protein L27a	RPL27A	NQSFC*PTVNLDK	0.9	1.0	0.9
138	P55060	CSE1L Exportin-2	CSE1L	IC*AVGITK	0.9	1.0	0.9
139	O95747	OXSR1 Serine/threonine-protein kinase OSR1	OXSR1	TFVGTPC*WMAPEVMEQVR	1.0	1.0	1.0
140	Q68CP9	ARID2 AT-rich interactive domain-containing protein 2	ARID2	SC*SNAAFALK	0.8	1.0	0.9
141	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	AVHQC*DR	1.0	1.1	1.1
142	O14980	XPO1 Exportin-1	XPO1	DLLGLC*EQK	1.1	0.9	1.0
143	Q06203	PPAT Amidophosphoribosyltransferase	PPAT	C*ELENCQPFVVETLHGK	0.8	1.1	1.0
144	P27448	MARK3 MAP/microtubule affinity-regulating kinase 3	MARK3	LDTFC*GSPPYAAPELFQGK	0.9	1.0	1.0
145	O95782	AP2A1 AP-2 complex subunit alpha-1	AP2A1	TVFEALQAPAC*HENMVK	1.0	1.1	1.1
146	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	EYLPIGGLAEFC*K	0.9	1.0	0.9
147	Q9BTZ2	DHRS4 Dehydrogenase/reductase SDR family member 4	DHRS4	VNC*LAPGLIK	0.9	1.0	1.0
148	P07384	CAPN1 Calpain-1 catalytic subunit	CAPN1	LEIC*NLTPDALK	0.8	0.9	0.9
149	Q9Y2R9	MRPS7 28S ribosomal protein S7, mitochondrial	MRPS7	NC*EPMIGLVPILK	0.9	0.9	0.9
150	Q04726	TLE3 Transducin-like enhancer protein 3	TLE3	FTVAESC*DR	0.9	1.0	1.0
151	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	LC*ALR	0.6	1.0	0.8
152	Q9H1K1	ISCU Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	ISCU	NVGTGLVGAPAC*GDVMK	0.8	1.1	1.0
153	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	GDEC*ELLGHSK	0.9	1.0	1.0
154	P62330	ARF6 ADP-ribosylation factor 6	ARF6	NWYVQPSC*ATSGDGLYEGLTWLTSNYK	0.9	0.9	0.9
155	P51610	HCFC1 Host cell factor 1	HCFC1	AC*AAGTPAVIR	0.9	0.9	0.9

1.8	1.8	2.2	2.3	1.9	2.0	ns	Mitochondrion {ECO Mitochondrion membrane {ECO Mitochondrion membrane {ECO	274	Yes	Yes	No	--	Yes	--	75.0
2.1	2.4	0.9	3.5	1.0	2.0	ns	Cytoplasm.	143	Yes	Yes	No	No	--	--	50.0
								147	Yes	Yes	Yes	Yes	--	--	100.0
2.1	2.0	1.8	2.3	1.6	2.0	ns	Cytoplasm, cytoskeleton.	1977	Yes	Yes	No	No	--	No	40.0
2.5	1.7	1.7	2.3	1.7	2.0	ns	Cell junction, desmosome {ECO	740	Yes	Yes	--	--	--	No	66.7
1.3	2.0	2.5	2.3	1.6	1.9	ns	Cytoplasm {ECO	375	Yes	Yes	--	--	--	--	100.0
2.0	1.8	1.9	2.1	2.0	1.9	ns	Nucleus {ECO	27	Yes	Yes	Yes	No	No	Yes	66.7
1.9	1.8	2.3	1.9	1.9	1.9	ns	Cytoplasm {ECO	246	Yes	Yes	Yes	--	No	No	60.0
2.1	1.7	1.8	2.1	2.0	1.9	ns	Cytoplasm.	134	Yes	No	No	No	No	No	16.7
1.8	1.8	2.0	2.3	1.8	1.9	ns	Cytoplasm. Nucleus {ECO	567	Yes	Yes	Yes	No	No	Yes	66.7
2.0	1.9	1.8	2.0	1.9	1.9	*	Mitochondrion matrix.	111	Yes	Yes	Yes	No	No	No	50.0
1.9	1.4	1.9	2.2	2.1	1.9	ns	Cytoplasm {ECO	197	Yes	Yes	No	--	--	--	66.7
2.0	1.7	2.1	2.2	1.7	1.9	*	Cytoplasm {ECO	181	Yes	Yes	Yes	No	No	No	50.0
2.3	1.8	1.8	1.9	1.8	1.9	ns		70	Yes	Yes	No	No	Yes	Yes	66.7
1.9	2.1	1.7	2.0	1.9	1.9	ns	Cytoplasm. Nucleus.	842	Yes	Yes	No	No	No	No	33.3
1.8	1.5	1.7	2.5	2.0	1.9	ns	Cytoplasm {ECO	191	Yes	Yes	Yes	No	Yes	Yes	83.3
2.2	1.6	1.4	1.9	2.5	1.9	ns	Nucleus.	82	Yes	Yes	Yes	--	No	No	60.0
2.0	1.8	1.8	2.2	1.7	1.9	ns	Nucleus {ECO	72	Yes	Yes	Yes	No	No	No	50.0
2.1	1.7	1.8	1.8	2.1	1.9	ns	Cytoplasm. Nucleus, nucleoplasm. Nucleus, Cajal body. Nucleus, nucleolus.	528	Yes	Yes	Yes	No	Yes	Yes	83.3
1.6	1.3	1.4	1.7	3.5	1.9	ns		100	Yes	Yes	No	No	No	No	33.3
1.5	1.6	1.6	3.1	1.7	1.9	ns	Cell membrane {ECO	213	Yes	Yes	Yes	Yes	Yes	Yes	100.0
2.0	1.5	2.0	1.7	2.2	1.9	ns	Cell membrane {ECO	492	Yes	Yes	Yes	No	No	Yes	66.7
1.6	1.8	1.9	2.3	1.7	1.9	ns	Mitochondrion matrix {ECO	106	Yes	Yes	No	No	No	No	33.3
2.1	1.8	1.8	1.9	1.7	1.9	ns	Peroxisome {ECO Nucleus {ECO	209	Yes	Yes	Yes	Yes	No	No	66.7
1.9	1.7	1.9	2.4	1.5	1.9	ns	Cytoplasm {ECO	351	Yes	Yes	Yes	--	Yes	Yes	100.0
2.0	1.8	1.8	1.9	1.9	1.9	ns	Mitochondrion {ECO	152	Yes	Yes	Yes	--	No	Yes	80.0
2.5	1.1	2.0	1.6	2.0	1.8	ns	Nucleus.	26	Yes	Yes	No	--	--	No	50.0
2.0	1.5	1.8	2.0	1.9	1.8	*		38	Yes	No	--	--	--	--	50.0
1.8	1.7	1.8	2.2	1.7	1.8	ns	Mitochondrion {ECO Cytoplasm. Nucleus {ECO	69	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.8	1.8	1.7	2.1	1.8	1.8	ns	Mitochondrion.	290	Yes	Yes	Yes	No	No	No	50.0
2.1	1.6	1.9	1.9	1.6	1.8	ns	Golgi apparatus. Cell membrane; Lipid- anchor. Endosome membrane; Lipid-anchor. Recycling endosome membrane {ECO	155	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.5	1.9	2.0	2.0	1.9	1.8	ns	Cytoplasm. Nucleus.	1139	Yes	No	--	--	--	--	50.0

156	P49327	FASN Fatty acid synthase	FASN	DPETLVGYSMVGC*QR	1.0	0.9	1.0
157	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	TIIPLISQC*TPK	0.9	1.0	0.9
158	P02795	MT2A Metallothionein-2	MT2A	SC*CSCC*PVGC*AK	1.0	0.9	1.0
159	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	FC*LDNGAK	1.1	1.0	1.0
160	O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	SFVQWLGC*R	1.1	0.9	1.0
161	P48047	ATP5O ATP synthase subunit O, mitochondrial	ATP5O	GEVPC*TVTSASPLEEATLSELK	1.0	1.0	1.0
162	Q27J81	INF2 Inverted formin-2	INF2	AVLLASDAQEC*TLEEVVER	0.8	0.8	0.8
163	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	AVASQLDC*NFLK	0.9	1.0	0.9
164	P82912	MRPS11 28S ribosomal protein S11, mitochondrial	MRPS11	ASHNNTQIQVVSASNEPLAFASC*GTEGFR	0.8	0.9	0.9
165	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	LVIVGDGAC*GK	1.0	0.9	1.0
166	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	NFILDQC*NVYNSGQR	0.8	0.9	0.9
167	Q9Y5Q8	GTF3C5 General transcription factor 3C polypeptide 5	GTF3C5	VC*TNPVDR	0.9	1.1	1.0
168	Q96CM8	ACSF2 Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	MVSTPIGGLSYVQGC*TK	1.4	1.8	1.6
169	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	AGAIAPC*EVTVPAQNTGLGPEK	0.9	1.0	0.9
170	P00966	ASS1 Argininosuccinate synthase	ASS1	FELSC*YSLAPQIK	1.1	1.0	1.0
171	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	C*AMTALSSK	0.9	1.1	1.0
172	P11802	CDK4 Cyclin-dependent kinase 4	CDK4	LMDVC*ATSR	1.0	1.0	1.0
173	Q969Z0	TBRG4 Protein TBRG4	TBRG4	LATDLLSLMPSLTSGEVAHC*AK	1.0	1.1	1.0
174	Q7Z406	MYH14 Myosin-14	MYH14	ADLLLEPC*SHYR	1.0	1.0	1.0
175	Q15019	SEPT2 Septin-2	2-Sep	LTVVDTPGYGDAINC*R	1.0	1.0	1.0
176	P23396	RPS3 40S ribosomal protein S3	RPS3	GLC*AIAQAESLR	0.9	1.0	1.0
177	P43246	MSH2 DNA mismatch repair protein Msh2	MSH2	HVIEC*AK	0.9	0.6	0.7
178	P56377	AP1S2 AP-1 complex subunit sigma-2	AP1S2	MC*SFLEWR	1.0	0.9	1.0
179	Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	FSIQTMC*PIEGEGNIAR	0.9	1.0	1.0
180	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	QLC*DNAGFDATNILNK	0.9	1.1	1.0
181	P21333	FLNA Filamin-A	FLNA	THEAEIVEGENHTYC*IR	1.1	1.0	1.0
182	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	PMC*VESFSQYPPLGR	0.9	1.0	0.9
183	P62910	RPL32 60S ribosomal protein L32	RPL32	SYC*AEIAHNVSSK	0.8	1.0	0.9
184	Q8WTW3	COG1 Conserved oligomeric Golgi complex subunit 1	COG1	AQAISPC*VQNFCSALDSK	0.9	1.0	0.9
185	Q13542	EIF4EBP2 Eukaryotic translation initiation factor 4E-binding protein 2	EIF4EBP2	TVAISDAAQLPHDYC*TTPGGTLFSTTPGGTR	0.8	0.7	0.7
186	P33992	MCM5 DNA replication licensing factor MCM5	MCM5	C*SPIGVYTSGK	1.0	1.0	1.0
187	A6NDG6	PGP Phosphoglycolate phosphatase	PGP	NNQESDC*VSK	1.0	1.0	1.0
188	P62318	SNRPD3 Small nuclear ribonucleoprotein Sm D3	SNRPD3	VLHEAEGHIVTC*ETNTGEVYR	0.9	1.0	0.9

1.8	1.8	1.6	2.0	1.8	1.8	ns	Cytoplasm {ECO	135	Yes	Yes	Yes	No	--	Yes	80.0
1.7	1.8	1.9	1.9	1.8	1.8	ns	Mitochondrion matrix.	212	Yes	Yes	No	No	No	No	33.3
1.4	1.6	1.8	2.7	1.6	1.8	ns		33/37/41	Yes	Yes	--	--	--	--	100.0
0.8	2.6	2.4	0.8	2.5	1.8	ns	Cytoplasm.	50	Yes	Yes	No	No	No	No	33.3
1.7	1.6	1.8	1.8	2.1	1.8	ns	Nucleus {ECO Cytoplasm {ECO	663	Yes	Yes	--	--	--	No	66.7
3.3	1.5	1.3	1.5	1.5	1.8	ns	Mitochondrion {ECO	141	Yes	Yes	Yes	No	No	No	50.0
1.8	0.9	2.0	2.7	1.5	1.8	ns	Cytoplasm, perinuclear region {ECO	332	Yes	--	--	--	--	No	50.0
1.7	1.8	1.7	1.9	1.7	1.8	ns	Cytoplasm {ECO	193	Yes	Yes	No	No	No	Yes	50.0
2.0	1.3	1.8	2.2	1.5	1.8	ns	Mitochondrion {ECO	112	Yes	Yes	Yes	--	No	Yes	80.0
2.3	1.6	1.6	1.8	1.6	1.8	ns	Cell membrane {ECO	16	Yes	Yes	Yes	Yes	No	Yes	83.3
1.7	1.5	1.7	2.2	1.8	1.8	ns	Nucleus {ECO	538	Yes	Yes	No	--	--	No	50.0
1.6	1.1	1.7	2.0	2.4	1.8	ns	Nucleus.	242	Yes	Yes	No	--	No	Yes	60.0
1.9	1.8	1.6	1.8	1.7	1.8	ns	Mitochondrion {ECO	64	Yes	No	No	--	--	Yes	50.0
1.8	1.6	1.7	2.0	1.8	1.8	ns	Nucleus {ECO	119	Yes	Yes	No	No	No	Yes	50.0
2.1	1.7	1.6	1.6	1.8	1.8	ns		132	Yes	Yes	No	No	No	--	40.0
1.8	2.4	1.5	1.7	1.4	1.8	ns	Cytoplasm {ECO	158	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.7	2.0	1.6	2.0	1.5	1.8	ns	Cytoplasm. Nucleus. Membrane.	78	Yes	Yes	Yes	No	No	No	50.0
1.7	1.8	1.7	2.0	1.6	1.7	ns	Mitochondrion {ECO	335	Yes	Yes	No	--	--	--	66.7
1.7	1.8	1.6	1.9	1.8	1.7	ns		324	Yes	Yes	No	No	No	No	33.3
1.8	1.6	1.6	1.9	1.8	1.7	ns	Cytoplasm {ECO	111	Yes	Yes	No	No	--	No	40.0
1.8	1.7	1.6	1.8	1.8	1.7	ns	Cytoplasm {ECO	97	Yes	Yes	Yes	No	Yes	Yes	83.3
1.8	1.8	1.2	2.0	1.9	1.7	ns	Nucleus {ECO	843	Yes	Yes	No	No	No	No	33.3
2.0	1.5	1.5	2.2	1.5	1.7	ns	Golgi apparatus. Cytoplasmic vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Membrane, clathrin-coated pit.	46	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.6	1.6	1.8	2.0	1.7	1.7	ns	Cytoplasm, cytosol {ECO	205	Yes	Yes	No	--	--	--	66.7
1.7	1.9	1.8	1.9	1.4	1.7	ns	Cytoplasm {ECO	450	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.6	1.6	1.6	2.3	1.4	1.7	ns	Cytoplasm, cell cortex. Cytoplasm, cytoskeleton.	2199	Yes	Yes	No	--	--	No	50.0
1.6	1.6	1.8	1.9	1.6	1.7	ns	Nucleus {ECO	411	Yes	Yes	Yes	Yes	No	Yes	83.3
1.6	1.7	1.7	1.7	1.8	1.7	ns		96	Yes	Yes	Yes	No	Yes	No	66.7
1.6	1.7	1.6	2.0	1.5	1.7	ns	Golgi apparatus membrane {ECO	513	Yes	Yes	No	--	No	--	50.0
1.5	1.4	1.9	2.1	1.7	1.7	ns		35	Yes	Yes	No	--	--	--	66.7
2.1	1.7	1.2	2.2	1.3	1.7	ns	Nucleus.	397	Yes	Yes	No	No	No	No	33.3
1.7	1.7	1.6	1.8	1.8	1.7	ns		297	Yes	Yes	No	No	No	No	33.3
1.6	1.6	1.7	2.2	1.5	1.7	ns	Cytoplasm, cytosol {ECO	20	Yes	Yes	Yes	No	No	No	50.0

189	O95340	PAPSS2 Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 2	PAPSS2	VWGTTC*TK	0.9	0.9	0.9
190	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	C*ATITPDEAR	0.8	1.0	0.9
191	P15880	RPS2 40S ribosomal protein S2	RPS2	GC*TATLGNFAK	1.0	1.0	1.0
192	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	C*TPSVISFGSK	0.9	1.0	0.9
193	P24385	CCND1 G1/S-specific cyclin-D1	CCND1	AEETC*APSVSYFK	0.8	1.1	1.0
194	P46782	RPS5 40S ribosomal protein S5	RPS5	TIAEC*LADELINAAK	0.9	1.0	0.9
195	Q53H96	PYCRL Pyrroline-5-carboxylate reductase 3	PYCRL	SDVC*TPGGTTIYGLHALEQGGLR	1.0	1.0	1.0
196	P53597	SUCLG1 Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	LIGPNC*PGVINPGEC*K	1.0	0.9	1.0
197	P35125	USP6 Ubiquitin carboxyl-terminal hydrolase 6	USP6	SGTSC*PSSK	0.9	1.0	0.9
198	O95685	PPP1R3D Protein phosphatase 1 regulatory subunit 3D	PPP1R3D	APPPTPAPSGC*DPR	0.9	1.4	1.1
199	Q9Y508	RNF114 RING finger protein 114	RNF114	DC*GGAAQLAGPAAEADPLGR	1.0	1.1	1.0
200	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	LQGATC*NNNK	0.9	0.9	0.9
201	O95757	HSPA4L Heat shock 70 kDa protein 4L	HSPA4L	GC*ALQC*AILSPAFK	0.9	0.9	0.9
202	Q9UHD8	SEPT9 Septin-9	9-Sep	LTVIDTPGFGDHINNENC*WQPIMK	0.9	0.9	0.9
203	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	ISAFGYLEC*SAK	0.7	0.7	0.7
204	Q9H1K1	ISCU Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	ISCU	LHC*SMLAEDAIK	0.9	1.0	1.0
205	P15924	DSP Desmoplakin	DSP	DANSENC*NK	0.8	1.0	0.9
206	Q99836	MYD88 Myeloid differentiation primary response protein MyD88	MYD88	FITVCDYTNPC*TK	0.9	0.9	0.9
207	P37198	NUP62 Nuclear pore glycoprotein p62	NUP62	DIIEHLNTSGAPADTSDPLQQIC*K	0.7	0.9	0.8
208	P10599	TXN Thioredoxin	TXN	C*MPTFQFFK	1.0	1.0	1.0
209	P16455	MGMT Methylated-DNA--protein-cysteine methyltransferase	MGMT	VVC*SSGAVGNYSGGLAVK	1.0	1.0	1.0
210	Q96RQ3	MCCC1 Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCC1	ESLC*QAALGLILK	1.0	0.9	1.0
211	Q9UBT2	UBA2 SUMO-activating enzyme subunit 2	UBA2	VLVVGAGGIGC*ELLK	0.9	0.9	0.9
212	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	GDEC*GLALGR	1.0	1.0	1.0
213	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	C*SFDVVK	0.8	0.9	0.8
214	Q9UL25	RAB21 Ras-related protein Rab-21	RAB21	VVLLGEGC*VGK	1.1	1.0	1.1
215	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	GNVC*GDSK	0.8	1.0	0.9
216	Q66K14	TBC1D9B TBC1 domain family member 9B	TBC1D9B	NEC*YR	1.1	1.2	1.2
217	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	ALDH6A1	AEMDAAIASC*K	0.9	1.0	1.0
218	P10599	TXN Thioredoxin	TXN	LVVVDFSATWC*GPC*K	1.1	1.0	1.0
219	Q96CD2	PPCDC Phosphopantothenoylcysteine decarboxylase	PPCDC	ASC*PAAAPLMER	1.0	1.2	1.1

1.8	1.7	1.3	1.9	1.8	1.7	ns		350	Yes	No	No	--	No	No	20.0
1.7	1.5	1.9	1.8	1.6	1.7	ns	Mitochondrion.	113	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.8	1.7	1.6	1.7	1.7	1.7	ns		229	Yes	Yes	No	No	No	No	33.3
1.6	1.6	1.6	1.8	1.7	1.7	ns	Cytoplasm {ECO	34	Yes	Yes	No	No	No	No	33.3
1.8	1.5	2.4	1.8	0.9	1.7	ns	Nucleus {ECO	38	Yes	Yes	No	No	--	No	40.0
1.7	1.6	1.6	1.8	1.7	1.7	ns		172	Yes	Yes	Yes	No	Yes	Yes	83.3
1.6	1.6	1.7	1.8	1.7	1.7	ns		235	Yes	No	No	Yes	No	No	33.3
1.7	1.6	1.6	1.7	1.8	1.7	ns	Mitochondrion.	172	Yes	Yes	Yes	Yes	Yes	Yes	100.0
								181	Yes	Yes	Yes	No	Yes	Yes	83.3
1.5	1.5	1.9	1.8	1.6	1.7	ns	Cell membrane. Cytoplasm. Endosome.	1185	Yes	Yes	--	--	--	--	100.0
1.0	3.1	1.1	0.8	2.2	1.6	ns		60	Yes	Yes	--	--	--	--	100.0
1.6	1.8	1.5	1.6	1.7	1.6	ns	Cytoplasm {ECO	8	Yes	No	--	--	--	--	50.0
1.8	1.9	1.5	2.2	0.7	1.6	ns	Cytoplasm, cytoskeleton.	4570	Yes	Yes	Yes	--	--	No	75.0
1.7	1.7	1.5	1.5	1.7	1.6	ns	Cytoplasm {ECO	376	Yes	Yes	No	No	Yes	No	50.0
								380	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.6	1.7	1.6	1.7	1.5	1.6	ns	Cytoplasm, cytoskeleton {ECO	375	Yes	Yes	No	No	--	Yes	60.0
1.9	1.2	1.8	1.8	1.5	1.6	ns	Cell membrane {ECO	159	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.6	1.3	1.6	1.9	1.7	1.6	ns	Mitochondrion {ECO Cytoplasm. Nucleus {ECO	138	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.2	1.6	1.8	2.1	1.4	1.6	ns	Cell junction, desmosome {ECO	1052	Yes	Yes	--	--	--	--	100.0
1.9	1.4	1.7	1.6	1.5	1.6	ns	Cytoplasm {ECO	280	Yes	Yes	No	--	--	--	66.7
1.8	1.6	1.5	1.7	1.6	1.6	ns	Nucleus, nuclear pore complex. Cytoplasm, cytoskeleton, spindle pole.	475	Yes	Yes	No	No	No	--	40.0
1.4	1.2	2.2	1.7	1.5	1.6	ns	Nucleus {ECO	73	Yes	Yes	No	No	No	No	33.3
1.7	1.6	1.4	1.6	1.7	1.6	ns	Nucleus.	150	Yes	No	No	No	--	No	20.0
1.4	2.0	1.4	1.6	1.6	1.6	ns	Mitochondrion matrix {ECO	509	Yes	Yes	No	--	No	No	40.0
1.6	1.5	1.6	1.7	1.5	1.6	ns	Cytoplasm. Nucleus.	30	Yes	Yes	Yes	No	Yes	Yes	83.3
1.7	1.5	1.5	1.7	1.6	1.6	ns	Mitochondrion inner membrane.	88	Yes	Yes	No	--	No	Yes	60.0
1.7	1.3	1.5	1.8	1.7	1.6	ns	Cytoplasm {ECO	169	Yes	Yes	No	No	No	No	33.3
1.8	1.4	1.5	1.6	1.6	1.6	ns	Endoplasmic reticulum membrane {ECO	29	Yes	Yes	Yes	No	No	Yes	66.7
1.5	1.5	1.6	1.9	1.4	1.6	ns	Nucleus {ECO	326	Yes	Yes	No	Yes	No	Yes	66.7
1.4	1.6	1.4	1.7	1.8	1.6	ns	Membrane {ECO	289	Yes	Yes	No	No	--	No	40.0
1.5	1.6	1.6	1.9	1.5	1.6	ns	Mitochondrion.	86	Yes	Yes	No	No	No	No	33.3
1.5	1.2	2.1	1.7	1.4	1.6	ns	Nucleus {ECO	32/35	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.4	1.5	1.7	1.8	1.6	1.6	ns		7	Yes	Yes	--	--	--	--	100.0

220	Q92879	CELF1 CUGBP Elav-like family member 1	CELF1	GC*AFVTFTTR	1.0	1.1	1.1
221	P61758	VBP1 Prefoldin subunit 3	VBP1	DSC*GK	0.9	0.9	0.9
222	A0MZ66	KIAA1598 Shootin-1	KIAA1598	VTFQPPSSIGC*R	1.0	1.1	1.0
223	O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	ANSSVVSVNC*K	0.9	1.0	1.0
224	Q8NFA0	USP32 Ubiquitin carboxyl-terminal hydrolase 32	USP32	VLAYTGC*FSR	1.0	0.9	0.9
225	Q9P2R7	SUCLA2 Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	ILAC*DDLDEAAR	0.7	1.0	0.9
226	P20810	CAST Calpastatin	CAST	AAAPAPVSEAVC*R	1.0	0.9	0.9
227	P62244	RPS15A 40S ribosomal protein S15a	RPS15A	C*GVISPR	0.9	0.9	0.9
228	P46782	RPS5 40S ribosomal protein S5	RPS5	AQC*PIVER	0.9	0.9	0.9
229	Q9NZA1	CLIC5 Chloride intracellular channel protein 5	CLIC5	AGIDGESIGNC*PFSQR	1.0	1.0	1.0
230	P38606	ATP6V1A V-type proton ATPase catalytic subunit A	ATP6V1A	VLDALFPCVQGGTTAIPGAFGC*GK	1.0	1.0	1.0
231	Q96I99	SUCLG2 Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SC*NGPVLVGSPQGGVDIEEVAASNPELIFK	0.8	1.0	0.9
232	Q6PKG0	LARP1 La-related protein 1	LARP1	TASISSSPSEGTPTVGSYGC*TPQSLPK	0.9	1.0	0.9
233	Q7Z2W4	ZC3HAV1 Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	NSNVDSSYLESLYQSC*PR	1.0	1.2	1.1
234	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	VC*VETVESGAMTK	0.9	0.9	0.9
235	Q9Y285	FARSA Phenylalanine--tRNA ligase alpha subunit	FARSA	VNLQMVYDSPLC*R	0.9	0.9	0.9
236	P60981	DSTN Destrin	DSTN	HEC*QANGPEDLNR	1.2	1.0	1.1
237	O75439	PMPCB Mitochondrial-processing peptidase subunit beta	PMPCB	LC*TSVTESEVAR	1.1	0.9	1.0
238	P55263	ADK Adenosine kinase	ADK	TGC*TFPEK	1.0	1.0	1.0
239	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	LFC*VGFTK	1.0	0.9	1.0
240	P35914	HMGCL Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	LLEAGNFIC*QALNR	0.8	1.0	0.9
241	P19838	NFKB1 Nuclear factor NF-kappa-B p105 subunit	NFKB1	YVC*EGPSHGGLPGASSEK	0.9	0.8	0.8
242	E9PPU0	EPPK1 Epiplakin	EPPK1	YLC*GLGAVGGVR	1.0	1.0	1.0
243	Q9BUL9	RPP25 Ribonuclease P protein subunit p25	RPP25	SEEAPAGC*GAEGGGPGSGPFADLAPGAVHMR	1.1	1.0	1.0
244	Q9BUH6	C9orf142 Uncharacterized protein C9orf142	C9orf142	C*PGESLINPGFK	1.0	1.0	1.0
245	P62191	PSMC1 26S protease regulatory subunit 4	PSMC1	AIC*TEAGLMALR	1.0	1.0	1.0
246	P22102	GART Trifunctional purine biosynthetic protein adenosine-3	GART	QVLVAPGNAGTAC*SEK	0.8	0.8	0.8
247	P55809	OXCT1 Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	OXCT1	C*TLPLTGK	0.8	1.0	0.9
248	Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	SC*ENLAPFNTALK	0.9	1.0	0.9
249	Q93052	LPP Lipoma-preferred partner	LPP	TYITDPVSAPC*APPLQPK	1.0	1.1	1.0
250	Q8TEX9	IPO4 Importin-4	IPO4	APAALPALC*DLLASAADPQIR	1.0	1.1	1.0
251	P11413	G6PD Glucose-6-phosphate 1-dehydrogenase	G6PD	TQVC*GILR	0.9	1.0	0.9

1.8	1.5	1.5	1.5	1.7	1.6	ns	Nucleus {ECO	150	Yes	Yes	Yes	No	Yes	Yes	83.3
3.5	1.0	1.2	1.1	1.1	1.6	ns	Cytoplasm. Nucleus.	8	Yes	Yes	--	--	--	--	100.0
1.5	1.7	1.7	1.5	1.5	1.6	ns	Perikaryon {ECO	565	Yes	No	--	--	--	--	50.0
1.7	1.4	1.4	1.8	1.7	1.6	ns	Nucleus {ECO Cytoplasm {ECO	596	Yes	Yes	--	--	--	No	66.7
1.7	1.2	1.5	1.8	1.7	1.6	ns	Membrane {ECO	641	Yes	Yes	No	--	No	Yes	60.0
1.2	1.7	1.4	2.1	1.5	1.6	ns	Mitochondrion.	430	Yes	Yes	No	No	No	Yes	50.0
1.6	1.5	1.6	1.6	1.5	1.6	ns		408	Yes	No	--	--	--	--	50.0
1.6	1.7	1.5	1.4	1.6	1.6	ns		72	Yes	Yes	Yes	Yes	Yes	No	83.3
1.6	1.6	1.3	1.7	1.6	1.6	ns		66	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.6	1.5	1.5	1.7	1.5	1.6	ns	Cytoplasm, cell cortex {ECO Golgi apparatus. Cytoplasm, cytoskeleton, microtubule organizing center, centrosome. Membrane; Single-pass membrane protein.	191	Yes	Yes	Yes	--	Yes	No	80.0
1.6	1.6	1.4	1.6	1.6	1.5	ns		254	Yes	Yes	Yes	--	Yes	Yes	100.0
1.6	1.4	1.4	1.7	1.6	1.5	ns	Mitochondrion.	162	Yes	No	No	No	No	No	16.7
1.4	1.5	1.4	1.9	1.6	1.5	ns	Cytoplasm {ECO	864	Yes	Yes	No	--	No	No	40.0
1.2	1.3	1.6	1.9	1.7	1.5	ns	Cytoplasm. Nucleus.	645	Yes	Yes	--	--	--	--	100.0
1.4	1.4	1.4	2.0	1.5	1.5	ns	Mitochondrion.	402	Yes	Yes	Yes	No	Yes	Yes	83.3
1.1	1.5	1.6	2.0	1.6	1.5	ns	Cytoplasm {ECO	493	Yes	Yes	Yes	No	Yes	Yes	83.3
1.5	1.4	1.7	1.6	1.5	1.5	ns		135	Yes	No	No	No	No	No	16.7
2.0	1.6	1.4	1.3	1.3	1.5	ns	Mitochondrion matrix {ECO	389	Yes	Yes	Yes	No	No	No	50.0
1.5	1.4	1.4	1.8	1.5	1.5	ns	Nucleus {ECO Cytoplasm {ECO	353	Yes	Yes	Yes	No	Yes	Yes	83.3
1.6	1.6	1.6	1.2	1.6	1.5	ns	Cytoplasm {ECO	139	Yes	Yes	Yes	No	Yes	No	66.7
1.4	1.4	1.6	1.7	1.5	1.5	ns	Mitochondrion matrix. Peroxisome.	307	Yes	Yes	Yes	No	No	No	50.0
1.5	1.5	1.5	1.5	1.5	1.5	ns	Nucleus. Cytoplasm.	61	Yes	Yes	Yes	--	--	--	100.0
1.4	1.6	1.3	1.5	1.6	1.5	ns		Bad ID	Error	Error	Error	Error	Error	Error	#DIV/0!
1.4	1.5	1.5	1.5	1.5	1.5	ns	Nucleus {ECO	16	Yes	No	--	--	--	--	50.0
1.4	1.4	1.5	1.7	1.5	1.5	ns	Nucleus {ECO	180	Yes	Yes	--	--	--	--	100.0
1.5	1.4	1.6	1.6	1.4	1.5	ns	Cytoplasm. Nucleus. Membrane {ECO	399	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.7	1.2	1.4	1.6	1.5	1.5	ns		41	Yes	Yes	No	No	No	No	33.3
1.4	1.5	1.4	1.6	1.5	1.5	ns	Mitochondrion matrix.	456	Yes	Yes	Yes	--	--	Yes	100.0
1.0	1.7	1.4	1.7	1.6	1.5	ns	Cytoplasm, cytosol {ECO	306	Yes	Yes	--	--	--	--	100.0
1.4	1.4	1.4	1.7	1.5	1.5	ns	Nucleus. Cytoplasm. Cell junction. Cell membrane.	364	Yes	Yes	--	--	--	--	100.0
1.3	1.4	1.4	1.6	1.6	1.5	ns	Cytoplasm {ECO	42	Yes	No	No	No	No	No	16.7
1.4	1.3	1.5	1.7	1.4	1.5	ns		13	Yes	Yes	Yes	--	--	--	100.0

252	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	DLAGC*IHGLSNVK	0.9	0.9	0.9
253	Q13636	RAB31 Ras-related protein Rab-31	RAB31	VC*LLGDTGVGK	0.8	1.0	0.9
254	Q00765	REEP5 Receptor expression-enhancing protein 5	REEP5	NC*MTDLLAK	1.1	1.0	1.0
255	P11498	PC Pyruvate carboxylase, mitochondrial	PC	FLYEC*PWR	1.2	1.1	1.1
256	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	ALDH6A1	VC*NLIDSGTK	0.9	1.0	0.9
257	O15355	PPM1G Protein phosphatase 1G	PPM1G	C*SGDGVGAPR	1.0	0.9	1.0
258	P0CW22	RPS17L 40S ribosomal protein S17-like	RPS17L	VC*EEIAIIPSK	0.9	0.9	0.9
259	O95747	OXSR1 Serine/threonine-protein kinase OSR1	OXSR1	C*QTSMDELLK	0.9	1.0	1.0
260	P09429	HMGB1 High mobility group protein B1	HMGB1	MSSYAFFVQTC*R	1.0	0.8	0.9
261	P30281	CCND3 G1/S-specific cyclin-D3	CCND3	ASYFQC*VQR	0.9	0.9	0.9
262	O00148	DDX39A ATP-dependent RNA helicase DDX39A	DDX39A	AIVDC*GFEHPSEVQHEC*IPQAILGMDVLC*QAK	0.9	1.5	1.2
263	P49327	FASN Fatty acid synthase	FASN	WVC*SSLR	1.0	0.9	0.9
264	Q00610	CLTC Clathrin heavy chain 1	CLTC	IHEGC*EEPATHNALAK	0.9	1.1	1.0
265	Q9Y3A3	MOB4 MOB-like protein phocein	MOB4	HTLDGAAC*LLNSNK	1.0	0.9	1.0
266	Q9UJU6	DBNL Drebrin-like protein	DBNL	AEEDVEPEC*IMEK	1.8	1.4	1.6
267	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	ADHQPLTEASYVNLPTIALC*NTDSPLR	0.9	0.9	0.9
268	Q9ULV4	CORO1C Coronin-1C	CORO1C	C*DLISIPK	0.9	1.0	1.0
269	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	HIIEDPC*TLR	1.1	0.9	1.0
270	P50552	VASP Vasodilator-stimulated phosphoprotein	VASP	SSSSVTTSETQPC*TPSSSDYSDLQR	0.7	1.4	1.1
271	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	TLSGMESYC*VR	0.8	1.0	0.9
272	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	PMC*VESFSDYPPLGR	1.0	1.0	1.0
273	Q15208	STK38 Serine/threonine-protein kinase 38	STK38	LSDFGLC*TGLK	1.1	1.0	1.1
274	O43390	HNRNPR Heterogeneous nuclear ribonucleoprotein R	HNRNPR	SAFLC*GVMK	0.9	1.0	0.9
275	P63220	RPS21 40S ribosomal protein S21	RPS21	TYAIC*GAIR	1.4	1.0	1.2
276	Q8IUR0	TRAPPC5 Trafficking protein particle complex subunit 5	TRAPPC5	ENSTLNC*ASFTAGIVEAVLTHSGFPAK	0.9	1.0	1.0
277	Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	NPVSQC*MR	0.9	1.1	1.0
278	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	QAVLGAGLPISTPC*TTINK	0.8	0.9	0.9
279	O15541	RNF113A RING finger protein 113A	RNF113A	AVDQVC*TFLFK	0.9	1.0	0.9
280	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	YC*SGTGWPSFSEAHGTSGSDESHTGILR	1.0	0.9	0.9
281	Q15813	TBCE Tubulin-specific chaperone E	TBCE	NCAVSC*AGEK	1.4	1.1	1.2
282	Q96EB1	ELP4 Elongator complex protein 4	ELP4	VEPC*SLTPGYTK	0.9	0.9	0.9
283	O43684	BUB3 Mitotic checkpoint protein BUB3	BUB3	TPC*NAGTFSQPEK	1.0	1.1	1.0
284	P30050	RPL12 60S ribosomal protein L12	RPL12	C*TGGEVGATSALAPK	0.9	0.9	0.9

1.5	1.4	1.4	1.6	1.5	1.5	ns	Mitochondrion.	418	Yes	Yes	Yes	No	No	Yes	66.7
1.6	1.3	1.5	1.5	1.4	1.5	ns	Golgi apparatus, trans-Golgi network {ECO	9	Yes	Yes	No	No	No	No	33.3
1.5	1.5	1.3	1.7	1.4	1.5	ns	Membrane {ECO	18	Yes	Yes	--	--	--	No	66.7
1.5	1.5	1.4	1.4	1.6	1.5	ns	Mitochondrion matrix.	622	Yes	Yes	Yes	No	--	Yes	80.0
1.5	1.4	1.4	1.7	1.3	1.5	ns	Mitochondrion.	368	Yes	Yes	No	No	Yes	No	50.0
1.3	1.5	1.5	1.5	1.5	1.4	ns	Cytoplasm {ECO	13	Yes	Yes	--	--	--	--	100.0
1.5	1.4	1.4	1.5	1.5	1.4	ns		35	Yes	Yes	Yes	Yes	No	Yes	83.3
1.4	1.0	2.0	1.2	1.6	1.4	ns	Cytoplasm {ECO	53	Yes	Yes	No	No	Yes	Yes	66.7
1.4	1.7	1.4	1.4	1.4	1.4	ns	Nucleus {ECO	23	Yes	Yes	Yes	--	No	Yes	80.0
1.5	1.4	1.3	1.5	1.5	1.4	ns	Nucleus {ECO	47	Yes	Yes	No	--	No	No	40.0
1.5	1.3	1.3	1.7	1.5	1.4	ns	Nucleus {ECO	62	Yes	Yes	Yes	Yes	No	Yes	83.3
								74	Yes	Yes	Yes	No	Yes	Yes	83.3
								86	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.5	1.2	1.5	1.4	1.5	1.4	ns	Cytoplasm {ECO	1548	Yes	No	--	--	--	No	33.3
1.6	1.1	1.4	1.6	1.5	1.4	ns	Cytoplasmic vesicle membrane {ECO	870	Yes	Yes	Yes	No	No	No	50.0
1.4	1.4	1.4	1.5	1.4	1.4	ns	Cytoplasm, perinuclear region {ECO	134	Yes	Yes	Yes	No	No	No	50.0
1.1	1.1	1.5	1.7	1.6	1.4	ns	Cytoplasm, cytoskeleton {ECO	127	Yes	Yes	No	--	--	No	50.0
1.4	1.3	1.5	1.7	1.3	1.4	ns		Bad ID	Error	Error	Error	Error	Error	Error	#DIV/0!
1.3	1.3	1.5	1.6	1.4	1.4	ns	Cell membrane {ECO	420	Yes	No	No	--	--	--	33.3
1.6	1.2	1.3	1.6	1.4	1.4	ns	Cytoplasm {ECO	1832	Yes	Yes	--	--	--	--	100.0
1.4	1.4	1.3	1.4	1.6	1.4	ns	Cytoplasm. Cytoplasm, cytoskeleton. Cell junction, focal adhesion. Cell junction, tight junction {ECO	334	Yes	No	--	--	--	--	50.0
1.3	1.4	1.4	1.6	1.3	1.4	ns	Cytoplasm {ECO	450	Yes	Yes	Yes	No	Yes	Yes	83.3
1.5	1.3	1.4	1.5	1.4	1.4	ns	Cytoplasm. Nucleus. Nucleus, nucleolus.	411	Yes	Yes	Yes	Yes	No	Yes	83.3
1.6	1.6	1.3	1.2	1.3	1.4	ns	Nucleus. Cytoplasm.	234	Yes	Yes	Yes	No	Yes	Yes	83.3
2.1	1.1	1.3	1.3	1.2	1.4	ns	Nucleus {ECO	99	Yes	Yes	Yes	--	--	No	75.0
1.2	1.7	1.2	1.4	1.5	1.4	ns		56	Yes	Yes	Yes	No	Yes	Yes	83.3
1.4	1.4	1.3	1.3	1.6	1.4	ns	Golgi apparatus, cis-Golgi network {ECO	139	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.5	1.3	1.3	1.5	1.4	1.4	ns	Nucleus {ECO	50	Yes	Yes	No	--	--	No	50.0
1.3	1.4	1.4	1.4	1.4	1.4	ns	Mitochondrion.	119	Yes	Yes	Yes	No	Yes	No	66.7
1.4	1.2	1.4	1.5	1.5	1.4	ns		15	Yes	Yes	--	--	Yes	--	100.0
1.7	1.3	1.1	1.4	1.4	1.4	ns	Mitochondrion {ECO	105	Yes	Yes	No	No	No	No	33.3
1.2	1.4	1.5	1.1	1.7	1.4	ns	Cytoplasm {ECO	141	Yes	No	No	No	No	No	16.7
1.1	1.3	1.4	1.6	1.5	1.4	ns	Cytoplasm. Nucleus.	218	Yes	Yes	--	No	Yes	No	60.0
1.2	1.5	1.3	1.6	1.2	1.4	ns	Nucleus. Chromosome, centromere, kinetochore {ECO	129	Yes	Yes	No	No	No	No	33.3
1.5	1.0	1.5	1.6	1.3	1.4	ns		17	Yes	Yes	Yes	No	No	Yes	66.7

285	Q9BXJ9	NAA15 N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	LFNTAVC*ESK	1.0	0.9	1.0
286	P18085	ARF4 ADP-ribosylation factor 4	ARF4	NIC*FTVWDVGGQDR	0.9	1.0	0.9
287	P62633	CNBP Cellular nucleic acid-binding protein	CNBP	TSEVNC*YR	0.8	1.0	0.9
288	Q5T4S7	UBR4 E3 ubiquitin-protein ligase UBR4	UBR4	AVQC*LNTSSK	1.0	1.0	1.0
289	P49915	GMPS GMP synthase	GMPS	VICAEEPYIC*K	0.9	1.1	1.0
290	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	SQETEC*TYFSTPLLLGK	0.9	1.0	1.0
291	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	YVDIAIPC*NNK	0.9	1.0	0.9
292	Q9GZZ9	UBA5 Ubiquitin-like modifier-activating enzyme 5	UBA5	EGVC*AASLPTTMGVVAGILVQNVLK	1.1	1.1	1.1
293	P20073	ANXA7 Annexin A7	ANXA7	LGTDESC*FNMILATR	0.9	0.9	0.9
294	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	C*IPALDSLTPANEDQK	1.0	1.0	1.0
295	O14545	TRAFD1 TRAF-type zinc finger domain-containing protein 1	TRAFD1	AVC*EADQSHGGPR	1.0	1.0	1.0
296	Q9NP73	ALG13 UDP-N-acetylglucosamine transferase subunit ALG13	ALG13	ADLVISHAGAGSC*LETLEK	1.0	1.0	1.0
297	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	FFSDC*K	1.0	1.1	1.0
298	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	IHMGSC*AENTAK	0.9	0.9	0.9
299	P60709	ACTB Actin, cytoplasmic 1	ACTB	C*PEALFQPSFLGMESC*GIHETTFNSIMK	0.9	0.9	0.9
300	Q9C0C9	UBE2O Ubiquitin-conjugating enzyme E2 O	UBE2O	C*YNEMALIR	0.9	1.0	1.0
301	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	NMITGTSQADC*AVLIVAAGVGEFEAGISK	0.9	1.0	1.0
302	P49327	FASN Fatty acid synthase	FASN	ADEASELAC*PTPK	1.0	1.0	1.0
303	P60866	RPS20 40S ribosomal protein S20	RPS20	TPC*GEGSK	1.1	1.0	1.0
304	P84085	ARF5 ADP-ribosylation factor 5	ARF5	NIC*FTVWDVGGQDK	0.9	1.1	1.0
305	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	LTFSC*LGGSDNFK	0.9	1.0	1.0
306	Q9NUU7	DDX19A ATP-dependent RNA helicase DDX19A	DDX19A	VLVTTNVC*AR	0.9	1.0	0.9
307	P15924	DSP Desmoplakin	DSP	NQC*TQVVQER	1.0	0.9	0.9
308	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	VDENFDC*VEADDVEGK	1.0	0.9	1.0
309	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	ISASC*QHPTAFEEAIPK	0.9	0.9	0.9
310	P49327	FASN Fatty acid synthase	FASN	AINC*ATSGVVGLVNC*LR	1.0	1.0	1.0
311	P13639	EEF2 Elongation factor 2	EEF2	VTDGALVVVDC*VSGVC*VQTETVLR	1.7	1.1	1.4
312	E7EQ34	GOSR2 Golgi SNAP receptor complex member 2	GOSR2	QVHEIQSC*MGR	1.0	1.0	1.0
313	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	MC*SMVK	0.8	0.9	0.9
314	P13639	EEF2 Elongation factor 2	EEF2	IWC*FGPDGTGPNILTDITK	1.0	1.1	1.0
315	Q04637	EIF4G1 Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	LQGINC*GPDFTPSFANLGR	1.0	1.0	1.0
316	Q9UHD8	SEPT9 Septin-9	9-Sep	SQEATEAAPSC*VGDMADTPR	1.2	1.0	1.1
317	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	AC*QSIYPLHDVFVR	1.0	0.7	0.8

1.3	1.7	1.2	1.3	1.3	1.4	ns	Cytoplasm. Nucleus.	721	Yes	Yes	No	--	No	No	40.0
1.4	1.2	1.3	1.5	1.5	1.4	ns	Golgi apparatus. Membrane {ECO	62	Yes	Yes	Yes	No	No	No	50.0
1.4	1.3	1.5	1.4	1.2	1.4	ns	Cytoplasm {ECO	158	Yes	Yes	Yes	Yes	Yes	--	100.0
2.0	1.2	1.3	0.9	1.3	1.4	ns	Membrane {ECO	2554	Yes	Yes	No	--	--	--	66.7
1.3	1.3	1.4	1.4	1.4	1.4	ns	Cytoplasm.	456	Yes	Yes	No	No	No	No	33.3
1.3	1.3	1.4	1.4	1.4	1.4	ns	Mitochondrion matrix.	285	Yes	Yes	No	No	No	No	33.3
1.4	1.2	1.4	1.5	1.3	1.3	ns		Bad ID	Error	Error	Error	Error	Error	Error	#DIV/0!
1.4	1.3	1.3	1.3	1.4	1.3	ns	Cytoplasm {ECO	250	Yes	Yes	Yes	--	Yes	Yes	100.0
1.5	1.3	1.2	1.4	1.4	1.3	ns		363	Yes	Yes	No	--	No	No	40.0
1.3	1.2	1.4	1.4	1.4	1.3	ns	Mitochondrion matrix.	447	Yes	Yes	Yes	No	No	No	50.0
1.2	1.2	1.3	1.5	1.6	1.3	ns		267	Yes	No	--	--	--	--	50.0
1.3	1.3	1.3	1.5	1.3	1.3	ns	Endoplasmic reticulum {ECO	86	Yes	Yes	--	No	No	Yes	60.0
1.4	1.2	1.5	1.3	1.3	1.3	ns	Nucleus, nucleoplasm.	34	Yes	Yes	No	--	No	No	40.0
1.4	1.2	1.3	1.4	1.4	1.3	ns	Mitochondrion.	196	Yes	Yes	Yes	No	Yes	Yes	83.3
1.3	1.5	1.4	1.1	1.4	1.3	ns	Cytoplasm, cytoskeleton {ECO	257	Yes	Yes	Yes	No	Yes	Yes	83.3
								272	Yes	Yes	Yes	No	No	No	50.0
1.2	1.3	1.2	1.5	1.5	1.3	ns	Cytoplasm {ECO	1099	Yes	Yes	No	--	No	No	40.0
1.3	1.4	1.4	1.4	1.3	1.3	ns	Cytoplasm. Nucleus.	111	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.3	1.3	1.3	1.4	1.4	1.3	ns	Cytoplasm {ECO	2202	Yes	No	--	--	--	No	33.3
1.5	1.5	1.2	1.2	1.3	1.3	ns	Cytoplasm {ECO	70	Yes	Yes	Yes	No	Yes	Yes	83.3
1.5	1.2	1.3	1.4	1.3	1.3	ns	Golgi apparatus {ECO	62	Yes	Yes	Yes	No	No	No	50.0
0.7	1.2	1.9	1.9	0.8	1.3	ns	Cytoplasm.	40	Yes	Yes	No	No	No	No	33.3
1.3	1.2	1.3	1.4	1.3	1.3	ns	Cytoplasm {ECO	392	Yes	Yes	No	No	No	No	33.3
1.1	1.4	1.3	1.3	1.4	1.3	ns	Cell junction, desmosome {ECO	1805	Yes	Yes	--	--	--	--	100.0
1.3	1.0	1.4	1.5	1.4	1.3	ns	Nucleus matrix. Cytoplasm. Nucleus. Nucleus matrix. Nucleus, nucleoplasm.	101	Yes	Yes	No	No	No	No	33.3
1.3	1.3	1.3	1.4	1.4	1.3	ns	Cytoplasm {ECO	327	Yes	No	--	No	No	No	20.0
1.3	1.4	1.3	1.5	1.1	1.3	ns	Cytoplasm {ECO	1448/1459	Yes	Yes	--	--	--	Yes	100.0
1.3	1.3	1.0	1.0	2.0	1.3	ns	Cytoplasm. Nucleus {ECO	131	Yes	Yes	Yes	No	Yes	Yes	83.3
								136	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.2	1.4	1.3	1.3	1.4	1.3	ns		18	Yes	No	No	--	--	No	25.0
1.4	1.3	1.3	1.4	1.3	1.3	ns	Cytoplasm {ECO	111	Yes	Yes	No	No	No	Yes	50.0
2.3	1.1	1.1	1.0	1.1	1.3	ns	Cytoplasm. Nucleus {ECO	651	Yes	Yes	Yes	Yes	No	Yes	83.3
1.6	1.2	1.2	1.2	1.3	1.3	ns		662	Yes	Yes	No	--	No	No	40.0
1.2	1.3	1.3	1.6	1.2	1.3	ns	Cytoplasm, cytoskeleton {ECO	248	Yes	Yes	--	--	--	--	100.0
1.2	1.6	1.3	1.4	1.1	1.3	ns	Cytoplasm {ECO	201	Yes	Yes	Yes	No	No	Yes	66.7

318	P21964	COMT Catechol O-methyltransferase	COMT	GSSC*FECTHYQSFLEYR	1.0	1.0	1.0
319	P13639	EEF2 Elongation factor 2	EEF2	STLTDSLVC*K	0.9	1.0	1.0
320	Q96CP2	FLYWCH2 FLYWCH family member 2	FLYWCH2	TEDSGLAAGPPEAAGENFAPC*SVAPGK	0.9	1.2	1.0
321	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	SSGGFVWAC*K	1.0	1.0	1.0
322	P55769	NHP2L1 NHP2-like protein 1	NHP2L1	LLDLVQQSC*NYK	0.9	0.9	0.9
323	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	AAVEEGIVLGGGC*ALLR	0.9	1.0	1.0
324	P40222	TXLNA Alpha-taxilin	TXLNA	VTEAPC*YPGAPSTEASGQTGPQEPTSAR	0.9	1.4	1.1
325	Q06323	PSME1 Proteasome activator complex subunit 1	PSME1	EDLC*TK	0.9	1.1	1.0
326	Q9P1F3	ABRACL Costars family protein ABRACL	ABRACL	C*ANLFEALVGTLK	1.0	1.0	1.0
327	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	AATGEEVSAEDLGGADLHC*R	0.9	0.9	0.9
328	O15075	DCLK1 Serine/threonine-protein kinase DCLK1	DCLK1	YQDDFLLDESEC*R	1.0	1.1	1.1
329	Q9NZL4	HSPBP1 Hsp70-binding protein 1	HSPBP1	DAC*DTVR	1.0	1.0	1.0
330	Q9NQC3	RTN4 Reticulon-4	RTN4	YSNSALGHVNC*TIK	1.1	1.1	1.1
331	Q7L1Q6	BZW1 Basic leucine zipper and W2 domain-containing protein 1	BZW1	FDPTQFQDC*IIQGLTETGTDLEAVAK	1.0	1.0	1.0
332	P23921	RRM1 Ribonucleoside-diphosphate reductase large subunit	RRM1	IIDINYYPVPEAC*LSNK	1.1	0.9	1.0
333	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	C*C*SGAIIVLTK	0.9	0.9	0.9
334	Q9P258	RCC2 Protein RCC2	RCC2	AVQDLC*GWR	1.1	1.2	1.1
335	Q13045	FLII Protein flightless-1 homolog	FLII	TGLC*YLPEELAALQK	0.8	1.1	1.0
336	P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	C*VVVGDGAVGK	0.9	0.9	0.9
337	Q7Z4W1	DCXR L-xylulose reductase	DCXR	AVTNHSVYC*STK	0.9	0.8	0.9
338	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	IGNC*PFSQR	1.0	1.0	1.0
339	O43865	AHCYL1 Putative adenosylhomocysteinase 2	AHCYL1	LC*VPAMNVNDSVTK	0.9	1.0	0.9
340	Q9UPM8	AP4E1 AP-4 complex subunit epsilon-1	AP4E1	SSC*STLPDYLLYQCQK	0.7	0.7	0.7
341	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	VFIMDSC*DELIPEYLNFIR	1.0	1.2	1.1
342	P49721	PSMB2 Proteasome subunit beta type-2	PSMB2	NLADC*LR	0.9	1.1	1.0
343	Q8NBF2	NHLRC2 NHL repeat-containing protein 2	NHLRC2	AILFSQPLQITDTQQGC*IAPVELR	0.9	1.0	1.0
344	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	EGC*TEVSLLR	1.0	1.0	1.0
345	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	IC*PVETLVEEAIQC*AEK	1.0	1.0	1.0
346	Q6IA69	NADSYN1 Glutamine-dependent NAD(+) synthetase	NADSYN1	NSSQETC*TR	1.3	1.3	1.3
347	P30042	C21orf33 ES1 protein homolog, mitochondrial	C21orf33	DC*K	0.9	1.0	0.9
348	Q99798	ACO2 Aconitate hydratase, mitochondrial	ACO2	DLGGIVLANAC*GPC*IGQWDR	1.1	0.9	1.0

1.4	1.2	1.2	1.3	1.3	1.3	ns	Cytoplasm. Cell membrane; Single-pass type II membrane protein; Extracellular side {ECO	238	Yes	No	--	--	--	--	50.0
1.3	1.1	1.2	1.3	1.5	1.3	ns	Cytoplasm. Nucleus {ECO	41	Yes	Yes	No	No	No	No	33.3
1.2	1.3	1.4	1.4	1.2	1.3	ns		132	Yes	--	--	--	--	--	100.0
1.4	1.3	1.1	1.3	1.4	1.3	ns	Mitochondrion.	308	Yes	Yes	Yes	No	Yes	Yes	83.3
1.3	1.3	1.2	1.3	1.3	1.3	ns	Nucleus, nucleolus {ECO	30	Yes	Yes	No	No	No	No	33.3
1.3	1.2	1.3	1.3	1.3	1.3	ns	Mitochondrion matrix.	442	Yes	Yes	No	No	No	No	33.3
1.1	1.5	1.2	1.3	1.4	1.3	ns		523	Yes	Yes	--	--	--	--	100.0
1.2	1.2	1.3	1.5	1.3	1.3	ns		22	Yes	Yes	No	--	--	No	50.0
1.1	1.3	1.3	1.4	1.3	1.3	ns		39	Yes	Yes	--	--	Yes	--	100.0
1.4	1.3	1.1	1.3	1.4	1.3	ns	Mitochondrion matrix {ECO	267	Yes	Yes	Yes	--	Yes	Yes	100.0
1.3	1.2	1.3	1.4	1.3	1.3	ns		276	Yes	Yes	No	--	--	No	50.0
1.2	1.2	1.4	1.3	1.3	1.3	ns		204	Yes	Yes	No	No	No	--	40.0
1.1	1.5	1.0	1.3	1.5	1.3	ns	Endoplasmic reticulum membrane; Multi-pass membrane protein.	1101	Yes	No	No	No	No	Yes	33.3
1.4	1.2	1.3	1.3	1.2	1.3	ns		35	Yes	Yes	No	--	No	--	50.0
1.4	1.2	1.2	1.3	1.3	1.3	ns	Cytoplasm.	492	Yes	No	No	No	No	No	16.7
1.2	1.3	1.3	1.3	1.2	1.3	ns	Cytoplasm. Nucleus.	423	Yes	Yes	No	No	No	Yes	50.0
								424	Yes	Yes	No	No	No	No	33.3
1.3	1.1	1.3	1.4	1.3	1.3	ns	Nucleus, nucleolus. Chromosome, centromere. Cytoplasm, cytoskeleton, spindle.	428	Yes	Yes	No	--	No	No	40.0
1.2	1.1	1.3	1.4	1.3	1.3	ns	Nucleus {ECO	46	Yes	Yes	No	No	--	No	40.0
1.2	1.3	1.5	1.1	1.3	1.3	ns	Cytoplasm.	6	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.3	1.5	1.3	1.2	1.1	1.3	ns	Membrane {ECO	150	Yes	Yes	No	No	No	Yes	50.0
1.3	1.2	1.2	1.3	1.4	1.3	ns	Nucleus. Nucleus membrane {ECO	24	Yes	Yes	Yes	--	Yes	No	80.0
1.2	1.0	1.4	1.2	1.4	1.3	ns	Endoplasmic reticulum {ECO	272	Yes	Yes	No	No	No	No	33.3
1.3	1.1	1.3	1.4	1.3	1.3	ns	Golgi apparatus, trans-Golgi network. Membrane, coated pit {ECO	1119	Yes	No	--	--	--	--	50.0
1.2	1.4	1.2	1.1	1.3	1.3	ns	Cytoplasm. Melanosome.	366	Yes	Yes	Yes	No	Yes	Yes	83.3
1.3	1.3	1.2	1.2	1.3	1.3	ns	Cytoplasm. Nucleus.	91	Yes	Yes	No	No	No	No	33.3
1.3	1.2	1.3	1.3	1.2	1.3	ns		716	Yes	Yes	--	--	--	--	100.0
1.3	1.2	1.2	1.2	1.4	1.3	ns	Nucleus {ECO	308	Yes	Yes	--	--	No	No	50.0
1.2	1.2	1.3	1.4	1.2	1.2	ns	Mitochondrion matrix.	213	Yes	No	No	No	No	No	16.7
1.1	1.1	1.0	1.8	1.1	1.2	ns		428	Yes	No	No	No	No	No	16.7
1.3	1.2	1.2	1.5	1.1	1.2	ns	Mitochondrion {ECO	153	Yes	Yes	--	--	--	--	100.0
1.0	1.3	1.1	1.4	1.4	1.2	ns	Mitochondrion {ECO	448/451	Yes	Yes	Yes	Yes	Yes	Yes	100.0

349	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	EQFSQGSPSNC*LETSLAEI FPLGK	0.9	1.0	1.0
350	Q15233	NONO Non-POU domain-containing octamer-binding protein	NONO	C*SEGSFLLTTFPR	0.9	1.1	1.0
351	Q8IXH7	TH1L Negative elongation factor C/D	TH1L	AC*QALGAMLSK	1.1	0.9	1.0
352	O00233	PSMD9 26S proteasome non-ATPase regulatory subunit 9	PSMD9	GIGMNEPLVDC*EGYPR	1.0	1.3	1.2
353	Q9UK41	VPS28 Vacuolar protein sorting-associated protein 28 homolog	VPS28	LDC*PLAMER	1.1	1.3	1.2
354	P49327	FASN Fatty acid synthase	FASN	LTPGC*EAEAETEAICFFVQ QFTDMEHNR	1.2	1.0	1.1
355	Q6P1X6	C8orf82 UPF0598 protein C8orf82	C8orf82	YEAAFPFLSPC*GR	1.2	1.0	1.1
356	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	DLNYC*FSGMSDHR	1.0	1.0	1.0
357	Q7L2H7	EIF3M Eukaryotic translation initiation factor 3 subunit	EIF3M	VAASC*GAIQYIPTELDQV R	0.9	1.0	0.9
358	O75934	BCAS2 Pre-mRNA-splicing factor SPF27	BCAS2	IENLELMSQHGC*NAWK	1.0	1.0	1.0
359	O43765	SGTA Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	AIC*IDPAYSK	1.0	1.0	1.0
360	P78406	RAE1 mRNA export factor	RAE1	VFTASC*DK	0.9	1.0	1.0
361	Q8IWX8	CHERP Calcium homeostasis endoplasmic reticulum protein	CHERP	LALEQQQLIC*K	0.8	1.1	0.9
362	Q7Z4W1	DCXR L-xylulose reductase	DCXR	GVPGAIVNVSSQC*SQR	0.9	0.9	0.9
363	O00267	SUPT5H Transcription elongation factor SPT5	SUPT5H	VELHSTC*QTISVDR	1.3	1.1	1.2
364	Q14694	USP10 Ubiquitin carboxyl-terminal hydrolase 10	USP10	TPSYSISSTLNPQAPEFILGC *TASK	1.1	1.0	1.0
365	P55263	ADK Adenosine kinase	ADK	SLIANLAAANC*YK	1.0	1.0	1.0
366	P19367	HK1 Hexokinase-1	HK1	AAQLC*GAGMAAVVDK	0.9	0.6	0.8
367	Q14181	POLA2 DNA polymerase alpha subunit B	POLA2	VLGC*PEALTGSYK	0.9	0.9	0.9
368	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit 2	PSMD2	GTLTLC*PYHSDR	0.8	1.0	0.9
369	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	GSDFDC*ELR	0.9	0.9	0.9
370	P49327	FASN Fatty acid synthase	FASN	DGLLENQTPEFFQDVC*K	0.9	0.9	0.9
371	Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	VGLGIC*YDMR	1.0	1.1	1.0
372	Q15004	KIAA0101 PCNA-associated factor	KIAA0101	AC*PLQPDHTNDEK	1.1	1.0	1.0
373	Q09666	AHNAK Neuroblast differentiation-associated protein AHNAK	AHNAK	LEGDLTGPSVDVEVPDVEL EC*PDAK	1.1	1.1	1.1
374	O75934	BCAS2 Pre-mRNA-splicing factor SPF27	BCAS2	NDITAWQEC*VNNSMAQL EHQAVR	1.0	1.0	1.0
375	O95336	PGLS 6-phosphogluconolactonase	PGLS	AAC*CLAGAR	1.0	1.0	1.0
376	P62195	PSMC5 26S protease regulatory subunit 8	PSMC5	NIDINDVTPNC*R	0.7	0.9	0.8
377	O75153	KIAA0664 Clustered mitochondria protein homolog	KIAA0664	C*LTQQAVALQR	0.9	1.0	1.0
378	Q9BX63	BRIP1 Fanconi anemia group J protein	BRIP1	LANNSDC*ILAK	0.9	1.0	0.9
379	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	SC*AHDWVYE	1.2	1.2	1.2
380	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	ENQWC*EEK	1.0	0.9	1.0
381	P15924	DSP Desmoplakin	DSP	AC*GSEIMQK	0.9	0.9	0.9
382	P20810	CAST Calpastatin	CAST	SEC*K	1.1	1.1	1.1
383	Q13185	CBX3 Chromobox protein homolog 3	CBX3	LTWHSC*PEDEAQ	0.9	1.0	1.0

1.3	1.4	1.2	1.0	1.2	1.2	ns	Cytoplasm {ECO	161	Yes	No	No	--	--	--	33.3
1.1	1.0	1.4	1.4	1.4	1.2	ns	Nucleus. Nucleus, nucleolus. Nucleus speckle.	208	Yes	Yes	Yes	--	No	No	60.0
0.6	1.4	1.3	1.3	1.7	1.2	ns	Nucleus {ECO	293	Yes	Yes	Yes	--	--	--	100.0
1.3	1.2	1.2	1.3	1.1	1.2	ns		59	Yes	Yes	No	No	No	No	33.3
1.2	1.2	1.3	1.3	1.2	1.2	ns	Cell membrane {ECO	103	Yes	Yes	Yes	No	Yes	Yes	83.3
1.2	1.2	1.1	1.4	1.3	1.2	ns	Cytoplasm {ECO	2359	Yes	Yes	--	--	--	No	66.7
1.3	1.1	1.2	1.3	1.2	1.2	ns		98	Yes	Yes	Yes	--	--	Yes	100.0
1.3	1.2	1.2	1.3	1.3	1.2	ns	Nucleus, nucleoplasm.	267	Yes	Yes	--	--	--	No	66.7
1.4	1.1	1.2	1.3	1.2	1.2	ns	Cytoplasm {ECO	134	Yes	Yes	Yes	--	No	No	60.0
1.3	1.0	1.2	1.4	1.2	1.2	ns	Nucleus, nucleolus {ECO	132	Yes	Yes	No	--	No	No	40.0
1.5	1.3	1.1	1.2	1.1	1.2	ns		153	Yes	No	No	No	No	No	16.7
0.7	0.9	1.2	2.2	1.1	1.2	ns	Cytoplasm {ECO	106	Yes	Yes	Yes	Yes	Yes	No	83.3
1.1	1.3	1.1	1.2	1.4	1.2	ns	Cytoplasm {ECO	69	Yes	Yes	--	--	No	--	66.7
1.3	1.2	1.1	1.2	1.3	1.2	ns	Membrane {ECO	138	Yes	No	No	No	No	No	16.7
1.3	1.1	1.3	1.4	1.0	1.2	ns	Nucleus {ECO	740	Yes	Yes	Yes	No	No	Yes	66.7
1.2	1.1	1.2	1.3	1.2	1.2	ns	Cytoplasm {ECO	94	Yes	Yes	--	--	--	--	100.0
1.0	1.4	1.2	1.3	1.1	1.2	ns	Nucleus {ECO Cytoplasm {ECO	160	Yes	Yes	No	No	Yes	No	50.0
2.0	1.2	1.0	0.9	1.1	1.2	ns	Mitochondrion outer membrane.	834	Yes	Yes	No	No	No	--	40.0
1.3	0.9	1.6	1.3	1.0	1.2	ns	Nucleus.	198	Yes	No	No	No	--	No	20.0
1.0	0.9	1.1	0.8	2.2	1.2	ns		779	Yes	Yes	No	No	No	--	40.0
1.1	1.3	1.3	1.2	1.3	1.2	ns	Cytoplasm {ECO	145	Yes	Yes	No	No	No	No	33.3
1.3	1.0	1.1	1.5	1.1	1.2	ns	Cytoplasm {ECO	1992	Yes	No	--	--	--	No	33.3
1.4	1.1	1.0	1.2	1.3	1.2	ns	Cytoplasm {ECO	153	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.3	1.0	1.2	1.4	1.1	1.2	ns	Nucleus {ECO	99	Yes	Yes	--	--	--	--	100.0
1.1	1.1	1.1	1.4	1.2	1.2	ns	Nucleus.	2162	Yes	No	--	--	--	--	50.0
0.8	1.3	1.2	1.5	1.3	1.2	ns	Nucleus, nucleolus {ECO	106	Yes	Yes	No	--	No	No	40.0
1.2	1.2	1.1	1.3	1.3	1.2	ns	Cytoplasm {ECO	32	Yes	No	No	No	No	No	16.7
1.0	1.0	1.4	1.4	1.2	1.2	ns	Cytoplasm {ECO	112	Yes	Yes	Yes	No	No	No	50.0
1.2	1.2	1.2	1.1	1.3	1.2	ns	Cytoplasm {ECO	1196	Yes	Yes	No	--	No	No	40.0
1.1	1.1	1.3	1.3	1.2	1.2	ns	Nucleus {ECO	1164	Yes	Yes	--	--	--	--	100.0
1.4	1.4	1.0	1.0	1.2	1.2	ns		130	Yes	Yes	No	No	No	No	33.3
1.2	1.2	1.2	1.2	1.2	1.2	ns		160	Yes	Yes	Yes	No	No	Yes	66.7
1.2	1.2	1.2	1.2	1.1	1.2	ns	Cell junction, desmosome {ECO	1280	Yes	Yes	--	--	--	--	100.0
1.0	1.1	1.5	1.3	1.1	1.2	ns		381	Yes	No	--	--	--	--	50.0
1.2	1.1	1.1	1.3	1.2	1.2	ns	Nucleus {ECO	177	Yes	Yes	--	--	--	--	100.0

384	Q9BV86	NTMT1 N-terminal Xaa-Pro-Lys N-methyltransferase 1	NTMT1	IIC*SAGLSLLAEER	1.0	1.1	1.0
385	Q09666	AHNAK Neuroblast differentiation-associated protein AHNAK	AHNAK	LEGDLTGPSVGVEVPDVELEC*PDAK	1.0	1.0	1.0
386	O15355	PPM1G Protein phosphatase 1G	PPM1G	GTEAGQVGEPGIPTGEAGPSC*SSASDK	1.0	1.0	1.0
387	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	LFQEC*C*PHSTDR	0.8	0.9	0.9
388	O15371	EIF3D Eukaryotic translation initiation factor 3 subunit	EIF3D	FMTPVIQDNPSGWGPC*AVPEQFR	1.0	1.0	1.0
389	O15382	BCAT2 Branched-chain-amino-acid aminotransferase, mitochondrial	BCAT2	EVFGSGTAC*QVCPVHR	0.9	1.0	0.9
390	P17844	DDX5 Probable ATP-dependent RNA helicase DDX5	DDX5	LIDFLEC*GK	1.1	1.0	1.1
391	Q9Y3F4	STRAP Serine-threonine kinase receptor-associated protein	STRAP	IGFPETTEEELEEIASENSDC*IFPSAPDVK	1.0	1.1	1.0
392	Q9Y696	CLIC4 Chloride intracellular channel protein 4	CLIC4	AGSDGESIGNC*PFSQR	1.0	1.0	1.0
393	Q2TAA2	IAH1 Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	VILITPTPLC*ETAWEEQCIIQGCK	0.9	0.9	0.9
394	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	YAGLSTC*FR	1.0	0.9	1.0
395	P33240	CSTF2 Cleavage stimulation factor subunit 2	CSTF2	LC*VQNSPQEAR	1.0	1.0	1.0
396	Q9BSU1	C16orf70 UPF0183 protein C16orf70	C16orf70	LLAAGC*GPGLLADAK	0.9	0.9	0.9
397	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	HSMNPFC*EIAVEEAVR	1.2	1.1	1.2
398	Q9UNE7	STUB1 E3 ubiquitin-protein ligase CHIP	STUB1	AQQAC*IEAK	1.0	1.1	1.1
399	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	C*EFQDAYVLLSEK	0.9	1.0	1.0
400	Q9UBF6	RNF7 RING-box protein 2	RNF7	VQVMDAC*LR	0.9	0.9	0.9
401	Q6YN16	HSDL2 Hydroxysteroid dehydrogenase-like protein 2	HSDL2	TAIHTAAMDMLGGPGIESQC*R	1.0	0.9	0.9
402	Q13526	PIN1 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	PIN1	SGEEDFESLASQFSDC*SSAK	1.0	0.9	1.0
403	O14980	XPO1 Exportin-1	XPO1	LDINLLDNVVNC*LYHGEGAQQR	1.0	1.0	1.0
404	Q9UQ35	SRRM2 Serine/arginine repetitive matrix protein 2	SRRM2	SVSPC*SNVESR	1.0	0.9	1.0
405	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	ASVGFGGSC*FQK	0.9	1.0	1.0
406	Q9BRA2	TXNDC17 Thioredoxin domain-containing protein 17	TXNDC17	SWC*PDCVQAEPVVR	1.0	1.0	1.0
407	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	TIC*AILENYQTEK	0.9	1.0	1.0
408	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	HLNEIDLFHC*IDPNDSK	1.1	1.0	1.0
409	E9PPU0	EPPK1 Epiplakin	EPPK1	TGGQALSTLEC*VK	0.9	1.0	0.9
410	P62306	SNRPF Small nuclear ribonucleoprotein F	SNRPF	C*NNVLYIR	1.0	1.0	1.0
411	P38646	HSPA9 Stress-70 protein, mitochondrial	HSPA9	C*ELSSSVQTDINLPYLTMDSSGPK	0.9	1.0	0.9
412	P07900	HSP90AA1 Heat shock protein HSP 90-alpha	HSP90AA1	VFIMDNC*EELIPEYLNFIR	1.1	1.0	1.0
413	Q15796	SMAD2 Mothers against decapentaplegic homolog 2	SMAD2	AITTQNC*NTK	0.9	1.1	1.0
414	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	LVVPATQC*GSLIGK	0.9	1.0	0.9
415	Q96RS6	NUDCD1 NudC domain-containing protein 1	NUDCD1	DSAQC*AAIAER	0.8	0.8	0.8

1.3	1.2	1.1	1.2	1.1	1.2	ns	Nucleus {ECO	195	Yes	No	No	No	No	No	16.7
1.1	1.1	1.2	1.5	1.1	1.2	ns	Nucleus.	1900	Yes	No	--	--	--	--	50.0
1.2	1.1	1.2	1.3	1.2	1.2	ns	Cytoplasm {ECO	241	Yes	Yes	--	--	--	--	100.0
1.2	1.1	1.3	1.3	1.2	1.2	ns	Cytoplasm {ECO	184	Yes	Yes	No	No	No	No	33.3
								185	Yes	Yes	No	No	Yes	No	50.0
1.3	1.1	1.1	1.3	1.2	1.2	ns	Cytoplasm {ECO	19	Yes	Yes	Yes	--	No	No	60.0
1.1	1.2	1.1	1.1	1.4	1.2	ns	Mitochondrion. Cytoplasm.	342	Yes	Yes	Yes	No	No	Yes	66.7
1.2	1.1	1.2	1.2	1.1	1.2	ns	Nucleus, nucleolus {ECO	234	Yes	Yes	No	No	No	No	33.3
1.0	1.1	1.3	1.4	1.2	1.2	ns	Cytoplasm. Nucleus.	340	Yes	No	--	--	--	--	50.0
1.1	1.3	1.0	1.3	1.1	1.2	ns	Cytoplasm, cytoskeleton, microtubule organizing center, centrosome. Cytoplasmic vesicle membrane {ECO	35	Yes	Yes	Yes	--	Yes	No	80.0
1.2	1.1	1.1	1.2	1.2	1.2	ns		137	Yes	Yes	--	No	No	--	50.0
1.2	1.1	1.1	1.3	1.2	1.2	ns	Cytoplasm.	300	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.3	1.1	1.2	1.2	1.2	1.2	ns	Nucleus {ECO	150	Yes	Yes	Yes	--	No	No	60.0
1.3	1.2	1.0	1.1	1.3	1.2	ns		222	Yes	Yes	No	--	No	No	40.0
1.1	1.0	1.3	1.3	1.2	1.2	ns	Mitochondrion matrix {ECO	42	Yes	Yes	No	No	Yes	No	50.0
1.1	1.3	1.0	1.4	1.0	1.2	ns	Cytoplasm {ECO	199	Yes	Yes	No	--	No	No	40.0
1.1	1.2	1.1	1.2	1.2	1.2	ns	Mitochondrion matrix.	237	Yes	Yes	No	No	Yes	No	50.0
1.1	1.4	1.1	1.1	1.1	1.2	ns	Cytoplasm {ECO	61	Yes	Yes	Yes	Yes	Yes	Yes	100.0
0.9	1.2	1.1	1.5	1.1	1.2	ns	Peroxisome {ECO	218	Yes	Yes	No	--	--	No	50.0
1.1	1.1	1.1	1.3	1.2	1.2	ns	Nucleus {ECO	113	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.2	1.1	1.2	1.2	1.2	1.2	ns	Cytoplasm. Nucleus, nucleoplasm. Nucleus, Cajal body. Nucleus, nucleolus	34	Yes	Yes	No	No	No	No	33.3
1.1	1.1	1.1	1.5	1.1	1.2	ns	Nucleus speckle.	956	Yes	Yes	--	--	--	--	100.0
1.2	1.0	1.6	1.0	1.1	1.2	ns		276	Yes	Yes	Yes	--	Yes	Yes	100.0
1.2	1.1	1.1	1.3	1.2	1.2	ns	Cytoplasm {ECO	43	Yes	Yes	Yes	--	Yes	Yes	100.0
1.2	1.2	1.1	1.2	1.2	1.2	ns	Cytoplasm.	438	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.2	1.1	1.1	1.2	1.2	1.2	ns	Cytoplasm.	58	Yes	Yes	No	No	No	No	33.3
1.2	1.2	1.0	1.4	1.1	1.2	ns		Bad ID	Error	Error	Error	Error	Error	Error	#DIV/0!
1.2	1.1	1.1	1.2	1.2	1.2	ns	Cytoplasm, cytosol {ECO	66	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.1	1.0	1.1	1.4	1.1	1.2	ns	Mitochondrion {ECO	317	Yes	Yes	Yes	No	No	Yes	66.7
1.2	1.1	1.2	1.3	1.1	1.2	ns	Cytoplasm. Melanosome. Cell membrane.	374	Yes	Yes	Yes	No	Yes	Yes	83.3
1.3	0.4	1.4	1.4	1.3	1.2	ns	Cytoplasm {ECO	70	Yes	Yes	No	--	--	No	50.0
1.2	1.1	1.2	1.2	1.2	1.2	ns	Nucleus. Cytoplasm.	109	Yes	Yes	Yes	No	Yes	Yes	83.3
1.2	1.4	1.1	1.0	1.1	1.2	ns	Cytoplasm. Nucleus. Cytoplasm. Cytoplasm. Nucleus.	376	Yes	Yes	No	--	--	No	50.0

416	Q16854	DGUOK Deoxyguanosine kinase, mitochondrial	DGUOK	AC*TAQSLGNLLDMMYR	1.0	1.2	1.1
417	P28838	LAP3 Cytosol aminopeptidase	LAP3	SAGAC*TAAAFLK	0.9	1.0	1.0
418	P37802	TAGLN2 Transgelin-2	TAGLN2	QYDADLEQILIQWITTQC*R	1.0	1.0	1.0
419	P07741	APRT Adenine phosphoribosyltransferase	APRT	VVVVDDLLATGGTMNAAC*ELLGR	1.1	1.1	1.1
420	Q86SX6	GLRX5 Glutaredoxin-related protein 5, mitochondrial	GLRX5	GTPEQPQC*GFSNAVVQILR	1.0	1.0	1.0
421	O60547	GMDS GDP-mannose 4,6 dehydratase	GMDS	PTEVDFLQGDC*TK	0.9	1.0	0.9
422	P53990	IST1 IST1 homolog	IST1	IVADQLC*AK	1.0	1.0	1.0
423	Q5MNZ6	WDR45L WD repeat domain phosphoinositide-interacting protein 3	WDR45L	C*NYLALVGGGK	1.0	1.0	1.0
424	Q9BV79	MECR Trans-2-enoyl-CoA reductase, mitochondrial	MECR	LALNC*VGGK	1.0	0.9	1.0
425	O75940	SMNDC1 Survival of motor neuron-related-splicing factor 3	SMNDC1	VGVGTC*GIADK	0.9	1.0	1.0
426	Q9H0C8	ILKAP Integrin-linked kinase-associated serine/threonine phosphatase 2C	ILKAP	FILLAC*DGLFK	0.9	1.0	0.9
427	P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	GFGFVC*FSSPEEATK	1.0	1.2	1.1
428	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	IAAYLQSDQFC*K	0.9	1.0	0.9
429	P78347	GTF2I General transcription factor II-I	GTF2I	SILSPGGSC*GPIK	0.9	0.9	0.9
430	P53602	MVD Diphosphomevalonate decarboxylase	MVD	DGDPLPSSLSC*K	1.0	1.3	1.1
431	P26641	EEF1G Elongation factor 1-gamma	EEF1G	AAAPAPEEEMDEC*EQALAAEPK	1.0	1.0	1.0
432	P49915	GMPS GMP synthase	GMPS	TVGVQGDC*R	0.5	1.1	0.8
433	P21964	COMT Catechol O-methyltransferase	COMT	IVDAVIQEHQPSVLLELGAYC*GYSAVR	0.9	1.0	1.0
434	P53396	ACLY ATP-citrate synthase	ACLY	FIC*TTSAIQNR	0.9	1.0	0.9
435	Q9UI30	TRMT112 tRNA methyltransferase 112 homolog	TRMT112	IC*PVEFNPNFVAR	1.0	1.0	1.0
436	Q9UNH7	SNX6 Sorting nexin-6	SNX6	IGSSLYALGTQDSTDIC*K	0.9	0.9	0.9
437	P49841	GSK3B Glycogen synthase kinase-3 beta	GSK3B	LC*DFGSAK	1.0	1.0	1.0
438	Q5TFE4	NT5DC1 5-nucleotidase domain-containing protein 1	NT5DC1	HFLSDTGMAC*R	1.0	1.1	1.0
439	Q9Y224	C14orf166 UPF0568 protein C14orf166	C14orf166	LTALDYHNPAGFNC*K	1.0	1.0	1.0
440	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	QEPLGSDSEGVNC*LAYDEAIMAQQDR	1.0	1.0	1.0
441	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	INISEGNC*PER	1.0	1.0	1.0
442	Q99873	PRMT1 Protein arginine N-methyltransferase 1	PRMT1	VIGIEC*SSISDYAVK	0.9	1.0	0.9
443	Q15181	PPA1 Inorganic pyrophosphatase	PPA1	GISC*MNTTLSESPFK	1.0	1.3	1.2
444	P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	AC*QIFVR	1.0	1.0	1.0
445	P00338	LDHA L-lactate dehydrogenase A chain	LDHA	VIGSGC*NLDSAR	1.0	1.0	1.0
446	Q14151	SAFB2 Scaffold attachment factor B2	SAFB2	ILDILGETC*K	1.0	0.7	0.8
447	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	GLLDVTC*K	1.0	0.9	1.0
448	Q9Y2Q3	GSTK1 Glutathione S-transferase kappa 1	GSTK1	ETTEAAC*R	1.0	1.0	1.0

1.1	1.0	1.1	1.4	1.2	1.2	ns	Mitochondrion.	87	Yes	No	No	--	No	--	25.0
1.1	0.9	1.2	1.4	1.1	1.2	ns	Cytoplasm.	462	Yes	Yes	Yes	--	No	No	60.0
0.8	1.8	1.2	1.0	0.9	1.2	ns		38	Yes	Yes	No	No	--	Yes	60.0
1.0	1.3	1.1	1.2	1.1	1.1	ns	Cytoplasm.	140	Yes	Yes	No	No	No	No	33.3
1.2	1.1	1.1	1.2	1.2	1.1	ns	Mitochondrion matrix {ECO	67	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.2	1.1	1.1	1.3	1.1	1.1	ns		336	Yes	Yes	No	--	No	No	40.0
1.1	1.1	1.3	1.2	1.0	1.1	ns	Cytoplasmic vesicle {ECO	125	Yes	Yes	No	No	No	No	33.3
1.1	1.2	1.0	1.1	1.2	1.1	ns		63	Yes	Yes	Yes	No	Yes	No	66.7
1.3	1.0	1.0	1.1	1.3	1.1	ns	Mitochondrion {ECO Cytoplasm {ECO	263	Yes	Yes	Yes	No	Yes	Yes	83.3
1.0	1.4	1.0	1.2	1.1	1.1	ns	Nucleus speckle. Nucleus, Cajal body.	214	Yes	Yes	Yes	--	No	--	75.0
1.0	1.1	1.4	1.2	0.9	1.1	ns	Cytoplasm {ECO	325	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.0	1.2	1.3	1.2	1.0	1.1	ns	Cytoplasm. Nucleus.	339	Yes	Yes	Yes	Yes	No	Yes	83.3
1.2	1.1	1.1	1.2	1.2	1.1	ns	Cytoplasm.	208	Yes	No	--	--	--	No	33.3
1.1	1.0	1.1	1.2	1.2	1.1	ns	Cytoplasm {ECO	215	Yes	Yes	--	--	--	--	100.0
1.1	1.1	1.1	1.2	1.1	1.1	ns		108	Yes	No	No	No	No	No	16.7
1.1	1.1	1.2	1.1	1.1	1.1	ns		266	Yes	Yes	No	No	No	No	33.3
1.3	0.7	1.1	1.3	1.4	1.1	ns	Cytoplasm.	523	Yes	Yes	No	No	No	No	33.3
1.1	1.1	1.2	1.1	1.2	1.1	ns	Cytoplasm. Cell membrane; Single-pass type II membrane protein; Extracellular side {ECO	119	Yes	Yes	--	--	No	--	66.7
1.3	1.0	1.0	1.2	1.2	1.1	ns	Cytoplasm.	20	Yes	Yes	No	--	--	No	50.0
0.9	1.2	1.2	1.2	1.2	1.1	ns		33	Yes	No	No	No	No	No	16.7
1.1	1.0	1.1	1.2	1.2	1.1	ns	Early endosome {ECO	264	Yes	Yes	No	--	No	No	40.0
1.0	1.2	1.0	1.2	1.2	1.1	ns	Cytoplasm. Nucleus. Cell membrane.	199	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.1	1.2	1.0	1.2	1.1	1.1	ns		119	Yes	Yes	No	--	No	No	40.0
1.1	1.1	1.1	1.2	1.1	1.1	ns	Nucleus. Cytoplasm, cytosol. Cytoplasm, perinuclear region. Cytoplasm, cytoskeleton, microtubule organizing center, centrosome.	19	Yes	Yes	--	--	--	No	66.7
1.1	1.1	1.2	1.1	1.1	1.1	ns	Cytoplasm {ECO	23	Yes	Yes	--	--	Yes	No	75.0
1.1	1.1	1.1	1.2	1.1	1.1	ns	Cytoplasm {ECO	86	Yes	Yes	Yes	No	No	Yes	66.7
1.1	1.1	1.0	1.2	1.2	1.1	ns	Nucleus {ECO	109	Yes	Yes	Yes	No	Yes	No	66.7
1.2	1.0	1.2	1.1	1.1	1.1	ns	Cytoplasm {ECO	242	Yes	Yes	No	No	--	No	40.0
1.2	1.1	1.1	1.0	1.2	1.1	ns	Nucleus, nucleolus {ECO	653	Yes	Yes	--	--	--	--	100.0
1.1	1.1	1.2	1.1	1.1	1.1	ns	Cytoplasm.	163	Yes	Yes	No	No	No	No	33.3
0.9	1.3	1.2	1.2	0.9	1.1	ns	Cytoplasm. Nucleus.	224	Yes	Yes	--	--	--	--	100.0
1.1	1.1	1.1	1.1	1.1	1.1	ns		120	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.1	1.1	1.2	1.1	1.1	1.1	ns	Peroxisome {ECO	176	Yes	Yes	--	--	--	No	66.7

449	P53041	PPP5C Serine/threonine-protein phosphatase 5	PPP5C	TEC*AEPPR	0.9	1.0	1.0
450	P36969	GPX4 Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	GPX4	YAEC*GLR	1.0	0.9	0.9
451	Q86YH6	PDSS2 Decaprenyl-diphosphate synthase subunit 2	PDSS2	C*LLSDELSNIAMQVR	0.8	1.0	0.9
452	Q9NYL2	MLTK Mitogen-activated protein kinase kinase kinase MLT	MLTK	IC*DFGASR	0.8	0.8	0.8
453	P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	IHDVLC*K	1.0	1.2	1.1
454	Q96HE7	ERO1L ERO1-like protein alpha	ERO1L	HDDSSDNFC*EADDIQSPEAEYVDLLLNPER	0.9	1.1	1.0
455	P60981	DSTN Destrin	DSTN	C*STPEEIK	1.0	1.0	1.0
456	P29401	TKT Transketolase	TKT	MAAISESNINLCGSHC*GVSIGEDGPSQMALEDLAMFR	1.1	1.0	1.1
457	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	LVVPASQC*GSLIGK	0.9	1.0	0.9
458	Q15149	PLEC Plectin	PLEC	AFC*GFEDPR	1.0	1.0	1.0
459	Q8WTW3	COG1 Conserved oligomeric Golgi complex subunit 1	COG1	C*AVGLVDAVK	0.9	1.2	1.1
460	P62258	YWHAE 14-3-3 protein epsilon	YWHAE	LIC*C*DILDVLDK	1.0	1.0	1.0
461	Q969T9	WBP2 WW domain-binding protein 2	WBP2	DC*EIK	0.9	0.9	0.9
462	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK	0.9	1.0	1.0
463	Q14247	CTTN Src substrate cortactin	CTTN	C*ALGWDHQEK	1.0	0.9	0.9
464	Q8TB45	DEPTOR DEP domain-containing mTOR-interacting protein	DEPTOR	SPSSQETHDSPFC*LR	0.7	1.0	0.9
465	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	LDFVC*SFLQK	1.0	0.8	0.9
466	Q9H773	DCTPP1 dCTP pyrophosphatase 1	DCTPP1	YTELPHGAISEDQAVGPADIPC*DSTGQTST	1.2	1.0	1.1
467	Q9BY32	ITPA Inosine triphosphate pyrophosphatase	ITPA	GC*QDFGWDPCFQPDGYEQTYAEMPK	1.0	1.0	1.0
468	P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	YLEC*SALTQR	1.0	1.1	1.0
469	P62826	RAN GTP-binding nuclear protein Ran	RAN	VC*ENIPIVLC*GNK	0.9	1.0	1.0
470	Q9BW61	DDA1 DET1- and DDB1-associated protein 1	DDA1	FHADSVC*K	1.0	1.2	1.1
471	P36507	MAP2K2 Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	LC*DFGVSGQLIDSMANSFVGTR	1.1	1.0	1.1
472	P49458	SRP9 Signal recognition particle 9 kDa protein	SRP9	VTDDLVC*LVYK	0.8	0.9	0.8
473	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	GQAGGGGPGTGPGLGEAGSLATC*ELPLAK	1.1	1.0	1.0
474	P55786	NPEPPS Puromycin-sensitive aminopeptidase	NPEPPS	DGVC*VR	0.9	0.8	0.9
475	P50990	CCT8 T-complex protein 1 subunit theta	CCT8	IAVYSC*PFDGMITETK	1.1	0.9	1.0
476	Q09666	AHNAK Neuroblast differentiation-associated protein AHNAK	AHNAK	GPFVEAEVPDVDLEC*PDAK	0.9	1.0	1.0
477	P51659	HSD17B4 Peroxisomal multifunctional enzyme type 2	HSD17B4	IC*DFENASK	1.1	1.1	1.1
478	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	AITIAGVPQSVTEC*VK	1.0	1.0	1.0
479	P62857	RPS28 40S ribosomal protein S28	RPS28	TGSQGQC*TQVR	0.9	0.9	0.9
480	Q8N987	NECAB1 N-terminal EF-hand calcium-binding protein 1	NECAB1	ETLNQLQSLQNSLEC*AMETTEEQTR	1.0	0.9	0.9
481	P37802	TAGLN2 Transgelin-2	TAGLN2	NMAC*VQR	1.0	1.0	1.0

1.0	0.8	1.2	1.3	1.1	1.1	ns	Nucleus {ECO	11	Yes	Yes	--	--	--	--	100.0
1.1	1.0	1.1	1.2	1.2	1.1	ns	Mitochondrion. Cytoplasm.	93	Yes	Yes	No	No	No	No	33.3
0.7	1.1	1.2	1.3	1.2	1.1	ns	Mitochondrion {ECO	71	Yes	Yes	No	--	--	--	66.7
1.0	1.2	0.9	1.2	1.2	1.1	ns	Cytoplasm {ECO	150	Yes	Yes	No	No	Yes	Yes	66.7
1.1	0.9	1.1	0.9	1.5	1.1	ns	Mitochondrion. Nucleus, nucleoplasm. Nucleus inner membrane. Nucleus outer membrane.	863	Yes	Yes	--	--	--	--	100.0
1.0	1.2	1.0	1.2	1.2	1.1	ns	Endoplasmic reticulum membrane {ECO	166	Yes	Yes	Yes	Yes	No	Yes	83.3
1.1	1.0	1.1	1.2	1.1	1.1	ns		23	Yes	Yes	No	No	No	No	33.3
1.0	1.1	1.1	1.2	1.2	1.1	ns		417	Yes	Yes	Yes	No	No	No	50.0
1.1	1.1	1.1	1.2	1.1	1.1	ns	Cytoplasm {ECO	141	Yes	Yes	Yes	No	Yes	Yes	83.3
1.1	1.1	1.0	1.2	1.1	1.1	ns	Cytoplasm, cytoskeleton {ECO	4494	Yes	Yes	--	--	--	--	100.0
1.1	1.0	1.0	1.4	1.0	1.1	ns	Golgi apparatus membrane {ECO	72	Yes	Yes	No	--	No	--	50.0
1.2	1.0	1.1	1.1	1.1	1.1	ns	Cytoplasm {ECO	97	Yes	Yes	Yes	No	Yes	Yes	83.3
								98	Yes	Yes	No	No	No	No	33.3
1.0	1.1	1.2	1.1	1.1	1.1	ns		80	Yes	Yes	No	--	--	No	50.0
1.1	1.0	1.0	1.1	1.1	1.1	ns	Cytoplasm {ECO	132	Yes	Yes	No	No	No	No	33.3
1.1	1.1	1.1	1.1	1.1	1.1	ns	Cytoplasm, cytoskeleton {ECO	246	Yes	Yes	No	--	--	--	66.7
1.0	1.2	1.2	1.0	1.0	1.1	ns		247	Yes	Yes	--	No	--	--	66.7
1.2	1.1	1.0	1.1	1.1	1.1	ns	Nucleus matrix {ECO Cytoplasm, cytosol {ECO Cytoplasm, cytosol {ECO	65	Yes	Yes	--	--	--	--	100.0
1.1	1.1	1.1	1.1	1.1	1.1	ns	Cytoplasm {ECO	162	Yes	No	--	--	--	--	50.0
1.3	1.0	0.9	1.2	1.1	1.1	ns	Cytoplasm {ECO	146	Yes	No	No	No	No	No	16.7
0.8	1.8	1.0	0.9	0.9	1.1	ns	Cytoplasm.	157	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.1	1.0	1.2	1.0	1.1	1.1	ns	Nucleus. Cytoplasm. Melanosome. Nucleus envelope {ECO	112/120	Yes	Yes	Yes	Yes	Yes	Yes	100.0
1.0	1.2	1.0	1.0	1.1	1.1	ns		25	Yes	Yes	No	--	No	--	50.0
1.1	1.0	1.0	1.1	1.2	1.1	ns	Cytoplasm {ECO	211	Yes	Yes	Yes	Yes	No	Yes	83.3
1.1	1.0	1.1	1.1	1.1	1.1	ns	Cytoplasm.	48	Yes	Yes	Yes	--	Yes	Yes	100.0
1.1	1.0	0.9	1.2	1.1	1.1	ns	Mitochondrion {ECO	45	Yes	No	--	--	--	--	50.0
1.2	0.9	1.2	1.1	1.0	1.1	ns	Cytoplasm, cytosol {ECO	265	Yes	Yes	No	No	No	No	33.3
1.1	1.0	1.0	1.2	1.1	1.1	ns	Cytoplasm {ECO	244	Yes	Yes	Yes	Yes	No	Yes	83.3
1.0	1.1	1.1	1.1	1.0	1.1	ns	Nucleus.	1833	Yes	No	--	--	--	--	50.0
0.9	1.0	1.3	1.1	1.1	1.1	ns	Peroxisome.	277	Yes	Yes	No	No	--	No	40.0
1.0	1.2	1.1	0.9	1.1	1.1	ns	Nucleus. Cytoplasm.	158	Yes	Yes	Yes	No	No	Yes	66.7
1.0	1.1	1.1	1.1	1.1	1.1	ns		27	Yes	Yes	Yes	No	No	Yes	66.7
1.1	0.9	1.0	1.2	1.2	1.1	ns	Cytoplasm {ECO	152	Yes	Yes	--	--	--	--	100.0
1.3	1.0	0.9	1.0	1.1	1.1	ns		124	Yes	Yes	No	No	--	No	40.0

482	Q9NZZ3	CHMP5 Charged multivesicular body protein 5	CHMP5	APPPSLTDC*IGTVDSR	1.0	0.9	0.9
483	P30153	PPP2R1A Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	LNIISNLDC*VNEVIGIR	0.8	1.0	0.9
484	P55735	SEC13 Protein SEC13 homolog	SEC13	FASGGC*DNLIK	1.0	1.0	1.0
485	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	EEFASTC*PDDEEIELAYEQVAK	1.3	1.3	1.3
486	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	FIC*EQDHQNFLR	1.1	1.2	1.1
487	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	LNEC*VDHTPK	1.0	0.9	1.0
488	Q96Q11	TRNT1 CCA tRNA nucleotidyltransferase 1, mitochondrial	TRNT1	YQGEHC*LLK	0.9	0.9	0.9
489	P13639	EEF2 Elongation factor 2	EEF2	YVEPIEDVPC*GNIVGLVGVDQFLVK	1.0	1.0	1.0
490	P35270	SPR Sepiapterin reductase	SPR	TVVNISSLC*ALQPFK	0.9	0.8	0.9
491	P60981	DSTN Destrin	DSTN	LGGSLIVAFEGC*PV	0.9	0.9	0.9
492	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	YTC*GEAPDYDR	0.9	0.9	0.9
493	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	LVSSPC*C*IVTSTYGWTANMER	0.8	1.0	0.9
494	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	LEVDAIVNAANSSLLGGGGVDGC*IHR	0.9	1.0	1.0
495	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	FC*PFAER	1.0	1.0	1.0
496	P31947	SFN 14-3-3 protein sigma	SFN	GEELSC*EER	0.9	0.9	0.9
497	P52943	CRIP2 Cysteine-rich protein 2	CRIP2	ASSVTTFTGEPNTC*PR	1.0	0.9	0.9
498	Q6KB66	KRT80 Keratin, type II cytoskeletal 80	KRT80	C*HIDLSGIVEEVK	0.9	1.0	1.0
499	P52597	HNRNPF Heterogeneous nuclear ribonucleoprotein F	HNRNPF	GLPFGC*TK	1.0	0.9	0.9
500	Q9Y5P6	GMPPB Mannose-1-phosphate guanyltransferase beta	GMPPB	LC*SGPGIVGNVLVDPSAR	0.9	1.1	1.0
501	Q14247	CTTN Src substrate cortactin	CTTN	HC*SQVDSVR	0.9	0.9	0.9
502	P13639	EEF2 Elongation factor 2	EEF2	TFC*QLILDPIFK	0.8	0.9	0.9
503	P33316	DUT Deoxyuridine 5-triphosphate nucleotidohydrolase, mitochondrial	DUT	TDIQIALPSGC*YGR	1.0	1.0	1.0
504	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	YLAEVAC*GDDR	0.9	1.0	0.9
505	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	C*LSVMEAK	0.9	0.9	0.9
506	Q9Y365	STARD10 PCTP-like protein	STARD10	MEC*C*DVPAETLYDVLHDIEYR	1.0	1.1	1.1
507	P23434	GCSH Glycine cleavage system H protein, mitochondrial	GCSH	SC*YEDGWLIK	1.3	0.8	1.1
508	Q01518	CAP1 Adenylyl cyclase-associated protein 1	CAP1	ALLVTASQC*QQPAENK	0.9	1.0	1.0
509	P13639	EEF2 Elongation factor 2	EEF2	C*LYASVLTAQPR	1.0	0.8	0.9
510	O95671	ASMTL N-acetylserotonin O-methyltransferase-like protein	ASMTL	LTAC*QVATAFNLSR	1.0	1.1	1.0
511	O00204	SULT2B1 Sulfotransferase family cytosolic 2B member 1	SULT2B1	APWC*ETIVGAFSLPDQYSPR	0.9	1.0	1.0

1.0	1.1	1.1	1.1	1.0	1.1	ns	Cytoplasm, cytosol. Endosome membrane {ECO	20	Yes	Yes	Yes	No	No	No	50.0
1.0	1.1	0.9	1.2	1.1	1.1	ns	Cytoplasm {ECO	390	Yes	Yes	Yes	No	No	No	50.0
1.1	1.0	1.0	1.1	1.1	1.1	ns	Cytoplasmic vesicle, COPII-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Endoplasmic reticulum membrane; Peripheral membrane protein; Cytoplasmic side. Nucleus, nuclear pore complex.	187	Yes	Yes	Yes	No	Yes	No	66.7
0.9	1.0	1.3	1.1	1.1	1.1	ns	Nucleus. Nucleus membrane {ECO	223	Yes	Yes	Yes	--	No	Yes	80.0
0.8	1.0	1.1	1.2	1.2	1.1	ns	Cytoplasm {ECO	658	Yes	Yes	--	No	No	No	40.0
1.0	1.3	1.0	1.0	1.0	1.1	ns	Cytoplasm, cytosol {ECO	192	Yes	Yes	No	No	--	No	40.0
1.3	1.0	1.1	1.1	0.9	1.1	ns	Mitochondrion {ECO	373	Yes	No	No	--	--	No	25.0
0.9	1.1	1.1	0.9	1.1	1.0	ns	Cytoplasm. Nucleus {ECO	466	Yes	Yes	No	No	Yes	No	50.0
1.1	1.0	1.1	1.0	1.1	1.0	ns	Cytoplasm.	159	Yes	Yes	No	No	No	No	33.3
1.1	1.0	1.0	1.1	1.0	1.0	ns		163	Yes	No	--	--	--	--	50.0
1.0	1.0	1.2	1.1	0.9	1.0	ns	Cytoplasm.	39	Yes	Yes	No	--	--	No	50.0
1.2	1.1	0.9	1.0	1.0	1.0	ns	Cytoplasm. Melanosome.	589	Yes	Yes	Yes	No	Yes	Yes	83.3
								590	Yes	Yes	Yes	No	Yes	Yes	83.3
1.1	1.0	1.0	1.0	1.2	1.0	ns	Nucleus {ECO	186	Yes	Yes	No	--	No	No	40.0
1.1	1.0	1.1	1.1	1.1	1.0	ns	Cytoplasm, cytosol {ECO	32	Yes	Yes	Yes	No	No	Yes	66.7
1.0	1.1	1.1	1.1	1.0	1.0	ns	Cytoplasm. Nucleus {ECO	38	Yes	Yes	No	No	No	No	33.3
1.1	0.9	1.1	1.2	1.0	1.0	ns		126	Yes	Yes	Yes	--	Yes	Yes	100.0
1.0	1.0	1.0	1.1	1.1	1.0	ns		244	Yes	Yes	No	--	--	No	50.0
1.0	1.1	1.1	1.0	1.0	1.0	ns	Nucleus, nucleoplasm.	122	Yes	Yes	No	--	No	Yes	60.0
1.0	1.0	1.0	1.0	1.1	1.0	ns	Cytoplasm {ECO	245	Yes	No	No	No	No	No	16.7
1.1	0.9	1.1	1.1	1.0	1.0	ns	Cytoplasm, cytoskeleton {ECO	112	Yes	Yes	No	--	--	--	66.7
1.0	1.1	1.0	1.1	1.0	1.0	ns	Cytoplasm. Nucleus {ECO	290	Yes	Yes	Yes	No	No	Yes	66.7
1.0	1.4	0.9	0.9	1.0	1.0	ns	Nucleus {ECO Mitochondrion {ECO	166	Yes	Yes	No	No	No	No	33.3
0.9	1.1	1.1	1.0	1.1	1.0	ns	Cytoplasm.	134	Yes	Yes	No	No	No	No	33.3
1.2	1.0	0.9	1.0	1.1	1.0	ns	Cytoplasm {ECO	773	Yes	No	No	No	No	No	16.7
1.0	1.0	1.1	1.0	1.0	1.0	ns	Cell projection, cilium, flagellum {ECO	74/75	Yes	Yes	No	--	No	No	40.0
0.9	1.2	0.6	1.0	1.4	1.0	ns	Mitochondrion.	138	Yes	Yes	Yes	No	No	No	50.0
0.9	1.1	1.0	0.9	1.2	1.0	ns	Cell membrane {ECO	93	Yes	Yes	No	No	No	No	33.3
1.1	1.2	1.2	1.0	0.8	1.0	ns	Cytoplasm. Nucleus {ECO	728	Yes	Yes	Yes	No	No	No	50.0
1.1	0.9	1.0	1.0	1.0	1.0	ns		441	Yes	No	--	--	No	--	33.3
1.3	1.0	1.1	0.8	0.9	1.0	ns	Cytoplasm. Microsome. Nucleus.	104	Yes	Yes	No	--	No	No	40.0

512	P51610	HCFC1 Host cell factor 1	HCFC1	LVIYGGMSGC*R	0.9	0.9	0.9
513	P47756	CAPZB F-actin-capping protein subunit beta	CAPZB	DETVSDC*SPHIANIGR	1.1	1.0	1.0
514	Q12765	SCRN1 Secernin-1	SCRN1	TQSPC*FGDDDPAK	0.9	1.0	1.0
515	Q8TAQ2	SMARCC2 SWI/SNF complex subunit SMARCC2	SMARCC2	NLAGDVC*AIMR	1.2	1.1	1.2
516	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	ISSINSISALC*EATGADVEEVATAIGMDQR	1.0	1.0	1.0
517	P00492	HPRT1 Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	SYC*NDQSTGDIK	1.0	0.8	0.9
518	P30086	PEBP1 Phosphatidylethanolamine-binding protein 1	PEBP1	APVAGTC*YQAEWDDYVPK	1.0	1.1	1.0
519	P35270	SPR Sepiapterin reductase	SPR	AVC*LLTGASR	1.0	1.0	1.0
520	Q96EY8	MMAB Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	MMAB	IQCTLQDVGSALATPC*SSAR	0.9	1.1	1.0
521	O75131	CPNE3 Copine-3	CPNE3	NC*LNPQFSK	0.9	1.0	1.0
522	Q9HAV7	GRPEL1 GrpE protein homolog 1, mitochondrial	GRPEL1	LYGIQAFC*K	1.0	0.8	0.9
523	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	IVDTPC*NEMNTDTFLEEINK	0.9	1.1	1.0
524	Q9H8M7	FAM188A Protein FAM188A	FAM188A	SSPGLSDTIFC*R	1.5	0.9	1.2
525	P26599	PTBP1 Polypyrimidine tract-binding protein 1	PTBP1	LSLDGQNIYNAC*C*TLR	0.9	1.1	1.0
526	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	NVGC*LQEALQLATSFAQLR	1.1	1.1	1.1
527	P14649	MYL6B Myosin light chain 6B	MYL6B	ILYSQC*GDVMR	1.0	0.9	1.0
528	P21964	COMT Catechol O-methyltransferase	COMT	LITIEINPDC*AAITQR	0.9	0.9	0.9
529	P30626	SRI Sorcin	SRI	DTAQQGVVNFPYDDFIQC*VMSV	1.0	0.9	0.9
530	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	ILSC*GEVIHVK	1.0	1.5	1.2
531	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	C*LDEFPNLK	1.0	1.1	1.1
532	P49753	ACOT2 Acyl-coenzyme A thioesterase 2, mitochondrial	ACOT2	SEFYANEAC*K	1.0	1.0	1.0
533	P12004	PCNA Proliferating cell nuclear antigen	PCNA	C*AGNEDIITLR	1.2	0.9	1.1
534	Q9NRF9	POLE3 DNA polymerase epsilon subunit 3	POLE3	AASVFVLYATSC*ANNFAMK	0.9	1.1	1.0
535	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	GDFC*IQVGR	1.0	0.9	0.9
536	Q7LG56	RRM2B Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	IEQEFLTEALPVGLIGMNC*ILMK	0.8	1.1	1.0
537	Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	AITIAGIPQSIIEC*VK	1.1	1.0	1.1
538	Q9BSH4	TACO1 Translational activator of cytochrome c oxidase 1	TACO1	LDSLGLCSVSC*ALEFIPNSK	0.8	1.1	1.0
539	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	NDTPC*GTTIGPILASR	1.0	1.0	1.0
540	Q96EY5	FAM125A Multivesicular body subunit 12A	FAM125A	GFSAISC*TVEGAPASFGK	0.9	1.0	0.9
541	P63167	DYNLL1 Dynein light chain 1, cytoplasmic	DYNLL1	NADMSEEMQQDSVEC*ATQALEK	1.0	0.9	0.9
542	Q96AT9	RPE Ribulose-phosphate 3-epimerase	RPE	IGPSILNSDLANLGAEC*LR	1.0	1.0	1.0
543	P51858	HDGF Hepatoma-derived growth factor	HDGF	C*GDLVFAK	1.0	1.0	1.0

1.1	1.0	1.2	1.0	0.9	1.0	ns	Cytoplasm. Nucleus.	227	Yes	Yes	Yes	No	No	No	50.0
1.0	1.0	1.2	1.0	0.9	1.0	ns	Cytoplasm, cytoskeleton {ECO	206	Yes	Yes	No	No	No	No	33.3
1.1	0.9	1.0	1.0	1.2	1.0	ns	Cytoplasm {ECO	324	Yes	Yes	No	--	--	--	66.7
1.0	0.9	1.0	1.1	1.0	1.0	ns	Nucleus.	495	Yes	Yes	Yes	No	No	Yes	66.7
1.0	1.1	1.0	0.9	1.1	1.0	ns		241	Yes	Yes	Yes	--	Yes	Yes	100.0
1.0	1.1	0.9	1.0	1.0	1.0	ns	Cytoplasm.	106	Yes	Yes	--	--	No	No	50.0
0.9	1.1	1.1	1.0	1.1	1.0	ns	Cytoplasm {ECO	168	Yes	Yes	No	--	No	No	40.0
1.0	1.1	1.1	0.9	0.9	1.0	ns	Cytoplasm.	10	Yes	Yes	No	No	No	--	40.0
1.1	0.9	0.9	1.1	1.1	1.0	ns	Mitochondrion {ECO	132	Yes	No	--	--	--	No	33.3
1.0	1.0	1.0	1.0	1.0	1.0	ns	Nucleus {ECO	54	Yes	No	No	--	No	No	20.0
0.8	1.0	1.1	1.0	1.1	1.0	ns	Mitochondrion matrix.	108	Yes	Yes	Yes	No	No	Yes	66.7
1.1	1.0	0.9	1.0	1.0	1.0	ns		189	Yes	Yes	Yes	--	No	No	60.0
0.5	1.2	1.0	1.0	1.4	1.0	ns	Nucleus {ECO	27	Yes	Yes	No	--	No	--	50.0
1.0	0.7	1.2	1.0	1.1	1.0	ns	Nucleus.	250/251	Yes	Yes	Yes	--	Yes	Yes	100.0
0.9	0.9	0.6	1.6	1.0	1.0	ns	Cytoplasm {ECO	947	Yes	Yes	No	--	No	No	40.0
0.9	1.0	1.1	1.0	1.0	1.0	ns		89	Yes	Yes	No	No	No	No	33.3
1.1	1.0	0.9	1.0	1.0	1.0	ns	Cytoplasm. Cell membrane; Single-pass type II membrane protein; Extracellular side {ECO	145	Yes	No	--	--	No	--	33.3
1.2	0.9	1.0	0.8	1.0	1.0	ns	Cytoplasm. Sarcoplasmic reticulum membrane; Peripheral membrane protein; Cytoplasmic side.	194	Yes	Yes	No	No	No	No	33.3
0.9	1.0	0.8	1.2	1.1	1.0	ns	Mitochondrion {ECO	180	Yes	No	No	No	No	No	16.7
0.9	1.0	1.1	1.0	1.0	1.0	ns	Cytoplasm.	178	Yes	Yes	No	--	--	No	50.0
1.0	1.0	0.8	0.9	1.2	1.0	ns	Mitochondrion {ECO	401	Yes	No	--	--	--	No	33.3
0.9	1.0	1.0	1.0	1.0	1.0	ns	Nucleus {ECO	81	Yes	Yes	Yes	Yes	Yes	Yes	100.0
0.9	0.9	1.0	1.1	0.9	1.0	ns	Nucleus {ECO	51	Yes	Yes	No	No	No	No	33.3
1.1	1.1	0.9	0.9	0.9	1.0	ns		94	Yes	Yes	Yes	No	No	Yes	66.7
1.0	1.1	1.0	1.1	0.7	1.0	ns	Cytoplasm. Nucleus.	279	Yes	Yes	Yes	No	No	Yes	66.7
1.0	1.1	1.0	0.9	1.0	1.0	ns	Nucleus {ECO	158	Yes	Yes	Yes	No	No	Yes	66.7
0.7	1.0	1.0	1.1	1.0	1.0	ns	Mitochondrion {ECO	256	Yes	Yes	No	No	No	No	33.3
0.9	0.9	1.0	1.0	0.9	1.0	ns	Cytoplasm {ECO	413	Yes	Yes	--	Yes	Yes	Yes	100.0
0.9	1.0	0.9	1.0	0.9	1.0	ns	Cytoplasm. Nucleus. Endosome. Cytoplasm, cytoskeleton, microtubule organizing center, centrosome. Late endosome membrane {ECO	33	Yes	Yes	No	--	--	Yes	75.0
0.9	1.0	0.9	0.9	1.0	1.0	ns	Cytoplasm, cytoskeleton.	24	Yes	Yes	Yes	No	No	Yes	66.7
0.8	1.0	1.4	0.8	0.9	1.0	ns		23	Yes	Yes	No	Yes	No	Yes	66.7
0.8	1.1	1.0	1.1	0.9	1.0	ns	Cytoplasm. Nucleus.	12	Yes	Yes	No	--	No	No	40.0

544	O43681	ASNA1 ATPase ASNA1	ASNA1	PC*K	1.0	1.2	1.1
545	P18669	PGAM1 Phosphoglycerate mutase 1	PGAM1	YADLTEDQLPSC*ESLK	0.9	0.9	0.9
546	Q04917	YWHAH 14-3-3 protein eta	YWHAH	NC*NDFQYESK	1.1	1.0	1.0
547	P11766	ADH5 Alcohol dehydrogenase class-3	ADH5	VC*LLGC*GISTGYGAAVN TAK	1.1	0.9	1.0
548	P40925	MDH1 Malate dehydrogenase, cytoplasmic	MDH1	AIC*DHVR	1.0	1.0	1.0
549	P08107	HSPA1B Heat shock 70 kDa protein 1A/1B	HSPA1B	FEELC*SDLFR	1.4	1.1	1.2
550	P61981	YWHAG 14-3-3 protein gamma	YWHAG	NC*SETQYESK	0.6	0.5	0.6
551	P30626	SRI Sorcin	SRI	PFNLETC*R	0.9	0.8	0.9
552	P62993	GRB2 Growth factor receptor-bound protein 2	GRB2	VLNEEC*DQNWYK	1.0	1.0	1.0
553	P23528	CFL1 Cofilin-1	CFL1	AVLFC*LSEDK	1.0	1.0	1.0
554	P52209	PGD 6-phosphogluconate dehydrogenase, decarboxylating	PGD	C*LSSLK	0.9	1.0	1.0
555	P10768	ESD S-formylglutathione hydrolase	ESD	CPALYWLSGLTC*TEQNFIS K	1.2	1.0	1.1
556	Q1KMD 3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL 2	LQEALDAEMLEDEAGGGG AGPGGAC*K	1.1	1.1	1.1
557	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	YLLQYQEPIPC*EQLVTALC *DIK	1.1	1.1	1.1
558	P31947	SFN 14-3-3 protein sigma	SFN	VETELQGVC*DTVLGLLDS HLIK	1.2	0.9	1.1
559	O14964	HGS Hepatocyte growth factor-regulated tyrosine kinase	HGS	AC*GQIFC*GK	0.8	0.8	0.8
560	P60174	TPI1 Triosephosphate isomerase	TPI1	IIYGGSVTGATC*K	1.1	1.0	1.1
561	P37802	TAGLN2 Transgelin-2	TAGLN2	DGTVLC*ELINALYPEGQA PVK	1.1	1.0	1.0
562	P21291	CSRP1 Cysteine and glycine-rich protein 1	CSRP1	SC*FLC*MVC*K	1.0	1.0	1.0
563	Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	GNGIVEC*LGPK	1.0	1.0	1.0
564	P22234	PAICS Multifunctional protein ADE2	PAICS	ITSC*IFQLLQEAGIK	1.0	1.0	1.0
565	P52788	SMS Spermine synthase	SMS	LYC*PVEFSK	1.1	1.0	1.1
566	O75874	IDH1 Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	SEGGFIWAC*K	0.9	1.0	1.0
567	P04632	CAPNS1 Calpain small subunit 1	CAPNS1	YSDESGNMDFDNFISC*LV R	1.1	1.3	1.2
568	P23528	CFL1 Cofilin-1	CFL1	HELQANC*YEEVK	1.0	1.0	1.0
569	P22061	PCMT1 Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	ALDVGSGSGILTAC*FAR	1.0	1.0	1.0
570	Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	LAAQSC*ALSLVR	0.8	0.7	0.8
571	Q96EI5	TCEAL4 Transcription elongation factor A protein-like 4	TCEAL4	PEVTC*TLEDK	0.9	0.5	0.7
572	P61970	NUTF2 Nuclear transport factor 2	NUTF2	NINDAWVC*TNDMFR	1.0	0.9	0.9
573	Q96FJ2	DYNLL2 Dynein light chain 2, cytoplasmic	DYNLL2	NADMSEDMQQDAVDC*AT QAMEK	1.1	0.9	1.0
574	P60174	TPI1 Triosephosphate isomerase	TPI1	VPADTEVVC*APPTAYIDFA R	1.1	1.0	1.1
575	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	IC*PVETLVEEAIQC*AEK	0.9	0.9	0.9

1.0	1.3	0.7	0.8	0.9	1.0	ns	Cytoplasm. Endoplasmic reticulum. Nucleus, nucleolus.	289	Yes	Yes	Yes	Yes	No	Yes	83.3
1.0	0.9	1.1	0.9	0.8	1.0	ns		153	Yes	Yes	No	No	No	--	40.0
0.9	1.1	0.9	0.9	1.0	0.9	ns		112	Yes	Yes	No	No	No	No	33.3
1.1	0.8	1.0	1.0	0.9	0.9	ns	Cytoplasm.	170	Yes	Yes	Yes	Yes	Yes	No	83.3
								174	Yes	Yes	Yes	Yes	Yes	Yes	100.0
0.9	1.1	1.0	0.8	1.0	0.9	ns	Cytoplasm.	251	Yes	No	Yes	No	Yes	Yes	66.7
0.9	1.0	1.0	0.9	1.0	0.9	ns		Bad ID	Error	Error	Error	Error	Error	Error	#DIV/0!
0.9	0.9	1.0	0.9	1.0	0.9	ns	Cytoplasm {ECO	112	Yes	Yes	No	No	No	No	33.3
1.0	0.8	1.0	0.9	1.0	0.9	ns	Cytoplasm. Sarcoplasmic reticulum membrane; Peripheral membrane protein; Cytoplasmic side.	75	Yes	Yes	No	No	No	Yes	50.0
0.9	0.8	1.0	0.9	1.0	0.9	ns	Nucleus {ECO	32	Yes	Yes	No	--	--	No	50.0
0.8	1.0	1.1	0.8	0.9	0.9	ns	Nucleus matrix {ECO	39	Yes	Yes	No	No	No	No	33.3
0.9	1.0	0.9	0.9	1.0	0.9	ns	Cytoplasm {ECO	289	Yes	Yes	Yes	Yes	No	Yes	83.3
1.0	0.9	0.9	1.0	0.9	0.9	ns	Cytoplasm. Cytoplasmic vesicle.	56	Yes	Yes	Yes	Yes	Yes	Yes	100.0
0.8	0.9	1.0	1.0	1.0	0.9	ns	Nucleus {ECO	57	Yes	Yes	--	--	--	--	100.0
0.8	1.0	1.0	0.9	0.9	0.9	ns	Cytoplasm. Nucleus. Cytoplasm, P-body {ECO	107	Yes	Yes	Yes	No	No	No	50.0
								115	Yes	Yes	Yes	No	Yes	Yes	83.3
0.8	1.0	1.1	0.9	0.9	0.9	ns	Cytoplasm. Nucleus {ECO	96	Yes	Yes	Yes	No	Yes	Yes	83.3
1.0	0.7	0.9	1.2	0.9	0.9	ns	Cytoplasm. Early endosome membrane; Peripheral membrane protein; Cytoplasmic side. Endosome, multivesicular body membrane {ECO	185/190	Yes	Yes	Yes	Yes	--	Yes	100.0
0.7	1.1	0.9	1.0	1.0	0.9	ns		255	Yes	Yes	No	No	No	No	33.3
0.9	1.0	1.0	0.8	0.9	0.9	ns		63	Yes	Yes	Yes	Yes	--	Yes	100.0
0.9	0.8	0.9	1.0	1.0	0.9	ns	Nucleus.	34/37/40	Yes	Yes	Yes	--	Yes	Yes	100.0
0.6	1.5	0.7	1.1	0.6	0.9	ns	Nucleus {ECO	342	Yes	Yes	No	--	No	No	40.0
1.0	0.8	0.9	0.9	0.9	0.9	ns		63	Yes	Yes	No	No	--	No	40.0
0.9	0.8	1.0	0.9	0.9	0.9	ns		337	Yes	Yes	No	--	No	No	40.0
0.9	0.9	0.8	0.9	1.0	0.9	ns	Cytoplasm {ECO	269	Yes	Yes	Yes	No	Yes	Yes	83.3
0.9	1.0	0.9	0.9	0.9	0.9	ns	Cytoplasm {ECO	232	Yes	Yes	Yes	--	Yes	No	80.0
0.9	0.9	0.9	0.9	1.0	0.9	ns	Nucleus matrix {ECO	139	Yes	Yes	--	No	--	No	50.0
0.9	0.9	0.9	0.8	0.9	0.9	ns	Cytoplasm.	95	Yes	Yes	Yes	--	Yes	Yes	100.0
0.9	0.7	1.0	1.0	0.9	0.9	ns	Nucleus, nucleolus. Cytoplasm.	242	Yes	Yes	Yes	--	--	Yes	100.0
0.8	0.8	1.0	0.9	0.9	0.9	ns	Nucleus {ECO	34	Yes	No	--	--	--	--	50.0
0.9	0.9	0.9	0.9	0.9	0.9	ns	Cytoplasm.	114	Yes	Yes	No	No	No	No	33.3
0.8	0.8	1.2	0.8	0.9	0.9	ns	Cytoplasm, cytoskeleton {ECO	24	Yes	Yes	Yes	No	No	Yes	66.7
0.8	1.0	1.0	0.8	0.9	0.9	ns		79	Yes	Yes	No	No	No	No	33.3
0.8	0.9	1.0	0.9	0.8	0.9	ns	Mitochondrion matrix.	213	Yes	No	No	No	No	No	16.7

576	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	ATC*IGNNSAAAVSMLK	0.9	0.9	0.9
577	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	NTGIIC*TIGPASR	0.8	1.0	0.9
578	P00491	PNP Purine nucleoside phosphorylase	PNP	AC*VMMQGR	1.2	1.2	1.2
579	Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	VVFC*PVK	1.0	0.9	1.0
580	Q9UL46	PSME2 Proteasome activator complex subunit 2	PSME2	C*GFLPGNEK	1.0	0.9	1.0
581	P60981	DSTN Destrin	DSTN	AVIFC*LSADK	0.8	0.9	0.8
582	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	YASIC*QQNGIVPIVEPEILP DGDHDLK	1.0	1.0	1.0
583	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	LNEDMAC*SVAGITSDANV LTNELR	0.9	0.9	0.9
584	Q9UHX 1	PUF60 Poly(U)-binding-splicing factor PUF60	PUF60	ALAIMC*R	1.0	1.0	1.0
585	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	SIC*TTVLELLDK	1.1	1.0	1.0
586	P07737	PFN1 Profilin-1	PFN1	C*YEMASHLR	1.0	0.9	1.0
587	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	FLDGNELTLADC*NLLPK	1.0	0.8	0.9
588	P00390	GSR Glutathione reductase, mitochondrial	GSR	LGGTC*VNVGCVPK	0.9	0.9	0.9
589	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	ALANSLAC*QGK	1.0	1.0	1.0
590	P14174	MIF Macrophage migration inhibitory factor	MIF	LLC*GLLAER	1.0	1.0	1.0
591	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	DIC*NDVLSLLEK	1.1	0.9	1.0
592	P60174	TPI1 Triosephosphate isomerase	TPI1	IAVAAQNC*YK	0.9	1.0	1.0
593	P31949	S100A11 Protein S100-A11	S100A11	C*IESLIAVFQK	1.0	0.9	1.0
594	F5H284	PPIAL4D Peptidyl-prolyl cis-trans isomerase A-like 4D	PPIAL4D	IIPGFMC*QGGDFTR	1.0	1.0	1.0
595	P09467	FBP1 Fructose-1,6-bisphosphatase 1	FBP1	GTGELTQLLNSLC*TAVK	0.9	1.2	1.0
596	P61158	ACTR3 Actin-related protein 3	ACTR3	LPACVVDC*GTGYTK	1.1	1.0	1.0
597	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	SC*YLSSLDLLLEHR	1.0	1.0	1.0
598	P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	DC*LIPMGITSENVAER	0.9	0.9	0.9
599	P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	ITIADC*GQLE	0.8	1.0	0.9
600	P21964	COMT Catechol O-methyltransferase	COMT	YLPDTLLLEEC*GLLR	0.9	1.0	0.9
601	P31150	GDI1 Rab GDP dissociation inhibitor alpha	GDI1	TDDYLDQPC*LETVNR	0.9	1.1	1.0
602	P30044	PRDX5 Peroxiredoxin-5, mitochondrial	PRDX5	ALNVEPDGTGLTC*SLAPN IISQL	1.0	1.0	1.0
603	P13489	RNH1 Ribonuclease inhibitor	RNH1	LSLQNC*C*LTGAGC*GVL SSTLR	0.9	1.0	0.9
604	Q15369	TCEB1 Transcription elongation factor B polypeptide 1	TCEB1	VC*MYFTYK	1.2	0.8	1.0
605	Q9Y3D0	FAM96B Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	VAAALENTHLLEVVNQC* LSAR	1.0	1.0	1.0

								225	Yes	Yes	No	--	No	No	40.0
0.8	0.8	0.9	0.9	0.9	0.9	ns	Cytoplasm. Nucleus. Cytoplasm, P-body {ECO	163	Yes	Yes	Yes	No	No	Yes	66.7
0.9	0.9	0.9	0.9	0.8	0.9	ns	Cytoplasm. Nucleus.	49	Yes	Yes	Yes	No	Yes	Yes	83.3
0.7	1.1	1.0	0.7	0.8	0.9	ns	Cytoplasm, cytoskeleton {ECO	78	Yes	Yes	No	No	--	No	40.0
1.0	0.8	0.8	1.0	0.8	0.9	ns	Nucleus {ECO	214	Yes	Yes	No	No	No	No	33.3
0.9	0.8	0.9	1.0	0.9	0.9	ns		91	Yes	Yes	No	--	--	No	50.0
0.7	1.0	0.9	0.8	0.9	0.9	ns		39	Yes	Yes	No	No	No	No	33.3
0.8	0.9	0.9	0.8	0.9	0.9	ns	Cytoplasm, myofibril, sarcomere, I band. Cytoplasm, myofibril, sarcomere, M line. sides of the Z line in the absence of Ca(2+). {ECO	178	Yes	Yes	Yes	--	Yes	Yes	100.0
0.7	0.9	0.9	1.0	0.8	0.9	ns	Cytoplasm. Nucleus. Cytoplasm, P-body {ECO	74	Yes	Yes	Yes	No	Yes	Yes	83.3
0.8	1.1	0.8	0.8	0.8	0.9	ns	Nucleus {ECO	129	Yes	Yes	Yes	--	--	No	75.0
0.8	1.0	0.9	0.8	0.8	0.9	ns	Cytoplasm.	94	Yes	Yes	Yes	No	Yes	Yes	83.3
0.9	0.9	0.8	0.8	0.9	0.9	ns	Cytoplasm, cytoskeleton.	128	Yes	Yes	--	No	--	--	66.7
0.9	0.8	1.0	0.7	0.9	0.9	ns	Nucleus. Nucleus membrane {ECO	178	Yes	Yes	Yes	--	No	Yes	80.0
0.8	0.9	0.8	0.9	0.9	0.9	ns	Mitochondrion. Cytoplasm.	102	Yes	Yes	Yes	Yes	Yes	Yes	100.0
0.8	0.9	1.0	0.8	0.9	0.9	ns	Cytoplasm, myofibril, sarcomere, I band. Cytoplasm, myofibril, sarcomere, M line.	339	Yes	Yes	No	--	No	No	40.0
0.9	0.9	0.9	0.8	0.9	0.9	ns	Secreted {ECO	81	Yes	Yes	--	--	No	No	50.0
0.7	1.0	1.0	0.8	0.8	0.8	ns	Cytoplasm {ECO	94	Yes	Yes	Yes	No	Yes	Yes	83.3
0.8	0.9	0.9	0.7	0.9	0.8	ns		104	Yes	Yes	No	No	No	Yes	50.0
0.6	1.0	0.9	0.9	0.8	0.8	ns	Cytoplasm {ECO	13	Yes	Yes	--	--	--	--	100.0
0.8	0.9	0.9	0.8	0.8	0.8	ns	Cytoplasm {ECO	62	Yes	Yes	Yes	No	Yes	No	66.7
0.8	0.9	0.8	0.8	0.8	0.8	ns		39	Yes	Yes	No	No	No	No	33.3
1.0	0.6	0.9	0.9	0.9	0.8	ns	Cytoplasm, cytoskeleton {ECO	12	Yes	Yes	No	No	No	No	33.3
0.8	0.9	0.8	0.8	0.9	0.8	ns	Nucleus {ECO	246	Yes	Yes	Yes	--	Yes	Yes	100.0
0.8	0.9	0.8	0.9	0.8	0.8	ns	Peroxisome.	177	Yes	Yes	No	Yes	Yes	No	66.7
0.8	1.0	0.8	0.8	0.8	0.8	ns	Cytoplasm {ECO	161	Yes	Yes	No	No	Yes	Yes	66.7
0.8	0.9	0.8	0.7	0.8	0.8	ns	Cytoplasm. Cell membrane; Single-pass type II membrane protein; Extracellular side {ECO	207	Yes	Yes	--	--	No	--	66.7
0.8	0.8	0.9	0.7	0.8	0.8	ns	Cytoplasm {ECO	202	Yes	Yes	No	No	No	No	33.3
0.7	0.8	0.9	0.8	0.8	0.8	ns	Mitochondrion. Cytoplasm. Peroxisome.	204	Yes	Yes	Yes	No	No	--	60.0
1.1	0.4	0.8	0.8	0.8	0.8	ns	Cytoplasm.	95	Yes	Yes	Yes	--	No	No	60.0
								96	Yes	No	No	--	No	No	20.0
								102	Yes	Yes	No	--	No	No	40.0
0.9	0.6	0.9	0.8	0.7	0.8	ns	Nucleus {ECO	74	Yes	Yes	Yes	No	Yes	Yes	83.3
0.6	0.8	0.6	0.6	0.7	0.7	ns	Nucleus {ECO	158	Yes	Yes	Yes	No	Yes	Yes	83.3

606	P25398	RPS12 40S ribosomal protein S12	RPS12	QAHLC*VLASNC*DEPMY VK	1.1	1.0	1.0
607	P25398	RPS12 40S ribosomal protein S12	RPS12	LVEALC*AEHQINLIK	1.0	1.0	1.0
608	Q14847	LASP1 LIM and SH3 domain protein 1	LASP1	ACFHC*ETC*K	1.0	1.0	1.0
609	P21291	CSRP1 Cysteine and glycine-rich protein 1	CSRP1	C*SQAVYAAEK	1.0	1.0	1.0
610	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	VPTANVSVVDLTC*R	0.9	1.0	0.9

0.6	0.6	0.6	0.7	0.7	0.6	ns	Cytoplasm.	50	Yes	Yes	Yes	No	Yes	Yes	83.3
								56	Yes	Yes	No	No	Yes	Yes	66.7
0.6	0.6	0.6	0.6	0.6	0.6	ns	Cytoplasm.	69	Yes	Yes	Yes	No	Yes	Yes	83.3
0.6	0.5	0.7	0.6	0.7	0.6	ns	Cytoplasm, cell cortex {ECO	32/35	Yes	Yes	Yes	--	Yes	Yes	100.0
0.5	0.4	0.5	0.6	0.5	0.5	ns	Nucleus.	122	Yes	Yes	Yes	--	Yes	--	100.0
0.4	0.5	0.5	0.5	0.4	0.5	ns	Cytoplasm, cytosol {ECO	247	Yes	Yes	No	No	Yes	No	50.0

(1) "--": cysteine is not found.

(2) "Conservation Ratio (%)" = (number of "Yes" / number of "Yes+No") × 100%

Table 2A-2. Evaluation of the data obtained by the current cysteine-profiling platform within the context of previously identified sites of S-nitrosation. The top 27 cysteine residues (R >3; Appendix I, Table 2A-1 in gray) was compaed to cysteines previously identified as S-nitrosated in the dbSNO database, and are denoted with Y (yes) and N (no), where Y* denotes presence of mouse homolog in dbSNO database. *In vitro* reflects an entry in dbSNO where GSNO treatment was performed *in vitro* and *in vivo* is a dbSNO entry where no exogenous treatment was applied.

Peptide #	Description	Sequence	Identified in dbSNO database	
			yes/no (Y/Y*(1)/N)	*in vitro*(2) /*in vivo*
1	ACO2 Aconitate hydratase, mitochondrial	VGLIGSC*TNSSYEDMGR	Y*	*in vitro*
2	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	IISNASC*TTNCLAPLAK	Y	*in vivo*
3	P4HA1 Prolyl 4-hydroxylase subunit alpha-1	PC*TLSELE	N	
4	PAFAH1B1 Platelet-activating factor acetylhydrolase IB subunit alpha	PNQDGTLIASC*SNDQTVR	Y*	*in vitro*
5	FN3K Fructosamine-3-kinase	AFGGPGAGC*ISEGR	N	
6	NTPCR Cancer-related nucleoside-triphosphatase	NADC*SSGPGQR	N	
7	CTSD Cathepsin D	AIGAVPLIQGEYMIPC*EK	Y*	*in vivo*
8	PFKP 6-phosphofructokinase type C	LPLMEC*VQMTQDVQK	N	
9	TUBB Tubulin beta chain	LTTPTYGDLNHLVSATMSGVTTC*LR	Y	*in vivo*
10	GFPT1 Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	C*QNALQQVVAR	N	
11	PCBP1 Poly(rC)-binding protein 1	VMTIPYQPMPASSPVIC*AGGQDR	N	
12	TCP1 T-complex protein 1 subunit alpha	IAC*LDFSLQK	Y	*in vivo*
13	TLE3 Transducin-like enhancer protein 3	SPISQLDC*LNR	N	
14	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	C*MALSTAVLVGEAK	N	
15	PCK2 Phosphoenolpyruvate carboxykinase	QC*PIMDPAWEAPEGVPIDAIIFGGR	N	
16	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-like 1	VWNLANC*K	Y	*in vivo*
17	TUBA4A Tubulin alpha-4A chain	AYHEQLSVAEITNAC*FEPANQMVK	Y	*in vivo*
18	ATOX1 Copper transport protein ATOX1	VC*IESEHSMDTLLATLK	Y*	*in vitro*
19	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	TSAPITC*ELLNK	Y	*in vitro*
20	RPL34 60S ribosomal protein L34	AYGGSMC*AK	N	
21	AKT1 RAC-alpha serine/threonine-protein kinase	TFC*GTPEYLAPEVLEDNDYGR	Y	
22	DLD Dihydrolipoyl dehydrogenase, mitochondrial	NETLGGTC*LNVGC*IPSK	Y*	*in vivo*
23	TK1 Thymidine kinase, cytosolic	NTMEALPAC*LLR	N	
24	GCDH Glutaryl-CoA dehydrogenase, mitochondrial	GYGC*AGVSSVAYGLLAR	Y*	*in vivo*
25	TUBA4A Tubulin alpha-4A chain	AVC*MLSNTTAIAEAWAR	Y	*in vivo*
26	PPP1CB Serine/threonine-protein phosphatase PP1-beta catalytic subunit	IC*GDIHGQYTDLLR	N	
27	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	LGNNC*VFAPADVTSEK	N	

(1) "Y*": SNO was identified in mouse.

(2) Identified *in vitro* : GSNO as NO source.

Table 2A-3. R-values from transnitrosation experiment at 0, 50, 100, 200 and 500 μM GSNO. A list of all identified peptides (* denotes labeled cysteine) is presented at each GSNO concentration together with calculated Heavy:Light Ratios (R).

Peptide #	Uniprot #	Description	Symbol	Sequence	Heavy : Light Ratio				
					GSNO concentration (μM)				
					0	50	100	200	500
1	P54136	RARS Arginine--tRNA ligase, cytoplasmic	RARS	NC*GC*LGASPNLEQLQEENLK	1.1	1.3	1.3	9.0	9.4
2	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	IISNASC*TTNCLAPLAK	1.1	1.7	2.7	6.5	9.3
3	P31749	AKT1 RAC-alpha serine/threonine-protein kinase	AKT1	TFC*GTPEYLAPEVLEDNDYGR	0.9	1.1	1.4	5.2	7.2
4	P07339	CTSD Cathepsin D	CTSD	AIGAVPLIQGEYMIPC*EK	1.1	1.5	1.5	4.0	6.6
5	Q9NXJ5	PGPEP1 Pyroglutamyl-peptidase 1	PGPEP1	YLC*DFTYYTSLYQSHGR	1.0	1.2	1.2	4.6	6.3
6	Q9UEW8	STK39 STE20/SPS1-related proline-alanine-rich protein kinase	STK39	DAYELQEVIGSGATAVVQAALC*K	1.1	1.9	2.0	5.1	6.1
7	Q06210	GFPT1 Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	VDSTTC*LFPVEEK	0.8	1.0	1.6	2.1	4.8
8	Q9NUU7	DDX19A ATP-dependent RNA helicase DDX19A	DDX19A	VLVTTNVC*AR	1.1	1.0	1.1	1.3	4.6
9	Q9Y3E2	BOLA1 BolA-like protein 1	BOLA1	VCLC*QGSAGSGAIGPVEAAIR	1.2	1.4	2.0	1.7	4.4
10	Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	MC*LFAGFQR	1.0	1.3	1.4	2.8	4.0
11	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	VGILDVDLC*GPSIPR	1.0	1.3	1.3	2.5	3.5
12	P62888	RPL30 60S ribosomal protein L30	RPL30	VC*TLAIIDPGDSDIIR	1.0	0.8	1.2	3.3	3.5
13	P07858	CTSB Cathepsin B	CTSB	GQDHC*GIESEVVAGIPR	0.9	1.3	1.3	3.0	3.5
14	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	LGNNC*VFAPADVTSEK	1.0	1.4	1.5	3.2	3.4
15	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	AVC*MLSNTTAIAEAWAR	1.0	1.3	1.8	2.8	3.4
16	P56192	MARS Methionine--tRNA ligase, cytoplasmic	MARS	LFVSDGVPGC*LPVLAAAGR	1.0	1.4	1.5	2.4	3.3
17	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	C*MTNTPVVVR	1.1	1.5	1.5	2.6	3.3
18	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	AYHEQLSVAEITNAC*FEPANQMVK	1.1	1.4	1.5	3.1	3.2
19	Q5JTZ9	AARS2 Alanine--tRNA ligase, mitochondrial	AARS2	HSTYDTDLFSPLLNAIQQGC*R	1.1	1.4	2.2	3.0	3.2
20	P07437	TUBB Tubulin beta chain	TUBB	VSDTVVEPYNATLSVHQLVENTDETYC*IDNEALYDICFR	1.1	1.4	1.4	2.2	3.2
21	P50213	IDH3A Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	C*SDFTEEICR	1.1	1.5	1.5	2.0	3.1
22	P51610	HCFC1 Host cell factor 1	HCFC1	VAGINAC*GR	1.1	0.9	1.2	2.1	3.1
23	Q6NXE6	ARMC6 Armadillo repeat-containing protein 6	ARMC6	AFLDNPGILSELC*GTLSR	1.0	1.5	1.3	2.5	3.1
24	P26440	IVD Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	AC*DEGHC*TAK	1.1	3.6	1.3	2.2	3.0
25	Q14318	FKBP8 Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8	C*LNNLAASQLK	1.0	1.1	1.8	2.1	3.0
26	Q01813	PFKP 6-phosphofructokinase type C	PFKP	AAC*NLLQR	1.0	1.3	1.4	3.0	3.0
27	Q05655	PRKCD Protein kinase C delta type	PRKCD	ASTFC*GTPDYIAPEILQGLK	1.0	1.1	1.2	2.4	3.0
28	Q8TCU6	PREX1 Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein	PREX1	LC*VLNEILGTER	1.1	1.3	1.2	2.0	2.9

29	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	LFC*VGFTK	1.4	1.3	1.2	2.1	2.9
30	Q9BVA1	TUBB2B Tubulin beta-2B chain	TUBB2B	ESESC*DCLQGFQLTHSLGGGTGSGMGTLLISK	1.0	1.5	1.6	2.4	2.9
31	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	YMACC*LLYR	1.0	1.2	1.3	2.4	2.9
32	P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	AC*GDSTLTQITAGLDPVGR	1.0	1.2	1.3	3.3	2.8
33	P53621	COPA Coatomer subunit alpha	COPA	VQVPNC*DEIFYAGTGNLLLR	1.4	1.3	1.1	2.0	2.8
34	P29401	TKT Transketolase	TKT	QAFTDVATGSLGQGLGAAC*GMAYTGK	1.1	1.4	1.3	2.6	2.7
35	P07437	TUBB Tubulin beta chain	TUBB	TAVC*DIPPR	1.0	1.3	1.4	2.4	2.7
36	P17858	PFKL 6-phosphofructokinase, liver type	PFKL	VFANAPDSAC*VIGLK	1.1	1.4	1.5	2.3	2.7
37	O60568	PLOD3 Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3	GLDYEGGGC*R	1.2	1.0	1.5	2.2	2.7
38	O95671	ASMTL N-acetylserotonin O-methyltransferase-like protein	ASMTL	AEAGEAGQATAEAEC*HR	0.9	0.8	0.9	1.2	2.7
39	P51553	IDH3G Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	TSLDLYANVIHC*K	1.2	1.5	1.5	2.4	2.7
40	Q14694	USP10 Ubiquitin carboxyl-terminal hydrolase 10	USP10	TPSYSISSTLNPQAPEFILGC*TASK	0.8	1.1	0.9	1.6	2.7
41	Q92947	GCDH Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	GYGC*AGVSSVAYGLLAR	1.1	1.2	1.5	2.8	2.7
42	Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	NVVAEC*LGK	1.0	1.3	0.8	2.6	2.7
43	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	AC*QSIYPLHDVFVR	1.1	1.1	1.2	2.2	2.7
44	P53384	NUBP1 Cytosolic Fe-S cluster assembly factor NUBP1	NUBP1	GASC*QGC*PNQR	0.9	1.0	1.0	1.7	2.7
45	Q13748	TUBA3D Tubulin alpha-3C/D chain	TUBA3D	TIQFVDWC*PTGFK	1.0	1.4	1.4	2.2	2.7
46	P49327	FASN Fatty acid synthase	FASN	AFDTAGNGYC*R	0.9	1.1	1.1	1.8	2.7
47	Q01813	PFKP 6-phosphofructokinase type C	PFKP	NESC*SENYTTDFIYQLYSEEGK	1.1	1.1	1.1	2.9	2.7
48	P35250	RFC2 Replication factor C subunit 2	RFC2	TTSILC*LAR	1.2	1.3	1.2	3.2	2.7
49	P07437	TUBB Tubulin beta chain	TUBB	NMMAAC*DPR	1.3	1.3	1.5	2.8	2.7
50	P07437	TUBB Tubulin beta chain	TUBB	LTTPTYGDLNHLVSATMSGVTTC*LR	1.1	1.4	1.5	2.6	2.7
51	P61163	ACTR1A Alpha-centractin	ACTR1A	AC*YLSINPQK	1.0	1.0	1.2	2.2	2.7
52	P62280	RPS11 40S ribosomal protein S11	RPS11	DVQIGDIVTVGEC*R	1.0	1.2	1.1	2.5	2.6
53	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	GEETPVIVGSALC*ALEGR	1.2	1.2	1.3	2.4	2.6
54	P62249	RPS16 40S ribosomal protein S16	RPS16	TATAVAHC*K	1.0	1.1	1.2	2.2	2.6
55	P42677	RPS27 40S ribosomal protein S27	RPS27	LTEGC*SFR	1.0	1.2	1.4	2.2	2.6
56	Q92616	GCN1L1 Translational activator GCN1	GCN1L1	PEC*VLDK	1.1	1.3	1.4	3.3	2.6
57	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	AVHQC*DR	1.1	1.2	1.3	2.2	2.6
58	P56192	MARS Methionine--tRNA ligase, cytoplasmic	MARS	AEVLISTVGPEDC*VVPFLTR	1.1	1.2	1.5	2.0	2.6
59	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	GC*LLYGPPGTGK	1.0	1.0	1.3	1.3	2.6
60	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	SIQFVDWC*PTGFK	1.1	1.2	1.3	2.4	2.6
61	Q6ISB3	GRHL2 Grainyhead-like protein 2 homolog	GRHL2	GQASQTQC*NSSSDGK	1.1	1.1	1.0	1.5	2.6
62	Q96RN5	MED15 Mediator of RNA polymerase II transcription subunit 15	MED15	QQYLC*QPLLDAVLANIR	0.9	1.1	1.4	1.7	2.5

63	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	HLYTLDGGDIINALC*FSPNR	1.2	1.3	1.5	2.5	2.5
64	Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	AVVVC*PK	1.0	1.1	1.2	2.4	2.5
65	Q8NBF2	NHLRC2 NHL repeat-containing protein 2	NHLRC2	AILFSQPLQITDTQQGC*IAPVELR	1.1	1.0	1.1	2.1	2.5
66	P50213	IDH3A Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	PC*VSIEGYK	1.0	1.3	1.1	1.8	2.5
67	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	QAVLGAGLPISTPC*TTINK	0.9	0.9	1.0	1.8	2.5
68	P12268	IMPDH2 Inosine-5-monophosphate dehydrogenase 2	IMPDH2	HGFC*GIPITDTGR	1.2	1.2	0.9	1.7	2.5
69	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	SLLINAVEASC*IR	1.0	1.2	1.3	2.3	2.5
70	P49327	FASN Fatty acid synthase	FASN	SFYGSTLFLC*R	1.3	1.2	1.1	2.1	2.5
71	P53597	SUCLG1 Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	IIC*QGFTGK	1.1	1.2	1.9	2.3	2.5
72	P50914	RPL14 60S ribosomal protein L14	RPL14	ALVDGPC*TQVR	1.0	1.2	1.4	2.8	2.4
73	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	QGEYGLASIC*NGGGGASAMLIQK	1.0	0.9	1.3	1.9	2.4
74	P15880	RPS2 40S ribosomal protein S2	RPS2	GC*TATLGNFAK	1.0	1.2	1.3	1.9	2.4
75	P46734	MAP2K3 Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	FSPEFVDFTAQC*LR	1.0	1.4	1.4	2.4	2.4
76	Q7Z7H8	MRPL10 39S ribosomal protein L10, mitochondrial	MRPL10	TVPFLPLLGGC*IDDTILSR	1.0	1.2	1.3	2.4	2.4
77	Q99460	PSMD1 26S proteasome non-ATPase regulatory subunit 1	PSMD1	TPEQC*PSVVSLLSESYNPHVR	1.2	1.3	1.1	2.4	2.4
78	Q8IU81	IRF2BP1 Interferon regulatory factor 2-binding protein 1	IRF2BP1	LFTEYPC*GSGNVYAGVLAVAR	1.0	0.9	0.8	1.4	2.4
79	P62701	RPS4X 40S ribosomal protein S4, X isoform	RPS4X	EC*LPLIIFLR	0.9	1.2	1.2	2.4	2.4
80	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	VLGPAAC*R	1.0	1.5	1.4	2.2	2.4
81	Q9C0C2	TNKS1BP1 182 kDa tankyrase-1-binding protein	TNKS1BP1	EAALPILEPVLGQEQPAAPDQPC*VLFADAPEPGQALPVEEEAVTLAR	1.1	1.3	1.0	2.0	2.4
82	P62829	RPL23 60S ribosomal protein L23	RPL23	ISLGLPVGAVINC*ADNTGAK	1.0	1.1	1.3	2.1	2.4
83	P49327	FASN Fatty acid synthase	FASN	DGLLENQTPEFFQDVC*K	1.0	1.1	1.3	2.0	2.4
84	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	NMITGTSQADC*AVLIVAAGVGEFEAGISK	1.2	1.3	1.4	1.8	2.4
85	Q14258	TRIM25 E3 ubiquitin/ISG15 ligase TRIM25	TRIM25	NTVLC*NVVEQFLQADLAR	1.0	1.0	1.0	1.7	2.4
86	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	ALDH6A1	C*MALSTAVLVGEAK	0.8	1.1	0.9	2.4	2.4
87	P51570	GALK1 Galactokinase	GALK1	GHALLIDC*R	0.9	1.1	0.9	2.3	2.4
88	O43264	ZW10 Centromere/kinetochore protein zw10 homolog	ZW10	LAPILC*DGTATFVDLVPGFR	1.9	1.1	1.3	2.1	2.4
89	P26641	EEF1G Elongation factor 1-gamma	EEF1G	FPEELTQTFMSC*NLITGMFQR	1.0	1.1	1.2	1.4	2.4
90	P46109	CRKL Crk-like protein	CRKL	VPC*AYDK	1.2	0.8	1.1	1.3	2.4
91	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	YNFFTGC*PK	1.4	1.1	1.2	1.8	2.3
92	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	GDEC*ELLGHSK	1.0	1.2	1.3	2.0	2.3
93	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	IC*DDELILIK	1.1	1.1	1.1	1.8	2.3
94	P22102	GART Trifunctional purine biosynthetic protein adenosine-3	GART	FGDPEC*QVILPLLK	1.1	1.3	1.1	2.2	2.3
95	P46782	RPS5 40S ribosomal protein S5	RPS5	TIAEC*LADELINAAK	1.1	1.0	1.1	1.6	2.3

96	Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	LSTLC*PSAVLQR	1.0	1.2	1.3	2.0	2.3
97	O75362	ZNF217 Zinc finger protein 217	ZNF217	C*IPQLDPFTTFQAWQLATK	0.9	0.9	1.0	1.0	2.3
98	P13804	ETFA Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	TIYAGNALC*TVK	1.1	1.2	1.4	1.9	2.3
99	P49327	FASN Fatty acid synthase	FASN	DPETLVGYSMVGC*QR	1.1	0.9	0.9	1.5	2.3
100	O43837	IDH3B Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	LGDGLFLQC*C*EEVAELYPK	1.4	1.3	1.7	1.7	2.2
101	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	CEYPAAC*NALETLLIHR	1.1	1.1	1.3	2.0	2.2
102	P60981	DSTN Destrin	DSTN	HEC*QANGPEDLNR	0.8	1.0	1.2	1.6	2.2
103	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	LC*PNSTGAEIR	1.2	1.2	1.2	2.1	2.2
104	Q96I99	SUCLG2 Succinyl-CoA ligase [GDP forming] subunit beta, mitochondrial	SUCLG2	IDATQVEVNPFGETPEGQVVC*FDAK	1.1	0.9	1.2	2.2	2.2
105	Q9UBS0	RPS6KB2 Ribosomal protein S6 kinase beta-2	RPS6KB2	PC*LQSEEDVSQFDTR	1.2	1.3	1.3	1.9	2.2
106	Q9ULV4	CORO1C Coronin-1C	CORO1C	C*DLISIPK	1.2	0.6	1.0	1.6	2.2
107	Q07020	RPL18 60S ribosomal protein L18	RPL18	GC*GTVLLSGPR	1.1	1.1	1.2	2.1	2.2
108	P63220	RPS21 40S ribosomal protein S21	RPS21	TYAIC*GAIR	1.0	1.0	1.1	1.7	2.2
109	Q9UPN9	TRIM33 E3 ubiquitin-protein ligase TRIM33	TRIM33	C*DPVPAANGAIR	1.0	1.0	1.0	1.0	2.2
110	P62241	RPS8 40S ribosomal protein S8	RPS8	NC*IVLIDSTPYR	1.2	1.4	1.2	3.2	2.2
111	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit 2	PSMD2	NEC*DPALALLSDYVLHNSNTMR	1.1	1.0	0.7	1.4	2.2
112	P60709	ACTB Actin, cytoplasmic 1	ACTB	C*DVDIR	1.0	1.2	1.5	2.2	2.2
113	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	AC*ALQVLSAILEGSK	1.0	1.2	1.4	1.7	2.2
114	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	GNVC*GDSK	1.0	1.1	1.1	1.8	2.2
115	P23610	F8A3 Factor VIII intron 22 protein	F8A3	LVC*PAAYGEPLQAAASALGAAVR	0.8	1.1	1.0	1.9	2.1
116	Q9BTZ2	DHRS4 Dehydrogenase/reductase SDR family member 4	DHRS4	VNC*LAPGLIK	1.1	1.2	1.3	1.9	2.1
117	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	C*FIVGADNVGSK	1.1	1.1	1.1	1.8	2.1
118	P51858	HDGF Hepatoma-derived growth factor	HDGF	C*GDLVFAK	1.0	0.9	1.3	1.6	2.1
119	Q9UL15	BAG5 BAG family molecular chaperone regulator 5	BAG5	NPC*IR	1.1	0.9	0.9	1.4	2.1
120	Q6P2I3	FAHD2B Fumarylacetoacetate hydrolase domain-containing protein 2B	FAHD2B	TFDTFC*PLGPALVTK	1.0	1.2	1.2	1.2	2.1
121	P13804	ETFA Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	LGGEVSC*LVAGTK	1.0	1.1	1.3	2.0	2.1
122	Q7L0Y3	TRMT10C Mitochondrial ribonuclease P protein 1	TRMT10C	NVDPFHIYFC*NLK	1.4	1.3	1.2	1.7	2.1
123	Q9UL25	RAB21 Ras-related protein Rab-21	RAB21	VVLLGEGC*VGK	1.1	1.1	1.2	1.4	2.1
124	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	AVASQLDC*NFLK	1.0	1.0	1.2	1.8	2.1
125	Q96T76	MMS19 MMS19 nucleotide excision repair protein homolog	MMS19	AC*DSVTSNVLPLLLEQFHK	1.0	1.4	1.5	2.1	2.1
126	P30042	C21orf33 ES1 protein homolog, mitochondrial	C21orf33	DC*K	1.0	0.9	0.9	1.8	2.1
127	Q8TEX9	IPO4 Importin-4	IPO4	AC*YALENFVENLGPK	0.9	1.0	1.3	2.1	2.1
128	P60763	RAC3 Ras-related C3 botulinum toxin substrate 3	RAC3	AVLC*PPPVK	1.0	1.0	1.1	1.3	2.1
129	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	C*PTSGR	1.0	1.1	1.2	1.8	2.1
130	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	AGAIAPC*EVTVPAQNTGLGPEK	0.9	1.0	1.2	1.8	2.1

131	Q9H773	DCTPP1 dCTP pyrophosphatase 1	DCTPP1	YTELPHGAISEDQAVGPADIPC*DSTGQTST	1.1	1.6	1.3	1.5	2.1
132	P21964	COMT Catechol O-methyltransferase	COMT	IVDAVIQEHQPSVLLELGAYC*GYSAVR	1.0	1.1	1.1	1.4	2.0
133	Q15393	SF3B3 Splicing factor 3B subunit 3	SF3B3	SEHPPLC*GR	1.1	1.0	1.1	1.3	2.0
134	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	EMQNLSFQDC*YSSK	1.2	1.1	1.1	2.0	2.0
135	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	C*ATITPDEAR	0.9	0.9	1.2	1.5	2.0
136	P35237	SERPINB6 Serpin B6	SERPINB6	SC*DFLSSFR	0.8	1.0	1.0	1.3	2.0
137	E9PPU0	EPPK1 Epiplakin	EPPK1	YLQGTGC*IAGLLLPGSQER	1.0	1.2	1.0	1.8	2.0
138	Q9P1F3	ABRACL Costars family protein ABRACL	ABRACL	C*ANLFEALVGTLK	1.2	1.0	1.2	1.3	2.0
139	Q8N163	KIAA1967 DBIRD complex subunit KIAA1967	KIAA1967	VHLTPYTVDSPIC*DFLELQR	1.1	1.1	1.1	1.5	2.0
140	P24468	NR2F2 COUP transcription factor 2	NR2F2	AIVLFTSDAC*GLSDVAHVESLQEK	1.1	1.0	1.2	1.3	2.0
141	P62280	RPS11 40S ribosomal protein S11	RPS11	C*PFTGNVSIR	1.0	1.2	1.2	1.9	2.0
142	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	IHMGSC*AENTAK	0.9	1.0	1.0	1.7	2.0
143	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	PMC*VESFSDYPPLGR	1.0	1.1	1.2	2.0	2.0
144	Q9Y3E2	BOLA1 BolA-like protein 1	BOLA1	ENSQLDTSPPC*LGGNK	0.9	0.9	1.1	1.5	2.0
145	Q9Y3D0	FAM96B Mitotic spindle-associated MMXD complex subunit MIP28	FAM96B	VAAALENTHLLEVVNQC*LSAR	1.0	0.8	1.1	0.9	2.0
146	P08243	ASNS Asparagine synthetase	ASNS	IGC*LLSGGLDSSLVAATLLK	1.1	1.2	1.2	1.8	1.9
147	P25398	RPS12 40S ribosomal protein S12	RPS12	LVEALC*AEHQINLIK	1.0	1.3	1.1	1.6	1.9
148	P48643	CCT5 T-complex protein 1 subunit epsilon	CCT5	VVNSC*HR	1.0	1.0	1.0	1.5	1.9
149	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	PVTDC*VISVPSFFTDAER	0.9	1.1	1.2	2.7	1.9
150	P60709	ACTB Actin, cytoplasmic 1	ACTB	LC*YVALDFEQEMATAASSSSLEK	1.2	1.3	1.3	1.9	1.9
151	Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	NC*IGDFLK	1.0	1.1	1.3	1.6	1.9
152	Q13636	RAB31 Ras-related protein Rab-31	RAB31	VC*LLGDTGVGK	1.1	1.1	1.4	1.3	1.9
153	P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	TFVSGAC*DASIK	1.0	1.3	1.3	2.3	1.9
154	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	GDEC*GLALGR	1.0	1.2	1.1	1.6	1.9
155	P82912	MRPS11 28S ribosomal protein S11, mitochondrial	MRPS11	ASHNNTQIQVVSASNEPLAFASC*GTEGFR	1.0	1.0	1.3	1.6	1.9
156	P62753	RPS6 40S ribosomal protein S6	RPS6	LNISFPATGC*QK	1.0	1.1	1.2	1.9	1.9
157	P22314	UBA1 Ubiquitin-like modifier-activating enzyme 1	UBA1	SIPIC*TLK	1.0	1.1	1.3	1.5	1.9
158	P41240	CSK Tyrosine-protein kinase CSK	CSK	SVLGGDC*LLK	1.1	1.1	1.0	1.4	1.9
159	P60866	RPS20 40S ribosomal protein S20	RPS20	TPC*GEGSK	1.0	1.1	1.0	1.6	1.9
160	B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	IFVGNVSAAC*TSQELR	1.0	1.1	1.3	1.6	1.9
161	Q8NEC7	GSTCD Glutathione S-transferase C-terminal domain-containing protein	GSTCD	LC*ELTIPLAIENFLR	1.2	0.9	1.0	1.5	1.9
162	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	GQPC*SQNYR	1.4	1.0	1.1	1.1	1.9
163	P83731	RPL24 60S ribosomal protein L24	RPL24	VELC*SFSGYK	1.6	0.8	1.8	2.2	1.9
164	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	ADHQPLTEASYVNLPTIALC*NTDSPLR	1.2	1.2	1.2	1.8	1.9
165	P01111	NRAS GTPase NRas	NRAS	TGEGFLC*VFAINNSK	1.1	1.0	1.1	1.3	1.9

166	P49321	NASP Nuclear autoantigenic sperm protein	NASP	PTDGASSSNC*VTDISHLVR	1.1	2.4	0.9	1.2	1.9
167	P05141	SLC25A5 ADP/ATP translocase 2	SLC25A5	GLGDC*LVK	1.0	0.9	1.2	1.7	1.9
168	P23396	RPS3 40S ribosomal protein S3	RPS3	GLC*AIAQAESLR	1.1	1.1	1.2	1.7	1.9
169	Q7L0Y3	TRMT10C Mitochondrial ribonuclease P protein 1	TRMT10C	SSVQEEC*VSTISSSK	1.5	1.3	1.0	1.6	1.9
170	Q13418	ILK Integrin-linked protein kinase	ILK	FSFQC*PGR	1.0	0.9	1.0	1.5	1.9
171	Q7Z2W4	ZC3HAV1 Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	NSNVDSSYLESLYQSC*PR	1.0	1.0	0.9	1.2	1.9
172	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	YVLC*TAPR	1.1	1.1	0.5	1.4	1.8
173	Q96CP2	FLYWCH2 FLYWCH family member 2	FLYWCH2	TEDSGLAAGPPEAAGENFAPC*SVAPGK	1.0	1.1	1.3	1.1	1.8
174	P07900	HSP90AA1 Heat shock protein HSP 90-alpha	HSP90AA1	VFIMDNC*EELIPEYLNFIR	1.1	1.0	1.0	1.1	1.8
175	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	SLHDALC*VVK	1.1	1.2	1.2	1.8	1.8
176	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	TGC*NVLLIQK	1.0	1.1	1.1	1.9	1.8
177	Q96CM8	ACSF2 Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	MVSTPIGGLSYVQGC*TK	1.0	1.2	1.1	1.6	1.8
178	P49327	FASN Fatty acid synthase	FASN	LGMLSPEGTC*K	0.9	1.2	1.7	2.5	1.8
179	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	NFILDQC*NVYNSGQR	1.0	1.1	1.1	1.7	1.8
180	P15924	DSP Desmoplakin	DSP	YC*YLQNEVFGLFQK	1.1	1.0	1.2	1.6	1.8
181	Q9NP73	ALG13 UDP-N-acetylglucosamine transferase subunit ALG13	ALG13	ADLVISHAGAGSC*LETLEK	1.0	0.9	0.9	1.4	1.8
182	O60547	GMDS GDP-mannose 4,6 dehydratase	GMDS	LHYGDLTDSTC*LVK	0.9	0.9	1.2	1.4	1.8
183	Q92879	CELF1 CUGBP Elav-like family member 1	CELF1	GC*AFVTFTTR	1.1	0.9	1.3	1.3	1.8
184	Q9H1B7	IRF2BPL Interferon regulatory factor 2-binding protein-like	IRF2BPL	AHGC*FQDGR	0.9	0.9	0.9	1.3	1.8
185	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	ITGC*ASPGK	1.1	1.2	1.7	1.6	1.8
186	Q16576	RBBP7 Histone-binding protein RBBP7	RBBP7	VHIPNDDAQFDASHC*DSDK	0.9	1.0	0.9	1.5	1.8
187	Q15723	ELF2 ETS-related transcription factor Elf-2	ELF2	IITIPATQLAQC*QLQTK	1.1	1.1	1.2	1.4	1.8
188	Q7RTV0	PHF5A PHD finger-like domain-containing protein 5A	PHF5A	PC*TLVR	1.0	1.1	1.0	1.4	1.8
189	Q9Y3F4	STRAP Serine-threonine kinase receptor-associated protein	STRAP	IGFPETTEEELEEIASENSDC*IFPSAPDVK	1.0	0.9	1.0	1.3	1.8
190	P50570	DNM2 Dynamin-2	DNM2	LQDAFSSIGQSC*HLDLPQIAVVGGQSAGK	1.0	1.0	1.1	1.3	1.8
191	Q15370	TCEB2 Transcription elongation factor B polypeptide 2	TCEB2	ADDTFEALC*IEPFSSPPELPDVMK	1.3	1.0	1.4	1.2	1.8
192	P48047	ATP5O ATP synthase subunit O, mitochondrial	ATP5O	GEVPC*TVTSASPLEEATLSELK	1.0	1.3	1.3	1.6	1.8
193	P55769	NHP2L1 NHP2-like protein 1	NHP2L1	LLDLVQQSC*NYK	1.0	1.0	1.0	1.6	1.8
194	O43175	PHGDH D-3-phosphoglycerate dehydrogenase	PHGDH	NAGNC*LSPAVIVGLLK	1.0	1.0	1.1	1.4	1.8
195	P49327	FASN Fatty acid synthase	FASN	ADEASELAC*PTPK	1.0	1.0	1.0	1.2	1.8
196	O15355	PPM1G Protein phosphatase 1G	PPM1G	C*SGDGVGAPR	1.0	1.1	1.1	1.3	1.7
197	Q9BQ61	C19orf43 Uncharacterized protein C19orf43	C19orf43	AHQC*GDDDK	1.1	1.0	1.0	0.8	1.7
198	Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	LQISHEAAAC*ITGLR	1.1	1.0	1.0	1.5	1.7
199	P51553	IDH3G Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	LGDGLFLQC*CR	1.1	1.4	1.3	1.9	1.7
200	Q15631	TSN Translin	TSN	ETAAAC*VEK	0.9	1.1	1.0	1.6	1.7

201	P09429	HMGB1 High mobility group protein B1	HMGB1	MSSYAFFVQTC*R	1.0	1.0	1.1	2.0	1.7
202	Q8TEX9	IPO4 Importin-4	IPO4	APAALPALC*DLLASAADPQIR	1.1	1.2	1.3	1.6	1.7
203	P13639	EEF2 Elongation factor 2	EEF2	STLTDSLVC*K	1.0	1.0	1.0	1.4	1.7
204	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	SVLDAAQIVGLNC*LR	1.2	1.2	1.2	1.6	1.7
205	Q06323	PSME1 Proteasome activator complex subunit 1	PSME1	EDLC*TK	1.2	1.0	1.2	1.6	1.7
206	P28838	LAP3 Cytosol aminopeptidase	LAP3	SAGAC*TAAAFLK	0.9	0.9	0.9	1.5	1.7
207	Q93052	LPP Lipoma-preferred partner	LPP	TYITDPVSAPC*APPLQPK	0.9	0.9	1.1	1.4	1.7
208	Q16186	ADRM1 Proteasomal ubiquitin receptor ADRM1	ADRM1	VPQC*PSGR	8.1	0.1	1.0	3.2	1.7
209	Q7Z4W1	DCXR L-xylulose reductase	DCXR	GVPGAIVNVSSQC*SQR	1.0	1.3	1.4	1.8	1.7
210	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	GNHEC*ASINR	1.0	1.0	1.1	1.7	1.7
211	P62316	SNRPD2 Small nuclear ribonucleoprotein Sm D2	SNRPD2	NNTQVLINC*R	1.0	1.2	1.3	10.4	1.7
212	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	YVDIAIPC*NNK	1.2	1.1	1.3	1.9	1.7
213	P00966	ASS1 Argininosuccinate synthase	ASS1	FELSC*YSLAPQIK	0.9	1.1	1.3	1.3	1.7
214	Q969Z0	TBRG4 Protein TBRG4	TBRG4	LATDLLSLMPSLTSGEVAHC*AK	1.1	1.2	0.2	1.6	1.7
215	P23921	RRM1 Ribonucleoside-diphosphate reductase large subunit	RRM1	IIDINYYPVPEAC*LSNK	1.1	0.9	1.5	1.4	1.6
216	Q04637	EIF4G1 Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	LQGINC*GPDFTPSFANLGR	0.9	1.0	1.1	1.3	1.6
217	Q96JB2	COG3 Conserved oligomeric Golgi complex subunit 3	COG3	ELLLGPSIAC*TVAELTSQNNR	1.0	1.0	1.0	1.2	1.6
218	P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	LNVC*VSK	1.0	1.0	1.0	1.3	1.6
219	P17676	CEBPB CCAAT/enhancer-binding protein beta	CEBPB	APPTAC*YAGAAPAPSQVK	1.0	1.1	1.0	1.2	1.6
220	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	IVDTPC*NEMNTDTFLEEINK	1.4	1.0	0.9	0.9	1.6
221	P21964	COMT Catechol O-methyltransferase	COMT	LITIEINPDC*AAITQR	1.0	1.2	1.1	1.2	1.6
222	P40227	CCT6A T-complex protein 1 subunit zeta	CCT6A	NAIDDGC*VVPGAGAVEVAMAEALIK	1.1	1.0	0.9	0.9	1.6
223	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	YVAAAFPSAC*GK	2.5	1.3	1.4	2.0	1.6
224	P52597	HNRNPF Heterogeneous nuclear ribonucleoprotein F	HNRNPF	DLSYC*LSGMYDHR	1.2	1.1	0.9	1.6	1.6
225	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	INALTAASEAAC*LIVSVDETIK	1.1	1.1	1.0	1.6	1.6
226	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	PDGNC*FYR	1.1	1.1	1.1	1.5	1.6
227	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	DLNYC*FSGMSDHR	1.0	1.1	1.0	1.5	1.6
228	O60716	CTNND1 Catenin delta-1	CTNND1	TPAILEASAGAIQNLC*AGR	1.1	1.2	1.4	1.7	1.6
229	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	DC*LINAAK	1.0	1.1	1.1	1.4	1.6
230	Q6P1X6	C8orf82 UPF0598 protein C8orf82	C8orf82	YEAAFPFLSPC*GR	1.0	1.0	1.1	1.3	1.6
231	P55786	NPEPPS Puromycin-sensitive aminopeptidase	NPEPPS	DGVC*VR	1.1	1.1	1.1	1.2	1.6
232	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	DLAGC*IHGLSNVK	1.0	1.1	1.2	1.6	1.6
233	P30153	PPP2R1A Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	LNIISNLDC*VNEVIGIR	0.9	1.0	1.1	1.3	1.6
234	O15355	PPM1G Protein phosphatase 1G	PPM1G	GTEAGQVGEPGIPTGEAGPSC*SSASDK	1.1	1.1	1.0	1.5	1.6

235	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	TLTSC*FLSCVVCVEGIVTK	1.1	1.1	1.2	1.4	1.6
236	P22061	PCMT1 Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	MVGC*TGK	0.9	0.9	0.9	1.4	1.6
237	erse_Q9N	CRIM1 Cysteine-rich motor neuron 1 protein	CRIM1	SCSLEPC*K	1.1	1.2	1.3	1.5	1.5
238	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	AEGSDVANAVLDGADC*IMLSGETAK	0.8	1.0	1.2	1.2	1.5
239	P11413	G6PD Glucose-6-phosphate 1-dehydrogenase	G6PD	LQFHDVAGDIFHQQC*K	1.3	1.1	1.1	1.3	1.5
240	Q9Y4L1	HYOU1 Hypoxia up-regulated protein 1	HYOU1	VEFEELC*ADLFER	1.2	0.9	1.1	1.1	1.5
241	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	EEFASTC*PDDEEIELAYEQVAK	1.6	1.6	1.5	1.4	1.5
242	P78346	RPP30 Ribonuclease P protein subunit p30	RPP30	LTIIVSDPSHC*NVLR	0.9	1.0	1.0	1.1	1.5
243	P53396	ACLY ATP-citrate synthase	ACLY	FIC*TTSAIQNR	1.0	0.7	0.9	1.1	1.5
244	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	FC*PFAER	1.1	1.0	1.1	1.0	1.5
245	Q9BXJ9	NAA15 N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	LFNTAVC*ESK	1.1	1.0	1.1	1.4	1.5
246	Q9GZZ9	UBA5 Ubiquitin-like modifier-activating enzyme 5	UBA5	EGVC*AASLPTTMGVVAGILVQNVLK	0.9	1.2	0.9	1.2	1.5
247	P10599	TXN Thioredoxin	TXN	C*MPTFQFFK	1.1	1.0	1.0	1.2	1.5
248	Q15149	PLEC Plectin	PLEC	LC*FEGLR	0.9	0.9	1.1	1.1	1.5
249	P31949	S100A11 Protein S100-A11	S100A11	C*IESLIAVFQK	1.4	0.9	1.3	1.0	1.5
250	Q96RQ3	MCCC1 Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCC1	ESLC*QAALGLILK	1.2	1.3	1.2	1.7	1.5
251	Q6P996	PDXDC1 Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	HAC*QLSQR	1.1	1.2	1.3	1.5	1.5
252	Q9HB40	SCPEP1 Retinoid-inducible serine carboxypeptidase	SCPEP1	TFFSC*HK	1.0	1.0	1.5	1.4	1.5
253	Q04760	GLO1 Lactoylglutathione lyase	GLO1	C*DFPIMK	1.2	0.8	0.9	1.3	1.5
254	O00233	PSMD9 26S proteasome non-ATPase regulatory subunit 9	PSMD9	GIGMNEPLVDC*EGYPR	0.9	1.1	1.3	1.2	1.5
255	Q8WU76	SCFD2 Sec1 family domain-containing protein 2	SCFD2	AVFVLSC*LLK	1.2	1.1	1.0	1.2	1.5
256	Q96EY5	FAM125A Multivesicular body subunit 12A	FAM125A	SC*SPLAFSAFGDLTIK	1.0	0.9	1.0	0.9	1.5
257	Q9UKV8	EIF2C2 Protein argonaute-2	EIF2C2	SFFTASEGC*SNPLGGGR	1.2	0.9	0.9	0.9	1.5
258	O60547	GMDS GDP-mannose 4,6 dehydratase	GMDS	IYLGQLEC*FSLGNLDAK	1.1	1.0	1.0	1.8	1.5
259	P49915	GMPS GMP synthase	GMPS	TVGVQGDC*R	0.9	1.1	1.0	1.1	1.5
260	P46782	RPS5 40S ribosomal protein S5	RPS5	AQC*PIVER	1.0	1.1	1.1	1.4	1.5
261	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	C*CSGAIIVLTK	1.0	1.0	1.1	1.3	1.5
262	Q09666	AHNAK Neuroblast differentiation-associated protein AHNAK	AHNAK	LEGDLTGPSVGVEVPDVELEC*PDAK	1.1	1.0	1.0	1.1	1.5
263	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	LVVPATQC*GSLIGK	1.0	0.9	1.0	1.1	1.5
264	P30040	ERP29 Endoplasmic reticulum resident protein 29	ERP29	GQGVYLGMPGC*LPVYDALAGEFIR	1.0	1.0	2.7	0.6	1.5
265	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	GC*DVVVIPAGVPR	1.0	1.2	1.3	1.4	1.5
266	Q99873	PRMT1 Protein arginine N-methyltransferase 1	PRMT1	VEDLTFTSPFC*LQVK	1.0	1.2	1.1	1.0	1.5
267	Q9H8M7	FAM188A Protein FAM188A	FAM188A	SSPGLSDTIFC*R	1.9	2.6	1.6	3.5	1.5
268	Q16555	DPYSL2 Dihydropyrimidinase-related protein 2	DPYSL2	FQLTDC*QIYEVLSVIR	0.9	1.1	0.9	2.6	1.5
269	O75083	WDR1 WD repeat-containing protein 1	WDR1	SIQC*LTVHK	1.0	1.2	1.3	1.6	1.5
270	O00515	LAD1 Ladinin-1	LAD1	GLPC*TELFVAPVGVASK	1.2	1.0	1.6	1.3	1.5

271	Q8IUR0	TRAPPC5 Trafficking protein particle complex subunit 5	TRAPPC5	ENSTLNC*ASFTAGIVEAVLTHSGFPAK	1.0	1.0	1.0	1.3	1.5
272	Q8TEX9	IPO4 Importin-4	IPO4	DNIC*GALAR	1.0	1.3	1.3	1.3	1.5
273	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	QEPLGSDSEGVNC*LAYDEAIMAQQDR	1.0	1.0	1.1	1.2	1.5
274	P45974	USP5 Ubiquitin carboxyl-terminal hydrolase 5	USP5	VC*ASEK	1.0	1.0	1.0	1.2	1.5
275	P62244	RPS15A 40S ribosomal protein S15a	RPS15A	C*GVISPR	0.9	1.1	1.2	1.3	1.4
276	Q96EY5	FAM125A Multivesicular body subunit 12A	FAM125A	GFSAISC*TVEGAPASFGK	1.0	0.8	0.9	0.9	1.4
277	P31153	MAT2A S-adenosylmethionine synthase isoform type-2	MAT2A	TC*NVLVALEQQSPDIAQGVHLDR	1.0	1.1	1.1	1.3	1.4
278	P67936	TPM4 Tropomyosin alpha-4 chain	TPM4	EENVGLHQTLDQTLNELNC*I	1.1	1.0	1.0	1.2	1.4
279	Q09666	AHNAK Neuroblast differentiation-associated protein AHNAK	AHNAK	GPFVEAEVPDVDLEC*PDAK	1.2	0.9	1.0	1.2	1.4
280	Q96IR7	HPDL 4-hydroxyphenylpyruvate dioxygenase-like protein	HPDL	HAVPSATNLC*FDVADAGAATR	1.2	1.1	0.9	2.2	1.4
281	P53597	SUCLG1 Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	LIGPNCPGVINPGEC*K	1.0	1.1	1.1	1.6	1.4
282	P38606	ATP6V1A V-type proton ATPase catalytic subunit A	ATP6V1A	VLDALFPCVQGGTTAIPGAFGC*GK	1.0	1.1	1.2	1.3	1.4
283	Q9Y3A3	MOB4 MOB-like protein phocein	MOB4	HTLDGAAC*LLNSNK	0.9	1.0	1.0	1.2	1.4
284	P49327	FASN Fatty acid synthase	FASN	AINC*ATSGVVGLVNCLR	1.1	1.1	1.0	1.4	1.4
285	P24298	GPT Alanine aminotransferase 1	GPT	LLEETGIC*VVPGSGFGQR	1.0	1.2	1.1	1.4	1.4
286	Q9HA64	FN3KRP Ketosamine-3-kinase	FN3KRP	ATGHSGGGC*ISQGR	1.0	1.2	1.0	1.4	1.4
287	P45985	MAP2K4 Dual specificity mitogen-activated protein kinase kinase 4	MAP2K4	LC*DFGISGQLVDSIAK	1.1	0.8	0.7	1.4	1.4
288	O60547	GMDS GDP-mannose 4,6 dehydratase	GMDS	PTEVDFLQGDC*TK	1.0	0.9	1.1	1.2	1.4
289	E9PPU0	EPPK1 Epiplakin	EPPK1	YLC*GLGAVGGVR	1.1	1.0	1.1	1.2	1.4
290	P36969	GPX4 Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	GPX4	YAEC*GLR	1.0	1.0	1.0	1.1	1.4
291	P61158	ACTR3 Actin-related protein 3	ACTR3	LGYAGNTEPQFIIPSC*IAIK	1.1	1.1	1.1	1.5	1.4
292	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	SSGGFVWAC*K	1.4	1.0	1.1	1.5	1.4
293	P16455	MGMT Methylated-DNA--protein-cysteine methyltransferase	MGMT	VVC*SSGAVGNYSGGLAVK	1.0	1.1	1.1	1.5	1.4
294	P12532	CKMT1B Creatine kinase U-type, mitochondrial	CKMT1B	LGYILTC*PSNLGTGLR	1.1	1.0	1.1	1.3	1.4
295	Q9H0C8	ILKAP Integrin-linked kinase-associated serine/threonine phosphatase 2C	ILKAP	FILLAC*DGLFK	1.0	0.9	1.1	1.3	1.4
296	P57081	WDR4 tRNA (guanine-N(7)-)-methyltransferase subunit WDR4	WDR4	SGDVYSFSVLEPHGC*GR	1.5	1.0	0.9	1.2	1.4
297	P18669	PGAM1 Phosphoglycerate mutase 1	PGAM1	YADLTEDQLPSC*ESLK	0.9	1.0	1.1	1.1	1.4
298	P30041	PRDX6 Peroxiredoxin-6	PRDX6	DFTPVC*TTELGR	1.0	0.8	1.0	0.9	1.4
299	A6NDG6	PGP Phosphoglycolate phosphatase	PGP	NNQESDC*VSK	1.0	0.9	1.1	1.3	1.4
300	O15382	BCAT2 Branched-chain-amino-acid aminotransferase, mitochondrial	BCAT2	EVFGSGTAC*QVCPVHR	1.1	1.0	1.1	1.1	1.4
301	Q08J23	NSUN2 tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	MVYSTC*SLNPIEDEAVIASLLEK	1.1	1.1	1.2	1.2	1.4
302	Q9Y508	RNF114 RING finger protein 114	RNF114	DC*GGAAQLAGPAAEADPLGR	1.0	1.0	1.1	1.2	1.4
303	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	QC*PIMDPAWEAPEGVPIDAIIFGGR	1.0	1.1	1.3	1.5	1.4
304	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	SVHYC*PATK	0.9	1.0	1.0	1.5	1.4

305	P00338	LDHA L-lactate dehydrogenase A chain	LDHA	VIGSGC*NLDSAR	1.0	1.1	1.0	1.4	1.4
306	P13489	RNH1 Ribonuclease inhibitor	RNH1	LDDC*GLTEAR	2.1	1.7	1.4	1.4	1.4
307	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	ALNALC*DGLIDELNQALK	1.0	1.0	1.0	1.3	1.4
308	P41250	GARS Glycine--tRNA ligase	GARS	SCYDLSC*HAR	1.1	1.1	1.3	1.3	1.4
309	Q7Z5L9	IRF2BP2 Interferon regulatory factor 2-binding protein 2	IRF2BP2	AHGC*FPEGR	0.9	0.9	0.9	1.2	1.4
310	Q86YH6	PDSS2 Decaprenyl-diphosphate synthase subunit 2	PDSS2	C*LLSDELSNIAMQVR	0.9	1.0	1.1	1.1	1.4
311	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	VC*VETVESGAMTK	1.1	0.9	1.0	1.8	1.3
312	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	LGGTIDDC*ELVEGLVLTQK	0.9	1.1	1.1	1.4	1.3
313	O15144	ARPC2 Actin-related protein 2/3 complex subunit 2	ARPC2	NC*FASVFEK	0.9	1.0	1.1	1.4	1.3
314	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	EGTDSSQGIPQLVSNISAC*QVIAEAVR	0.9	1.1	1.0	1.4	1.3
315	P13489	RNH1 Ribonuclease inhibitor	RNH1	ELDLSNNC*LGDAGILQLVESVR	1.0	1.0	1.1	1.4	1.3
316	P60709	ACTB Actin, cytoplasmic 1	ACTB	CPEALFQPSFLGMESC*GIHETTFNSIMK	1.0	1.1	1.2	1.3	1.3
317	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	AATGEEVSAEDLGGADLHC*R	0.9	1.0	1.1	1.2	1.3
318	Q9UI30	TRMT112 tRNA methyltransferase 112 homolog	TRMT112	IC*PVEFNPNFVAR	1.1	1.0	1.0	1.2	1.3
319	Q9NZZ3	CHMP5 Charged multivesicular body protein 5	CHMP5	APPPSLTDC*IGTVDSR	1.2	1.0	1.2	1.1	1.3
320	P49458	SRP9 Signal recognition particle 9 kDa protein	SRP9	VTDDLVC*LVYK	1.0	1.0	1.1	1.1	1.3
321	Q9P0W2	HMG20B SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related	HMG20B	GGDC*DGFSTFDVPIFTEEFLDQNK	1.0	0.9	0.9	1.9	1.3
322	Q9UBT2	UBA2 SUMO-activating enzyme subunit 2	UBA2	VLVVGAGGIGC*ELLK	1.1	1.0	1.1	1.3	1.3
323	Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGAC*GLR	1.3	0.9	1.2	1.3	1.3
324	Q8N806	UBR7 Putative E3 ubiquitin-protein ligase UBR7	UBR7	VEQNSEPC*AGSSSESDLQTVFK	1.1	1.1	1.1	1.2	1.3
325	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	GLLDVTC*K	1.1	0.9	1.0	1.0	1.3
326	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	AAVEEGIVLGGGC*ALLR	1.0	1.0	1.0	1.1	1.3
327	Q14247	CTTN Src substrate cortactin	CTTN	HC*SQVDSVR	1.0	0.9	1.0	1.1	1.3
328	Q96EP5	DAZAP1 DAZ-associated protein 1	DAZAP1	PC*TPR	1.0	0.9	1.2	1.0	1.3
329	O75223	GGCT Gamma-glutamylcyclotransferase	GGCT	NPSAAFFC*VAR	1.0	0.9	1.0	0.9	1.3
330	P36405	ARL3 ADP-ribosylation factor-like protein 3	ARL3	LSC*VPVLIFANK	1.0	0.9	1.0	1.1	1.3
331	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	AC*ANPAAGSVILLENLR	1.8	1.0	1.2	0.9	1.3
332	Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	AFAFVTFADDQIAQSLC*GEDLIIK	1.7	1.3	0.8	1.7	1.3
333	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	GIFPVLC*K	1.1	1.0	1.1	1.3	1.3
334	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	YLAEVAC*GDDR	0.8	0.8	0.8	1.0	1.3
335	Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	YCFSEMAPVC*AVVGGILAQEIVK	1.1	1.0	1.0	1.2	1.3
336	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	GCITIIGGGDTATC*CAK	0.9	0.9	0.6	1.0	1.3
337	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	ISAFGYLEC*SAK	0.9	0.7	0.8	1.0	1.3
338	Q9BQ52	ELAC2 Zinc phosphodiesterase ELAC protein 2	ELAC2	GPSGC*SGGPNTVYLQVVAAGSR	0.9	1.2	1.5	1.7	1.3

339	P13639	EEF2 Elongation factor 2	EEF2	TFC*QLILDPIFK	1.0	1.0	1.0	1.2	1.3
340	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	LDFVC*SFLQK	1.1	0.8	1.0	1.1	1.3
341	P60981	DSTN Destrin	DSTN	LGGSLIVAFEGC*PV	1.0	1.0	1.0	1.0	1.3
342	Q96GX2	ATXN7L3B Putative ataxin-7-like protein 3B	ATXN7L3B	LPLC*SLPGEPGNGPDQQLQR	1.1	1.2	1.0	0.7	1.3
343	Q9Y263	PLAA Phospholipase A-2-activating protein	PLAA	AINC*PEDIVFPALDILR	1.0	1.0	1.1	1.2	1.3
344	O14980	XPO1 Exportin-1	XPO1	LDINLLDNVVNC*LYHGEGAQQR	1.1	1.0	1.0	1.2	1.3
345	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	VC*NFLASQVPFPSR	1.1	1.0	0.9	1.1	1.3
346	P26641	EEF1G Elongation factor 1-gamma	EEF1G	AAAPAPEEEMDEC*EQALAAEPK	1.0	1.0	1.0	1.1	1.3
347	P60981	DSTN Destrin	DSTN	C*STPEEIK	1.0	1.0	1.0	1.1	1.3
348	P49840	GSK3A Glycogen synthase kinase-3 alpha	GSK3A	LC*DFGSAK	1.0	0.8	0.9	1.3	1.3
349	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	VDENFDC*VEADDVEGK	1.0	0.9	0.9	1.2	1.3
350	Q96RS6	NUDCD1 NudC domain-containing protein 1	NUDCD1	DSAQC*AAIAER	1.0	0.9	1.0	1.2	1.3
351	P26639	TARS Threonine--tRNA ligase, cytoplasmic	TARS	DQELYFFHELSPGSC*FFLPK	1.0	1.0	1.0	1.2	1.3
352	P78371	CCT2 T-complex protein 1 subunit beta	CCT2	SLHDALC*VLAQTVK	1.1	0.9	1.0	1.1	1.3
353	P62306	SNRPF Small nuclear ribonucleoprotein F	SNRPF	C*NNVLYIR	1.1	1.0	1.0	1.1	1.3
354	P35914	HMGCL Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	VAQATC*K	0.9	0.9	1.0	1.1	1.2
355	P61158	ACTR3 Actin-related protein 3	ACTR3	TLTGTVIDSGDGVTHVIPVAEGYVIGSC*IK	1.0	1.3	1.1	1.4	1.2
356	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	VFIMDSC*DELIPEYLNFIR	1.2	1.1	1.0	1.3	1.2
357	Q9BV86	NTMT1 N-terminal Xaa-Pro-Lys N-methyltransferase 1	NTMT1	IIC*SAGLSLLAEER	1.0	1.0	1.0	1.2	1.2
358	P48431	SOX2 Transcription factor SOX-2	SOX2	APC*QAGDLR	1.0	0.9	0.9	1.2	1.2
359	P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	SC*GSLLPELK	1.0	1.1	1.2	1.2	1.2
360	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	HLNEIDLFHC*IDPNDSK	1.0	1.0	1.0	1.1	1.2
361	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	NTGIIC*TIGPASR	1.0	1.1	1.1	1.1	1.2
362	P53602	MVD Diphosphomevalonate decarboxylase	MVD	DGDPLPSSLSC*K	1.0	0.9	1.0	1.1	1.2
363	Q96HE7	ERO1L ERO1-like protein alpha	ERO1L	HDDSSDNFC*EADDIQSPEAEYVDLLLNPER	1.1	1.1	1.0	1.1	1.2
364	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	QLC*DNAGFDATNILNK	0.9	0.9	0.9	1.1	1.2
365	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	LEVDAIVNAANSSLLGGGGVDGC*IHR	1.0	1.0	1.0	1.1	1.2
366	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	C*IPALDSLTPANEDQK	1.2	1.0	1.0	1.0	1.2
367	Q7L1Q6	BZW1 Basic leucine zipper and W2 domain-containing protein 1	BZW1	FDPTQFQDC*IIQGLTETGTDLEAVAK	1.0	1.0	1.0	1.1	1.2
368	P33240	CSTF2 Cleavage stimulation factor subunit 2	CSTF2	LC*VQNSPQEAR	1.1	1.0	1.0	1.0	1.2
369	Q9Y5R8	TRAPPC1 Trafficking protein particle complex subunit 1	TRAPPC1	NPLC*PLGQTVQSELFR	0.9	1.1	1.1	1.3	1.2
370	Q9Y296	TRAPPC4 Trafficking protein particle complex subunit 4	TRAPPC4	C*ELFDQNLK	1.0	1.0	1.1	1.2	1.2
371	Q8IVH4	MMAA Methylmalonic aciduria type A protein, mitochondrial	MMAA	AC*LAEAITLVESTHSR	0.8	1.0	1.0	1.1	1.2
372	P11413	G6PD Glucose-6-phosphate 1-dehydrogenase	G6PD	TQVC*GILR	1.0	1.0	0.9	1.1	1.2
373	O75131	CPNE3 Copine-3	CPNE3	NC*LNPQFSK	1.2	1.0	0.9	1.1	1.2
374	Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	LVVPASQC*GSLIGK	1.0	0.9	0.9	1.0	1.2

375	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	AITIAGVPQSVTEC*VK	1.2	1.1	1.0	0.9	1.2
376	P12004	PCNA Proliferating cell nuclear antigen	PCNA	C*AGNEDIITLR	1.0	1.0	1.0	0.9	1.2
377	P21333	FLNA Filamin-A	FLNA	VGTEC*GNQK	1.0	0.9	1.0	1.1	1.2
378	Q09666	AHNAK Neuroblast differentiation-associated protein AHNAK	AHNAK	LEGDLTGPSVDVEVPDVELEC*PDAK	1.1	1.0	1.0	1.1	1.2
379	P62258	YWHAE 14-3-3 protein epsilon	YWHAE	LIC*C*DILDVLDK	1.3	1.0	1.1	1.1	1.2
380	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	APVPSTC*SSTFPEELSPPSHQAK	1.0	0.9	1.0	1.0	1.2
381	Q9NS86	LANCL2 LanC-like protein 2	LANCL2	AFVNPFPDYEAAAGALLASGAAEETGC*VR	1.1	0.9	0.8	0.9	1.2
382	Q8WVV9	HNRPLL Heterogeneous nuclear ribonucleoprotein L-like	HNRPLL	GLC*ESVVEADLVEALEK	1.4	1.1	1.1	1.8	1.2
383	Q9NYL2	MLTK Mitogen-activated protein kinase kinase kinase MLT	MLTK	FDDLQFFENC*GGGSFGSVYR	1.0	1.0	1.3	1.4	1.2
384	P49327	FASN Fatty acid synthase	FASN	LSIPTYGLQC*TR	1.0	1.0	1.0	1.3	1.2
385	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	EQFSQGSPSNC*LETSLAEIFPLGK	0.9	1.2	1.0	1.2	1.2
386	Q9Y2Q3	GSTK1 Glutathione S-transferase kappa 1	GSTK1	ETTEAAC*R	1.0	0.9	1.0	1.1	1.2
387	P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	LC*FSTAQHAS	1.1	1.0	1.1	1.0	1.2
388	Q6IA69	NADSYN1 Glutamine-dependent NAD(+) synthetase	NADSYN1	NSSQETC*TR	1.0	1.0	0.9	1.2	1.2
389	Q15149	PLEC Plectin	PLEC	AFC*GFEDPR	1.0	0.9	1.0	1.1	1.2
390	P78347	GTF2I General transcription factor II-I	GTF2I	SILSPGGSC*GPIK	1.0	0.9	1.0	1.1	1.2
391	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	EYLPIGGLAEFC*K	0.9	1.1	1.1	1.3	1.2
392	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	TIIPLISQC*TPK	1.2	1.1	1.0	1.1	1.2
393	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	INISEGNC*PER	1.0	1.0	1.0	1.0	1.2
394	Q9Y224	C14orf166 UPF0568 protein C14orf166	C14orf166	LTALDYHNPAGFNC*K	1.1	0.9	1.1	1.0	1.2
395	Q7Z4W1	DCXR L-xylulose reductase	DCXR	AVTNHSVYC*STK	1.1	1.2	1.2	1.2	1.2
396	P13639	EEF2 Elongation factor 2	EEF2	YVEPIEDVPC*GNIVGLVGVDQFLVK	1.2	1.3	0.9	1.1	1.2
397	Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	VGLGIC*YDMR	1.1	1.0	0.9	1.1	1.2
398	P21333	FLNA Filamin-A	FLNA	AHVVPC*FDASK	1.1	1.0	1.0	1.1	1.2
399	P49915	GMPS GMP synthase	GMPS	AC*TTEEDQEK	1.2	0.9	1.0	1.0	1.2
400	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	IC*PVETLVEEAIQCAEK	1.1	1.0	1.0	1.0	1.2
401	O60610	DIAPH1 Protein diaphanous homolog 1	DIAPH1	AGC*AVTSLLASELTK	0.9	0.9	2.3	1.0	1.2
402	P14678	SNRPB Small nuclear ribonucleoprotein-associated protein B and B'	SNRPB	C*ILQDGR	1.2	1.1	1.1	1.3	1.2
403	P49721	PSMB2 Proteasome subunit beta type-2	PSMB2	NLADC*LR	1.2	1.1	1.1	1.3	1.2
404	Q9NVS9	PNPO Pyridoxine-5-phosphate oxidase	PNPO	LPEEEAEC*YFHSR	1.2	1.1	1.3	1.2	1.2
405	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	NDTPC*GTTIGPILASR	1.3	1.2	1.3	1.1	1.2
406	Q00796	SORD Sorbitol dehydrogenase	SORD	YNLSPSIFFCATPPDDGNLC*R	1.0	1.0	0.9	1.1	1.2
407	Q5TC12	ATPAF1 ATP synthase mitochondrial F1 complex assembly factor 1	ATPAF1	C*AQNQNK	0.9	0.9	1.6	1.1	1.1
408	P47756	CAPZB F-actin-capping protein subunit beta	CAPZB	DETVSDC*SPHIANIGR	1.0	1.0	1.0	1.0	1.1
409	P53582	METAP1 Methionine aminopeptidase 1	METAP1	LGIQGSYFCSQEC*FK	1.0	1.0	1.1	1.0	1.1

410	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	IIPTLEEGLQLPSPTATSQLP LESDAVEC*LNYQHYK	1.0	1.0	1.0	1.1	1.1
411	O95861	BPNT1 3(2),5-bisphosphate nucleotidase 1	BPNT1	TC*ATDLQTK	1.0	1.0	1.0	1.0	1.1
412	Q9Y365	STARD10 PCTP-like protein	STARD10	MECC*DVPAETLYDVLHD IEYR	1.1	1.0	1.0	1.0	1.1
413	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit 2	PSMD2	GTLTLC*PYHSDR	1.0	1.1	1.0	1.0	1.1
414	Q9NTK5	OLA1 Obg-like ATPase 1	OLA1	STFFNVLTNSQASAENFPF C*TIDPNESR	1.0	0.9	0.9	1.0	1.1
415	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	NVGC*LQEALQLATSFAQ LR	0.9	0.9	1.0	1.0	1.1
416	P21964	COMT Catechol O-methyltransferase	COMT	GSSC*FEC*THYQSFLEYR	1.1	1.0	1.0	1.4	1.1
417	P20810	CAST Calpastatin	CAST	SEC*K	1.1	1.0	1.1	1.2	1.1
418	Q9NZL4	HSPBP1 Hsp70-binding protein 1	HSPBP1	ALFAISC*LVR	1.3	1.1	1.1	1.0	1.1
419	Q96Q11	TRNT1 CCA tRNA nucleotidyltransferase 1, mitochondrial	TRNT1	YQGEHC*LLK	1.0	1.0	1.0	1.0	1.1
420	Q96EY8	MMAB Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	MMAB	IQCTLQDVGSALATPC*SS AR	1.1	1.0	0.9	1.0	1.1
421	O14561	NDUFAB1 Acyl carrier protein, mitochondrial	NDUFAB 1	LMC*PQEIVDYIADK	1.1	1.0	1.1	0.9	1.1
422	Q53T59	HS1BP3 HCLS1-binding protein 3	HS1BP3	LFDDPDLGGAIPLGDSLLL PAAC*ESGGPTPSLSHR	0.9	0.8	0.9	0.8	1.1
423	P43897	TSFM Elongation factor Ts, mitochondrial	TSFM	FEC*GEGEEAAETE	1.3	1.1	1.1	1.2	1.1
424	Q9NZL4	HSPBP1 Hsp70-binding protein 1	HSPBP1	DAC*DTVR	1.0	0.8	1.0	1.2	1.1
425	O95336	PGLS 6-phosphogluconolactonase	PGLS	AAC*CLAGAR	1.1	1.0	1.0	1.2	1.1
426	O95671	ASMTL N-acetylserotonin O-methyltransferase-like protein	ASMTL	LTAC*QVATAFNLSR	1.0	0.9	0.8	1.0	1.1
427	Q14566	MCM6 DNA replication licensing factor MCM6	MCM6	LGFSEYC*R	1.1	1.0	0.9	1.0	1.1
428	Q9BSH4	TACO1 Translational activator of cytochrome c oxidase 1	TACO1	LDSLGLCSVSC*ALEFIPNS K	1.0	0.9	0.9	1.0	1.1
429	Q9UJ70	NAGK N-acetyl-D-glucosamine kinase	NAGK	FAGFC*R	1.2	1.2	1.0	1.3	1.1
430	Q9BT78	COPS4 COP9 signalosome complex subunit 4	COPS4	QIQSLC*FQVNNLLEK	1.4	1.1	1.1	1.1	1.1
431	P62826	RAN GTP-binding nuclear protein Ran	RAN	VC*ENIPIVLC*GNK	1.0	1.1	1.2	1.1	1.1
432	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	HSMNPFC*EIAVEEAVR	1.0	1.0	1.0	1.1	1.1
433	P00492	HPRT1 Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	SYC*NDQSTGDIK	1.4	1.1	1.1	1.1	1.1
434	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	C*EFQDAYVLLSEK	1.1	0.9	1.0	1.0	1.1
435	P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	AC*QIFVR	1.0	1.0	0.9	1.0	1.1
436	P61981	YWHAG 14-3-3 protein gamma	YWHAG	NC*SETQYESK	1.2	1.2	1.3	0.9	1.1
437	P55036	PSMD4 26S proteasome non-ATPase regulatory subunit 4	PSMD4	SNPENNVGLITLANDC*EV LTTLTPDTGR	1.1	0.9	1.0	0.6	1.1
438	Q06587	RING1 E3 ubiquitin-protein ligase RING1	RING1	FC*SDCIVTALR	1.1	1.3	0.9	1.3	1.1
439	P49327	FASN Fatty acid synthase	FASN	LTPGC*EAEAETEAICFFV QQFTDMEHNR	1.0	1.0	1.2	1.2	1.1
440	Q9NXG2	THUMPD1 THUMP domain-containing protein 1	THUMPD 1	C*DAGGPR	1.1	1.0	1.0	1.1	1.1
441	Q9BV79	MECR Trans-2-enoyl-CoA reductase, mitochondrial	MECR	LALNC*VGGK	1.1	1.1	1.0	1.0	1.1
442	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	EEC*PVFTPPGGETLDQVK	1.0	1.2	0.9	1.2	1.1
443	Q99873	PRMT1 Protein arginine N-methyltransferase 1	PRMT1	VIGIEC*SSISDYAVK	1.1	1.1	1.0	1.2	1.1

444	P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	AALEALGSC*LNNK	1.1	0.9	0.9	1.2	1.1
445	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	FLDGNELTLADC*NLLPK	1.3	1.1	0.9	1.0	1.1
446	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	SVC*TEAGMFAIR	1.2	1.3	1.1	0.9	1.1
447	P14649	MYL6B Myosin light chain 6B	MYL6B	ILYSQC*GDVMR	0.9	1.3	0.9	0.9	1.1
448	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	LPC*IYLVDSGGAYLPR	1.0	1.1	1.1	1.3	1.1
449	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	GSDFDC*ELR	1.2	1.1	1.0	1.1	1.1
450	Q9Y5P6	GMPPB Mannose-1-phosphate guanyltransferase beta	GMPPB	LC*SGPGIVGNVLVDPSAR	1.1	0.9	0.9	1.1	1.1
451	Q969H4	CNKSR1 Connector enhancer of kinase suppressor of ras 1	CNKSR1	NLLQLC*PQSLEALAVR	1.0	1.0	1.0	1.4	1.1
452	Q15019	SEPT2 Septin-2	2-Sep	LTVVDTPGYGDAINC*R	1.0	1.0	1.0	1.2	1.1
453	Q6PI48	DARS2 Aspartate--tRNA ligase, mitochondrial	DARS2	LIC*LVTGSPSIR	1.2	1.0	1.0	1.1	1.1
454	O75390	CS Citrate synthase, mitochondrial	CS	LPC*VAAK	1.2	1.0	1.1	1.1	1.1
455	Q13526	PIN1 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	PIN1	SGEEDFESLASQFSDC*SSAK	0.9	1.0	1.0	1.1	1.1
456	P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	GFGFVC*FSSPEEATK	1.4	0.9	0.9	1.0	1.1
457	P55210	CASP7 Caspase-7	CASP7	LFFIQAC*R	1.0	0.8	0.8	0.9	1.1
458	Q9P2R7	SUCLA2 Succinyl-CoA ligase [ADP forming] subunit beta, mitochondrial	SUCLA2	ILAC*DDLDEAAR	1.2	1.2	1.0	1.2	1.1
459	P36507	MAP2K2 Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	LC*DFGVSGQLIDSMANSFVGTR	1.0	0.8	1.0	1.1	1.1
460	P31947	SFN 14-3-3 protein sigma	SFN	GEELSC*EER	1.1	1.0	1.0	1.0	1.1
461	P00338	LDHA L-lactate dehydrogenase A chain	LDHA	DDVFLSVPC*ILGQNGISDLVK	0.9	1.1	1.2	1.3	1.0
462	O95571	ETHE1 Protein ETHE1, mitochondrial	ETHE1	TDFQQGC*AK	1.0	1.1	1.1	1.3	1.0
463	P13639	EEF2 Elongation factor 2	EEF2	C*LYASVLTAQPR	1.1	1.0	1.1	1.0	1.0
464	P37802	TAGLN2 Transgelin-2	TAGLN2	NMAC*VQR	1.0	0.9	1.0	1.0	1.0
465	Q96AT9	RPE Ribulose-phosphate 3-epimerase	RPE	IGPSILNSDLANLGAEC*LR	1.2	1.0	1.0	0.8	1.0
466	Q02543	RPL18A 60S ribosomal protein L18a	RPL18A	DLTTAGAVTQC*YR	1.1	0.9	2.1	3.7	1.0
467	Q9HAV7	GRPEL1 GrpE protein homolog 1, mitochondrial	GRPEL1	ATQC*VPK	1.0	0.9	0.9	1.0	1.0
468	O00268	TAF4 Transcription initiation factor TFIID subunit 4	TAF4	SC*K	1.0	1.2	0.9	0.8	1.0
469	Q04917	YWHAH 14-3-3 protein eta	YWHAH	NC*NDFQYESK	1.0	0.9	1.1	0.7	1.0
470	Q9UNH7	SNX6 Sorting nexin-6	SNX6	IGSSLYALGTQDSTDIC*K	0.9	1.0	0.9	1.2	1.0
471	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	YAGLSTC*FR	1.0	1.1	1.0	1.1	1.0
472	Q9Y530	C6orf130 O-acetyl-ADP-ribose deacetylase C6orf130	C6orf130	IGC*GLDR	0.9	0.9	0.9	1.1	1.0
473	P61158	ACTR3 Actin-related protein 3	ACTR3	YSYVC*PDLVK	0.8	1.0	1.0	1.0	1.0
474	P55735	SEC13 Protein SEC13 homolog	SEC13	FASGGC*DNLIK	1.0	1.0	1.0	1.0	1.0
475	Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	AITIAGIPQSIIEC*VK	1.2	1.0	1.0	1.0	1.0
476	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	LSSC*DSFTSTINELNHCLSLR	1.1	0.9	0.9	1.0	1.0
477	Q9BW61	DDA1 DET1- and DDB1-associated protein 1	DDA1	FHADSVC*K	1.1	1.0	1.0	1.0	1.0
478	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	SQETEC*TYFSTPLLLGK	1.4	1.0	1.1	0.9	1.0

479	P26440	IVD Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	GSNTCELIFEDC*K	1.0	1.1	0.9	1.6	1.0
480	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	FIC*EQDHQNFLR	1.0	1.1	0.9	1.0	1.0
481	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	C*LSVMEAK	0.9	1.0	1.0	1.0	1.0
482	P24941	CDK2 Cyclin-dependent kinase 2	CDK2	APEILLGC*K	1.0	1.0	0.9	1.0	1.0
483	P51659	HSD17B4 Peroxisomal multifunctional enzyme type 2	HSD17B4	IC*DFENASK	0.9	1.0	1.0	1.0	1.0
484	Q9UL46	PSME2 Proteasome activator complex subunit 2	PSME2	C*GFLPGNEK	0.9	0.8	0.9	0.9	1.0
485	Q14738	PPP2R5D Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	C*TAK	1.0	1.0	1.4	1.0	1.0
486	P23528	CFL1 Cofilin-1	CFL1	AVLFC*LSEDK	4.5	0.9	0.8	0.8	1.0
487	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	IGNC*PFSQR	1.0	1.0	1.0	1.1	1.0
488	P13489	RNH1 Ribonuclease inhibitor	RNH1	LSLQNC*C*LTGAGC*GVLSSTLR	1.2	0.9	0.7	0.9	1.0
489	P52597	HNRNPF Heterogeneous nuclear ribonucleoprotein F	HNRNPF	GLPFGC*TK	1.3	1.0	1.0	1.1	1.0
490	P50990	CCT8 T-complex protein 1 subunit theta	CCT8	IAVYSC*PFDGMITETK	1.0	1.0	0.9	0.9	1.0
491	P37837	TALDO1 Transaldolase	TALDO1	ALAGC*DFLTISPK	1.3	1.0	1.0	0.9	1.0
492	P37802	TAGLN2 Transgelin-2	TAGLN2	DGTVLC*ELINALYPEGQAPVK	1.5	1.1	1.0	0.9	1.0
493	P28838	LAP3 Cytosol aminopeptidase	LAP3	QVVDC*QLADVNNIGK	0.9	1.0	0.9	0.8	1.0
494	P31942	HNRNPH3 Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	GLPFGC*SK	1.2	1.1	1.0	1.1	1.0
495	Q12765	SCRN1 Secernin-1	SCRN1	TQSPC*FGDDDPAK	1.1	1.1	0.9	0.9	1.0
496	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	YTC*GEAPDYDR	1.0	1.2	1.1	1.1	0.9
497	P49327	FASN Fatty acid synthase	FASN	AAPLDSIHSLAAYYIDC*IR	1.3	1.0	1.1	1.1	0.9
498	Q9HAV7	GRPEL1 GrpE protein homolog 1, mitochondrial	GRPEL1	LYGIQAFC*K	1.1	0.7	1.0	1.0	0.9
499	Q86SX6	GLRX5 Glutaredoxin-related protein 5, mitochondrial	GLRX5	GTPEQPQC*GFSNAVVQILR	1.0	0.9	1.0	1.0	0.9
500	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	EGVVEC*SFVK	1.3	1.0	1.0	0.9	0.9
501	P30044	PRDX5 Peroxiredoxin-5, mitochondrial	PRDX5	ALNVEPDGTGLTC*SLAPNIISQL	1.1	0.9	0.9	0.8	0.9
502	Q96EK6	GNPNAT1 Glucosamine 6-phosphate N-acetyltransferase	GNPNAT1	ITLEC*LPQNVGFYK	1.1	0.9	0.7	0.9	0.9
503	Q9NS86	LANCL2 LanC-like protein 2	LANCL2	SVVC*QESDLPDELLYGR	1.1	0.9	0.9	0.9	0.9
504	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	TIC*AILENYQTEK	1.1	1.0	1.0	1.0	0.9
505	P52209	PGD 6-phosphogluconate dehydrogenase, decarboxylating	PGD	AVSTGVQAGIPMPC*FTTALSFYDGYR	1.4	1.0	0.9	1.0	0.9
506	P35270	SPR Sepiapterin reductase	SPR	TVVNISSLC*ALQPFK	1.0	0.9	1.0	1.0	0.9
507	Q5TFE4	NT5DC1 5-nucleotidase domain-containing protein 1	NT5DC1	HFLSDTGMAC*R	0.9	1.0	0.9	1.0	0.9
508	Q04917	YWHAH 14-3-3 protein eta	YWHAH	ELETVC*NDVLSLLDK	1.4	1.0	1.2	1.0	0.9
509	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	DIC*NDVLSLLEK	1.4	1.0	1.0	0.8	0.9
510	P60174	TPI1 Triosephosphate isomerase	TPI1	IIYGGSVTGATC*K	1.4	1.0	1.0	0.8	0.9
511	P39687	ANP32A Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A	SLDLFNC*EVTNLNDYR	1.3	1.0	1.3	0.8	0.9
512	Q7L8W6	ATPBD4 ATP-binding domain-containing protein 4	ATPBD4	C*EGDEVEDLYELLK	1.4	0.6	0.9	0.8	0.9
513	P31948	STIP1 Stress-induced-phosphoprotein 1	STIP1	ALSVGNIDDALQC*YSEAIK	1.2	1.1	1.1	1.2	0.9

514	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	LVIVGDGAC*GK	1.0	1.4	1.1	1.1	0.9
515	P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	ALYDTFSAFGNILSC*K	1.1	0.7	0.8	0.9	0.9
516	P15927	RPA2 Replication protein A 32 kDa subunit	RPA2	AC*PR	1.1	0.8	1.0	0.8	0.9
517	P60174	TPI1 Triosephosphate isomerase	TPI1	VAHALAEGLGVIAC*IGEK	1.4	0.9	1.0	0.8	0.9
518	Q9Y696	CLIC4 Chloride intracellular channel protein 4	CLIC4	AGSDGESIGNC*PFSQR	1.0	1.0	1.0	1.1	0.9
519	Q9NUQ9	FAM49B Protein FAM49B	FAM49B	VLTC*TDLEQGPNFFLDFE NAQPTESEK	0.9	0.6	1.2	1.0	0.9
520	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	GQAGGGGPGTGPGLGEA GSLATC*ELPLAK	1.0	0.8	0.8	0.9	0.9
521	P60174	TPI1 Triosephosphate isomerase	TPI1	IAVAAQNC*YK	1.3	0.9	1.0	0.8	0.9
522	Q92945	KHSRP Far upstream element-binding protein 2	KHSRP	C*EHAAR	1.0	0.9	0.8	0.9	0.9
523	P21964	COMT Catechol O-methyltransferase	COMT	YLPDTLLLEEC*GLLR	1.3	1.0	1.0	0.9	0.9
524	P13489	RNH1 Ribonuclease inhibitor	RNH1	SNELGDVGVHCVLQGLQT PSC*K	1.0	0.8	0.9	0.7	0.9
525	Q9NRF9	POLE3 DNA polymerase epsilon subunit 3	POLE3	AASVFVLYATSC*ANNFA MK	1.1	1.0	0.9	0.9	0.9
526	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	SIC*TTVLELLDK	1.4	0.9	1.1	0.9	0.9
527	Q9BWD1	ACAT2 Acetyl-CoA acetyltransferase, cytosolic	ACAT2	ATVAPEDVSEVIFGHVLAA GC*GQNPVR	1.0	0.8	0.8	0.8	0.9
528	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	YIEAC*AR	1.2	0.8	1.0	1.3	0.9
529	Q96S19	C16orf13 UPF0585 protein C16orf13	C16orf13	C*TEGLFR	1.1	0.8	1.0	1.3	0.9
530	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	GDFC*IQVGR	1.1	0.9	0.9	0.9	0.9
531	P52907	CAPZA1 F-actin-capping protein subunit alpha-1	CAPZA1	TIDGQQTIIAC*IESHQFQP K	1.5	1.0	1.0	0.9	0.9
532	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	ISSINSISALC*EATGADVE EVATAIGMDQR	1.1	1.1	1.1	0.9	0.9
533	P23528	CFL1 Cofilin-1	CFL1	HELQANC*YEEVK	1.0	0.9	0.9	0.9	0.9
534	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	YASIC*QQNGIVPIVEPEILP DGDHDLK	1.3	1.0	1.0	0.9	0.9
535	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	FC*LDNGAK	0.9	1.1	1.4	0.8	0.9
536	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	ASVGFGGSC*FQK	1.0	1.0	1.0	0.8	0.9
537	P31948	STIP1 Stress-induced-phosphoprotein 1	STIP1	ALDLDSSC*K	1.0	0.9	1.0	1.0	0.9
538	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	ALANSLAC*QGK	1.1	0.9	1.0	0.9	0.9
539	P34896	SHMT1 Serine hydroxymethyltransferase, cytosolic	SHMT1	NTC*PGDR	1.0	0.7	0.7	0.9	0.9
540	P11142	HSPA8 Heat shock cognate 71 kDa protein	HSPA8	VC*NPIITK	1.5	1.1	1.1	0.9	0.9
541	Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	GNGIVEC*LGPK	1.0	0.9	0.7	0.7	0.9
542	Q9NZA1	CLIC5 Chloride intracellular channel protein 5	CLIC5	AGIDGESIGNC*PFSQR	1.0	1.0	0.9	0.9	0.8
543	Q12849	GRSF1 G-rich sequence factor 1	GRSF1	YIELFLNSC*PK	0.8	1.0	0.9	0.9	0.8
544	P09467	FBP1 Fructose-1,6-bisphosphatase 1	FBP1	GTGELTQLLNSLC*TAVK	1.4	1.0	1.0	0.9	0.8
545	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	LTFSC*LGGSDNFK	1.3	0.9	0.9	1.0	0.8
546	P07237	P4HB Protein disulfide-isomerase	P4HB	ITEFC*HR	1.4	1.0	1.0	0.8	0.8
547	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	FFSDC*K	1.2	0.9	1.0	1.1	0.8
548	P60174	TPI1 Triosephosphate isomerase	TPI1	VPADTEVVC*APPTAYIDF AR	1.3	1.0	1.0	0.9	0.8

549	F5H284	PPIAL4D Peptidyl-prolyl cis-trans isomerase A-like 4D	PPIAL4D	IIPGFMC*QGGDFTR	1.0	1.0	0.9	0.9	0.8
550	O75874	IDH1 Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	DLAAC*IK	1.3	0.9	1.0	0.8	0.8
551	P61158	ACTR3 Actin-related protein 3	ACTR3	LPACVVDC*GTGYTK	0.8	1.0	0.8	1.0	0.8
552	P22234	PAICS Multifunctional protein ADE2	PAICS	ITSC*IFQLLQEAGIK	1.3	1.0	1.0	0.9	0.8
553	P24534	EEF1B2 Elongation factor 1-beta	EEF1B2	SYIEGYVPSQADVAVFEAV SSPPPADLC*HALR	1.1	1.0	1.1	0.9	0.8
554	P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	ITIADC*GQLE	1.4	0.9	1.0	0.9	0.8
555	P14174	MIF Macrophage migration inhibitory factor	MIF	LLC*GLLAER	1.4	1.0	1.0	0.9	0.8
556	P22061	PCMT1 Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	ALDVGSGSGILTAC*FAR	1.4	1.0	1.1	0.8	0.8
557	P50395	GDI2 Rab GDP dissociation inhibitor beta	GDI2	TDDYLDQPC*YETINR	1.6	1.2	1.2	0.9	0.8
558	O95571	ETHE1 Protein ETHE1, mitochondrial	ETHE1	QMFEPVSC*TFTYLLGDR	1.0	1.0	0.8	0.9	0.8
559	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	YLLQYQEPIPC*EQLVTAL CDIK	1.2	0.7	1.2	1.1	0.8
560	Q9BS40	LXN Latexin	LXN	VNC*TAEVLYPSTGQETAP EVNFTFEGETGK	1.4	1.2	1.1	1.0	0.8
561	P55212	CASP6 Caspase-6	CASP6	GTC*ADR	1.0	0.9	1.0	0.8	0.8
562	P52788	SMS Spermine synthase	SMS	YFTQGNC*VNLTEALSLYE EQLGR	1.3	0.8	0.9	0.6	0.8
563	P04632	CAPNS1 Calpain small subunit 1	CAPNS1	TDGFGIDTC*R	1.2	1.5	1.2	4.7	0.7
564	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	ILSC*GEVIHVK	1.3	1.0	1.0	0.9	0.7
565	P29373	CRABP2 Cellular retinoic acid-binding protein 2	CRABP2	PC*K	1.4	0.8	0.9	0.9	0.7
566	P49419	ALDH7A1 Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A 1	GSDC*GIVNVNIPTSGAEI GGAFGGEK	1.1	1.1	0.9	0.9	0.7
567	P07737	PFN1 Profilin-1	PFN1	C*YEMASHLR	1.3	0.9	1.0	0.9	0.7
568	P04632	CAPNS1 Calpain small subunit 1	CAPNS1	YSDESGNMDFDNFISC*LV R	2.2	1.4	1.1	1.0	0.7
569	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	DVLNLVYLC*EALNLPEV AR	1.3	1.1	0.9	0.9	0.7
570	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	LC*YSSDHEK	0.8	0.8	1.2	0.6	0.7
571	P26641	EEF1G Elongation factor 1-gamma	EEF1G	VPAFEGDDGFC*VFESNAI AYYVSNEELR	1.0	1.2	0.9	0.6	0.7
572	Q7Z5L9	IRF2BP2 Interferon regulatory factor 2-binding protein 2	IRF2BP2	LEDTHFVQC*PSVPSHK	1.0	1.2	1.1	1.1	0.7
573	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACRO D1	SC*YLSSLDLLLEHR	1.2	1.0	0.9	0.8	0.6
574	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	VPTANVSVVDLTC*R	1.1	0.7	0.6	0.5	0.6
575	P34896	SHMT1 Serine hydroxymethyltransferase, cytosolic	SHMT1	AVLEALGSC*LNNK	1.0	0.4	0.4	1.1	0.3
576	P23443	RPS6KB1 Ribosomal protein S6 kinase beta-1	RPS6KB1	PEC*FELLR	1.4	1.0	1.1	1.1	0.3

Table 2A-4. R-values from time-dependent transnitrosation experiment at 500 μM GSNO (0, 5, 10, 20, 30 and 60 mins treatment). 0 μM GSNO with 60 mins treatment was performed as a control. A list of all identified peptides (* denotes labeled cysteine) is presented at GSNO treatment time together with calculated Heavy:Light Ratios (R).

Peptide #	Uniprot #	Description	Symbol	Sequence	Heavy : Light Ratio					
					control	GSNO (500 μM) transnitrosation time (min)				
					60	5	10	20	30	60
1	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	IISNASC*TTNCLAPLAK	0.9	2.1	2.9	4.5	7.9	9.0
2	Q9NUU7	DDX19A ATP-dependent RNA helicase DDX19A	DDX19A	VLVTTNVC*AR	0.9	1.8	0.8	1.9	2.6	4.6
3	P23396	RPS3 40S ribosomal protein S3	RPS3	GC*EVVVSGK	1.0	3.0	2.1	3.9	2.6	3.7
4	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	LGNNC*VFAPADVTSEK	0.9	4.4	3.1	2.5	4.8	3.7
5	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	AVC*MLSNTTAIAEAWAR	0.9	2.5	2.1	3.2	3.1	3.4
6	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	YMACC*LLYR	0.9	2.1	1.7	2.1	2.2	3.0
7	P49327	FASN Fatty acid synthase	FASN	AFDTAGNGYC*R	1.0	3.3	2.7	3.1	3.4	2.9
8	O14561	NDUFAB1 Acyl carrier protein, mitochondrial	NDUFAB1	LMC*PQEIVDYIADK	0.9	1.7	1.0	1.1	1.5	2.8
9	P07437	TUBB Tubulin beta chain	TUBB	NMMAAC*DPR	0.9	3.7	2.6	3.2	3.5	2.8
10	P07437	TUBB Tubulin beta chain	TUBB	TAVC*DIPPR	0.9	3.1	2.7	3.7	3.5	2.8
11	P29401	TKT Transketolase	TKT	QAFTDVATGSLGQGLGAAC*GMAYTGK	0.9	3.2	2.7	4.4	3.1	2.7
12	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	GC*LLYGPPGTGK	0.9	3.7	2.2	20.0	2.8	2.6
13	P62249	RPS16 40S ribosomal protein S16	RPS16	TATAVAHC*K	0.9	3.2	3.1	3.5	4.1	2.6
14	P53621	COPA Coatomer subunit alpha	COPA	TTYQALPC*LPSMYGYPNR	0.8	11.2	2.2	1.7	4.1	2.6
15	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	SIQFVDWC*PTGFK	0.9	2.3	2.1	2.6	2.7	2.5
16	Q71U36	TUBA1A Tubulin alpha-1A chain	TUBA1A	TIQFVDWC*PTGFK	0.9	2.4	2.1	2.5	2.8	2.5
17	P60709	ACTB Actin, cytoplasmic 1	ACTB	C*DVDIR	1.0	1.5	1.9	2.1	1.6	2.5
18	P62701	RPS4X 40S ribosomal protein S4, X isoform	RPS4X	EC*LPLIIFLR	0.9	0.8	2.3	2.5	3.8	2.5
19	P50914	RPL14 60S ribosomal protein L14	RPL14	ALVDGPC*TQVR	0.9	2.9	2.1	2.8	2.6	2.4
20	P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	YLEC*SALTQR	1.0	0.6	1.0	6.0	0.8	2.4
21	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	C*MALSTAVLVGEAK	0.9	1.3	2.0	2.9	5.2	2.4
22	O95757	HSPA4L Heat shock 70 kDa protein 4L	HSPA4L	GC*ALQCAILSPAFK	0.9	2.2	2.0	2.1	2.8	2.3
23	Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	LSTLC*PSAVLQR	1.0	1.9	1.7	1.9	1.9	2.3
24	P46782	RPS5 40S ribosomal protein S5	RPS5	TIAEC*LADELINAAK	0.9	2.6	2.5	3.4	6.5	2.3
25	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	AVASQLDC*NFLK	0.9	2.8	2.0	2.4	2.8	2.1
26	P60763	RAC3 Ras-related C3 botulinum toxin substrate 3	RAC3	AVLC*PPPVK	1.0	1.9	2.6	3.5	3.2	2.1
27	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	PMC*VESFSQYPPLGR	1.0	2.3	2.1	2.4	2.3	2.0
28	P60709	ACTB Actin, cytoplasmic 1	ACTB	LC*YVALDFEQEMATAASSSSLEK	0.9	1.3	1.3	1.2	1.6	2.0
29	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	EMQNLSFQDC*YSSK	0.9	2.8	2.3	3.6	4.5	1.9

30	Q9P1F3	ABRACL Costars family protein ABRACL	ABRACL	C*ANLFEALVGTLK	1.0	1.0	1.8	2.3	3.8	1.9
31	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	GDEC*GLALGR	1.0	2.2	2.1	2.9	3.2	1.9
32	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	GQPC*SQNYR	1.5	1.4	1.5	1.9	2.2	1.9
33	P23396	RPS3 40S ribosomal protein S3	RPS3	GLC*AIAQAESLR	0.9	2.3	2.2	2.6	2.9	1.8
34	Q9BRA2	TXNDC17 Thioredoxin domain-containing protein 17	TXNDC17	SWCPDC*VQAEPVVR	1.0	5.6	2.5	2.6	2.2	1.8
35	P63220	RPS21 40S ribosomal protein S21	RPS21	TYAIC*GAIR	1.4	3.1	2.6	3.5	3.8	1.8
36	Q96CM8	ACSF2 Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	MVSTPIGGLSYVQGC*TK	1.4	1.6	1.8	2.1	2.6	1.8
37	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	ITGC*ASPGK	0.9	1.9	1.8	1.8	2.2	1.8
38	O43175	PHGDH D-3-phosphoglycerate dehydrogenase	PHGDH	NAGNC*LSPAVIVGLLK	1.0	2.4	2.3	2.8	4.4	1.7
39	O15355	PPM1G Protein phosphatase 1G	PPM1G	C*SGDGVGAPR	1.0	2.3	2.6	2.8	3.1	1.7
40	P50570	DNM2 Dynamin-2	DNM2	LQDAFSSIGQSC*HLDLPQIAVVGGQSAGK	1.0	2.2	2.0	2.6	2.6	1.7
41	O43765	SGTA Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	AIC*IDPAYSK	1.0	0.7	0.8	0.8	3.8	1.7
42	P55769	NHP2L1 NHP2-like protein 1	NHP2L1	LLDLVQQSC*NYK	0.9	1.5	1.6	2.2	2.9	1.7
43	P13639	EEF2 Elongation factor 2	EEF2	STLTDSLVC*K	0.9	7.9	4.8	7.3	6.8	1.7
44	Q15370	TCEB2 Transcription elongation factor B polypeptide 2	TCEB2	ADDTFEALC*IEPFSSPPELPDVMK	1.0	1.8	2.8	3.4	3.3	1.7
45	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	GNHEC*ASINR	0.9	1.1	1.1	1.4	1.3	1.7
46	Q6YN16	HSDL2 Hydroxysteroid dehydrogenase-like protein 2	HSDL2	TAIHTAAMDMLGGPGIESQC*R	1.0	3.0	2.5	2.0	3.2	1.7
47	Q8TEX9	IPO4 Importin-4	IPO4	APAALPAL*CDLLASAADPQIR	1.0	1.6	1.5	1.7	1.7	1.6
48	P28838	LAP3 Cytosol aminopeptidase	LAP3	SAGAC*TAAAFLK	0.9	2.0	1.7	2.5	2.1	1.6
49	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	DLNYC*FSGMSDHR	1.0	3.5	2.6	2.8	3.2	1.6
50	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	PDGNC*FYR	0.9	1.8	1.7	2.7	2.1	1.6
51	Q6P1X6	C8orf82 UPF0598 protein C8orf82	C8orf82	YEAAFPFLSPC*GR	1.2	2.8	2.7	3.4	3.1	1.6
52	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	AEGSDVANAVLDGADC*IMLSGETAK	0.9	0.8	1.0	1.2	1.0	1.5
53	P10599	TXN Thioredoxin	TXN	C*MPTFQFFK	1.0	4.0	4.5	4.5	4.2	1.5
54	Q96I99	SUCLG2 Succinyl-CoA ligase	SUCLG2	SC*NGPVLVGSPQGGVDIEEVAASNPELIFK	0.8	3.5	3.2	4.0	3.3	1.5
55	P48735	IDH2 Isocitrate dehydrogenase	IDH2	DLAGC*IHGLSNVK	0.9	2.2	2.0	2.7	2.6	1.5
56	P53396	ACLY ATP-citrate synthase	ACLY	FIC*TTSAIQNR	0.9	1.7	1.7	1.8	2.1	1.5
57	Q9BXJ9	NAA15 N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	LFNTAVC*ESK	1.0	2.5	2.0	2.2	2.6	1.5
58	P31949	S100A11 Protein S100-A11	S100A11	C*IESLIAVFQK	1.0	0.8	1.3	1.3	1.0	1.5
59	Q04760	GLO1 Lactoylglutathione lyase	GLO1	C*DFPIMK	0.9	1.3	1.6	1.2	1.7	1.5
60	Q09666	AHNAK Neuroblast differentiation-associated protein AHNAK	AHNAK	GPFVEAEVPDVDLEC*PDAK	0.9	3.6	6.4	4.6	3.7	1.5
61	P49915	GMPS GMP synthase	GMPS	TVGVQGDC*R	0.5	1.8	2.4	3.6	3.5	1.5
62	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	LVVPATQC*GSLIGK	0.9	2.7	2.9	3.6	3.4	1.5
63	P11766	ADH5 Alcohol dehydrogenase class-3	ADH5	VCLLGC*GISTGYGAAVNTAK	1.1	2.0	2.0	20.0	2.6	1.5
64	P46782	RPS5 40S ribosomal protein S5	RPS5	AQC*PIVER	0.9	2.1	2.0	1.9	2.0	1.5

65	Q9GZZ9	UBA5 Ubiquitin-like modifier-activating enzyme 5	UBA5	EGVC*AASLPTTMGVVAGILVQNVLK	1.1	2.1	2.7	0.9	1.5	1.4
66	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	EEFASTC*PDDEEIELAYEQVAK	1.3	0.8	0.9	0.6	0.9	1.4
67	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	TC*GFDFTGAVEDISK	1.1	3.3	3.0	3.0	3.9	1.4
68	P49327	FASN Fatty acid synthase	FASN	AINC*ATSGVVGLVNCLR	1.0	1.4	1.5	1.6	2.5	1.4
69	P40925	MDH1 Malate dehydrogenase, cytoplasmic	MDH1	AIC*DHVR	1.0	1.2	1.3	1.3	1.4	1.4
70	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	C*CSGAIIVLTK	1.0	1.1	1.1	1.1	1.3	1.4
71	Q09666	AHNAK Neuroblast differentiation-associated protein AHNAK	AHNAK	LEGDLTGPSVGVEVPDVELEC*PDAK	1.0	4.2	4.4	5.4	4.9	1.4
72	P16455	MGMT Methylated-DNA--protein-cysteine methyltransferase	MGMT	VVC*SSGAVGNYSGGLAVK	1.0	1.9	1.5	1.9	1.9	1.4
73	P18669	PGAM1 Phosphoglycerate mutase 1	PGAM1	YADLTEDQLPSC*ESLK	0.9	1.3	1.3	1.5	1.5	1.4
74	O00233	PSMD9 26S proteasome non-ATPase regulatory subunit 9	PSMD9	GIGMNEPLVDC*EGYPR	1.0	2.2	2.0	2.5	2.2	1.4
75	Q9NZZ3	CHMP5 Charged multivesicular body protein 5	CHMP5	APPPSLTDC*IGTVDSR	1.0	2.3	2.8	3.0	3.0	1.3
76	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	ALNALC*DGLIDELNQALK	0.9	2.0	2.0	2.4	2.9	1.3
77	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	EGTDSSQGIPQLVSNISAC*QVIAEAVR	1.0	2.5	2.3	2.8	2.8	1.3
78	P60709	ACTB Actin, cytoplasmic 1	ACTB	CPEALFQPSFLGMESC*GIHETTFNSIMK	0.9	1.5	1.3	1.5	1.6	1.3
79	P12532	CKMT1B Creatine kinase U-type, mitochondrial	CKMT1B	LGYILTC*PSNLGTGLR	0.9	1.6	1.4	1.5	1.6	1.3
80	Q9UBT2	UBA2 SUMO-activating enzyme subunit 2	UBA2	VLVVGAGGIGC*ELLK	0.9	1.8	1.7	2.1	2.2	1.3
81	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	GLLDVTC*K	1.0	1.7	1.5	1.8	2.0	1.3
82	P49721	PSMB2 Proteasome subunit beta type-2	PSMB2	NLADC*LR	0.9	1.5	0.8	0.7	1.1	1.3
83	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	GCITIIGGGDTATC*CAK	1.0	0.9	0.8	1.0	0.8	1.3
84	P60981	DSTN Destrin	DSTN	LGGSLIVAFEGC*PV	0.9	3.1	2.8	0.8	3.1	1.3
85	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	YLAEVAC*GDDR	0.9	1.9	2.1	2.3	2.7	1.3
86	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	LEVDAIVNAANSSLLGGGGVDGC*IHR	0.9	1.7	1.8	2.0	2.1	1.3
87	Q2TAA2	IAH1 Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	VILITPTPLC*ETAWEEQCIIQGCK	0.9	2.0	1.9	2.5	2.3	1.3
88	P13639	EEF2 Elongation factor 2	EEF2	TFC*QLILDPIFK	0.8	0.8	1.2	1.0	1.2	1.3
89	P07900	HSP90AA1 Heat shock protein HSP 90-alpha	HSP90AA1	VFIMDNC*EELIPEYLNFIR	0.9	0.8	0.8	0.9	1.0	1.3
90	O14980	XPO1 Exportin-1	XPO1	LDINLLDNVVNC*LYHGEGAQQR	1.0	1.4	1.5	1.9	2.3	1.3
91	Q9NQC3	RTN4 Reticulon-4	RTN4	YSNSALGHVNC*TIK	1.1	1.2	1.5	2.3	2.2	1.3
92	Q12849	GRSF1 G-rich sequence factor 1	GRSF1	YIELFLNSC*PK	0.9	2.2	2.0	3.1	3.7	1.2
93	P60981	DSTN Destrin	DSTN	C*STPEEIK	1.0	2.4	2.5	2.9	2.6	1.2
94	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	ENQWC*EEK	1.0	1.7	1.6	2.6	2.3	1.2
95	P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	SC*GSLLPELK	0.9	0.7	1.8	1.3	1.2	1.2
96	P26641	EEF1G Elongation factor 1-gamma	EEF1G	AAAPAPEEEMDEC*EQALAAEPK	1.0	2.3	2.2	2.8	2.8	1.2
97	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	HLNEIDLFHC*IDPNDSK	1.0	1.9	1.8	2.3	2.2	1.2
98	P49458	SRP9 Signal recognition particle 9 kDa protein	SRP9	VTDDLVC*LVYK	0.8	1.8	1.8	1.9	2.2	1.2
99	Q7L1Q6	BZW1 Basic leucine zipper and W2 domain-containing protein 1	BZW1	FDPTQFQDC*IIQGLTETGTDLEAVAK	1.0	1.6	1.5	1.8	1.8	1.2

100	Q9Y5R8	TRAPPC1 Trafficking protein particle complex subunit 1	TRAPPC1	NPLC*PLGQTVQSELFR	0.9	0.5	1.9	1.6	1.7	1.2
101	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	IVDTPC*NEMNTDTFLEEINK	1.1	1.4	1.4	1.6	1.7	1.2
102	P51812	RPS6KA3 Ribosomal protein S6 kinase alpha-3	RPS6KA3	AENGLLMTPC*YTANFVAPEVLK	0.9	2.1	1.7	2.5	3.1	1.2
103	P12004	PCNA Proliferating cell nuclear antigen	PCNA	C*AGNEDIITLR	1.2	1.1	1.1	1.1	1.2	1.2
104	P62258	YWHAE 14-3-3 protein epsilon	YWHAE	LIC*C*DILDVLDK	1.0	1.0	1.0	1.2	1.3	1.2
105	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	EEC*PVFTPPGGETLDQVK	0.9	2.5	2.1	2.8	3.4	1.2
106	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	NTGIIC*TIGPASR	0.8	0.6	0.7	0.5	0.7	1.2
107	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	VDENFDC*VEADDVEGK	1.0	2.0	3.5	2.6	5.5	1.2
108	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	INISEGNC*PER	1.0	2.1	2.4	1.9	2.4	1.2
109	P60842	EIF4A1 Eukaryotic initiation factor 4A-I	EIF4A1	VVMALGDYMGASCHAC*IGGTNVR	1.0	1.0	1.0	1.4	1.4	1.2
110	P13639	EEF2 Elongation factor 2	EEF2	YVEPIEDVPC*GNIVGLVGVDQFLVK	1.0	0.8	1.1	1.0	1.1	1.2
111	Q7Z4W1	DCXR L-xylulose reductase	DCXR	AVTNHSVYC*STK	0.9	1.0	0.9	0.8	1.0	1.2
112	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	EYLPIGGLAEFC*K	0.9	2.7	2.7	3.1	3.6	1.2
113	P14678	SNRPB Small nuclear ribonucleoprotein-associated protein	SNRPB	C*ILQDGR	1.0	2.3	2.4	0.7	2.6	1.2
114	P21333	FLNA Filamin-A	FLNA	AHVVPC*FDASK	1.0	1.5	1.5	1.8	2.0	1.2
115	O95861	BPNT1 3(2),5-bisphosphate nucleotidase 1	BPNT1	TC*ATDLQTK	0.8	1.8	2.3	2.4	2.7	1.1
116	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK	1.0	2.0	2.1	2.6	2.6	1.1
117	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	IC*PVETLVEEAIQCAEK	0.9	1.0	1.2	2.3	1.3	1.1
118	Q96EY8	MMAB Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	MMAB	IQCTLQDVGSALATPC*SSAR	0.9	2.0	2.0	3.5	2.6	1.1
119	O95671	ASMTL N-acetylserotonin O-methyltransferase-like protein	ASMTL	LTAC*QVATAFNLSR	1.0	2.3	2.1	2.7	2.8	1.1
120	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	HSMNPFC*EIAVEEAVR	1.2	2.3	2.5	2.7	2.6	1.1
121	O95336	PGLS 6-phosphogluconolactonase	PGLS	AAC*CLAGAR	1.0	1.6	1.9	2.8	2.2	1.1
122	P52943	CRIP2 Cysteine-rich protein 2	CRIP2	ASSVTTFTGEPNTC*PR	1.0	1.7	1.4	1.4	1.3	1.1
123	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	LPC*IYLVDSGGAYLPR	0.9	0.8	0.8	0.9	0.9	1.1
124	P00492	HPRT1 Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	SYC*NDQSTGDIK	1.0	2.5	2.8	3.6	2.5	1.1
125	P31947	SFN 14-3-3 protein sigma	SFN	GEELSC*EER	0.9	1.7	1.5	2.9	1.9	1.1
126	Q99873	PRMT1 Protein arginine N-methyltransferase 1	PRMT1	VIGIEC*SSISDYAVK	0.9	1.2	1.0	1.2	1.2	1.1
127	P23528	CFL1 Cofilin-1	CFL1	MLPDKDC*R	1.0	1.1	1.2	1.4	1.1	1.1
128	P14649	MYL6B Myosin light chain 6B	MYL6B	ILYSQC*GDVMR	1.0	0.8	0.9	1.0	0.9	1.1
129	Q9Y365	STARD10 PCTP-like protein	STARD10	MECC*DVPAETLYDVLHDIEYR	1.0	1.6	1.6	2.1	1.9	1.1
130	P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	AALEALGSC*LNNK	0.7	0.9	1.0	1.3	1.2	1.1
131	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	FLDGNELTLADC*NLLPK	1.1	0.7	0.8	0.7	0.7	1.1
132	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	LSSC*DSFTSTINELNHCLSLR	1.0	1.9	2.4	3.4	2.0	1.1

133	Q6PI48	DARS2 Aspartate--tRNA ligase, mitochondrial	DARS2	LIC*LVTGSPSIR	0.9	1.1	1.1	1.3	1.2	1.1
134	Q13526	PIN1 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	PIN1	SGEEDFESLASQFSDC*SSAK	1.0	1.1	0.9	1.1	1.1	1.1
135	P37802	TAGLN2 Transgelin-2	TAGLN2	NMAC*VQR	1.0	1.2	1.4	1.5	1.4	1.0
136	Q9UNH7	SNX6 Sorting nexin-6	SNX6	IGSSLYALGTQDSTDIC*K	0.9	1.2	1.4	1.3	1.2	1.0
137	P62826	RAN GTP-binding nuclear protein Ran	RAN	VC*ENIPIVLC*GNK	1.0	1.0	1.0	1.1	1.2	1.0
138	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	SQETEC*TYFSTPLLLGK	1.0	0.8	1.1	0.9	0.9	1.0
139	P55735	SEC13 Protein SEC13 homolog	SEC13	FASGGC*DNLIK	1.0	1.0	1.0	1.1	1.2	1.0
140	Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	AITIAGIPQSIIEC*VK	1.1	1.0	1.3	1.1	1.1	1.0
141	P07237	P4HB Protein disulfide-isomerase	P4HB	EEC*PAVR	1.1	0.7	1.1	1.1	0.7	1.0
142	Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	VGLGIC*YDMR	1.0	1.0	0.8	0.9	1.0	1.0
143	P60953	CDC42 Cell division control protein 42 homolog	CDC42	YVEC*SALTQK	0.8	0.7	0.7	0.7	0.7	1.0
144	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	IAAYLQSDQFC*K	0.9	2.8	1.4	2.6	2.5	1.0
145	P50990	CCT8 T-complex protein 1 subunit theta	CCT8	IAVYSC*PFDGMITETK	1.1	1.0	1.1	1.5	1.2	1.0
146	P17931	LGALS3 Galectin-3	LGALS3	VIVC*NTK	1.1	0.9	1.0	1.1	0.9	1.0
147	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	IGNC*PFSQR	1.0	0.9	0.8	0.9	1.0	1.0
148	P08107	HSPA1B Heat shock 70 kDa protein 1A/1B	HSPA1B	FEELC*SDLFR	1.4	0.8	1.0	0.8	1.0	1.0
149	P36507	MAP2K2 Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	LC*DFGVSGQLIDSMANSFVGTR	1.2	1.1	1.0	1.2	1.3	1.0
150	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	TIC*AILENYQTEK	0.9	0.9	0.8	1.1	1.2	1.0
151	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	DIC*NDVLSLLEK	1.1	0.6	0.9	1.3	0.8	1.0
152	P51610	HCFC1 Host cell factor 1	HCFC1	LVIYGGMSGC*R	0.9	1.4	1.3	1.1	1.4	0.9
153	Q86SX6	GLRX5 Glutaredoxin-related protein 5, mitochondrial	GLRX5	GTPEQPQC*GFSNAVVQILR	1.0	1.2	1.1	1.2	1.2	0.9
154	P30044	PRDX5 Peroxiredoxin-5, mitochondrial	PRDX5	ALNVEPDGTGLTC*SLAPNIISQL	1.0	0.9	0.9	0.9	0.8	0.9
155	P37802	TAGLN2 Transgelin-2	TAGLN2	DGTVLC*ELINALYPEGQAPVK	1.1	0.7	0.9	0.7	0.7	0.9
156	P60174	TPI1 Triosephosphate isomerase	TPI1	VPADTEVVC*APPTAYIDFAR	1.1	0.7	0.8	0.7	0.7	0.9
157	P61158	ACTR3 Actin-related protein 3	ACTR3	YSYVC*PDLVK	0.9	1.4	1.4	1.6	1.6	0.9
158	P35270	SPR Sepiapterin reductase	SPR	TVVNISSLC*ALQPFK	0.9	0.8	0.8	0.8	0.8	0.9
159	P23528	CFL1 Cofilin-1	CFL1	AVLFC*LSEDK	1.2	0.8	1.1	0.9	0.8	0.9
160	P60174	TPI1 Triosephosphate isomerase	TPI1	IIYGGSVTGATC*K	1.1	0.7	0.9	0.7	0.8	0.9
161	Q00610	CLTC Clathrin heavy chain 1	CLTC	IHEGC*EEPATHNALAK	0.9	1.1	0.8	1.2	1.5	0.9
162	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	YTC*GEAPDYDR	0.9	1.4	1.1	1.1	1.2	0.9
163	P60174	TPI1 Triosephosphate isomerase	TPI1	IAVAAQNC*YK	1.0	0.7	0.8	0.7	0.7	0.9
164	Q9Y696	CLIC4 Chloride intracellular channel protein 4	CLIC4	AGSDGESIGNC*PFSQR	1.0	1.0	0.9	0.9	1.0	0.9
165	P49189	ALDH9A1 4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	GALMANFLTQGQVC*CNGTR	0.9	0.9	0.9	1.2	1.4	0.9
166	Q9BWD1	ACAT2 Acetyl-CoA acetyltransferase, cytosolic	ACAT2	ATVAPEDVSEVIFGHVLAAGC*GQNPVR	0.8	3.4	2.0	5.2	3.8	0.9
167	P23528	CFL1 Cofilin-1	CFL1	HELQANC*YEEVK	1.0	1.2	1.2	1.5	1.5	0.9
168	P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	ITIADC*GQLE	1.0	0.9	1.0	1.0	0.9	0.9

169	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	SC*AHDWVYE	1.2	1.0	1.0	1.2	1.0	0.9
170	P52907	CAPZA1 F-actin-capping protein subunit alpha-1	CAPZA1	TIDGQQTIIAC*IESHQFQPK	0.9	0.8	1.0	0.8	0.9	0.9
171	P04632	CAPNS1 Calpain small subunit 1	CAPNS1	YSDESGNMDFDNFISC*LVR	1.1	0.6	0.7	0.6	0.8	0.9
172	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	ISSINSISALC*EATGADVEEVATAIGMDQR	1.0	0.7	0.7	0.6	0.8	0.9
173	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	ALANSLAC*QGK	1.0	0.7	0.8	0.7	0.8	0.9
174	P31948	STIP1 Stress-induced-phosphoprotein 1	STIP1	ALDLDSSC*K	0.8	1.3	1.1	1.3	10.9	0.9
175	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	ASVGFGGSC*FQK	0.9	0.9	1.1	1.0	1.0	0.9
176	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	YASIC*QQNGIVPIVEPEILPDGDHDLK	1.0	0.7	0.7	0.7	0.8	0.9
177	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	FC*PFAER	1.0	1.0	0.9	1.4	1.3	0.8
178	P09467	FBP1 Fructose-1,6-bisphosphatase 1	FBP1	GTGELTQLLNSLC*TAVK	0.9	0.7	0.8	0.5	0.8	0.8
179	P36969	GPX4 Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	GPX4	ILAFPC*NQFGK	0.8	0.7	0.8	0.8	0.8	0.8
180	B4DXR9	ZNF732 Zinc finger protein 732	ZNF732	C*LDPAQQNLYR	1.0	0.9	1.0	1.0	1.0	0.8
181	P22234	PAICS Multifunctional protein ADE2	PAICS	ITSC*IFQLLQEAGIK	0.9	0.7	0.7	0.6	0.9	0.8
182	P14174	MIF Macrophage migration inhibitory factor	MIF	LLC*GLLAER	0.9	0.7	0.7	0.7	0.7	0.8
183	P22061	PCMT1 Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	ALDVGSGSGILTAC*FAR	1.0	0.8	0.8	0.8	0.8	0.8
184	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	SLLINAVEASC*IR	0.9	3.0	2.6	3.4	3.3	0.7
185	P07737	PFN1 Profilin-1	PFN1	C*YEMASHLR	1.0	0.7	0.9	0.8	0.8	0.7
186	Q99798	ACO2 Aconitate hydratase, mitochondrial	ACO2	DLGGIVLANACGPC*IGQWDR	1.1	1.8	2.6	3.5	2.9	0.7
187	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	LC*YSSDHEK	1.1	1.0	1.1	1.2	0.9	0.7
188	P07741	APRT Adenine phosphoribosyltransferase	APRT	VVVVDDLLATGGTMNAAC*ELLGR	1.0	0.7	0.9	0.8	0.8	0.6
189	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	VPTANVSVVDLTC*R	0.9	1.0	0.9	0.9	0.9	0.6
190	P30626	SRI Sorcin	SRI	DTAQQGVVNFPYDDFIQC*VMSV	1.2	1.6	1.1	0.9	1.0	0.5

Table 2A-5. Primers used for sub-cloning and mutagenesis of GSTO1, HADH2 and CTSD.

Constructs	Vector	Primers	
GSTO1-WT	pcDNA3.1(+)	forward	5’-TTACTCGAGATGTCCGGGGAGTCAGCCA-3’
		reverse	5’-TTAGGTACCAGGCCTGTGACTATGGGCTC-3’
HADH2-WT	pET23a	forward	5’-TATGGATCCATGGCAGCAGCGTGTCG-3’
		reverse	5’-TATCTCGAGAGGCTGCATACGAATGGCCC-3’
HADH2-C58S	pET23a	forward	5’-GTTAGGAAACAACTCCGTTTTCGCCCCAG-3’
		reverse	5’-CTGGGGCGAAAACGGAGTTGTTTCCTAAC-3’
HADH2-C58A	pET23a	forward	5’-CAAGAAGTTAGGAAACAACGCCGTTTTCGCCCCAGCCGAC-3’
		reverse	5’-GTCGGCTGGGGCGAAAACGGCGTTGTTTCCTAACTTCTTG-3’
CTSD-WT	pcDNA3.1(+)	forward	5’-TTACTCGAGATGCAGCCCTCCAGCCTTCTG-3’
		reverse	5’-TTAAAGCTTGAGGCTGCCCGCCTC-3’
CTSD-C91A	pcDNA3.1(+)	forward	5’-GACGCCCCCCCAGGCCTTCACAGTCGTC-3’
		reverse	5’-GACGACTGTGAAGGCCTGGGGGGGCGTC-3’
CTSD-C329A	pcDNA3.1(+)	forward	5’-GAGTACATGATCCAGAAGGTGTCCAC-3’
		reverse	5’-GTGGACACCTTCTGGATCATGTACTC-3’
CTSD-C366A	pcDNA3.1(+)	forward	5’-GCCGGGAAGACCCTCGCCCTGAGCGGCTTCATG-3’
		reverse	5’-CATGAAGCCGCTCAGGGCGAGGGTCTTCCCGGC-3’

Table 3A-1. R-values from transnitrosation experiment at 500 μM GSNO. A list of all identified peptides (* denotes labeled cysteine) is presented together with calculated Heavy:Light Ratios (R-values) in untreated (0 μM) (n=2) versus GSNO-treated (500 μM) (n=5) MS analysis. Date were sorted by their average R-values of GSNO-treated experiments and numbered as "Peptide #".

Peptide #	Uniprot #	Description	Symbol	Sequence	Heavy : Light Ratio								significance
					0 μM GSNO			500 μM GSNO					
					1	2	average	1	2	3	4	5	average
1	Q99798	ACO2 Aconitate hydratase, mitochondrial	ACO2	VGLIGSC*TNSSYEDMGR	0.9	1.0	0.9	5.5	5.1	6.8	10.6	5.3	6.6	***
2	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	IISNASC*TTNCLAPLAK	0.9	0.9	0.9	5.4	4.8	4.2	5.0	5.1	4.9	***
3	P13674	P4HA1 Prolyl 4-hydroxylase subunit alpha-1	P4HA1	PC*TLSELE	0.9	1.0	1.0	5.0	4.0	4.4	5.9	4.2	4.7	***
4	P43034	PAFAH1B1 Platelet-activating factor acetylhydrolase IB subunit alpha	PAFAH1B1	PNQDGTLIASC*SNDQTVR	1.0	0.9	0.9	4.9	4.4	3.4	3.8	4.2	4.1	***
5	Q9H479	FN3K Fructosamine-3-kinase	FN3K	AFGGPGAGC*ISEGR	1.1	1.1	1.1	10.8	1.4	5.0	1.8	1.3	4.1	***
6	Q9BSD7	NTPCR Cancer-related nucleoside-triphosphatase	NTPCR	NADC*SSGPGQR	0.9	0.9	0.9	3.6	3.5	3.9	4.7	4.1	3.9	***
7	P07339	CTSD Cathepsin D	CTSD	AIGAVPLIQGEYMIPC*EK	0.8	0.9	0.9	3.4	3.2	4.0	4.7	3.7	3.8	***
8	Q01813	PFKP 6-phosphofructokinase type C	PFKP	LPLMEC*VQMTQDVQK	0.9	1.0	0.9	3.9	3.5	3.4	4.0	3.7	3.7	***
9	P07437	TUBB Tubulin beta chain	TUBB	LTTPTYGDLNHLVSATMSGVTTC*LR	1.0	1.0	1.0	3.8	3.5	3.5	4.0	3.6	3.7	***
10	Q06210	GFPT1 Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	C*QNALQQVVAR	1.0	1.0	1.0	4.2	3.0	3.4	4.3	2.8	3.5	***
11	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	VMTIPYQPMPASSPVIC*AGGQDR	1.0	1.0	1.0	3.2	3.2	3.4	3.9	3.4	3.4	***
12	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	IAC*LDFSLQK	0.9	1.1	1.0	3.8	2.9	3.4	3.5	3.2	3.4	***
13	Q04726	TLE3 Transducin-like enhancer protein 3	TLE3	SPISQLDC*LNR	1.0	1.0	1.0	4.6	3.4	2.3	2.9	3.5	3.3	***
14	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	ALDH6A1	C*MALSTAVLVGEAK	0.9	1.0	1.0	3.0	3.2	2.8	4.2	3.4	3.3	***
15	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	QC*PIMDPAWEAPEGVPIDAIIFGGR	0.8	1.1	1.0	3.5	3.1	3.1	3.7	3.2	3.3	***
16	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	VWNLANC*K	1.0	1.1	1.0	3.0	4.1	2.6	3.3	3.5	3.3	***
17	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	AYHEQLSVAEITNAC*FEPANQMVK	1.0	1.0	1.0	3.3	3.0	3.1	3.5	3.3	3.2	***
18	O00244	ATOX1 Copper transport protein ATOX1	ATOX1	VC*IESEHSMDTLLATLK	1.0	1.1	1.0	2.8	3.1	3.6	3.1	3.5	3.2	***
19	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	TSAPITC*ELLNK	0.9	0.9	0.9	3.8	3.3	2.4	3.3	3.3	3.2	***
20	P49207	RPL34 60S ribosomal protein L34	RPL34	AYGGSMC*AK	0.9	1.1	1.0	2.5	2.3	2.5	6.0	2.3	3.1	***

21	P31749	AKT1 RAC-alpha serine/threonine-protein kinase	AKT1	TFC*GTPEYLAPEVLEDNDYGR	1.0	1.0	1.0	3.6	2.9	2.9	3.2	2.9	3.1	***
22	P09622	DLD Dihydrolipoyl dehydrogenase, mitochondrial	DLD	NETLGGTC*LNVGCIPSK	0.9	0.9	0.9	3.0	3.5	3.4	1.8	3.7	3.1	***
23	P04183	TK1 Thymidine kinase, cytosolic	TK1	NTMEALPAC*LLR	0.9	0.9	0.9	3.0	2.4	3.0	3.7	3.1	3.0	***
24	Q92947	GCDH Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	GYGC*AGVSSVAYGLLAR	0.9	1.0	0.9	2.5	3.4	2.9	3.2	3.1	3.0	***
25	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	AVC*MLSNTTAIAEAWAR	0.9	1.0	0.9	3.0	2.9	2.8	3.3	3.0	3.0	***
26	P62140	PPP1CB Serine/threonine-protein phosphatase PP1-beta catalytic subunit	PPP1CB	IC*GDIHGQYTDLLR	1.1	1.0	1.0	3.2	1.5	3.0	3.6	3.5	3.0	***
27	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	LGNNC*VFAPADVTSEK	0.9	1.0	0.9	2.9	2.6	3.0	3.7	2.8	3.0	***
28	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	GC*DVVVIPAGVPR	0.9	0.9	0.9	3.3	2.5	3.0	3.6	2.2	2.9	***
29	P04183	TK1 Thymidine kinase, cytosolic	TK1	YSSSFC*THDR	1.0	1.0	1.0	2.8	2.6	2.8	3.0	3.1	2.9	***
30	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	VDVAVNC*AGIAVASK	1.0	1.1	1.1	3.3	2.5	3.0	2.8	2.5	2.8	***
31	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	NMITGTAPLDGC*ILVVAANDGPMPQTR	0.9	1.0	1.0	2.7	2.7	2.5	3.0	3.2	2.8	***
32	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	AEPPQC*TSLAWSADGQTLFAGYTDNLVR	1.0	0.9	0.9	2.4	2.1	2.9	3.4	3.2	2.8	***
33	P07437	TUBB Tubulin beta chain	TUBB	NMMAAC*DPR	0.9	1.0	0.9	2.9	2.6	2.6	3.0	2.8	2.8	***
34	Q09028	RBBP4 Histone-binding protein RBBP4	RBBP4	YMPQNPC*IIATK	1.0	0.9	0.9	2.5	2.9	2.6	3.0	2.9	2.8	***
35	P49327	FASN Fatty acid synthase	FASN	LGMLSPEGTC*K	0.9	1.0	1.0	2.7	2.8	2.6	3.3	2.4	2.8	***
36	P60709	ACTB Actin, cytoplasmic 1	ACTB	C*DVDIR	1.0	1.0	1.0	2.6	2.8	2.7	3.1	2.6	2.8	***
37	P62280	RPS11 40S ribosomal protein S11	RPS11	DVQIGDIVTVGEC*R	0.9	1.0	0.9	2.9	2.5	2.5	3.1	2.7	2.7	***
38	Q9Y5M8	SRPRB Signal recognition particle receptor subunit beta	SRPRB	NTPSFLIAC*NK	1.0	1.1	1.1	2.6	1.4	2.7	3.4	3.3	2.7	***
39	P07437	TUBB Tubulin beta chain	TUBB	VSDTVVEPYNATLSVHQLVENTDETYC*IDNEALYDICFR	0.9	1.0	1.0	2.7	2.7	2.6	2.7	2.7	2.7	***
40	P51610	HCFC1 Host cell factor 1	HCFC1	VAGINAC*GR	1.0	1.0	1.0	2.5	2.2	2.8	3.4	2.5	2.7	***
41	P17858	PFKL 6-phosphofructokinase, liver type	PFKL	VFANAPDSAC*VIGLK	0.9	1.0	0.9	3.0	2.5	2.6	3.0	2.4	2.7	***
42	P07437	TUBB Tubulin beta chain	TUBB	TAVC*DIPPR	0.9	1.0	0.9	2.6	2.6	2.5	2.9	2.7	2.7	***
43	P29401	TKT Transketolase	TKT	QAFTDVATGSLGQGLGAAC*GMAYTGK	0.9	1.1	1.0	3.2	2.5	2.5	2.6	2.4	2.6	***
44	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta--like 1	GNB2L1	LWNTLGVC*K	1.0	1.0	1.0	2.9	2.1	2.7	2.8	2.6	2.6	***
45	P23396	RPS3 40S ribosomal protein S3	RPS3	GC*EVVVSGK	1.0	1.0	1.0	2.3	3.1	2.5	2.5	2.7	2.6	***
46	P83731	RPL24 60S ribosomal protein L24	RPL24	VELC*SFSGYK	0.9	1.1	1.0	2.6	2.5	2.1	2.6	3.2	2.6	***
47	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	ALC*QITDSTMLQAIER	1.0	1.0	1.0	2.8	2.7	2.1	3.1	2.4	2.6	***
48	P10644	PRKAR1A cAMP-dependent protein kinase type I-alpha regulatory subunit	PRKAR1A	EC*ELYVQK	0.9	1.0	1.0	2.2	3.1	2.4	2.5	2.8	2.6	***

49	Q01813	PFKP 6-phosphofructokinase type C	PFKP	NESC*SENYTTDFIYQLYSEEGK	1.0	1.0	1.0	2.7	2.3	2.3	2.9	2.8	2.6	***
50	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	SLLINAVEASC*IR	0.9	1.0	0.9	2.7	2.2	2.6	2.9	2.6	2.6	***
51	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	C*PTSGR	0.9	0.9	0.9	2.6	2.5	2.5	2.6	2.8	2.6	***
52	O95833	CLIC3 Chloride intracellular channel protein 3	CLIC3	ASEDGESVGHC*PSCQR	0.9	1.0	1.0	2.4	1.8	4.2	2.3	2.3	2.6	***
53	Q9BUF5	TUBB6 Tubulin beta-6 chain	TUBB6	EIVHIQAGQC*GNQIGTK	0.8	1.0	0.9	3.1	1.7	2.0	4.7	1.3	2.6	***
54	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	FSPNSSNPIIVSC*GWDK	0.9	1.0	0.9	2.8	2.3	2.6	2.8	2.4	2.6	***
55	P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	VEQLFQVMNGILAQDSAC*SQR	0.9	1.0	1.0	1.8	2.0	2.5	3.5	3.0	2.6	***
56	P42677	RPS27 40S ribosomal protein S27	RPS27	LTEGC*SFR	0.9	1.0	0.9	2.5	2.5	2.4	2.8	2.5	2.5	***
57	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	VVVVQAISALC*QK	0.9	1.0	0.9	2.6	2.6	2.2	2.9	2.4	2.5	***
58	Q92616	GCN1L1 Translational activator GCN1	GCN1L1	C*GLALALNK	0.9	0.9	0.9	3.2	2.0	2.4	2.8	2.4	2.5	***
59	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	SIQFVDWC*PTGFK	0.9	1.0	1.0	2.5	2.4	2.4	2.8	2.5	2.5	***
60	P11498	PC Pyruvate carboxylase, mitochondrial	PC	ADFAQAC*QDAGVR	1.0	0.7	0.9	1.6	1.7	2.7	3.7	2.9	2.5	***
61	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	C*MTNTPVVVR	1.0	1.0	1.0	2.7	2.4	2.5	2.7	2.3	2.5	***
62	P27635	RPL10 60S ribosomal protein L10	RPL10	MLSC*AGADR	0.9	1.0	0.9	2.4	2.2	2.5	2.9	2.5	2.5	***
63	P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	TFVSGAC*DASIK	0.8	1.0	0.9	1.8	3.0	1.7	4.1	1.9	2.5	***
64	Q9BQ52	ELAC2 Zinc phosphodiesterase ELAC protein 2	ELAC2	C*VLSGPPQLEK	0.8	0.9	0.9	2.6	2.1	2.4	2.4	2.9	2.5	***
65	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	GANDFMC*DEMER	0.9	0.8	0.8	2.8	2.0	2.0	2.8	2.8	2.5	***
66	P35250	RFC2 Replication factor C subunit 2	RFC2	VC*DEPHPLLVK	1.0	0.9	0.9	2.2	2.8	2.1	2.7	2.4	2.4	***
67	Q71U36	TUBA1A Tubulin alpha-1A chain	TUBA1A	TIQFVDWC*PTGFK	0.9	1.0	0.9	2.4	2.3	2.2	2.7	2.5	2.4	***
68	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	YVAAAFPSAC*GK	1.0	0.9	0.9	2.8	2.1	2.3	2.6	2.4	2.4	***
69	P25398	RPS12 40S ribosomal protein S12	RPS12	LGEWVGLC*K	1.0	1.0	1.0	2.1	2.4	2.4	2.9	2.3	2.4	***
70	P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	AC*GDSTLTQITAGLDPVGR	1.0	0.9	0.9	2.6	2.2	2.2	2.7	2.3	2.4	***
71	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	YMACC*LLYR	0.9	1.0	1.0	2.4	2.3	2.3	2.6	2.4	2.4	***
72	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	SLHDALC*VVK	1.0	1.2	1.1	1.9	2.0	2.5	3.3	2.3	2.4	***
73	P50914	RPL14 60S ribosomal protein L14	RPL14	C*MQLTDFILK	0.9	1.0	0.9	2.5	2.3	2.2	2.5	2.4	2.4	***
74	Q16576	RBBP7 Histone-binding protein RBBP7	RBBP7	VHIPNDDAQFDASHC*DSDK	0.9	1.0	0.9	1.7	1.6	1.4	1.9	5.3	2.4	***
75	P49327	FASN Fatty acid synthase	FASN	AFDTAGNGYC*R	1.0	1.0	1.0	2.5	1.9	2.2	2.9	2.3	2.4	***
76	P53582	METAP1 Methionine aminopeptidase 1	METAP1	VCETDGC*SSEAK	0.9	1.1	1.0	2.3	2.6	1.6	2.8	2.5	2.4	***

77	P53597	SUCLG1 Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	IIC*QGFTGK	1.0	0.9	1.0	2.0	2.3	2.4	2.6	2.5	2.4	***
78	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	GYLGPEQLPDC*LK	0.9	0.9	0.9	2.2	2.1	2.3	2.8	2.4	2.4	***
79	O00567	NOP56 Nucleolar protein 56	NOP56	IINDNATYC*R	1.0	1.0	1.0	2.3	2.2	2.4	2.6	2.2	2.4	***
80	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	GNHEC*ASINR	0.9	1.1	1.0	2.8	2.0	2.2	2.5	2.2	2.3	***
81	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	LC*PNSTGAEIR	0.9	1.0	0.9	2.6	2.1	2.2	2.4	2.4	2.3	***
82	P31153	MAT2A S-adenosylmethionine synthase isoform type-2	MAT2A	TC*NVLVALEQQSPDIAQGVHLDR	1.1	1.1	1.1	2.3	2.0	2.2	2.6	2.6	2.3	***
83	P62280	RPS11 40S ribosomal protein S11	RPS11	C*PFTGNVSIR	1.0	1.0	1.0	2.3	2.2	1.9	2.4	2.8	2.3	***
84	P50914	RPL14 60S ribosomal protein L14	RPL14	ALVDGPC*TQVR	0.9	1.0	1.0	2.5	2.1	2.1	2.7	2.3	2.3	***
85	P40939	HADHA Trifunctional enzyme subunit alpha, mitochondrial	HADHA	C*LAPMMSEVIR	0.9	1.0	0.9	2.6	1.8	2.3	2.6	2.3	2.3	***
86	Q16555	DPYSL2 Dihydropyrimidinase-related protein 2	DPYSL2	FQLTDC*QIYEVLSVIR	1.1	0.9	1.0	3.0	2.5	1.9	2.3	1.9	2.3	***
87	P53384	NUBP1 Cytosolic Fe-S cluster assembly factor NUBP1	NUBP1	GASC*QGC*PNQR	1.0	1.1	1.0	2.2	2.2	2.2	2.8	2.1	2.3	***
88	E9PPU0	EPPK1 Epiplakin	EPPK1	LLDAQLATGGLVC*PAR	0.9	1.0	1.0	2.5	2.1	2.4	2.2	2.3	2.3	***
89	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	VGAFTMVC*K	0.9	1.0	1.0	3.0	2.8	1.3	3.1	1.2	2.3	***
90	P36578	RPL4 60S ribosomal protein L4	RPL4	SGQGAFGNMC*R	0.8	0.9	0.8	1.9	2.1	2.2	2.6	2.5	2.3	***
91	P11586	MTHFD1 C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	GC*LELIK	0.8	0.9	0.9	1.9	1.8	2.7	2.8	2.1	2.3	***
92	Q96I99	SUCLG2 Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	IDATQVEVNPFGETPEGQVVC*FDAK	1.0	1.0	1.0	2.3	2.0	1.7	2.9	2.5	2.3	***
93	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	GEETPVIVGSALC*ALEGR	1.0	0.9	1.0	2.2	2.1	2.2	2.5	2.3	2.3	***
94	P33992	MCM5 DNA replication licensing factor MCM5	MCM5	C*SVLAAANSVFGR	1.3	1.0	1.1	2.2	2.8	1.9	2.5	1.9	2.2	**
95	P60709	ACTB Actin, cytoplasmic 1	ACTB	LC*YVALDFEQEMATAASSSSLEK	0.9	1.0	1.0	2.2	2.1	2.2	2.4	2.1	2.2	**
96	P26440	IVD Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	GSNTCELIFEDC*K	1.0	0.9	1.0	2.2	2.1	2.2	2.5	2.0	2.2	**
97	P10589	NR2F1 COUP transcription factor 1	NR2F1	SQC*ALEEYVR	0.8	1.0	0.9	2.1	2.0	2.1	2.5	2.4	2.2	***
98	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	YNFFTGC*PK	0.9	1.1	1.0	2.2	2.0	2.1	2.6	2.1	2.2	**
99	P45984	MAPK9 Mitogen-activated protein kinase 9	MAPK9	TAC*TNFMMTPYVVTR	2.7	1.0	1.9	4.6	1.4	1.6	1.6	1.7	2.2	ns
100	P07384	CAPN1 Calpain-1 catalytic subunit	CAPN1	C*LQSGTLFR	0.8	1.0	0.9	2.3	2.2	1.9	2.4	2.1	2.2	***
101	Q8N163	KIAA1967 DBIRD complex subunit KIAA1967	KIAA1967	VVTQNIC*QYR	0.9	0.8	0.9	1.8	2.4	1.9	2.4	2.5	2.2	***
102	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	CEYPAAC*NALETLLIHR	0.9	1.1	1.0	2.3	2.1	2.0	2.0	2.5	2.2	**
103	P13804	ETFA Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	LGGEVSC*LVAGTK	0.9	1.0	0.9	2.3	1.9	2.2	2.4	2.0	2.2	**

104	P46734	MAP2K3 Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	FSPEFVDFTAQC*LR	1.9	1.2	1.6	1.7	2.0	2.2	2.8	2.2	2.2	ns
105	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	ALNALC*DGLIDELNQALK	0.9	1.0	1.0	2.3	2.1	2.1	2.3	2.1	2.2	**
106	P13804	ETFA Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	TIYAGNALC*TVK	1.0	1.0	1.0	1.9	2.1	2.3	2.5	2.0	2.2	**
107	O43719	HTATSF1 HIV Tat-specific factor 1	HTATSF1	GFEGSC*SQK	1.1	1.2	1.1	1.7	1.8	2.0	2.2	3.1	2.1	ns
108	Q9Y399	MRPS2 28S ribosomal protein S2, mitochondrial	MRPS2	DC*GEYAHTR	0.8	0.9	0.9	1.0	1.7	2.9	2.7	2.4	2.1	***
109	P42025	ACTR1B Beta-centractin	ACTR1B	AC*YLSINPQK	0.9	1.0	0.9	2.3	2.1	1.9	2.5	1.9	2.1	**
110	P62829	RPL23 60S ribosomal protein L23	RPL23	ISLGLPVGAVINC*ADNTGAK	0.9	1.0	1.0	2.2	1.9	2.0	2.3	2.2	2.1	**
111	P62249	RPS16 40S ribosomal protein S16	RPS16	TATAVAHC*K	1.0	1.0	1.0	2.2	1.9	2.2	2.3	1.9	2.1	*
112	Q9NZB2	FAM120A Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	VAAASGHC*GAFSGSDSSR	1.0	1.1	1.0	2.3	1.7	2.0	2.5	2.0	2.1	*
113	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	VGILDVDLC*GPSIPR	1.0	1.0	1.0	2.1	1.7	2.0	2.7	1.9	2.1	**
114	P53618	COPB1 Coatomer subunit beta	COPB1	ALSGYC*GFMAANLYAR	0.7	1.0	0.8	2.1	1.5	1.9	2.3	2.3	2.0	**
115	Q14152	EIF3A Eukaryotic translation initiation factor 3 subunit	EIF3A	NIC*QQVNIK	0.9	1.0	0.9	2.3	1.7	2.0	2.2	2.0	2.0	*
116	P62714	PPP2CB Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	PPP2CB	NVVTIFSAPNYC*YR	0.9	1.0	1.0	2.3	1.8	2.2	2.0	1.9	2.0	*
117	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	AC*ALQVLSAILEGSK	0.9	1.3	1.1	2.1	1.6	2.0	2.3	2.1	2.0	ns
118	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	GQPC*SQNYR	1.5	1.3	1.4	1.7	1.7	2.5	2.1	2.2	2.0	ns
119	P24468	NR2F2 COUP transcription factor 2	NR2F2	FGSQC*MQPNNIMGIENICELAAR	1.2	1.0	1.1	2.2	2.1	2.2	1.7	1.9	2.0	ns
120	P21333	FLNA Filamin-A	FLNA	LQVEPAVDTSGVQC*YGPGIEGQGVFR	1.0	1.1	1.1	1.8	2.0	1.8	2.8	1.6	2.0	ns
121	P62888	RPL30 60S ribosomal protein L30	RPL30	VC*TLAIIDPGDSDIIR	0.9	0.9	0.9	2.1	1.9	1.8	2.2	2.0	2.0	*
122	P62753	RPS6 40S ribosomal protein S6	RPS6	LNISFPATGC*QK	0.9	0.9	0.9	2.0	1.9	1.9	2.2	2.0	2.0	*
123	P53384	NUBP1 Cytosolic Fe-S cluster assembly factor NUBP1	NUBP1	NC*DK	1.0	1.0	1.0	2.0	2.1	1.6	2.5	1.7	2.0	ns
124	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	DLLVQQASQC*LSK	1.1	1.0	1.0	2.0	1.5	2.1	2.4	1.9	2.0	ns
125	Q14318	FKBP8 Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8	C*LNNLAASQLK	1.1	1.0	1.1	1.8	1.8	2.2	2.3	1.9	2.0	ns
126	P11586	MTHFD1 C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	GDLNDCFIPC*TPK	1.1	1.0	1.1	2.1	2.4	0.9	3.5	1.0	2.0	ns
127	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	MLSAVSQQVQC*IQEALR	1.0	0.9	1.0	2.1	2.0	1.8	2.3	1.6	2.0	ns
128	P15924	DSP Desmoplakin	DSP	YC*YLQNEVFGLFQK	1.0	1.0	1.0	2.5	1.7	1.7	2.3	1.7	2.0	ns
129	Q9C0C9	UBE2O Ubiquitin-conjugating enzyme E2 O	UBE2O	NC*AQGEGSMAK	1.0	1.0	1.0	1.3	2.0	2.5	2.3	1.6	1.9	ns
130	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	C*FIVGADNVGSK	0.9	1.0	1.0	2.0	1.8	1.9	2.1	2.0	1.9	ns
131	Q92616	GCN1L1 Translational activator GCN1	GCN1L1	YLLDSC*APLLR	0.8	1.3	1.0	1.9	1.8	2.3	1.9	1.9	1.9	ns

132	Q07020	RPL18 60S ribosomal protein L18	RPL18	GC*GTVLLSGPR	0.9	1.0	1.0	2.1	1.7	1.8	2.1	2.0	1.9	ns
133	P13639	EEF2 Elongation factor 2	EEF2	DLEEDHAC*IPIK	0.9	1.0	1.0	1.8	1.8	2.0	2.3	1.8	1.9	ns
134	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	EMQNLSFQDC*YSSK	0.9	0.9	0.9	2.0	1.9	1.8	2.0	1.9	1.9	*
135	Q8TC07	TBC1D15 TBC1 domain family member 15	TBC1D15	TLLVNC*QNK	1.1	1.0	1.1	1.9	1.4	1.9	2.2	2.1	1.9	ns
136	P62701	RPS4X 40S ribosomal protein S4, X isoform	RPS4X	FDTGNLC*MVTGGANLGR	0.9	0.9	0.9	2.0	1.7	2.1	2.2	1.7	1.9	*
137	P46776	RPL27A 60S ribosomal protein L27a	RPL27A	NQSFC*PTVNLDK	0.9	1.0	0.9	2.3	1.8	1.8	1.9	1.8	1.9	ns
138	P55060	CSE1L Exportin-2	CSE1L	IC*AVGITK	0.9	1.0	0.9	1.9	2.1	1.7	2.0	1.9	1.9	ns
139	O95747	OXSR1 Serine/threonine-protein kinase OSR1	OXSR1	TFVGTPC*WMAPEVMEQVR	1.0	1.0	1.0	1.8	1.5	1.7	2.5	2.0	1.9	ns
140	Q68CP9	ARID2 AT-rich interactive domain-containing protein 2	ARID2	SC*SNAAFALK	0.8	1.0	0.9	2.2	1.6	1.4	1.9	2.5	1.9	ns
141	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	AVHQC*DR	1.0	1.1	1.1	2.0	1.8	1.8	2.2	1.7	1.9	ns
142	O14980	XPO1 Exportin-1	XPO1	DLLGLC*EQK	1.1	0.9	1.0	2.1	1.7	1.8	1.8	2.1	1.9	ns
143	Q06203	PPAT Amidophosphoribosyltransferase	PPAT	C*ELENCQPFVVETLHGK	0.8	1.1	1.0	1.6	1.3	1.4	1.7	3.5	1.9	ns
144	P27448	MARK3 MAP/microtubule affinity-regulating kinase 3	MARK3	LDTFC*GSPPYAAPELFQGK	0.9	1.0	1.0	1.5	1.6	1.6	3.1	1.7	1.9	ns
145	O95782	AP2A1 AP-2 complex subunit alpha-1	AP2A1	TVFEALQAPAC*HENMVK	1.0	1.1	1.1	2.0	1.5	2.0	1.7	2.2	1.9	ns
146	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	EYLPIGGLAEFC*K	0.9	1.0	0.9	1.6	1.8	1.9	2.3	1.7	1.9	ns
147	Q9BTZ2	DHRS4 Dehydrogenase/reductase SDR family member 4	DHRS4	VNC*LAPGLIK	0.9	1.0	1.0	2.1	1.8	1.8	1.9	1.7	1.9	ns
148	P07384	CAPN1 Calpain-1 catalytic subunit	CAPN1	LEIC*NLTPDALK	0.8	0.9	0.9	1.9	1.7	1.9	2.4	1.5	1.9	ns
149	Q9Y2R9	MRPS7 28S ribosomal protein S7, mitochondrial	MRPS7	NC*EPMIGLVPILK	0.9	0.9	0.9	2.0	1.8	1.8	1.9	1.9	1.9	ns
150	Q04726	TLE3 Transducin-like enhancer protein 3	TLE3	FTVAESC*DR	0.9	1.0	1.0	2.5	1.1	2.0	1.6	2.0	1.8	ns
151	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	LC*ALR	0.6	1.0	0.8	2.0	1.5	1.8	2.0	1.9	1.8	*
152	Q9H1K1	ISCU Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	ISCU	NVGTGLVGAPAC*GDVMK	0.8	1.1	1.0	1.8	1.7	1.8	2.2	1.7	1.8	ns
153	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	GDEC*ELLGHSK	0.9	1.0	1.0	1.8	1.8	1.7	2.1	1.8	1.8	ns
154	P62330	ARF6 ADP-ribosylation factor 6	ARF6	NWYVQPSC*ATSGDGLYEGLTWLTSNYK	0.9	0.9	0.9	2.1	1.6	1.9	1.9	1.6	1.8	ns
155	P51610	HCFC1 Host cell factor 1	HCFC1	AC*AAGTPAVIR	0.9	0.9	0.9	1.5	1.9	2.0	2.0	1.9	1.8	ns
156	P49327	FASN Fatty acid synthase	FASN	DPETLVGYSMVGC*QR	1.0	0.9	1.0	1.8	1.8	1.6	2.0	1.8	1.8	ns
157	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	TIIPLISQC*TPK	0.9	1.0	0.9	1.7	1.8	1.9	1.9	1.8	1.8	ns
158	P02795	MT2A Metallothionein-2	MT2A	SC*CSCCPVGC*AK	1.0	0.9	1.0	1.4	1.6	1.8	2.7	1.6	1.8	ns
159	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	FC*LDNGAK	1.1	1.0	1.0	0.8	2.6	2.4	0.8	2.5	1.8	ns
160	O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	SFVQWLGC*R	1.1	0.9	1.0	1.7	1.6	1.8	1.8	2.1	1.8	ns
161	P48047	ATP5O ATP synthase subunit O, mitochondrial	ATP5O	GEVPC*TVTSASPLEEATLSELK	1.0	1.0	1.0	3.3	1.5	1.3	1.5	1.5	1.8	ns
162	Q27J81	INF2 Inverted formin-2	INF2	AVLLASDAQEC*TLEEVVER	0.8	0.8	0.8	1.8	0.9	2.0	2.7	1.5	1.8	ns

163	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	AVASQLDC*NFLK	0.9	1.0	0.9	1.7	1.8	1.7	1.9	1.7	1.8	ns
164	P82912	MRPS11 28S ribosomal protein S11, mitochondrial	MRPS11	ASHNNTQIQVVSASNEPLAFASC*GTEGFR	0.8	0.9	0.9	2.0	1.3	1.8	2.2	1.5	1.8	ns
165	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	LVIVGDGAC*GK	1.0	0.9	1.0	2.3	1.6	1.6	1.8	1.6	1.8	ns
166	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	NFILDQC*NVYNSGQR	0.8	0.9	0.9	1.7	1.5	1.7	2.2	1.8	1.8	ns
167	Q9Y5Q8	GTF3C5 General transcription factor 3C polypeptide 5	GTF3C5	VC*TNPVDR	0.9	1.1	1.0	1.6	1.1	1.7	2.0	2.4	1.8	ns
168	Q96CM8	ACSF2 Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	MVSTPIGGLSYVQGC*TK	1.4	1.8	1.6	1.9	1.8	1.6	1.8	1.7	1.8	ns
169	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	AGAIAPC*EVTVPAQNTGLGPEK	0.9	1.0	0.9	1.8	1.6	1.7	2.0	1.8	1.8	ns
170	P00966	ASS1 Argininosuccinate synthase	ASS1	FELSC*YSLAPQIK	1.1	1.0	1.0	2.1	1.7	1.6	1.6	1.8	1.8	ns
171	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	C*AMTALSSK	0.9	1.1	1.0	1.8	2.4	1.5	1.7	1.4	1.8	ns
172	P11802	CDK4 Cyclin-dependent kinase 4	CDK4	LMDVC*ATSR	1.0	1.0	1.0	1.7	2.0	1.6	2.0	1.5	1.8	ns
173	Q969Z0	TBRG4 Protein TBRG4	TBRG4	LATDLLSLMPSLTSGEVAHC*AK	1.0	1.1	1.0	1.7	1.8	1.7	2.0	1.6	1.7	ns
174	Q7Z406	MYH14 Myosin-14	MYH14	ADLLLEPC*SHYR	1.0	1.0	1.0	1.7	1.8	1.6	1.9	1.8	1.7	ns
175	Q15019	SEPT2 Septin-2	2-Sep	LTVVDTPGYGDAINC*R	1.0	1.0	1.0	1.8	1.6	1.6	1.9	1.8	1.7	ns
176	P23396	RPS3 40S ribosomal protein S3	RPS3	GLC*AIAQAESLR	0.9	1.0	1.0	1.8	1.7	1.6	1.8	1.8	1.7	ns
177	P43246	MSH2 DNA mismatch repair protein Msh2	MSH2	HVIEC*AK	0.9	0.6	0.7	1.8	1.8	1.2	2.0	1.9	1.7	ns
178	P56377	AP1S2 AP-1 complex subunit sigma-2	AP1S2	MC*SFLEWR	1.0	0.9	1.0	2.0	1.5	1.5	2.2	1.5	1.7	ns
179	Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	FSIQTMC*PIEGEGNIAR	0.9	1.0	1.0	1.6	1.6	1.8	2.0	1.7	1.7	ns
180	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	QLC*DNAGFDATNILNK	0.9	1.1	1.0	1.7	1.9	1.8	1.9	1.4	1.7	ns
181	P21333	FLNA Filamin-A	FLNA	THEAEIVEGENHTYC*IR	1.1	1.0	1.0	1.6	1.6	1.6	2.3	1.4	1.7	ns
182	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	PMC*VESFSQYPPLGR	0.9	1.0	0.9	1.6	1.6	1.8	1.9	1.6	1.7	ns
183	P62910	RPL32 60S ribosomal protein L32	RPL32	SYC*AEIAHNVSSK	0.8	1.0	0.9	1.6	1.7	1.7	1.7	1.8	1.7	ns
184	Q8WTW3	COG1 Conserved oligomeric Golgi complex subunit 1	COG1	AQAISPC*VQNFCSALDSK	0.9	1.0	0.9	1.6	1.7	1.6	2.0	1.5	1.7	ns
185	Q13542	EIF4EBP2 Eukaryotic translation initiation factor 4E-binding protein 2	EIF4EBP2	TVAISDAAQLPHDYC*TTPGGTLFSTTPGGTR	0.8	0.7	0.7	1.5	1.4	1.9	2.1	1.7	1.7	ns
186	P33992	MCM5 DNA replication licensing factor MCM5	MCM5	C*SPIGVYTSGK	1.0	1.0	1.0	2.1	1.7	1.2	2.2	1.3	1.7	ns
187	A6NDG6	PGP Phosphoglycolate phosphatase	PGP	NNQESDC*VSK	1.0	1.0	1.0	1.7	1.7	1.6	1.8	1.8	1.7	ns
188	P62318	SNRPD3 Small nuclear ribonucleoprotein Sm D3	SNRPD3	VLHEAEGHIVTC*ETNTGEVYR	0.9	1.0	0.9	1.6	1.6	1.7	2.2	1.5	1.7	ns
189	O95340	PAPSS2 Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 2	PAPSS2	VWGTTC*TK	0.9	0.9	0.9	1.8	1.7	1.3	1.9	1.8	1.7	ns
190	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	C*ATITPDEAR	0.8	1.0	0.9	1.7	1.5	1.9	1.8	1.6	1.7	ns
191	P15880	RPS2 40S ribosomal protein S2	RPS2	GC*TATLGNFAK	1.0	1.0	1.0	1.8	1.7	1.6	1.7	1.7	1.7	ns

192	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	C*TPSVISFGSK	0.9	1.0	0.9	1.6	1.6	1.6	1.8	1.7	1.7	ns
193	P24385	CCND1 G1/S-specific cyclin-D1	CCND1	AEETC*APSVSYFK	0.8	1.1	1.0	1.8	1.5	2.4	1.8	0.9	1.7	ns
194	P46782	RPS5 40S ribosomal protein S5	RPS5	TIAEC*LADELINAAK	0.9	1.0	0.9	1.7	1.6	1.6	1.8	1.7	1.7	ns
195	Q53H96	PYCRL Pyrroline-5-carboxylate reductase 3	PYCRL	SDVC*TPGGTTIYGLHALEQGGLR	1.0	1.0	1.0	1.6	1.6	1.7	1.8	1.7	1.7	ns
196	P53597	SUCLG1 Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	LIGPNCPGVINPGEC*K	1.0	0.9	1.0	1.7	1.6	1.6	1.7	1.8	1.7	ns
197	P35125	USP6 Ubiquitin carboxyl-terminal hydrolase 6	USP6	SGTSC*PSSK	0.9	1.0	0.9	1.5	1.5	1.9	1.8	1.6	1.7	ns
198	O95685	PPP1R3D Protein phosphatase 1 regulatory subunit 3D	PPP1R3D	APPPTPAPSGC*DPR	0.9	1.4	1.1	1.0	3.1	1.1	0.8	2.2	1.6	ns
199	Q9Y508	RNF114 RING finger protein 114	RNF114	DC*GGAAQLAGPAAEADPLGR	1.0	1.1	1.0	1.6	1.8	1.5	1.6	1.7	1.6	ns
200	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	LQGATC*NNNK	0.9	0.9	0.9	1.8	1.9	1.5	2.2	0.7	1.6	ns
201	O95757	HSPA4L Heat shock 70 kDa protein 4L	HSPA4L	GC*ALQCAILSPAFK	0.9	0.9	0.9	1.7	1.7	1.5	1.5	1.7	1.6	ns
202	Q9UHD8	SEPT9 Septin-9	9-Sep	LTVIDTPGFGDHINNENC*WQPIMK	0.9	0.9	0.9	1.6	1.7	1.6	1.7	1.5	1.6	ns
203	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	ISAFGYLEC*SAK	0.7	0.7	0.7	1.9	1.2	1.8	1.8	1.5	1.6	ns
204	Q9H1K1	ISCU Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	ISCU	LHC*SMLAEDAIK	0.9	1.0	1.0	1.6	1.3	1.6	1.9	1.7	1.6	ns
205	P15924	DSP Desmoplakin	DSP	DANSENC*NK	0.8	1.0	0.9	1.2	1.6	1.8	2.1	1.4	1.6	ns
206	Q99836	MYD88 Myeloid differentiation primary response protein MyD88	MYD88	FITVCDYTNPC*TK	0.9	0.9	0.9	1.9	1.4	1.7	1.6	1.5	1.6	ns
207	P37198	NUP62 Nuclear pore glycoprotein p62	NUP62	DIIEHLNTSGAPADTSDPLQQIC*K	0.7	0.9	0.8	1.8	1.6	1.5	1.7	1.6	1.6	ns
208	P10599	TXN Thioredoxin	TXN	C*MPTFQFFK	1.0	1.0	1.0	1.4	1.2	2.2	1.7	1.5	1.6	ns
209	P16455	MGMT Methylated-DNA--protein-cysteine methyltransferase	MGMT	VVC*SSGAVGNYSGGLAVK	1.0	1.0	1.0	1.7	1.6	1.4	1.6	1.7	1.6	ns
210	Q96RQ3	MCCC1 Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCC1	ESLC*QAALGLILK	1.0	0.9	1.0	1.4	2.0	1.4	1.6	1.6	1.6	ns
211	Q9UBT2	UBA2 SUMO-activating enzyme subunit 2	UBA2	VLVVGAGGIGC*ELLK	0.9	0.9	0.9	1.6	1.5	1.6	1.7	1.5	1.6	ns
212	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	GDEC*GLALGR	1.0	1.0	1.0	1.7	1.5	1.5	1.7	1.6	1.6	ns
213	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	C*SFDVVK	0.8	0.9	0.8	1.7	1.3	1.5	1.8	1.7	1.6	ns
214	Q9UL25	RAB21 Ras-related protein Rab-21	RAB21	VVLLGEGC*VGK	1.1	1.0	1.1	1.8	1.4	1.5	1.6	1.6	1.6	ns
215	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	GNVC*GDSK	0.8	1.0	0.9	1.5	1.5	1.6	1.9	1.4	1.6	ns
216	Q66K14	TBC1D9B TBC1 domain family member 9B	TBC1D9B	NEC*YR	1.1	1.2	1.2	1.4	1.6	1.4	1.7	1.8	1.6	ns
217	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	ALDH6A1	AEMDAAIASC*K	0.9	1.0	1.0	1.5	1.6	1.6	1.9	1.5	1.6	ns
218	P10599	TXN Thioredoxin	TXN	LVVVDFSATWC*GPCK	1.1	1.0	1.0	1.5	1.2	2.1	1.7	1.4	1.6	ns
219	Q96CD2	PPCDC Phosphopantothenoylcysteine decarboxylase	PPCDC	ASC*PAAAPLMER	1.0	1.2	1.1	1.4	1.5	1.7	1.8	1.6	1.6	ns
220	Q92879	CELF1 CUGBP Elav-like family member 1	CELF1	GC*AFVTFTTR	1.0	1.1	1.1	1.8	1.5	1.5	1.5	1.7	1.6	ns

221	P61758	VBP1 Prefoldin subunit 3	VBP1	DSC*GK	0.9	0.9	0.9	3.5	1.0	1.2	1.1	1.1	1.6	ns
222	A0MZ66	KIAA1598 Shootin-1	KIAA1598	VTFQPPSSIGC*R	1.0	1.1	1.0	1.5	1.7	1.7	1.5	1.5	1.6	ns
223	O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	ANSSVVSVNC*K	0.9	1.0	1.0	1.7	1.4	1.4	1.8	1.7	1.6	ns
224	Q8NFA0	USP32 Ubiquitin carboxyl-terminal hydrolase 32	USP32	VLAYTGC*FSR	1.0	0.9	0.9	1.7	1.2	1.5	1.8	1.7	1.6	ns
225	Q9P2R7	SUCLA2 Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	ILAC*DDLDEAAR	0.7	1.0	0.9	1.2	1.7	1.4	2.1	1.5	1.6	ns
226	P20810	CAST Calpastatin	CAST	AAAPAPVSEAVC*R	1.0	0.9	0.9	1.6	1.5	1.6	1.6	1.5	1.6	ns
227	P62244	RPS15A 40S ribosomal protein S15a	RPS15A	C*GVISPR	0.9	0.9	0.9	1.6	1.7	1.5	1.4	1.6	1.6	ns
228	P46782	RPS5 40S ribosomal protein S5	RPS5	AQC*PIVER	0.9	0.9	0.9	1.6	1.6	1.3	1.7	1.6	1.6	ns
229	Q9NZA1	CLIC5 Chloride intracellular channel protein 5	CLIC5	AGIDGESIGNC*PFSQR	1.0	1.0	1.0	1.6	1.5	1.5	1.7	1.5	1.6	ns
230	P38606	ATP6V1A V-type proton ATPase catalytic subunit A	ATP6V1A	VLDALFPCVQGGTTAIPGAFGC*GK	1.0	1.0	1.0	1.6	1.6	1.4	1.6	1.6	1.5	ns
231	Q96I99	SUCLG2 Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	SC*NGPVLVGSPQGGVDIEEVAASNPELIFK	0.8	1.0	0.9	1.6	1.4	1.4	1.7	1.6	1.5	ns
232	Q6PKG0	LARP1 La-related protein 1	LARP1	TASISSSPSEGTPTVGSYGC*TPQSLPK	0.9	1.0	0.9	1.4	1.5	1.4	1.9	1.6	1.5	ns
233	Q7Z2W4	ZC3HAV1 Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	NSNVDSSYLESLYQSC*PR	1.0	1.2	1.1	1.2	1.3	1.6	1.9	1.7	1.5	ns
234	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	VC*VETVESGAMTK	0.9	0.9	0.9	1.4	1.4	1.4	2.0	1.5	1.5	ns
235	Q9Y285	FARSA Phenylalanine--tRNA ligase alpha subunit	FARSA	VNLQMVYDSPLC*R	0.9	0.9	0.9	1.1	1.5	1.6	2.0	1.6	1.5	ns
236	P60981	DSTN Destrin	DSTN	HEC*QANGPEDLNR	1.2	1.0	1.1	1.5	1.4	1.7	1.6	1.5	1.5	ns
237	O75439	PMPCB Mitochondrial-processing peptidase subunit beta	PMPCB	LC*TSVTESEVAR	1.1	0.9	1.0	2.0	1.6	1.4	1.3	1.3	1.5	ns
238	P55263	ADK Adenosine kinase	ADK	TGC*TFPEK	1.0	1.0	1.0	1.5	1.4	1.4	1.8	1.5	1.5	ns
239	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	LFC*VGFTK	1.0	0.9	1.0	1.6	1.6	1.6	1.2	1.6	1.5	ns
240	P35914	HMGCL Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	LLEAGNFIC*QALNR	0.8	1.0	0.9	1.4	1.4	1.6	1.7	1.5	1.5	ns
241	P19838	NFKB1 Nuclear factor NF-kappa-B p105 subunit	NFKB1	YVC*EGPSHGGLPGASSEK	0.9	0.8	0.8	1.5	1.5	1.5	1.5	1.5	1.5	ns
242	E9PPU0	EPPK1 Epiplakin	EPPK1	YLC*GLGAVGGVR	1.0	1.0	1.0	1.4	1.6	1.3	1.5	1.6	1.5	ns
243	Q9BUL9	RPP25 Ribonuclease P protein subunit p25	RPP25	SEEAPAGC*GAEGGGPGSGPFADLAPGAVHMR	1.1	1.0	1.0	1.4	1.5	1.5	1.5	1.5	1.5	ns
244	Q9BUH6	C9orf142 Uncharacterized protein C9orf142	C9orf142	C*PGESLINPGFK	1.0	1.0	1.0	1.4	1.4	1.5	1.7	1.5	1.5	ns
245	P62191	PSMC1 26S protease regulatory subunit 4	PSMC1	AIC*TEAGLMALR	1.0	1.0	1.0	1.5	1.4	1.6	1.6	1.4	1.5	ns
246	P22102	GART Trifunctional purine biosynthetic protein adenosine-3	GART	QVLVAPGNAGTAC*SEK	0.8	0.8	0.8	1.7	1.2	1.4	1.6	1.5	1.5	ns
247	P55809	OXCT1 Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	OXCT1	C*TLPLTGK	0.8	1.0	0.9	1.4	1.5	1.4	1.6	1.5	1.5	ns
248	Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	SC*ENLAPFNTALK	0.9	1.0	0.9	1.0	1.7	1.4	1.7	1.6	1.5	ns

249	Q93052	LPP Lipoma-preferred partner	LPP	TYITDPVSAPC*APPLQPK	1.0	1.1	1.0	1.4	1.4	1.4	1.7	1.5	1.5	ns
250	Q8TEX9	IPO4 Importin-4	IPO4	APAALPALC*DLLASAADPQIR	1.0	1.1	1.0	1.3	1.4	1.4	1.6	1.6	1.5	ns
251	P11413	G6PD Glucose-6-phosphate 1-dehydrogenase	G6PD	TQVC*GILR	0.9	1.0	0.9	1.4	1.3	1.5	1.7	1.4	1.5	ns
252	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	DLAGC*IHGLSNVK	0.9	0.9	0.9	1.5	1.4	1.4	1.6	1.5	1.5	ns
253	Q13636	RAB31 Ras-related protein Rab-31	RAB31	VC*LLGDTGVGK	0.8	1.0	0.9	1.6	1.3	1.5	1.5	1.4	1.5	ns
254	Q00765	REEP5 Receptor expression-enhancing protein 5	REEP5	NC*MTDLLAK	1.1	1.0	1.0	1.5	1.5	1.3	1.7	1.4	1.5	ns
255	P11498	PC Pyruvate carboxylase, mitochondrial	PC	FLYEC*PWR	1.2	1.1	1.1	1.5	1.5	1.4	1.4	1.6	1.5	ns
256	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	ALDH6A1	VC*NLIDSGTK	0.9	1.0	0.9	1.5	1.4	1.4	1.7	1.3	1.5	ns
257	O15355	PPM1G Protein phosphatase 1G	PPM1G	C*SGDGVGAPR	1.0	0.9	1.0	1.3	1.5	1.5	1.5	1.5	1.4	ns
258	P0CW22	RPS17L 40S ribosomal protein S17-like	RPS17L	VC*EEIAIIPSK	0.9	0.9	0.9	1.5	1.4	1.4	1.5	1.5	1.4	ns
259	O95747	OXSR1 Serine/threonine-protein kinase OSR1	OXSR1	C*QTSMDELLK	0.9	1.0	1.0	1.4	1.0	2.0	1.2	1.6	1.4	ns
260	P09429	HMGB1 High mobility group protein B1	HMGB1	MSSYAFFVQTC*R	1.0	0.8	0.9	1.4	1.7	1.4	1.4	1.4	1.4	ns
261	P30281	CCND3 G1/S-specific cyclin-D3	CCND3	ASYFQC*VQR	0.9	0.9	0.9	1.5	1.4	1.3	1.5	1.5	1.4	ns
262	O00148	DDX39A ATP-dependent RNA helicase DDX39A	DDX39A	AIVDC*GFEHPSEVQHECIPQAILGMDVLCQAK	0.9	1.5	1.2	1.5	1.3	1.3	1.7	1.5	1.4	ns
263	P49327	FASN Fatty acid synthase	FASN	WVC*SSLR	1.0	0.9	0.9	1.5	1.2	1.5	1.4	1.5	1.4	ns
264	Q00610	CLTC Clathrin heavy chain 1	CLTC	IHEGC*EEPATHNALAK	0.9	1.1	1.0	1.6	1.1	1.4	1.6	1.5	1.4	ns
265	Q9Y3A3	MOB4 MOB-like protein phocein	MOB4	HTLDGAAC*LLNSNK	1.0	0.9	1.0	1.4	1.4	1.4	1.5	1.4	1.4	ns
266	Q9UJU6	DBNL Drebrin-like protein	DBNL	AEEDVEPEC*IMEK	1.8	1.4	1.6	1.1	1.1	1.5	1.7	1.6	1.4	ns
267	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	ADHQPLTEASYVNLPTIALC*NTDSPLR	0.9	0.9	0.9	1.4	1.3	1.5	1.7	1.3	1.4	ns
268	Q9ULV4	CORO1C Coronin-1C	CORO1C	C*DLISIPK	0.9	1.0	1.0	1.3	1.3	1.5	1.6	1.4	1.4	ns
269	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	HIIEDPC*TLR	1.1	0.9	1.0	1.6	1.2	1.3	1.6	1.4	1.4	ns
270	P50552	VASP Vasodilator-stimulated phosphoprotein	VASP	SSSSVTTSETQPC*TPSSSDYSDLQR	0.7	1.4	1.1	1.4	1.4	1.3	1.4	1.6	1.4	ns
271	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	TLSGMESYC*VR	0.8	1.0	0.9	1.3	1.4	1.4	1.6	1.3	1.4	ns
272	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	PMC*VESFSDYPPLGR	1.0	1.0	1.0	1.5	1.3	1.4	1.5	1.4	1.4	ns
273	Q15208	STK38 Serine/threonine-protein kinase 38	STK38	LSDFGLC*TGLK	1.1	1.0	1.1	1.6	1.6	1.3	1.2	1.3	1.4	ns
274	O43390	HNRNPR Heterogeneous nuclear ribonucleoprotein R	HNRNPR	SAFLC*GVMK	0.9	1.0	0.9	2.1	1.1	1.3	1.3	1.2	1.4	ns
275	P63220	RPS21 40S ribosomal protein S21	RPS21	TYAIC*GAIR	1.4	1.0	1.2	1.2	1.7	1.2	1.4	1.5	1.4	ns
276	Q8IUR0	TRAPPC5 Trafficking protein particle complex subunit 5	TRAPPC5	ENSTLNC*ASFTAGIVEAVLTHSGFPAK	0.9	1.0	1.0	1.4	1.4	1.3	1.3	1.6	1.4	ns
277	Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	NPVSQC*MR	0.9	1.1	1.0	1.5	1.3	1.3	1.5	1.4	1.4	ns
278	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	QAVLGAGLPISTPC*TTINK	0.8	0.9	0.9	1.3	1.4	1.4	1.4	1.4	1.4	ns

279	O15541	RNF113A RING finger protein 113A	RNF113A	AVDQVC*TFLFK	0.9	1.0	0.9	1.4	1.2	1.4	1.5	1.5	1.4	ns
280	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	YC*SGTGWPSFSEAHGTSGSDESHTGILR	1.0	0.9	0.9	1.7	1.3	1.1	1.4	1.4	1.4	ns
281	Q15813	TBCE Tubulin-specific chaperone E	TBCE	NCAVSC*AGEK	1.4	1.1	1.2	1.2	1.4	1.5	1.1	1.7	1.4	ns
282	Q96EB1	ELP4 Elongator complex protein 4	ELP4	VEPC*SLTPGYTK	0.9	0.9	0.9	1.1	1.3	1.4	1.6	1.5	1.4	ns
283	O43684	BUB3 Mitotic checkpoint protein BUB3	BUB3	TPC*NAGTFSQPEK	1.0	1.1	1.0	1.2	1.5	1.3	1.6	1.2	1.4	ns
284	P30050	RPL12 60S ribosomal protein L12	RPL12	C*TGGEVGATSALAPK	0.9	0.9	0.9	1.5	1.0	1.5	1.6	1.3	1.4	ns
285	Q9BXJ9	NAA15 N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	LFNTAVC*ESK	1.0	0.9	1.0	1.3	1.7	1.2	1.3	1.3	1.4	ns
286	P18085	ARF4 ADP-ribosylation factor 4	ARF4	NIC*FTVWDVGGQDR	0.9	1.0	0.9	1.4	1.2	1.3	1.5	1.5	1.4	ns
287	P62633	CNBP Cellular nucleic acid-binding protein	CNBP	TSEVNC*YR	0.8	1.0	0.9	1.4	1.3	1.5	1.4	1.2	1.4	ns
288	Q5T4S7	UBR4 E3 ubiquitin-protein ligase UBR4	UBR4	AVQC*LNTSSK	1.0	1.0	1.0	2.0	1.2	1.3	0.9	1.3	1.4	ns
289	P49915	GMPS GMP synthase	GMPS	VICAEEPYIC*K	0.9	1.1	1.0	1.3	1.3	1.4	1.4	1.4	1.4	ns
290	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	SQETEC*TYFSTPLLLGK	0.9	1.0	1.0	1.3	1.3	1.4	1.4	1.4	1.4	ns
291	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	YVDIAIPC*NNK	0.9	1.0	0.9	1.4	1.2	1.4	1.5	1.3	1.3	ns
292	Q9GZZ9	UBA5 Ubiquitin-like modifier-activating enzyme 5	UBA5	EGVC*AASLPTTMGVVAGILVQNVLK	1.1	1.1	1.1	1.4	1.3	1.3	1.3	1.4	1.3	ns
293	P20073	ANXA7 Annexin A7	ANXA7	LGTDESC*FNMILATR	0.9	0.9	0.9	1.5	1.3	1.2	1.4	1.4	1.3	ns
294	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	C*IPALDSLTPANEDQK	1.0	1.0	1.0	1.3	1.2	1.4	1.4	1.4	1.3	ns
295	O14545	TRAFD1 TRAF-type zinc finger domain-containing protein 1	TRAFD1	AVC*EADQSHGGPR	1.0	1.0	1.0	1.2	1.2	1.3	1.5	1.6	1.3	ns
296	Q9NP73	ALG13 UDP-N-acetylglucosamine transferase subunit ALG13	ALG13	ADLVISHAGAGSC*LETLEK	1.0	1.0	1.0	1.3	1.3	1.3	1.5	1.3	1.3	ns
297	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	FFSDC*K	1.0	1.1	1.0	1.4	1.2	1.5	1.3	1.3	1.3	ns
298	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	IHMGSC*AENTAK	0.9	0.9	0.9	1.4	1.2	1.3	1.4	1.4	1.3	ns
299	P60709	ACTB Actin, cytoplasmic 1	ACTB	CPEALFQPSFLGMESC*GIHETTFNSIMK	0.9	0.9	0.9	1.3	1.5	1.4	1.1	1.4	1.3	ns
300	Q9C0C9	UBE2O Ubiquitin-conjugating enzyme E2 O	UBE2O	C*YNEMALIR	0.9	1.0	1.0	1.2	1.3	1.2	1.5	1.5	1.3	ns
301	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	NMITGTSQADC*AVLIVAAGVGEFEAGISK	0.9	1.0	1.0	1.3	1.4	1.4	1.4	1.3	1.3	ns
302	P49327	FASN Fatty acid synthase	FASN	ADEASELAC*PTPK	1.0	1.0	1.0	1.3	1.3	1.3	1.4	1.4	1.3	ns
303	P60866	RPS20 40S ribosomal protein S20	RPS20	TPC*GEGSK	1.1	1.0	1.0	1.5	1.5	1.2	1.2	1.3	1.3	ns
304	P84085	ARF5 ADP-ribosylation factor 5	ARF5	NIC*FTVWDVGGQDK	0.9	1.1	1.0	1.5	1.2	1.3	1.4	1.3	1.3	ns
305	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	LTFSC*LGGSDNFK	0.9	1.0	1.0	0.7	1.2	1.9	1.9	0.8	1.3	ns
306	Q9NUU7	DDX19A ATP-dependent RNA helicase DDX19A	DDX19A	VLVTTNVC*AR	0.9	1.0	0.9	1.3	1.2	1.3	1.4	1.3	1.3	ns
307	P15924	DSP Desmoplakin	DSP	NQC*TQVVQER	1.0	0.9	0.9	1.1	1.4	1.3	1.3	1.4	1.3	ns

308	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	VDENFDC*VEADDVEGK	1.0	0.9	1.0	1.3	1.0	1.4	1.5	1.4	1.3	ns
309	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	ISASC*QHPTAFEEAIPK	0.9	0.9	0.9	1.3	1.3	1.3	1.4	1.4	1.3	ns
310	P49327	FASN Fatty acid synthase	FASN	AINC*ATSGVVGLVNCLR	1.0	1.0	1.0	1.3	1.4	1.3	1.5	1.1	1.3	ns
311	P13639	EEF2 Elongation factor 2	EEF2	VTDGALVVVDCVSGVC*VQTETVLR	1.7	1.1	1.4	1.3	1.3	1.0	1.0	2.0	1.3	ns
312	E7EQ34	GOSR2 Golgi SNAP receptor complex member 2	GOSR2	QVHEIQSC*MGR	1.0	1.0	1.0	1.2	1.4	1.3	1.3	1.4	1.3	ns
313	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	MC*SMVK	0.8	0.9	0.9	1.4	1.3	1.3	1.4	1.3	1.3	ns
314	P13639	EEF2 Elongation factor 2	EEF2	IWC*FGPDGTGPNILTDITK	1.0	1.1	1.0	2.3	1.1	1.1	1.0	1.1	1.3	ns
315	Q04637	EIF4G1 Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	LQGINC*GPDFTPSFANLGR	1.0	1.0	1.0	1.6	1.2	1.2	1.2	1.3	1.3	ns
316	Q9UHD8	SEPT9 Septin-9	9-Sep	SQEATEAAPSC*VGDMADTPR	1.2	1.0	1.1	1.2	1.3	1.3	1.6	1.2	1.3	ns
317	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	AC*QSIYPLHDVFVR	1.0	0.7	0.8	1.2	1.6	1.3	1.4	1.1	1.3	ns
318	P21964	COMT Catechol O-methyltransferase	COMT	GSSC*FECTHYQSFLEYR	1.0	1.0	1.0	1.4	1.2	1.2	1.3	1.3	1.3	ns
319	P13639	EEF2 Elongation factor 2	EEF2	STLTDSLVC*K	0.9	1.0	1.0	1.3	1.1	1.2	1.3	1.5	1.3	ns
320	Q96CP2	FLYWCH2 FLYWCH family member 2	FLYWCH2	TEDSGLAAGPPEAAGENFAPC*SVAPGK	0.9	1.2	1.0	1.2	1.3	1.4	1.4	1.2	1.3	ns
321	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	SSGGFVWAC*K	1.0	1.0	1.0	1.4	1.3	1.1	1.3	1.4	1.3	ns
322	P55769	NHP2L1 NHP2-like protein 1	NHP2L1	LLDLVQQSC*NYK	0.9	0.9	0.9	1.3	1.3	1.2	1.3	1.3	1.3	ns
323	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	AAVEEGIVLGGGC*ALLR	0.9	1.0	1.0	1.3	1.2	1.3	1.3	1.3	1.3	ns
324	P40222	TXLNA Alpha-taxilin	TXLNA	VTEAPC*YPGAPSTEASGQTGPQEPTSAR	0.9	1.4	1.1	1.1	1.5	1.2	1.3	1.4	1.3	ns
325	Q06323	PSME1 Proteasome activator complex subunit 1	PSME1	EDLC*TK	0.9	1.1	1.0	1.2	1.2	1.3	1.5	1.3	1.3	ns
326	Q9P1F3	ABRACL Costars family protein ABRACL	ABRACL	C*ANLFEALVGTLK	1.0	1.0	1.0	1.1	1.3	1.3	1.4	1.3	1.3	ns
327	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	AATGEEVSAEDLGGADLHC*R	0.9	0.9	0.9	1.4	1.3	1.1	1.3	1.4	1.3	ns
328	O15075	DCLK1 Serine/threonine-protein kinase DCLK1	DCLK1	YQDDFLLDESEC*R	1.0	1.1	1.1	1.3	1.2	1.3	1.4	1.3	1.3	ns
329	Q9NZL4	HSPBP1 Hsp70-binding protein 1	HSPBP1	DAC*DTVR	1.0	1.0	1.0	1.2	1.2	1.4	1.3	1.3	1.3	ns
330	Q9NQC3	RTN4 Reticulon-4	RTN4	YSNSALGHVNC*TIK	1.1	1.1	1.1	1.1	1.5	1.0	1.3	1.5	1.3	ns
331	Q7L1Q6	BZW1 Basic leucine zipper and W2 domain-containing protein 1	BZW1	FDPTQFQDC*IIQGLTETGTDLEAVAK	1.0	1.0	1.0	1.4	1.2	1.3	1.3	1.2	1.3	ns
332	P23921	RRM1 Ribonucleoside-diphosphate reductase large subunit	RRM1	IIDINYYPVPEAC*LSNK	1.1	0.9	1.0	1.4	1.2	1.2	1.3	1.3	1.3	ns
333	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	C*C*SGAIIVLTK	0.9	0.9	0.9	1.2	1.3	1.3	1.3	1.2	1.3	ns
334	Q9P258	RCC2 Protein RCC2	RCC2	AVQDLC*GWR	1.1	1.2	1.1	1.3	1.1	1.3	1.4	1.3	1.3	ns
335	Q13045	FLII Protein flightless-1 homolog	FLII	TGLC*YLPEELAALQK	0.8	1.1	1.0	1.2	1.1	1.3	1.4	1.3	1.3	ns
336	P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	C*VVVGDGAVGK	0.9	0.9	0.9	1.2	1.3	1.5	1.1	1.3	1.3	ns
337	Q7Z4W1	DCXR L-xylulose reductase	DCXR	AVTNHSVYC*STK	0.9	0.8	0.9	1.3	1.5	1.3	1.2	1.1	1.3	ns

338	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	IGNC*PFSQR	1.0	1.0	1.0	1.3	1.2	1.2	1.3	1.4	1.3	ns
339	O43865	AHCYL1 Putative adenosylhomocysteinase 2	AHCYL1	LC*VPAMNVNDSVTK	0.9	1.0	0.9	1.2	1.0	1.4	1.2	1.4	1.3	ns
340	Q9UPM8	AP4E1 AP-4 complex subunit epsilon-1	AP4E1	SSC*STLPDYLLYQCQK	0.7	0.7	0.7	1.3	1.1	1.3	1.4	1.3	1.3	ns
341	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	VFIMDSC*DELIPEYLNFIR	1.0	1.2	1.1	1.2	1.4	1.2	1.1	1.3	1.3	ns
342	P49721	PSMB2 Proteasome subunit beta type-2	PSMB2	NLADC*LR	0.9	1.1	1.0	1.3	1.3	1.2	1.2	1.3	1.3	ns
343	Q8NBF2	NHLRC2 NHL repeat-containing protein 2	NHLRC2	AILFSQPLQITDTQQGC*IAPVELR	0.9	1.0	1.0	1.3	1.2	1.3	1.3	1.2	1.3	ns
344	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	EGC*TEVSLLR	1.0	1.0	1.0	1.3	1.2	1.2	1.2	1.4	1.3	ns
345	Q6IA69	NADSYN1 Glutamine-dependent NAD(+) synthetase	NADSYN1	NSSQETC*TR	1.3	1.3	1.3	1.1	1.1	1.0	1.8	1.1	1.2	ns
346	P30042	C21orf33 ES1 protein homolog, mitochondrial	C21orf33	DC*K	0.9	1.0	0.9	1.3	1.2	1.2	1.5	1.1	1.2	ns
347	Q99798	ACO2 Aconitate hydratase, mitochondrial	ACO2	DLGGIVLANACGPC*IGQWDR	1.1	0.9	1.0	1.0	1.3	1.1	1.4	1.4	1.2	ns
348	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	EQFSQGSPSNC*LETSLAEIFPLGK	0.9	1.0	1.0	1.3	1.4	1.2	1.0	1.2	1.2	ns
349	Q15233	NONO Non-POU domain-containing octamer-binding protein	NONO	C*SEGSFLLTTFPR	0.9	1.1	1.0	1.1	1.0	1.4	1.4	1.4	1.2	ns
350	Q8IXH7	TH1L Negative elongation factor C/D	TH1L	AC*QALGAMLSK	1.1	0.9	1.0	0.6	1.4	1.3	1.3	1.7	1.2	ns
351	O00233	PSMD9 26S proteasome non-ATPase regulatory subunit 9	PSMD9	GIGMNEPLVDC*EGYPR	1.0	1.3	1.2	1.3	1.2	1.2	1.3	1.1	1.2	ns
352	Q9UK41	VPS28 Vacuolar protein sorting-associated protein 28 homolog	VPS28	LDC*PLAMER	1.1	1.3	1.2	1.2	1.2	1.3	1.3	1.2	1.2	ns
353	P49327	FASN Fatty acid synthase	FASN	LTPGC*EAEAETEAICFFVQQFTDMEHNR	1.2	1.0	1.1	1.2	1.2	1.1	1.4	1.3	1.2	ns
354	Q6P1X6	C8orf82 UPF0598 protein C8orf82	C8orf82	YEAAFPFLSPC*GR	1.2	1.0	1.1	1.3	1.1	1.2	1.3	1.2	1.2	ns
355	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	DLNYC*FSGMSDHR	1.0	1.0	1.0	1.3	1.2	1.2	1.3	1.3	1.2	ns
356	Q7L2H7	EIF3M Eukaryotic translation initiation factor 3 subunit	EIF3M	VAASC*GAIQYIPTELDQVR	0.9	1.0	0.9	1.4	1.1	1.2	1.3	1.2	1.2	ns
357	O75934	BCAS2 Pre-mRNA-splicing factor SPF27	BCAS2	IENLELMSQHGC*NAWK	1.0	1.0	1.0	1.3	1.0	1.2	1.4	1.2	1.2	ns
358	O43765	SGTA Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	AIC*IDPAYSK	1.0	1.0	1.0	1.5	1.3	1.1	1.2	1.1	1.2	ns
359	P78406	RAE1 mRNA export factor	RAE1	VFTASC*DK	0.9	1.0	1.0	0.7	0.9	1.2	2.2	1.1	1.2	ns
360	Q8IWX8	CHERP Calcium homeostasis endoplasmic reticulum protein	CHERP	LALEQQQLIC*K	0.8	1.1	0.9	1.1	1.3	1.1	1.2	1.4	1.2	ns
361	Q7Z4W1	DCXR L-xylulose reductase	DCXR	GVPGAIVNVSSQC*SQR	0.9	0.9	0.9	1.3	1.2	1.1	1.2	1.3	1.2	ns
362	O00267	SUPT5H Transcription elongation factor SPT5	SUPT5H	VELHSTC*QTISVDR	1.3	1.1	1.2	1.3	1.1	1.3	1.4	1.0	1.2	ns
363	Q14694	USP10 Ubiquitin carboxyl-terminal hydrolase 10	USP10	TPSYSISSTLNPQAPEFILGC*TASK	1.1	1.0	1.0	1.2	1.1	1.2	1.3	1.2	1.2	ns
364	P55263	ADK Adenosine kinase	ADK	SLIANLAAANC*YK	1.0	1.0	1.0	1.0	1.4	1.2	1.3	1.1	1.2	ns
365	P19367	HK1 Hexokinase-1	HK1	AAQLC*GAGMAAVVDK	0.9	0.6	0.8	2.0	1.2	1.0	0.9	1.1	1.2	ns
366	Q14181	POLA2 DNA polymerase alpha subunit B	POLA2	VLGC*PEALTGSYK	0.9	0.9	0.9	1.3	0.9	1.6	1.3	1.0	1.2	ns

367	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit 2	PSMD2	GTLTLC*PYHSDR	0.8	1.0	0.9	1.0	0.9	1.1	0.8	2.2	1.2	ns
368	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	GSDFDC*ELR	0.9	0.9	0.9	1.1	1.3	1.3	1.2	1.3	1.2	ns
369	P49327	FASN Fatty acid synthase	FASN	DGLLENQTPEFFQDVC*K	0.9	0.9	0.9	1.3	1.0	1.1	1.5	1.1	1.2	ns
370	Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	VGLGIC*YDMR	1.0	1.1	1.0	1.4	1.1	1.0	1.2	1.3	1.2	ns
371	Q15004	KIAA0101 PCNA-associated factor	KIAA0101	AC*PLQPDHTNDEK	1.1	1.0	1.0	1.3	1.0	1.2	1.4	1.1	1.2	ns
372	Q09666	AHNAK Neuroblast differentiation-associated protein AHNAK	AHNAK	LEGDLTGPSVDVEVPDVELEC*PDAK	1.1	1.1	1.1	1.1	1.1	1.1	1.4	1.2	1.2	ns
373	O75934	BCAS2 Pre-mRNA-splicing factor SPF27	BCAS2	NDITAWQEC*VNNSMAQLEHQAVR	1.0	1.0	1.0	0.8	1.3	1.2	1.5	1.3	1.2	ns
374	O95336	PGLS 6-phosphogluconolactonase	PGLS	AAC*CLAGAR	1.0	1.0	1.0	1.2	1.2	1.1	1.3	1.3	1.2	ns
375	P62195	PSMC5 26S protease regulatory subunit 8	PSMC5	NIDINDVTPNC*R	0.7	0.9	0.8	1.0	1.0	1.4	1.4	1.2	1.2	ns
376	O75153	KIAA0664 Clustered mitochondria protein homolog	KIAA0664	C*LTQQAVALQR	0.9	1.0	1.0	1.2	1.2	1.2	1.1	1.3	1.2	ns
377	Q9BX63	BRIP1 Fanconi anemia group J protein	BRIP1	LANNSDC*ILAK	0.9	1.0	0.9	1.1	1.1	1.3	1.3	1.2	1.2	ns
378	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	SC*AHDWVYE	1.2	1.2	1.2	1.4	1.4	1.0	1.0	1.2	1.2	ns
379	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	ENQWC*EEK	1.0	0.9	1.0	1.2	1.2	1.2	1.2	1.2	1.2	ns
380	P15924	DSP Desmoplakin	DSP	AC*GSEIMQK	0.9	0.9	0.9	1.2	1.2	1.2	1.2	1.1	1.2	ns
381	P20810	CAST Calpastatin	CAST	SEC*K	1.1	1.1	1.1	1.0	1.1	1.5	1.3	1.1	1.2	ns
382	Q13185	CBX3 Chromobox protein homolog 3	CBX3	LTWHSC*PEDEAQ	0.9	1.0	1.0	1.2	1.1	1.1	1.3	1.2	1.2	ns
383	Q9BV86	NTMT1 N-terminal Xaa-Pro-Lys N-methyltransferase 1	NTMT1	IIC*SAGLSLLAEER	1.0	1.1	1.0	1.3	1.2	1.1	1.2	1.1	1.2	ns
384	Q09666	AHNAK Neuroblast differentiation-associated protein AHNAK	AHNAK	LEGDLTGPSVGVEVPDVELEC*PDAK	1.0	1.0	1.0	1.1	1.1	1.2	1.5	1.1	1.2	ns
385	O15355	PPM1G Protein phosphatase 1G	PPM1G	GTEAGQVGEPGIPTGEAGPSC*SSASDK	1.0	1.0	1.0	1.2	1.1	1.2	1.3	1.2	1.2	ns
386	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	LFQECC*PHSTDR	0.8	0.9	0.9	1.2	1.1	1.3	1.3	1.2	1.2	ns
387	O15371	EIF3D Eukaryotic translation initiation factor 3 subunit	EIF3D	FMTPVIQDNPSGWGPC*AVPEQFR	1.0	1.0	1.0	1.3	1.1	1.1	1.3	1.2	1.2	ns
388	O15382	BCAT2 Branched-chain-amino-acid aminotransferase, mitochondrial	BCAT2	EVFGSGTAC*QVCPVHR	0.9	1.0	0.9	1.1	1.2	1.1	1.1	1.4	1.2	ns
389	P17844	DDX5 Probable ATP-dependent RNA helicase DDX5	DDX5	LIDFLEC*GK	1.1	1.0	1.1	1.2	1.1	1.2	1.2	1.1	1.2	ns
390	Q9Y3F4	STRAP Serine-threonine kinase receptor-associated protein	STRAP	IGFPETTEEELEEIASENSDC*IFPSAPDVK	1.0	1.1	1.0	1.0	1.1	1.3	1.4	1.2	1.2	ns
391	Q9Y696	CLIC4 Chloride intracellular channel protein 4	CLIC4	AGSDGESIGNC*PFSQR	1.0	1.0	1.0	1.1	1.3	1.0	1.3	1.1	1.2	ns
392	Q2TAA2	IAH1 Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	VILITPTPLC*ETAWEEQCIIQGCK	0.9	0.9	0.9	1.2	1.1	1.1	1.2	1.2	1.2	ns
393	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	YAGLSTC*FR	1.0	0.9	1.0	1.2	1.1	1.1	1.3	1.2	1.2	ns

394	P33240	CSTF2 Cleavage stimulation factor subunit 2	CSTF2	LC*VQNSPQEAR	1.0	1.0	1.0	1.3	1.1	1.2	1.2	1.2	1.2	ns
395	Q9BSU1	C16orf70 UPF0183 protein C16orf70	C16orf70	LLAAGC*GPGLLADAK	0.9	0.9	0.9	1.3	1.2	1.0	1.1	1.3	1.2	ns
396	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	HSMNPFC*EIAVEEAVR	1.2	1.1	1.2	1.1	1.0	1.3	1.3	1.2	1.2	ns
397	Q9UNE7	STUB1 E3 ubiquitin-protein ligase CHIP	STUB1	AQQAC*IEAK	1.0	1.1	1.1	1.1	1.3	1.0	1.4	1.0	1.2	ns
398	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	C*EFQDAYVLLSEK	0.9	1.0	1.0	1.1	1.2	1.1	1.2	1.2	1.2	ns
399	Q9UBF6	RNF7 RING-box protein 2	RNF7	VQVMDAC*LR	0.9	0.9	0.9	1.1	1.4	1.1	1.1	1.1	1.2	ns
400	Q6YN16	HSDL2 Hydroxysteroid dehydrogenase-like protein 2	HSDL2	TAIHTAAMDMLGGPGIESQC*R	1.0	0.9	0.9	0.9	1.2	1.1	1.5	1.1	1.2	ns
401	Q13526	PIN1 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	PIN1	SGEEDFESLASQFSDC*SSAK	1.0	0.9	1.0	1.1	1.1	1.1	1.3	1.2	1.2	ns
402	O14980	XPO1 Exportin-1	XPO1	LDINLLDNVVNC*LYHGEGAQQR	1.0	1.0	1.0	1.2	1.1	1.2	1.2	1.2	1.2	ns
403	Q9UQ35	SRRM2 Serine/arginine repetitive matrix protein 2	SRRM2	SVSPC*SNVESR	1.0	0.9	1.0	1.1	1.1	1.1	1.5	1.1	1.2	ns
404	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	ASVGFGGSC*FQK	0.9	1.0	1.0	1.2	1.0	1.6	1.0	1.1	1.2	ns
405	Q9BRA2	TXNDC17 Thioredoxin domain-containing protein 17	TXNDC17	SWC*PDCVQAEPVVR	1.0	1.0	1.0	1.2	1.1	1.1	1.3	1.2	1.2	ns
406	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	TIC*AILENYQTEK	0.9	1.0	1.0	1.2	1.2	1.1	1.2	1.2	1.2	ns
407	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	HLNEIDLFHC*IDPNDSK	1.1	1.0	1.0	1.2	1.1	1.1	1.2	1.2	1.2	ns
408	E9PPU0	EPPK1 Epiplakin	EPPK1	TGGQALSTLEC*VK	0.9	1.0	0.9	1.2	1.2	1.0	1.4	1.1	1.2	ns
409	P62306	SNRPF Small nuclear ribonucleoprotein F	SNRPF	C*NNVLYIR	1.0	1.0	1.0	1.2	1.1	1.1	1.2	1.2	1.2	ns
410	P38646	HSPA9 Stress-70 protein, mitochondrial	HSPA9	C*ELSSSVQTDINLPYLTMDSSGPK	0.9	1.0	0.9	1.1	1.0	1.1	1.4	1.1	1.2	ns
411	P07900	HSP90AA1 Heat shock protein HSP 90-alpha	HSP90AA1	VFIMDNC*EELIPEYLNFIR	1.1	1.0	1.0	1.2	1.1	1.2	1.3	1.1	1.2	ns
412	Q15796	SMAD2 Mothers against decapentaplegic homolog 2	SMAD2	AITTQNC*NTK	0.9	1.1	1.0	1.3	0.4	1.4	1.4	1.3	1.2	ns
413	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	LVVPATQC*GSLIGK	0.9	1.0	0.9	1.2	1.1	1.2	1.2	1.2	1.2	ns
414	Q96RS6	NUDCD1 NudC domain-containing protein 1	NUDCD1	DSAQC*AAIAER	0.8	0.8	0.8	1.2	1.4	1.1	1.0	1.1	1.2	ns
415	Q16854	DGUOK Deoxyguanosine kinase, mitochondrial	DGUOK	AC*TAQSLGNLLDMMYR	1.0	1.2	1.1	1.1	1.0	1.1	1.4	1.2	1.2	ns
416	P28838	LAP3 Cytosol aminopeptidase	LAP3	SAGAC*TAAAFLK	0.9	1.0	1.0	1.1	0.9	1.2	1.4	1.1	1.2	ns
417	P37802	TAGLN2 Transgelin-2	TAGLN2	QYDADLEQILIQWITTQC*R	1.0	1.0	1.0	0.8	1.8	1.2	1.0	0.9	1.2	ns
418	P07741	APRT Adenine phosphoribosyltransferase	APRT	VVVVDDLLATGGTMNAAC*ELLGR	1.1	1.1	1.1	1.0	1.3	1.1	1.2	1.1	1.1	ns
419	Q86SX6	GLRX5 Glutaredoxin-related protein 5, mitochondrial	GLRX5	GTPEQPQC*GFSNAVVQILR	1.0	1.0	1.0	1.2	1.1	1.1	1.2	1.2	1.1	ns
420	O60547	GMDS GDP-mannose 4,6 dehydratase	GMDS	PTEVDFLQGDC*TK	0.9	1.0	0.9	1.2	1.1	1.1	1.3	1.1	1.1	ns
421	P53990	IST1 IST1 homolog	IST1	IVADQLC*AK	1.0	1.0	1.0	1.1	1.1	1.3	1.2	1.0	1.1	ns
422	Q5MNZ6	WDR45L WD repeat domain phosphoinositide-interacting protein 3	WDR45L	C*NYLALVGGGK	1.0	1.0	1.0	1.1	1.2	1.0	1.1	1.2	1.1	ns
423	Q9BV79	MECR Trans-2-enoyl-CoA reductase, mitochondrial	MECR	LALNC*VGGK	1.0	0.9	1.0	1.3	1.0	1.0	1.1	1.3	1.1	ns
424	O75940	SMNDC1 Survival of motor neuron-related-splicing factor 3	SMNDC1	VGVGTC*GIADK	0.9	1.0	1.0	1.0	1.4	1.0	1.2	1.1	1.1	ns

425	Q9H0C8	ILKAP Integrin-linked kinase-associated serine/threonine phosphatase 2C	ILKAP	FILLAC*DGLFK	0.9	1.0	0.9	1.0	1.1	1.4	1.2	0.9	1.1	ns
426	P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	GFGFVC*FSSPEEATK	1.0	1.2	1.1	1.0	1.2	1.3	1.2	1.0	1.1	ns
427	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	IAAYLQSDQFC*K	0.9	1.0	0.9	1.2	1.1	1.1	1.2	1.2	1.1	ns
428	P78347	GTF2I General transcription factor II-I	GTF2I	SILSPGGSC*GPIK	0.9	0.9	0.9	1.1	1.0	1.1	1.2	1.2	1.1	ns
429	P53602	MVD Diphosphomevalonate decarboxylase	MVD	DGDPLPSSLSC*K	1.0	1.3	1.1	1.1	1.1	1.1	1.2	1.1	1.1	ns
430	P26641	EEF1G Elongation factor 1-gamma	EEF1G	AAAPAPEEEMDEC*EQALAAEPK	1.0	1.0	1.0	1.1	1.1	1.2	1.1	1.1	1.1	ns
431	P49915	GMPS GMP synthase	GMPS	TVGVQGDC*R	0.5	1.1	0.8	1.3	0.7	1.1	1.3	1.4	1.1	ns
432	P21964	COMT Catechol O-methyltransferase	COMT	IVDAVIQEHQPSVLLELGAYC*GYSAVR	0.9	1.0	1.0	1.1	1.1	1.2	1.1	1.2	1.1	ns
433	P53396	ACLY ATP-citrate synthase	ACLY	FIC*TTSAIQNR	0.9	1.0	0.9	1.3	1.0	1.0	1.2	1.2	1.1	ns
434	Q9UI30	TRMT112 tRNA methyltransferase 112 homolog	TRMT112	IC*PVEFNPNFVAR	1.0	1.0	1.0	0.9	1.2	1.2	1.2	1.2	1.1	ns
435	Q9UNH7	SNX6 Sorting nexin-6	SNX6	IGSSLYALGTQDSTDIC*K	0.9	0.9	0.9	1.1	1.0	1.1	1.2	1.2	1.1	ns
436	P49841	GSK3B Glycogen synthase kinase-3 beta	GSK3B	LC*DFGSAK	1.0	1.0	1.0	1.0	1.2	1.0	1.2	1.2	1.1	ns
437	Q5TFE4	NT5DC1 5-nucleotidase domain-containing protein 1	NT5DC1	HFLSDTGMAC*R	1.0	1.1	1.0	1.1	1.2	1.0	1.2	1.1	1.1	ns
438	Q9Y224	C14orf166 UPF0568 protein C14orf166	C14orf166	LTALDYHNPAGFNC*K	1.0	1.0	1.0	1.1	1.1	1.1	1.2	1.1	1.1	ns
439	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	QEPLGSDSEGVNC*LAYDEAIMAQQDR	1.0	1.0	1.0	1.1	1.1	1.2	1.1	1.1	1.1	ns
440	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	INISEGNC*PER	1.0	1.0	1.0	1.1	1.1	1.1	1.2	1.1	1.1	ns
441	Q99873	PRMT1 Protein arginine N-methyltransferase 1	PRMT1	VIGIEC*SSISDYAVK	0.9	1.0	0.9	1.1	1.1	1.0	1.2	1.2	1.1	ns
442	Q15181	PPA1 Inorganic pyrophosphatase	PPA1	GISC*MNTTLSESPFK	1.0	1.3	1.2	1.2	1.0	1.2	1.1	1.1	1.1	ns
443	P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	AC*QIFVR	1.0	1.0	1.0	1.2	1.1	1.1	1.0	1.2	1.1	ns
444	P00338	LDHA L-lactate dehydrogenase A chain	LDHA	VIGSGC*NLDSAR	1.0	1.0	1.0	1.1	1.1	1.2	1.1	1.1	1.1	ns
445	Q14151	SAFB2 Scaffold attachment factor B2	SAFB2	ILDILGETC*K	1.0	0.7	0.8	0.9	1.3	1.2	1.2	0.9	1.1	ns
446	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	GLLDVTC*K	1.0	0.9	1.0	1.1	1.1	1.1	1.1	1.1	1.1	ns
447	Q9Y2Q3	GSTK1 Glutathione S-transferase kappa 1	GSTK1	ETTEAAC*R	1.0	1.0	1.0	1.1	1.1	1.2	1.1	1.1	1.1	ns
448	P53041	PPP5C Serine/threonine-protein phosphatase 5	PPP5C	TEC*AEPPR	0.9	1.0	1.0	1.0	0.8	1.2	1.3	1.1	1.1	ns
449	P36969	GPX4 Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	GPX4	YAEC*GLR	1.0	0.9	0.9	1.1	1.0	1.1	1.2	1.2	1.1	ns
450	Q86YH6	PDSS2 Decaprenyl-diphosphate synthase subunit 2	PDSS2	C*LLSDELSNIAMQVR	0.8	1.0	0.9	0.7	1.1	1.2	1.3	1.2	1.1	ns
451	Q9NYL2	MLTK Mitogen-activated protein kinase kinase kinase MLT	MLTK	IC*DFGASR	0.8	0.8	0.8	1.0	1.2	0.9	1.2	1.2	1.1	ns
452	P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	IHDVLC*K	1.0	1.2	1.1	1.1	0.9	1.1	0.9	1.5	1.1	ns

453	Q96HE7	ERO1L ERO1-like protein alpha	ERO1L	HDDSSDNFC*EADDIQSPEAEYVDLLLNPER	0.9	1.1	1.0	1.0	1.2	1.0	1.2	1.2	1.1	ns
454	P60981	DSTN Destrin	DSTN	C*STPEEIK	1.0	1.0	1.0	1.1	1.0	1.1	1.2	1.1	1.1	ns
455	P29401	TKT Transketolase	TKT	MAAISESNINLCGSHC*GVSIGEDGPSQMALEDLAMFR	1.1	1.0	1.1	1.0	1.1	1.1	1.2	1.2	1.1	ns
456	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	LVVPASQC*GSLIGK	0.9	1.0	0.9	1.1	1.1	1.1	1.2	1.1	1.1	ns
457	Q15149	PLEC Plectin	PLEC	AFC*GFEDPR	1.0	1.0	1.0	1.1	1.1	1.0	1.2	1.1	1.1	ns
458	Q8WTW3	COG1 Conserved oligomeric Golgi complex subunit 1	COG1	C*AVGLVDAVK	0.9	1.2	1.1	1.1	1.0	1.0	1.4	1.0	1.1	ns
459	P62258	YWHAE 14-3-3 protein epsilon	YWHAE	LIC*C*DILDVLDK	1.0	1.0	1.0	1.2	1.0	1.1	1.1	1.1	1.1	ns
460	Q969T9	WBP2 WW domain-binding protein 2	WBP2	DC*EIK	0.9	0.9	0.9	1.0	1.1	1.2	1.1	1.1	1.1	ns
461	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK	0.9	1.0	1.0	1.1	1.0	1.0	1.1	1.1	1.1	ns
462	Q14247	CTTN Src substrate cortactin	CTTN	C*ALGWDHQEK	1.0	0.9	0.9	1.1	1.1	1.1	1.1	1.1	1.1	ns
463	Q8TB45	DEPTOR DEP domain-containing mTOR-interacting protein	DEPTOR	SPSSQETHDSPFC*LR	0.7	1.0	0.9	1.0	1.2	1.2	1.0	1.0	1.1	ns
464	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	LDFVC*SFLQK	1.0	0.8	0.9	1.2	1.1	1.0	1.1	1.1	1.1	ns
465	Q9H773	DCTPP1 dCTP pyrophosphatase 1	DCTPP1	YTELPHGAISEDQAVGPADIPC*DSTGQTST	1.2	1.0	1.1	1.1	1.1	1.1	1.1	1.1	1.1	ns
466	Q9BY32	ITPA Inosine triphosphate pyrophosphatase	ITPA	GC*QDFGWDPCFQPDGYEQTYAEMPK	1.0	1.0	1.0	1.3	1.0	0.9	1.2	1.1	1.1	ns
467	P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	YLEC*SALTQR	1.0	1.1	1.0	0.8	1.8	1.0	0.9	0.9	1.1	ns
468	P62826	RAN GTP-binding nuclear protein Ran	RAN	VC*ENIPIVLC*GNK	0.9	1.0	1.0	1.1	1.0	1.2	1.0	1.1	1.1	ns
469	Q9BW61	DDA1 DET1- and DDB1-associated protein 1	DDA1	FHADSVC*K	1.0	1.2	1.1	1.0	1.2	1.0	1.0	1.1	1.1	ns
470	P36507	MAP2K2 Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	LC*DFGVSGQLIDSMANSFVGTR	1.1	1.0	1.1	1.1	1.0	1.0	1.1	1.2	1.1	ns
471	P49458	SRP9 Signal recognition particle 9 kDa protein	SRP9	VTDDLVC*LVYK	0.8	0.9	0.8	1.1	1.0	1.1	1.1	1.1	1.1	ns
472	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	GQAGGGGPGTGPGLGEAGSLATC*ELPLAK	1.1	1.0	1.0	1.1	1.0	0.9	1.2	1.1	1.1	ns
473	P55786	NPEPPS Puromycin-sensitive aminopeptidase	NPEPPS	DGVC*VR	0.9	0.8	0.9	1.2	0.9	1.2	1.1	1.0	1.1	ns
474	P50990	CCT8 T-complex protein 1 subunit theta	CCT8	IAVYSC*PFDGMITETK	1.1	0.9	1.0	1.1	1.0	1.0	1.2	1.1	1.1	ns
475	Q09666	AHNAK Neuroblast differentiation-associated protein AHNAK	AHNAK	GPFVEAEVPDVDLEC*PDAK	0.9	1.0	1.0	1.0	1.1	1.1	1.1	1.0	1.1	ns
476	P51659	HSD17B4 Peroxisomal multifunctional enzyme type 2	HSD17B4	IC*DFENASK	1.1	1.1	1.1	0.9	1.0	1.3	1.1	1.1	1.1	ns
477	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	AITIAGVPQSVTEC*VK	1.0	1.0	1.0	1.0	1.2	1.1	0.9	1.1	1.1	ns
478	P62857	RPS28 40S ribosomal protein S28	RPS28	TGSQGQC*TQVR	0.9	0.9	0.9	1.0	1.1	1.1	1.1	1.1	1.1	ns
479	Q8N987	NECAB1 N-terminal EF-hand calcium-binding protein 1	NECAB1	ETLNQLQSLQNSLEC*AMETTEEQTR	1.0	0.9	0.9	1.1	0.9	1.0	1.2	1.2	1.1	ns
480	P37802	TAGLN2 Transgelin-2	TAGLN2	NMAC*VQR	1.0	1.0	1.0	1.3	1.0	0.9	1.0	1.1	1.1	ns

481	Q9NZZ3	CHMP5 Charged multivesicular body protein 5	CHMP5	APPPSLTDC*IGTV DSR	1.0	0.9	0.9	1.0	1.1	1.1	1.1	1.0	1.1	ns
482	P30153	PPP2R1A Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	LNIISNLDC*VNEVI GIR	0.8	1.0	0.9	1.0	1.1	0.9	1.2	1.1	1.1	ns
483	P55735	SEC13 Protein SEC13 homolog	SEC13	FASGGC*DNLIK	1.0	1.0	1.0	1.1	1.0	1.0	1.1	1.1	1.1	ns
484	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	EEFASTC*PDDEEIE LAYEQVAK	1.3	1.3	1.3	0.9	1.0	1.3	1.1	1.1	1.1	ns
485	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	FIC*EQDHQNFLR	1.1	1.2	1.1	0.8	1.0	1.1	1.2	1.2	1.1	ns
486	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	LNEC*VDHTPK	1.0	0.9	1.0	1.0	1.3	1.0	1.0	1.0	1.1	ns
487	Q96Q11	TRNT1 CCA tRNA nucleotidyltransferase 1, mitochondrial	TRNT1	YQGEHC*LLK	0.9	0.9	0.9	1.3	1.0	1.1	1.1	0.9	1.1	ns
488	P13639	EEF2 Elongation factor 2	EEF2	YVEPIEDVPC*GNI VGLVGVDQFLVK	1.0	1.0	1.0	0.9	1.1	1.1	0.9	1.1	1.0	ns
489	P35270	SPR Sepiapterin reductase	SPR	TVVNISSLC*ALQP FK	0.9	0.8	0.9	1.1	1.0	1.1	1.0	1.1	1.0	ns
490	P60981	DSTN Destrin	DSTN	LGGSLIVAFEGC*P V	0.9	0.9	0.9	1.1	1.0	1.0	1.1	1.0	1.0	ns
491	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	YTC*GEAPDYDR	0.9	0.9	0.9	1.0	1.0	1.2	1.1	0.9	1.0	ns
492	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	LVSSPCC*IVTSTY GWTANMER	0.8	1.0	0.9	1.2	1.1	0.9	1.0	1.0	1.0	ns
493	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	LEVDAIVNAANSS LLGGGGVDGC*IH R	0.9	1.0	1.0	1.1	1.0	1.0	1.0	1.2	1.0	ns
494	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	FC*PFAER	1.0	1.0	1.0	1.1	1.0	1.1	1.1	1.1	1.0	ns
495	P31947	SFN 14-3-3 protein sigma	SFN	GEELSC*EER	0.9	0.9	0.9	1.0	1.1	1.1	1.1	1.0	1.0	ns
496	P52943	CRIP2 Cysteine-rich protein 2	CRIP2	ASSVTTFTGEPNTC *PR	1.0	0.9	0.9	1.1	0.9	1.1	1.2	1.0	1.0	ns
497	Q6KB66	KRT80 Keratin, type II cytoskeletal 80	KRT80	C*HIDLSGIVEEVK	0.9	1.0	1.0	1.0	1.0	1.0	1.1	1.1	1.0	ns
498	P52597	HNRNPF Heterogeneous nuclear ribonucleoprotein F	HNRNPF	GLPFGC*TK	1.0	0.9	0.9	1.0	1.1	1.1	1.0	1.0	1.0	ns
499	Q9Y5P6	GMPPB Mannose-1-phosphate guanyltransferase beta	GMPPB	LC*SGPGIVGNVLV DPSAR	0.9	1.1	1.0	1.0	1.0	1.0	1.0	1.1	1.0	ns
500	Q14247	CTTN Src substrate cortactin	CTTN	HC*SQVDSVR	0.9	0.9	0.9	1.1	0.9	1.1	1.1	1.0	1.0	ns
501	P13639	EEF2 Elongation factor 2	EEF2	TFC*QLILDPIFK	0.8	0.9	0.9	1.0	1.1	1.0	1.1	1.0	1.0	ns
502	P33316	DUT Deoxyuridine 5-triphosphate nucleotidohydrolase, mitochondrial	DUT	TDIQIALPSGC*YG R	1.0	1.0	1.0	1.0	1.4	0.9	0.9	1.0	1.0	ns
503	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	YLAEVAC*GDDR	0.9	1.0	0.9	0.9	1.1	1.1	1.0	1.1	1.0	ns
504	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	C*LSVMEAK	0.9	0.9	0.9	1.2	1.0	0.9	1.0	1.1	1.0	ns
505	Q9Y365	STARD10 PCTP-like protein	STARD10	MECC*DVPAETLY DVLHDIEYR	1.0	1.1	1.1	1.0	1.0	1.1	1.0	1.0	1.0	ns
506	P23434	GCSH Glycine cleavage system H protein, mitochondrial	GCSH	SC*YEDGWLIK	1.3	0.8	1.1	0.9	1.2	0.6	1.0	1.4	1.0	ns
507	Q01518	CAP1 Adenylyl cyclase-associated protein 1	CAP1	ALLVTASQC*QQPA ENK	0.9	1.0	1.0	0.9	1.1	1.0	0.9	1.2	1.0	ns
508	P13639	EEF2 Elongation factor 2	EEF2	C*LYASVLTAQPR	1.0	0.8	0.9	1.1	1.2	1.2	1.0	0.8	1.0	ns
509	O95671	ASMTL N-acetylserotonin O-methyltransferase-like protein	ASMTL	LTAC*QVATAFNLS R	1.0	1.1	1.0	1.1	0.9	1.0	1.0	1.0	1.0	ns

510	O00204	SULT2B1 Sulfotransferase family cytosolic 2B member 1	SULT2B1	APWC*ETIVGAFSLPDQYSPR	0.9	1.0	1.0	1.3	1.0	1.1	0.8	0.9	1.0	ns
511	P51610	HCFC1 Host cell factor 1	HCFC1	LVIYGGMSGC*R	0.9	0.9	0.9	1.1	1.0	1.2	1.0	0.9	1.0	ns
512	P47756	CAPZB F-actin-capping protein subunit beta	CAPZB	DETVSDC*SPHIANIGR	1.1	1.0	1.0	1.0	1.0	1.2	1.0	0.9	1.0	ns
513	Q12765	SCRN1 Secernin-1	SCRN1	TQSPC*FGDDDPAK	0.9	1.0	1.0	1.1	0.9	1.0	1.0	1.2	1.0	ns
514	Q8TAQ2	SMARCC2 SWI/SNF complex subunit SMARCC2	SMARCC2	NLAGDVC*AIMR	1.2	1.1	1.2	1.0	0.9	1.0	1.1	1.0	1.0	ns
515	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	ISSINSISALC*EATGADVEEVATAIGMDQR	1.0	1.0	1.0	1.0	1.1	1.0	0.9	1.1	1.0	ns
516	P00492	HPRT1 Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	SYC*NDQSTGDIK	1.0	0.8	0.9	1.0	1.1	0.9	1.0	1.0	1.0	ns
517	P30086	PEBP1 Phosphatidylethanolamine-binding protein 1	PEBP1	APVAGTC*YQAEWDDYVPK	1.0	1.1	1.0	0.9	1.1	1.1	1.0	1.1	1.0	ns
518	P35270	SPR Sepiapterin reductase	SPR	AVC*LLTGASR	1.0	1.0	1.0	1.0	1.1	1.1	0.9	0.9	1.0	ns
519	Q96EY8	MMAB Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	MMAB	IQCTLQDVGSALATPC*SSAR	0.9	1.1	1.0	1.1	0.9	0.9	1.1	1.1	1.0	ns
520	O75131	CPNE3 Copine-3	CPNE3	NC*LNPQFSK	0.9	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	ns
521	Q9HAV7	GRPEL1 GrpE protein homolog 1, mitochondrial	GRPEL1	LYGIQAFC*K	1.0	0.8	0.9	0.8	1.0	1.1	1.0	1.1	1.0	ns
522	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	IVDTPC*NEMNTDTFLEEINK	0.9	1.1	1.0	1.1	1.0	0.9	1.0	1.0	1.0	ns
523	Q9H8M7	FAM188A Protein FAM188A	FAM188A	SSPGLSDTIFC*R	1.5	0.9	1.2	0.5	1.2	1.0	1.0	1.4	1.0	ns
524	P26599	PTBP1 Polypyrimidine tract-binding protein 1	PTBP1	LSLDGQNIYNAC*CTLR	0.9	1.1	1.0	1.0	0.7	1.2	1.0	1.1	1.0	ns
525	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	NVGC*LQEALQLATSFAQLR	1.1	1.1	1.1	0.9	0.9	0.6	1.6	1.0	1.0	ns
526	P14649	MYL6B Myosin light chain 6B	MYL6B	ILYSQC*GDVMR	1.0	0.9	1.0	0.9	1.0	1.1	1.0	1.0	1.0	ns
527	P21964	COMT Catechol O-methyltransferase	COMT	LITIEINPDC*AAITQR	0.9	0.9	0.9	1.1	1.0	0.9	1.0	1.0	1.0	ns
528	P30626	SRI Sorcin	SRI	DTAQQGVVNFPYDDFIQC*VMSV	1.0	0.9	0.9	1.2	0.9	1.0	0.8	1.0	1.0	ns
529	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	ILSC*GEVIHVK	1.0	1.5	1.2	0.9	1.0	0.8	1.2	1.1	1.0	ns
530	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	C*LDEFPNLK	1.0	1.1	1.1	0.9	1.0	1.1	1.0	1.0	1.0	ns
531	P49753	ACOT2 Acyl-coenzyme A thioesterase 2, mitochondrial	ACOT2	SEFYANEAC*K	1.0	1.0	1.0	1.0	1.0	0.8	0.9	1.2	1.0	ns
532	P12004	PCNA Proliferating cell nuclear antigen	PCNA	C*AGNEDIITLR	1.2	0.9	1.1	0.9	1.0	1.0	1.0	1.0	1.0	ns
533	Q9NRF9	POLE3 DNA polymerase epsilon subunit 3	POLE3	AASVFVLYATSC*ANNFAMK	0.9	1.1	1.0	0.9	0.9	1.0	1.1	0.9	1.0	ns
534	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	GDFC*IQVGR	1.0	0.9	0.9	1.1	1.1	0.9	0.9	0.9	1.0	ns
535	Q7LG56	RRM2B Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	IEQEFLTEALPVGLIGMNC*ILMK	0.8	1.1	1.0	1.0	1.1	1.0	1.1	0.7	1.0	ns
536	Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	AITIAGIPQSIIEC*VK	1.1	1.0	1.1	1.0	1.1	1.0	0.9	1.0	1.0	ns
537	Q9BSH4	TACO1 Translational activator of cytochrome c oxidase 1	TACO1	LDSLGLCSVSC*ALEFIPNSK	0.8	1.1	1.0	0.7	1.0	1.0	1.1	1.0	1.0	ns
538	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	NDTPC*GTTIGPILASR	1.0	1.0	1.0	0.9	0.9	1.0	1.0	0.9	1.0	ns

539	Q96EY5	FAM125A Multivesicular body subunit 12A	FAM125A	GFSAISC*TVEGAPASFGK	0.9	1.0	0.9	0.9	1.0	0.9	1.0	0.9	1.0	ns
540	P63167	DYNLL1 Dynein light chain 1, cytoplasmic	DYNLL1	NADMSEEMQQDSVEC*ATQALEK	1.0	0.9	0.9	0.9	1.0	0.9	0.9	1.0	1.0	ns
541	Q96AT9	RPE Ribulose-phosphate 3-epimerase	RPE	IGPSILNSDLANLGAEC*LR	1.0	1.0	1.0	0.8	1.0	1.4	0.8	0.9	1.0	ns
542	P51858	HDGF Hepatoma-derived growth factor	HDGF	C*GDLVFAK	1.0	1.0	1.0	0.8	1.1	1.0	1.1	0.9	1.0	ns
543	O43681	ASNA1 ATPase ASNA1	ASNA1	PC*K	1.0	1.2	1.1	1.0	1.3	0.7	0.8	0.9	1.0	ns
544	P18669	PGAM1 Phosphoglycerate mutase 1	PGAM1	YADLTEDQLPSC*ESLK	0.9	0.9	0.9	1.0	0.9	1.1	0.9	0.8	1.0	ns
545	Q04917	YWHAH 14-3-3 protein eta	YWHAH	NC*NDFQYESK	1.1	1.0	1.0	0.9	1.1	0.9	0.9	1.0	0.9	ns
546	P11766	ADH5 Alcohol dehydrogenase class-3	ADH5	VCLLGC*GISTGYGAAVNTAK	1.1	0.9	1.0	1.1	0.8	1.0	1.0	0.9	0.9	ns
547	P40925	MDH1 Malate dehydrogenase, cytoplasmic	MDH1	AIC*DHVR	1.0	1.0	1.0	0.9	1.1	1.0	0.8	1.0	0.9	ns
548	P08107	HSPA1B Heat shock 70 kDa protein 1A/1B	HSPA1B	FEELC*SDLFR	1.4	1.1	1.2	0.9	1.0	1.0	0.9	1.0	0.9	ns
549	P61981	YWHAG 14-3-3 protein gamma	YWHAG	NC*SETQYESK	0.6	0.5	0.6	0.9	0.9	1.0	0.9	1.0	0.9	ns
550	P30626	SRI Sorcin	SRI	PFNLETC*R	0.9	0.8	0.9	1.0	0.8	1.0	0.9	1.0	0.9	ns
551	P62993	GRB2 Growth factor receptor-bound protein 2	GRB2	VLNEEC*DQNWYK	1.0	1.0	1.0	0.9	0.8	1.0	0.9	1.0	0.9	ns
552	P23528	CFL1 Cofilin-1	CFL1	AVLFC*LSEDK	1.0	1.0	1.0	0.8	1.0	1.1	0.8	0.9	0.9	ns
553	P52209	PGD 6-phosphogluconate dehydrogenase, decarboxylating	PGD	C*LSSLK	0.9	1.0	1.0	0.9	1.0	0.9	0.9	1.0	0.9	ns
554	P10768	ESD S-formylglutathione hydrolase	ESD	CPALYWLSGLTC*TEQNFISK	1.2	1.0	1.1	1.0	0.9	0.9	1.0	0.9	0.9	ns
555	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	LQEALDAEMLEDEAGGGGAGPGGAC*K	1.1	1.1	1.1	0.8	0.9	1.0	1.0	1.0	0.9	ns
556	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	YLLQYQEPIPC*EQLVTALCDIK	1.1	1.1	1.1	0.8	1.0	1.0	0.9	0.9	0.9	ns
557	P31947	SFN 14-3-3 protein sigma	SFN	VETELQGVC*DTVLGLLDSHLIK	1.2	0.9	1.1	0.8	1.0	1.1	0.9	0.9	0.9	ns
558	O14964	HGS Hepatocyte growth factor-regulated tyrosine kinase	HGS	AC*GQIFC*GK	0.8	0.8	0.8	1.0	0.7	0.9	1.2	0.9	0.9	ns
559	P60174	TPI1 Triosephosphate isomerase	TPI1	IIYGGSVTGATC*K	1.1	1.0	1.1	0.7	1.1	0.9	1.0	1.0	0.9	ns
560	P37802	TAGLN2 Transgelin-2	TAGLN2	DGTVLC*ELINALYPEGQAPVK	1.1	1.0	1.0	0.9	1.0	1.0	0.8	0.9	0.9	ns
561	P21291	CSRP1 Cysteine and glycine-rich protein 1	CSRP1	SCFLCMVC*K	1.0	1.0	1.0	0.9	0.8	0.9	1.0	1.0	0.9	ns
562	Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	GNGIVEC*LGPK	1.0	1.0	1.0	0.6	1.5	0.7	1.1	0.6	0.9	ns
563	P22234	PAICS Multifunctional protein ADE2	PAICS	ITSC*IFQLLQEAGIK	1.0	1.0	1.0	1.0	0.8	0.9	0.9	0.9	0.9	ns
564	P52788	SMS Spermine synthase	SMS	LYC*PVEFSK	1.1	1.0	1.1	0.9	0.8	1.0	0.9	0.9	0.9	ns
565	O75874	IDH1 Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	SEGGFIWAC*K	0.9	1.0	1.0	0.9	0.9	0.8	0.9	1.0	0.9	ns
566	P04632	CAPNS1 Calpain small subunit 1	CAPNS1	YSDESGNMDFDNFISC*LVR	1.1	1.3	1.2	0.9	1.0	0.9	0.9	0.9	0.9	ns
567	P23528	CFL1 Cofilin-1	CFL1	HELQANC*YEEVK	1.0	1.0	1.0	0.9	0.9	0.9	0.9	1.0	0.9	ns
568	P22061	PCMT1 Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	ALDVGSGSGILTAC*FAR	1.0	1.0	1.0	0.9	0.9	0.9	0.8	0.9	0.9	ns
569	Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	LAAQSC*ALSLVR	0.8	0.7	0.8	0.9	0.7	1.0	1.0	0.9	0.9	ns

570	Q96EI5	TCEAL4 Transcription elongation factor A protein-like 4	TCEAL4	PEVTC*TLEDK	0.9	0.5	0.7	0.8	0.8	1.0	0.9	0.9	0.9	ns
571	P61970	NUTF2 Nuclear transport factor 2	NUTF2	NINDAWVC*TNDMFR	1.0	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	ns
572	Q96FJ2	DYNLL2 Dynein light chain 2, cytoplasmic	DYNLL2	NADMSEDMQQDAVDC*ATQAMEK	1.1	0.9	1.0	0.8	0.8	1.2	0.8	0.9	0.9	ns
573	P60174	TPI1 Triosephosphate isomerase	TPI1	VPADTEVVC*APPTAYIDFAR	1.1	1.0	1.1	0.8	1.0	1.0	0.8	0.9	0.9	ns
574	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	IC*PVETLVEEAIQCAEK	0.9	0.9	0.9	0.8	0.9	1.0	0.9	0.8	0.9	ns
575	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	ATC*IGNNSAAAVSMLK	0.9	0.9	0.9	0.8	0.8	0.9	0.9	0.9	0.9	ns
576	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	NTGIIC*TIGPASR	0.8	1.0	0.9	0.9	0.9	0.9	0.9	0.8	0.9	ns
577	P00491	PNP Purine nucleoside phosphorylase	PNP	AC*VMMQGR	1.2	1.2	1.2	0.7	1.1	1.0	0.7	0.8	0.9	ns
578	Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	VVFC*PVK	1.0	0.9	1.0	1.0	0.8	0.8	1.0	0.8	0.9	ns
579	Q9UL46	PSME2 Proteasome activator complex subunit 2	PSME2	C*GFLPGNEK	1.0	0.9	1.0	0.9	0.8	0.9	1.0	0.9	0.9	ns
580	P60981	DSTN Destrin	DSTN	AVIFC*LSADK	0.8	0.9	0.8	0.7	1.0	0.9	0.8	0.9	0.9	ns
581	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	YASIC*QQNGIVPIVEPEILPDGDHDLK	1.0	1.0	1.0	0.8	0.9	0.9	0.8	0.9	0.9	ns
582	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	LNEDMAC*SVAGITSDANVLTNELR	0.9	0.9	0.9	0.7	0.9	0.9	1.0	0.8	0.9	ns
583	Q9UHX1	PUF60 Poly(U)-binding-splicing factor PUF60	PUF60	ALAIMC*R	1.0	1.0	1.0	0.8	1.1	0.8	0.8	0.8	0.9	ns
584	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	SIC*TTVLELLDK	1.1	1.0	1.0	0.8	1.0	0.9	0.8	0.8	0.9	ns
585	P07737	PFN1 Profilin-1	PFN1	C*YEMASHLR	1.0	0.9	1.0	0.9	0.9	0.8	0.8	0.9	0.9	ns
586	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	FLDGNELTLADC*NLLPK	1.0	0.8	0.9	0.9	0.8	1.0	0.7	0.9	0.9	ns
587	P00390	GSR Glutathione reductase, mitochondrial	GSR	LGGTC*VNVGCVPK	0.9	0.9	0.9	0.8	0.9	0.8	0.9	0.9	0.9	ns
588	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	ALANSLAC*QGK	1.0	1.0	1.0	0.8	0.9	1.0	0.8	0.9	0.9	ns
589	P14174	MIF Macrophage migration inhibitory factor	MIF	LLC*GLLAER	1.0	1.0	1.0	0.9	0.9	0.9	0.8	0.9	0.9	ns
590	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	DIC*NDVLSLLEK	1.1	0.9	1.0	0.7	1.0	1.0	0.8	0.8	0.8	ns
591	P60174	TPI1 Triosephosphate isomerase	TPI1	IAVAAQNC*YK	0.9	1.0	1.0	0.8	0.9	0.9	0.7	0.9	0.8	ns
592	P31949	S100A11 Protein S100-A11	S100A11	C*IESLIAVFQK	1.0	0.9	1.0	0.6	1.0	0.9	0.9	0.8	0.8	ns
593	F5H284	PPIAL4D Peptidyl-prolyl cis-trans isomerase A-like 4D	PPIAL4D	IIPGFMC*QGGDFTR	1.0	1.0	1.0	0.8	0.9	0.9	0.8	0.8	0.8	ns
594	P09467	FBP1 Fructose-1,6-bisphosphatase 1	FBP1	GTGELTQLLNSLC*TAVK	0.9	1.2	1.0	0.8	0.9	0.8	0.8	0.8	0.8	ns
595	P61158	ACTR3 Actin-related protein 3	ACTR3	LPACVVDC*GTGYTK	1.1	1.0	1.0	1.0	0.6	0.9	0.9	0.9	0.8	ns
596	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	SC*YLSSLDLLLEHR	1.0	1.0	1.0	0.8	0.9	0.8	0.8	0.9	0.8	ns
597	P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	DC*LIPMGITSENVAER	0.9	0.9	0.9	0.8	0.9	0.8	0.9	0.8	0.8	ns
598	P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	ITIADC*GQLE	0.8	1.0	0.9	0.8	1.0	0.8	0.8	0.8	0.8	ns
599	P21964	COMT Catechol O-methyltransferase	COMT	YLPDTLLLEEC*GLLR	0.9	1.0	0.9	0.8	0.9	0.8	0.7	0.8	0.8	ns
600	P31150	GDI1 Rab GDP dissociation inhibitor alpha	GDI1	TDDYLDQPC*LETVNR	0.9	1.1	1.0	0.8	0.8	0.9	0.7	0.8	0.8	ns
601	P30044	PRDX5 Peroxiredoxin-5, mitochondrial	PRDX5	ALNVEPDGTGLTC*SLAPNIISQL	1.0	1.0	1.0	0.7	0.8	0.9	0.8	0.8	0.8	ns

602	P13489	RNH1 Ribonuclease inhibitor	RNH1	LSLQNC*C*LTGAGC*GVLSSTLR	0.9	1.0	0.9	1.1	0.4	0.8	0.8	0.8	0.8	ns
603	Q15369	TCEB1 Transcription elongation factor B polypeptide 1	TCEB1	VC*MYFTYK	1.2	0.8	1.0	0.9	0.6	0.9	0.8	0.7	0.8	ns
604	Q9Y3D0	FAM96B Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	VAAALENTHLLEVVNQC*LSAR	1.0	1.0	1.0	0.6	0.8	0.6	0.6	0.7	0.7	ns
605	P25398	RPS12 40S ribosomal protein S12	RPS12	QAHLCVLASNC*DEPMYVK	1.1	1.0	1.0	0.6	0.6	0.6	0.7	0.7	0.6	ns
606	P25398	RPS12 40S ribosomal protein S12	RPS12	LVEALC*AEHQINLIK	1.0	1.0	1.0	0.6	0.6	0.6	0.6	0.6	0.6	ns
607	Q14847	LASP1 LIM and SH3 domain protein 1	LASP1	ACFHC*ETC*K	1.0	1.0	1.0	0.6	0.5	0.7	0.6	0.7	0.6	ns
608	P21291	CSRP1 Cysteine and glycine-rich protein 1	CSRP1	C*SQAVYAAEK	1.0	1.0	1.0	0.5	0.4	0.5	0.6	0.5	0.5	ns
609	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	VPTANVSVVDLTC*R	0.9	1.0	0.9	0.4	0.5	0.5	0.5	0.4	0.5	ns

Table 3A-2. R-values from transnitrosation experiment at 500 μM CoA-SNO. A list of all identified peptides (* denotes labeled cysteine) is presented together with calculated Heavy:LightRatios (R-values) in untreated (0 μM) (n=2) versus CoA-SNO-treated (500 μM) (n=5) MS analysis. Date were sorted by their average R-values of CoA-SNO-treated experiments and numbered as "Peptide #".

Peptide #	Uniprot #	Description	Symbol	Sequence	Heavy : Light Ratio								significance
					0 μM CoA-SNO			500 μM CoA-SNO					
					1	2	average	1	2	3	4	5	average	
1	P31749	AKT1 RAC-alpha serine/threonine-protein kinase	AKT1	K.TFC*GTPEYLAPEVLEDNDYGR.A	0.9	0.9	0.9	14.4	20.0	17.3	15.8	3.0	14.1	***
2	Q9NZB2	FAM120A Constitutive coactivator of PPAR-gamma-like protei	FAM120A	R.VAAASGHC*GAFSGSDSSR.T	0.9	0.9	0.9	20.0	14.4	10.9	8.8	7.0	12.2	***
3	Q9BRA2	TXNDC17 Thioredoxin domain-containing protein 17	TXNDC17	K.DAGGKSWC*PDCVQAEPVVR.E	0.9	0.9	0.9	11.1	14.0	6.5	11.7	11.0	10.8	***
4	Q92947	GCDH Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	K.GYGC*AGVSSVAYGLLAR.E	0.9	0.8	0.9	7.9	13.0	12.9	13.2	5.3	10.5	***
5	P25398	RPS12 40S ribosomal protein S12	RPS12	K.KLGEWVGLC*K.I	0.7	0.9	0.8	11.5	10.6	9.3	12.1	6.4	10.0	***
6	Q01813	PFKP 6-phosphofructokinase type C	PFKP	R.LPLMEC*VQMTQDVQK.A	0.9	0.9	0.9	8.7	10.6	9.4	10.7	9.2	9.7	***
7	P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB2	K.AC*GDSTLTQITAGLDPVGR.I	0.9	0.9	0.9	4.9	20.0	9.1	6.4	5.9	9.2	***
8	P62888	RPL30 60S ribosomal protein L30	RPL30	R.VC*TLAIIDPGDSDIIR.S	0.8	0.8	0.8	11.1	8.2	8.4	8.7	9.6	9.2	***
9	Q53H96	PYCRL Pyrroline-5-carboxylate reductase 3	PYCRL	R.SDVC*TPGGTTIYGLHALEQGGLR.A	0.9	0.8	0.9	11.5	8.9	8.5	8.8	7.8	9.1	***
10	Q8TCU6	PREX1 Phosphatidylinositol 3,4,5-trisphosphate-dependent	PREX1	R.LC*VLNEILGTER.D	0.9	0.8	0.8	9.0	20.0	4.0	5.5	4.4	8.6	***
11	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.AFAAGADIKEMQNLSFQDC*YSSK.F	0.9	0.9	0.9	9.3	8.3	8.1	10.0	7.1	8.5	***
12	P04183	TK1 Thymidine kinase, cytosolic	TK1	R.NTMEALPAC*LLR.D	0.9	0.8	0.8	3.7	14.6	8.5	7.0	7.5	8.3	***

13	P13674	P4HA1 Prolyl 4-hydroxylase subunit alpha-1	P4HA1	R.RPC*TLSELE.-	0.9	0.8	0.9	9.9	8.2	7.5	7.2	8.3	8.2	***
14	P15924	DSP Desmoplakin	DSP	R.DANSENC*NK.N	1.0	0.9	0.9	19.6	6.8	5.4	4.4	4.4	8.1	***
15	Q01813	PFKP 6-phosphofructokinase type C	PFKP	R.NESC*SENYTTDFIYQLYSEEGK.G	1.0	0.9	0.9	7.2	13.9	6.5	6.4	5.9	8.0	***
16	P53384	NUBP1 Cytosolic Fe-S cluster assembly factor NUBP1	NUBP1	R.GASC*QGCPNQR.L	0.8	0.8	0.8	6.9	7.2	7.1	7.4	8.9	7.5	***
17	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.FGRVDVAVNC*AGIAVASK.T	0.8	0.8	0.8	4.7	5.5	8.8	4.7	13.4	7.4	***
18	P46734	MAP2K3 Dual specificity mitogen-activated protein kinase	MAP2K3	R.FSPEFVDFTAQC*LR.K	1.0	0.8	0.9	6.3	6.8	5.0	6.4	12.5	7.4	***
19	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	K.VGILDVDLC*GPSIPR.M	0.9	0.8	0.9	9.3	8.0	6.0	5.9	6.1	7.0	***
20	Q9Y5M8	SRPRB Signal recognition particle receptor subunit beta	SRPRB	K.NTPSFLIAC*NK.Q	0.8	1.0	0.9	5.8	5.7	5.0	13.6	5.0	7.0	***
21	P35270	SPR Sepiapterin reductase	SPR	R.TVVNISSLC*ALQPFK.G	0.8	0.9	0.8	12.1	7.3	4.0	6.0	5.0	6.9	***
22	Q9Y3A3	MOB4 MOB-like protein phocein	MOB4	R.HTLDGAAC*LLNSNK.Y	0.9	0.9	0.9	6.5	7.6	6.4	7.8	6.0	6.9	***
23	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.SLHDALC*VVK.R	0.7	0.9	0.8	5.5	7.5	6.3	6.2	8.9	6.9	***
24	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.KLGNNC*VFAPADVTSEK.D	0.9	0.8	0.9	3.6	8.0	7.3	7.9	7.3	6.8	***
25	Q14203	DCTN1 Dynactin subunit 1	DCTN1	K.VTFSC*AAGFGQR.H	1.2	1.1	1.2	2.0	9.0	2.4	17.6	3.0	6.8	***
26	P15924	DSP Desmoplakin	DSP	K.YQAEC*SQFK.A	0.9	0.9	0.9	7.4	9.9	6.7	4.6	5.1	6.7	***
27	P21281	ATP6V1B2 V-type proton ATPase subunit B, brain isoform	ATP6V1B2	K.KTSC*EFTGDILR.T	0.9	0.9	0.9	2.7	4.1	15.3	7.0	2.2	6.3	***
28	P07339	CTSD Cathepsin D	CTSD	K.AIGAVPLIQGEYMIPC*EK.V	0.9	0.8	0.8	9.1	5.0	5.7	6.0	4.5	6.1	***
29	P49327	FASN Fatty acid synthase	FASN	R.LGMLSPEGTC*K.A	0.9	0.8	0.8	3.7	5.9	12.5	5.2	2.9	6.1	***
30	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	K.IISNASC*TTNCLAPLAK.V	0.9	0.9	0.9	6.1	4.3	6.5	7.2	5.7	6.0	***
31	O15371	EIF3D Eukaryotic translation initiation factor 3 subunit	EIF3D	R.NLAMEATYINHNFSQQC*LR.M	0.9	0.9	0.9	2.7	2.5	2.0	20.0	1.9	5.8	***
32	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.AYHEQLSVAEITNAC*FEPANQMVK.C	0.9	0.9	0.9	6.5	5.7	5.6	5.7	5.2	5.7	***
33	Q86Y56	HEATR2 HEAT repeat-containing protein 2	HEATR2	R.C*SLLDPFAAVR.R	0.9	0.9	0.9	7.4	6.8	3.5	7.1	3.6	5.7	***
34	P54136	RARS Arginine--tRNA ligase, cytoplasmic	RARS	K.NC*GCLGASPNLEQLQEENLK.L	1.2	0.7	1.0	5.9	6.6	4.9	6.0	4.7	5.6	***
35	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.ALNALC*DGLIDELNQALK.T	0.9	0.9	0.9	6.3	5.5	5.4	5.9	4.7	5.6	***
36	P17858	PFKL 6-phosphofructokinase, liver type	PFKL	R.VFANAPDSAC*VIGLK.K	0.9	0.8	0.8	5.6	5.9	5.6	5.5	5.2	5.5	***
37	Q09028	RBBP4 Histone-binding protein RBBP4	RBBP4	R.YMPQNPC*IIATK.T	0.8	0.8	0.8	4.6	5.8	5.9	6.0	5.2	5.5	***
38	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	R.YVAAAFPSAC*GK.T	0.8	0.8	0.8	5.6	6.3	5.3	4.4	5.6	5.4	***
39	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.NMITGTAPLDGC*ILVVAANDGPMPQTR.E	0.9	0.9	0.9	5.5	4.8	5.4	5.5	5.3	5.3	***
40	P42677	RPS27 40S ribosomal protein S27	RPS27	K.ARLTEGC*SFR.R	0.8	0.9	0.8	5.6	5.8	5.0	5.3	4.8	5.3	***

41	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	R.QC*PIMDPAWEAPEGVPIDAIIFGGR.R	0.9	0.7	0.8	4.5	2.8	11.9	3.4	3.8	5.3	***
42	P43034	PAFAH1B1 Platelet-activating factor acetylhydrolase IB subu	PAFAH1B1	R.MVRPNQDGTLIASC*SNDQTVR.V	0.7	0.7	0.7	5.1	5.7	4.6	5.6	5.3	5.3	***
43	P07437	TUBB Tubulin beta chain	TUBB	K.LTTPTYGDLNHLVSATMSGVTTC*LR.F	0.9	0.9	0.9	5.3	5.5	5.2	5.3	4.8	5.2	***
44	P07437	TUBB Tubulin beta chain	TUBB	K.TAVC*DIPPR.G	0.9	0.8	0.9	5.3	5.1	5.0	5.7	5.0	5.2	***
45	P15924	DSP Desmoplakin	DSP	K.YC*YLQNEVFGLFQK.L	1.0	0.9	1.0	5.7	5.6	5.2	5.5	3.7	5.1	**
46	P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	K.IIC*QGFTGK.Q	0.9	0.9	0.9	4.8	5.3	5.8	4.5	5.1	5.1	**
47	Q96CM8	ACSF2 Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	R.MVSTPIGGLSYVQGC*TK.K	1.5	1.4	1.4	8.5	5.5	3.5	4.9	3.1	5.1	*
48	Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	K.AVVVC*PK.D	0.9	0.8	0.9	11.7	3.8	3.5	3.2	3.1	5.0	**
49	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.GEETPVIVGSALC*ALEGR.D	0.8	0.8	0.8	5.5	5.8	4.4	4.7	4.6	5.0	**
50	P31153	MAT2A S-adenosylmethionine synthase isoform type-2	MAT2A	K.TC*NVLVALEQQSPDIAQGVHLDR.N	0.9	0.8	0.9	6.0	5.5	4.8	4.9	3.6	5.0	**
51	P60709	ACTB Actin, cytoplasmic 1	ACTB	K.C*DVDIRK.D	0.9	0.8	0.8	3.8	5.3	5.3	4.9	5.4	4.9	**
52	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	R.C*MTNTPVVVR.E	0.8	0.8	0.8	5.6	4.9	4.5	4.7	4.1	4.8	**
53	P33992	MCM5 DNA replication licensing factor MCM5	MCM5	R.C*SVLAAANSVFGR.W	1.1	0.9	1.0	4.7	6.5	4.1	5.1	3.4	4.7	*
54	P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	R.TIYAGNALC*TVK.C	1.0	0.9	0.9	5.1	4.6	4.4	5.2	4.1	4.7	*
55	P62280	RPS11 40S ribosomal protein S11	RPS11	R.DVQIGDIVTVGEC*RPLSK.T	0.8	0.8	0.8	4.9	4.8	4.4	5.1	4.2	4.7	**
56	P36578	RPL4 60S ribosomal protein L4	RPL4	R.SGQGAFGNMC*R.G	0.9	0.8	0.8	5.0	5.2	4.9	4.2	4.0	4.6	*
57	P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	R.LGGEVSC*LVAGTK.C	0.9	0.8	0.8	3.8	4.9	4.5	5.4	4.6	4.6	*
58	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	R.AGGIETIANEFSDRC*TPSVISFGSK.N	0.9	0.8	0.9	3.8	5.3	4.7	5.5	3.9	4.6	*
59	P07437	TUBB Tubulin beta chain	TUBB	K.NMMAAC*DPR.H	0.9	0.8	0.8	5.1	4.8	4.5	4.6	4.2	4.6	*
60	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	R.LC*PNSTGAEIR.S	0.9	0.8	0.8	4.7	4.1	4.9	4.6	4.6	4.6	*
61	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	R.AVC*MLSNTTAIAEAWAR.L	0.9	0.9	0.9	4.8	4.8	4.6	4.6	4.3	4.6	*
62	P27635	RPL10 60S ribosomal protein L10	RPL10	K.MLSC*AGADR.L	0.9	0.8	0.9	5.6	4.8	4.4	4.2	4.1	4.6	*
63	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	K.LWNTLGVC*K.Y	0.8	0.8	0.8	3.7	4.8	5.2	4.9	4.2	4.6	*
64	P16455	MGMT Methylated-DNA--protein-cysteine methyltransferase	MGMT	R.VVC*SSGAVGNYSGGLAVK.E	0.9	0.8	0.9	6.1	5.1	3.3	4.1	4.1	4.6	*
65	P62857	RPS28 40S ribosomal protein S28	RPS28	R.TGSQGQC*TQVR.V	0.9	1.0	1.0	4.7	5.1	4.2	4.7	3.6	4.5	*
66	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	R.SVC*TEAGMFAIR.A	0.9	0.9	0.9	5.2	4.6	4.3	4.5	3.7	4.5	*
67	Q9UHD8	SEPT9 Septin-9	9-Sep	K.LTVIDTPGFGDHINNENC*WQPIMK.F	0.9	0.8	0.9	11.5	2.7	2.6	2.9	2.5	4.4	*
68	P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	R.LIGPNC*PGVINPGECK.I	0.9	0.8	0.8	6.2	4.8	3.5	3.8	3.8	4.4	*

69	Q92616	GCN1L1 Translational activator GCN1	GCN1L1	R.C*GLALALNK.L	0.8	0.7	0.8	4.1	5.0	4.9	3.9	4.2	4.4	*
70	P62241	RPS8 40S ribosomal protein S8	RPS8	K.NC*IVLIDSTPYR.Q	0.9	0.9	0.9	4.2	4.5	4.5	4.8	4.0	4.4	*
71	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	R.FSPNSSNPIIVSC*GWDK.L	0.9	0.8	0.8	3.5	5.1	4.5	4.9	3.9	4.4	*
72	O95757	HSPA4L Heat shock 70 kDa protein 4L	HSPA4L	R.GC*ALQCAILSPAFK.V	0.8	0.8	0.8	4.4	4.2	4.4	4.5	4.4	4.4	*
73	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	K.ERVC*NLIDSGTK.E	0.9	0.8	0.9	3.4	5.2	3.9	5.5	3.9	4.4	*
74	P46734	MAP2K3 Dual specificity mitogen-activated protein kinase	MAP2K3	K.TMDAGC*KPYMAPER.I	0.9	0.8	0.9	3.0	3.2	2.7	10.4	2.2	4.3	ns
75	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	R.QAVLGAGLPISTPC*TTINK.V	0.9	0.9	0.9	3.9	4.9	3.7	6.0	3.0	4.3	ns
76	Q5MNZ6	WDR45L WD repeat domain phosphoinositide-interacting prot	WDR45L	R.C*NYLALVGGGK.K	1.0	0.9	1.0	4.0	6.1	3.0	4.9	3.1	4.2	ns
77	Q13509	TUBB3 Tubulin beta-3 chain	TUBB3	K.VAVC*DIPPR.G	0.9	0.8	0.8	3.8	4.0	4.3	4.5	4.4	4.2	ns
78	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	K.ELAPAVSVLQLFC*SSPK.A	0.9	0.9	0.9	3.5	4.0	4.2	4.0	5.1	4.2	ns
79	P23396	RPS3 40S ribosomal protein S3	RPS3	K.GC*EVVVSGK.L	0.9	1.0	0.9	3.9	4.8	3.5	4.3	4.2	4.2	ns
80	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.KGDEC*ELLGHSK.N	1.0	0.9	0.9	3.7	5.0	3.9	4.3	3.8	4.1	ns
81	P61163	ACTR1A Alpha-centractin	ACTR1A	R.AC*YLSINPQK.D	0.7	0.8	0.8	4.1	5.0	3.7	4.3	3.6	4.1	ns
82	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	R.SLLINAVEASC*IR.T	0.8	0.9	0.8	4.4	4.8	3.7	4.1	3.6	4.1	ns
83	P40939	HADHA Trifunctional enzyme subunit alpha, mitochondrial	HADHA	R.C*LAPMMSEVIR.I	0.8	0.7	0.8	3.3	4.3	4.4	3.8	4.4	4.0	ns
84	Q14694	USP10 Ubiquitin carboxyl-terminal hydrolase 10	USP10	R.TPSYSISSTLNPQAPEFILGC*TASK.I	1.0	0.9	0.9	7.0	3.5	3.5	3.6	2.6	4.0	ns
85	P09622	DLD Dihydrolipoyl dehydrogenase, mitochondrial	DLD	K.NETLGGTC*LNVGCIPSK.A	0.9	0.9	0.9	1.9	2.4	2.8	10.6	2.6	4.0	ns
86	Q9BYG5	PARD6B Partitioning defective 6 homolog beta	PARD6B	R.HGAGSGC*LGTMEVK.S	0.9	0.9	0.9	3.5	1.9	1.9	11.1	1.6	4.0	ns
87	Q14152	EIF3A Eukaryotic translation initiation factor 3 subunit	EIF3A	K.NIC*QQVNIK.S	0.8	0.9	0.9	3.0	3.3	3.2	7.6	2.7	4.0	ns
88	P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	K.ARDC*LIPMGITSENVAER.F	0.9	0.9	0.9	4.7	5.0	3.3	3.6	3.1	3.9	ns
89	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.RSIQFVDWC*PTGFK.V	0.9	0.8	0.9	4.3	4.1	3.8	3.9	3.5	3.9	ns
90	P49207	RPL34 60S ribosomal protein L34	RPL34	R.AYGGSMC*AK.C	1.0	0.7	0.8	4.1	3.4	3.2	5.6	3.2	3.9	ns
91	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.GYLGPEQLPDC*LK.G	0.8	0.8	0.8	3.5	4.1	4.3	3.8	3.5	3.8	ns
92	Q8NBF2	NHLRC2 NHL repeat-containing protein 2	NHLRC2	K.AILFSQPLQITDTQQGC*IAPVELR.Y	1.2	0.9	1.1	4.0	4.4	3.1	4.8	2.9	3.8	ns
93	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	R.GNVC*GDSK.S	0.7	0.9	0.8	3.5	3.5	4.6	2.7	4.7	3.8	ns
94	O95747	OXSR1 Serine/threonine-protein kinase OSR1	OXSR1	K.TFVGTPC*WMAPEVMEQVR.G	0.9	0.8	0.9	2.7	4.6	4.0	3.8	3.8	3.8	ns
95	Q9ULV4	CORO1C Coronin-1C	CORO1C	K.C*DLISIPK.K	0.9	0.8	0.8	4.2	4.5	3.3	3.7	3.2	3.8	ns

96	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.GC*DVVVIPAGVPR.K	0.8	0.7	0.7	3.8	2.3	3.5	3.9	5.3	3.8	ns
97	P62249	RPS16 40S ribosomal protein S16	RPS16	K.TATAVAHC*K.R	0.7	0.8	0.8	4.0	4.1	3.5	3.9	3.3	3.8	ns
98	B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	K.IFVGNVSAAC*TSQELR.S	1.0	0.9	0.9	4.5	4.0	2.9	4.2	3.0	3.7	ns
99	Q9Y3F4	STRAP Serine-threonine kinase receptor-associated protei	STRAP	K.IGFPETTEEELEEIASENSDC*IFPSAPDVK.A	0.8	1.0	0.9	10.8	2.2	1.8	2.0	1.9	3.7	ns
100	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.IC*DDELILIK.N	0.9	0.9	0.9	3.6	4.0	3.7	2.9	4.4	3.7	ns
101	Q71U36	TUBA1A Tubulin alpha-1A chain	TUBA1A	R.TIQFVDWC*PTGFK.V	0.8	0.8	0.8	4.2	3.8	3.4	3.7	3.4	3.7	ns
102	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	K.SGDAAIVEMVPGKPMC*VESFSQYPPLGR.F	0.7	0.8	0.8	2.2	3.8	4.2	4.7	3.2	3.6	ns
103	P60709	ACTB Actin, cytoplasmic 1	ACTB	K.EKLC*YVALDFEQEMATAASSSSLEK.S	0.9	0.8	0.9	3.0	3.6	3.8	3.8	3.7	3.6	ns
104	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	K.AEMDAAIASC*K.R	0.9	0.8	0.9	2.8	4.0	3.9	3.7	3.5	3.6	ns
105	Q9Y265	RUVBL1 RuvB-like 1	RUVBL1	K.VPFC*PMVGSEVYSTEIK.K	0.9	0.8	0.8	2.0	5.8	3.6	2.4	4.1	3.6	ns
106	Q13185	CBX3 Chromobox protein homolog 3	CBX3	R.LTWHSC*PEDEAQ.-	1.0	1.0	1.0	3.9	5.0	2.4	3.2	3.0	3.5	ns
107	P62829	RPL23 60S ribosomal protein L23	RPL23	R.ISLGLPVGAVINC*ADNTGAK.N	0.9	0.8	0.8	3.9	3.6	3.3	3.3	3.3	3.5	ns
108	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	R.AC*ALQVLSAILEGSK.Q	0.9	0.9	0.9	4.3	3.3	3.8	3.1	3.1	3.5	ns
109	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	R.AAVEEGIVLGGGC*ALLR.C	0.8	0.9	0.8	4.1	3.6	3.2	3.8	2.6	3.5	ns
110	Q86YS7	KIAA0528 Uncharacterized protein KIAA0528	KIAA0528	R.SAPPC*ANSTVGVVK.M	0.8	0.8	0.8	4.5	3.2	3.3	2.8	3.4	3.5	ns
111	O75934	BCAS2 Pre-mRNA-splicing factor SPF27	BCAS2	K.NDITAWQEC*VNNSMAQLEHQAVR.I	0.9	0.9	0.9	3.9	3.6	3.4	3.4	2.8	3.4	ns
112	P60866	RPS20 40S ribosomal protein S20	RPS20	R.KTPC*GEGSK.T	1.0	0.8	0.9	3.9	3.6	3.2	3.3	3.0	3.4	ns
113	P50914	RPL14 60S ribosomal protein L14	RPL14	K.C*MQLTDFILK.F	0.9	0.8	0.9	3.3	3.7	3.2	3.4	3.2	3.4	ns
114	P13639	EEF2 Elongation factor 2	EEF2	K.STLTDSLVC*K.A	0.9	1.0	0.9	4.1	3.4	2.9	3.4	2.8	3.3	ns
115	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	R.GDEC*GLALGR.L	0.9	0.9	0.9	2.8	3.6	3.3	3.7	3.2	3.3	ns
116	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	K.VQYPQSQAC*K.M	0.8	1.0	0.9	3.9	3.6	2.8	3.1	3.1	3.3	ns
117	P49327	FASN Fatty acid synthase	FASN	K.AFDTAGNGYC*R.S	0.8	0.9	0.9	3.6	4.1	2.7	2.9	3.1	3.3	ns
118	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	K.VVVVQAISALC*QK.Y	0.9	0.9	0.9	2.9	3.2	3.7	3.2	3.3	3.3	ns
119	P53618	COPB1 Coatomer subunit beta	COPB1	K.ALSGYC*GFMAANLYAR.S	0.7	0.7	0.7	3.1	3.7	3.7	2.9	3.0	3.3	ns
120	P51553	IDH3G Isocitrate dehydrogenase	IDH3G	K.LGDGLFLQC*CR.E	1.1	0.8	0.9	3.1	4.3	3.0	2.9	3.1	3.3	ns
121	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	K.SRDLLVQQASQC*LSK.L	1.1	0.7	0.9	3.7	3.3	3.7	2.9	2.7	3.3	ns
122	Q8N163	KIAA1967 DBIRD complex subunit KIAA1967	KIAA1967	R.VVTQNIC*QYR.S	0.8	0.8	0.8	3.6	3.4	3.6	3.0	2.7	3.2	ns
123	Q02543	RPL18A 60S ribosomal protein L18a	RPL18A	R.DLTTAGAVTQC*YR.D	0.8	0.8	0.8	4.3	0.8	4.0	5.7	1.4	3.2	ns

124	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	R.NFILDQC*NVYNSGQR.R	0.9	0.9	0.9	3.3	3.8	2.8	3.4	2.8	3.2	ns
125	Q8TC07	TBC1D15 TBC1 domain family member 15	TBC1D15	R.TLLVNC*QNK.S	1.0	0.8	0.9	3.4	4.6	3.2	2.1	2.8	3.2	ns
126	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.YMAC*CLLYR.G	0.9	0.9	0.9	3.4	3.2	3.3	3.2	3.0	3.2	ns
127	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	R.SVLDAAQIVGLNC*LR.L	0.8	0.8	0.8	2.2	3.4	4.2	3.2	3.2	3.2	ns
128	P50914	RPL14 60S ribosomal protein L14	RPL14	R.ALVDGPC*TQVR.R	0.9	0.8	0.9	3.2	3.5	3.1	3.2	3.1	3.2	ns
129	P62280	RPS11 40S ribosomal protein S11	RPS11	K.C*PFTGNVSIR.G	0.9	0.9	0.9	3.2	3.5	3.2	3.2	2.9	3.2	ns
130	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	R.ISAFGYLEC*SAK.T	0.8	0.8	0.8	3.0	3.1	3.0	3.8	3.0	3.2	ns
131	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	R.QFC*STQAALQAMER.E	0.8	0.9	0.9	3.5	3.2	2.7	3.7	2.6	3.1	ns
132	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	R.AGAIAPC*EVTVPAQNTGLGPEK.T	0.9	0.8	0.9	3.3	3.3	3.0	3.5	2.6	3.1	ns
133	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.DGLTDVYNKIHMGSC*AENTAK.K	0.9	0.9	0.9	3.3	3.4	2.7	3.2	3.0	3.1	ns
134	P28838	LAP3 Cytosol aminopeptidase	LAP3	R.SAGAC*TAAAFLK.E	0.8	0.9	0.8	2.8	3.7	3.0	3.1	3.0	3.1	ns
135	Q13636	RAB31 Ras-related protein Rab-31	RAB31	K.VC*LLGDTGVGK.S	0.9	0.8	0.9	5.9	2.7	2.2	2.3	2.1	3.0	ns
136	P62753	RPS6 40S ribosomal protein S6	RPS6	K.LNISFPATGC*QK.L	0.9	0.8	0.8	3.0	3.0	2.7	2.8	3.7	3.0	ns
137	P45984	MAPK9 Mitogen-activated protein kinase 9	MAPK9	R.TAC*TNFMMTPYVVTR.Y	0.9	0.9	0.9	3.0	3.6	2.9	2.8	2.8	3.0	ns
138	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	K.C*FIVGADNVGSK.Q	0.8	0.9	0.9	3.6	3.0	2.8	3.0	2.6	3.0	ns
139	P13639	EEF2 Elongation factor 2	EEF2	K.EGALC*EENMR.G	0.7	0.8	0.7	1.0	3.2	3.5	3.4	3.9	3.0	ns
140	Q13526	PIN1 Peptidyl-prolyl cis-trans isomerase NIMA-interacti	PIN1	K.IKSGEEDFESLASQFSDC*SSAK.A	0.9	0.9	0.9	3.7	2.9	2.4	3.7	2.3	3.0	ns
141	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	R.LC*ALRPDDSSSAR.T	0.8	0.9	0.8	3.4	3.4	2.7	3.2	2.3	3.0	ns
142	O00743	PPP6C Serine/threonine-protein phosphatase 6 catalytic s	PPP6C	R.C*GNIASIMVFK.D	0.7	0.7	0.7	2.2	2.6	3.3	3.7	3.0	3.0	ns
143	O43264	ZW10 Centromere/kinetochore protein zw10 homolog	ZW10	R.LAPILC*DGTATFVDLVPGFR.R	0.8	0.8	0.8	2.8	3.6	3.0	2.8	2.5	3.0	ns
144	P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	R.AALEALGSC*LNNK.Y	0.7	0.9	0.8	1.3	4.3	3.7	2.2	3.2	3.0	ns
145	Q8TAQ2	SMARCC2 SWI/SNF complex subunit SMARCC2	SMARCC2	R.NLAGDVC*AIMR.V	1.1	0.9	1.0	2.0	3.9	2.6	3.2	3.0	2.9	ns
146	Q07020	RPL18 60S ribosomal protein L18	RPL18	K.GC*GTVLLSGPR.K	0.9	0.8	0.9	3.0	3.3	2.7	2.8	3.0	2.9	ns
147	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.AEGSDVANAVLDGADC*IMLSGETAK.G	0.6	0.8	0.7	0.8	3.2	3.7	4.2	2.8	2.9	ns
148	P55060	CSE1L Exportin-2	CSE1L	K.IC*AVGITK.L	0.8	0.9	0.8	3.1	3.4	3.4	1.9	2.8	2.9	ns
149	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	R.C*IPALDSLTPANEDQK.I	0.9	0.9	0.9	3.2	3.3	2.7	3.1	2.4	2.9	ns
150	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.TIIPLISQC*TPK.V	0.7	0.8	0.8	2.7	3.0	3.2	3.1	2.6	2.9	ns
151	Q6P1X6	C8orf82 UPF0598 protein C8orf82	C8orf82	R.YEAAFPFLSPC*GR.E	0.9	0.9	0.9	2.8	3.2	2.8	3.1	2.6	2.9	ns
152	Q9BX63	BRIP1 Fanconi anemia group J protein	BRIP1	R.LANNSDC*ILAK.D	0.8	0.8	0.8	3.4	2.8	3.7	1.7	2.8	2.9	ns

153	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	R.AVASQLDC*NFLK.V	0.8	0.9	0.9	2.9	3.2	2.8	2.7	2.6	2.8	ns
154	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	K.KLVIVGDGAC*GK.T	0.9	0.9	0.9	2.5	3.1	3.1	3.0	2.5	2.8	ns
155	P62910	RPL32 60S ribosomal protein L32	RPL32	K.SYC*AEIAHNVSSK.N	0.8	0.8	0.8	2.8	2.5	2.9	3.6	2.4	2.8	ns
156	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	R.VGAFTMVC*K.D	0.8	0.8	0.8	3.2	2.9	1.7	3.0	3.5	2.8	ns
157	P62244	RPS15A 40S ribosomal protein S15a	RPS15A	K.C*GVISPR.F	0.7	0.8	0.7	3.8	2.9	2.7	2.4	2.3	2.8	ns
158	P63220	RPS21 40S ribosomal protein S21	RPS21	K.TYAIC*GAIR.R	0.9	1.0	0.9	3.6	3.1	2.8	2.4	2.3	2.8	ns
159	P67936	TPM4 Tropomyosin alpha-4 chain	TPM4	K.EENVGLHQTLDQTLNELNC*I.-	1.0	1.0	1.0	5.1	2.2	2.2	2.7	1.8	2.8	ns
160	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	R.ADHQPLTEASYVNLPTIALC*NTDSPLR.Y	1.0	0.8	0.9	1.8	3.1	2.9	2.9	3.2	2.8	ns
161	P55769	NHP2L1 NHP2-like protein 1	NHP2L1	K.KLLDLVQQSC*NYK.Q	0.9	0.8	0.9	3.2	3.2	2.5	2.9	2.2	2.8	ns
162	Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.GVPGAIVNVSSQC*SQR.A	1.0	0.8	0.9	2.5	3.2	2.7	2.9	2.6	2.8	ns
163	Q93052	LPP Lipoma-preferred partner	LPP	K.TYITDPVSAPC*APPLQPK.G	0.9	1.0	1.0	3.6	3.4	2.5	2.7	1.8	2.8	ns
164	Q96I99	SUCLG2 Succinyl-CoA ligase	SUCLG2	R.SC*NGPVLVGSPQGGVDIEEVAASNPELIFK.E	0.9	0.8	0.9	2.8	2.8	2.9	2.7	2.7	2.8	ns
165	E9PPU0	EPPK1 Epiplakin	EPPK1	R.LLDAQLATGGLVC*PAR.R	0.9	0.9	0.9	3.0	4.0	2.5	2.5	2.0	2.8	ns
166	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.IC*PVETLVEEAIQCAEK.I	0.9	0.9	0.9	1.8	2.3	3.0	3.6	3.1	2.8	ns
167	Q7Z2W4	ZC3HAV1 Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	K.NSNVDSSYLESLYQSC*PR.G	1.0	1.2	1.1	3.8	2.5	2.3	2.9	2.3	2.8	ns
168	Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	R.NPVSQC*MR.G	0.8	1.0	0.9	2.9	3.5	2.6	2.5	2.2	2.7	ns
169	P10599	TXN Thioredoxin	TXN	K.C*MPTFQFFK.K	1.2	0.9	1.1	3.8	3.6	1.6	3.0	1.7	2.7	ns
170	P62195	PSMC5 26S protease regulatory subunit 8	PSMC5	K.GVC*TEAGMYALR.E	0.9	0.8	0.9	2.3	2.7	3.4	2.5	2.6	2.7	ns
171	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.PMC*VESFSDYPPLGR.F	0.8	0.9	0.8	3.0	2.8	2.5	3.0	2.2	2.7	ns
172	P49327	FASN Fatty acid synthase	FASN	K.SFYGSTLFLC*R.R	0.9	0.8	0.9	1.5	3.9	2.9	3.0	2.2	2.7	ns
173	Q9NP73	ALG13 UDP-N-acetylglucosamine transferase subunit ALG13	ALG13	K.ADLVISHAGAGSC*LETLEK.G	1.0	0.9	0.9	3.1	3.4	2.6	2.3	2.1	2.7	ns
174	P46782	RPS5 40S ribosomal protein S5	RPS5	K.TIAEC*LADELINAAK.G	0.9	0.9	0.9	3.3	2.8	2.5	2.5	2.3	2.7	ns
175	Q9UN37	VPS4A Vacuolar protein sorting-associated protein 4A	VPS4A	K.LLEPVVC*MSDMLR.S	1.2	1.1	1.1	2.9	3.2	2.8	2.4	2.1	2.7	ns
176	P29401	TKT Transketolase	TKT	K.QAFTDVATGSLGQGLGAAC*GMAYTGK.Y	1.0	0.9	0.9	1.8	2.7	3.0	3.2	2.7	2.7	ns
177	P49327	FASN Fatty acid synthase	FASN	R.LLSAAC*R.L	0.8	0.7	0.8	1.9	3.0	3.0	2.9	2.7	2.7	ns
178	O15355	PPM1G Protein phosphatase 1G	PPM1G	R.GTEAGQVGEPGIPTGEAGPSC*SSASDK.L	0.9	0.9	0.9	3.2	3.0	2.6	2.5	2.0	2.7	ns
179	O14980	XPO1 Exportin-1	XPO1	K.DLLGLC*EQKR.G	0.8	0.9	0.8	3.2	2.4	2.2	3.0	2.5	2.7	ns
180	P15880	RPS2 40S ribosomal protein S2	RPS2	R.GC*TATLGNFAK.A	0.9	0.9	0.9	3.1	2.8	2.4	2.7	2.3	2.7	ns
181	Q9P258	RCC2 Protein RCC2	RCC2	K.AVQDLC*GWR.I	1.0	1.1	1.0	3.9	2.6	1.8	3.3	1.6	2.6	ns
182	P35270	SPR Sepiapterin reductase	SPR	R.AVC*LLTGASR.G	0.5	0.8	0.6	3.1	2.8	2.8	2.1	2.4	2.6	ns

183	Q5T1V6	DDX59 Probable ATP-dependent RNA helicase DDX59	DDX59	K.NLPC*ANVR.Q	0.8	0.5	0.6	3.0	1.7	1.5	1.7	5.4	2.6	ns
184	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.GIFPVLC*K.D	0.6	0.9	0.7	1.2	2.6	3.3	3.6	2.5	2.6	ns
185	P55263	ADK Adenosine kinase	ADK	R.SLIANLAAANC*YK.K	0.7	0.7	0.7	1.7	3.0	2.5	3.9	2.0	2.6	ns
186	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	R.GNHEC*ASINR.I	0.9	0.9	0.9	3.2	2.6	2.6	2.5	2.3	2.6	ns
187	P13639	EEF2 Elongation factor 2	EEF2	R.C*LYASVLTAQPR.L	0.7	0.7	0.7	0.9	3.0	2.9	3.1	3.2	2.6	ns
188	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.QGEYGLASIC*NGGGGASAMLIQK.L	0.9	0.9	0.9	2.9	2.8	2.4	2.5	2.5	2.6	ns
189	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	K.ITGC*ASPGK.T	0.9	0.9	0.9	3.0	3.1	2.2	2.3	2.5	2.6	ns
190	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	R.GDFC*IQVGR.N	0.8	0.9	0.8	1.0	3.1	3.2	3.2	2.5	2.6	ns
191	Q9Y508	RNF114 RING finger protein 114	RNF114	R.DC*GGAAQLAGPAAEADPLGR.F	0.8	0.9	0.9	3.9	2.3	2.1	2.8	1.9	2.6	ns
192	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	R.YVDIAIPC*NNK.G	1.0	0.8	0.9	1.8	3.0	2.7	2.7	2.7	2.6	ns
193	Q9Y2R9	MRPS7 28S ribosomal protein S7, mitochondrial	MRPS7	K.NC*EPMIGLVPILK.G	0.9	0.8	0.9	2.6	2.6	2.7	2.5	2.5	2.6	ns
194	P49327	FASN Fatty acid synthase	FASN	R.LSIPTYGLQC*TR.A	0.7	0.8	0.7	2.4	3.0	2.5	2.6	2.3	2.6	ns
195	P22695	UQCRC2 Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	R.NALANPLYC*PDYR.I	0.9	0.8	0.8	2.5	2.8	2.6	2.8	2.1	2.6	ns
196	Q15796	SMAD2 Mothers against decapentaplegic homolog 2	SMAD2	K.AITTQNC*NTK.C	1.2	0.7	1.0	3.9	2.1	1.8	3.0	2.0	2.6	ns
197	Q9Y285	FARSA Phenylalanine--tRNA ligase alpha subunit	FARSA	K.VNLQMVYDSPLC*R.L	0.8	0.9	0.9	2.9	3.0	2.5	2.4	2.0	2.5	ns
198	P35914	HMGCL Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	K.LLEAGNFIC*QALNR.K	0.8	0.8	0.8	2.4	2.5	2.6	2.7	2.5	2.5	ns
199	Q9NUU7	DDX19A ATP-dependent RNA helicase DDX19A	DDX19A	K.VLVTTNVC*AR.G	1.0	0.9	1.0	2.8	2.7	2.7	2.4	2.2	2.5	ns
200	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.NTGIIC*TIGPASR.S	0.6	0.8	0.7	0.9	2.8	3.2	3.4	2.4	2.5	ns
201	O43707	ACTN4 Alpha-actinin-4	ACTN4	K.EGLLLWC*QR.K	0.9	0.9	0.9	1.8	3.0	2.4	3.0	2.5	2.5	ns
202	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.C*ATITPDEAR.V	0.7	0.8	0.7	2.5	2.3	2.6	2.8	2.5	2.5	ns
203	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.DLAGC*IHGLSNVK.L	0.8	0.7	0.8	2.7	2.9	1.8	2.9	2.3	2.5	ns
204	Q9UL25	RAB21 Ras-related protein Rab-21	RAB21	K.VVLLGEGC*VGK.T	1.1	0.9	1.0	2.9	2.7	2.4	2.4	2.0	2.5	ns
205	P62316	SNRPD2 Small nuclear ribonucleoprotein Sm D2	SNRPD2	K.NNTQVLINC*R.N	0.6	0.6	0.6	1.8	2.8	2.8	2.9	2.0	2.5	ns
206	Q9UHD8	SEPT9 Septin-9	9-Sep	R.SQEATEAAPSC*VGDMADTPR.D	1.0	0.9	0.9	3.3	2.4	1.9	2.5	2.1	2.5	ns
207	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	K.LEVDAIVNAANSSLLGGGGVDGC*IHR.A	0.9	0.9	0.9	3.2	3.0	2.2	2.2	1.7	2.5	ns
208	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.LGVENC*YFPMFVSQSALEK.E	1.0	0.9	0.9	2.6	2.8	2.4	2.3	2.2	2.4	ns
209	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	K.GC*LLYGPPGTGK.T	0.9	0.8	0.8	2.1	3.0	0.9	3.0	3.0	2.4	ns
210	P62191	PSMC1 26S protease regulatory subunit 4	PSMC1	K.AIC*TEAGLMALR.E	0.9	0.9	0.9	2.3	2.5	2.5	2.5	2.1	2.4	ns
211	P38606	ATP6V1A V-type proton ATPase catalytic subunit A	ATP6V1A	R.VLDALFPCVQGGTTAIPGAFGC*GK.T	0.9	0.8	0.9	2.2	2.9	2.4	2.4	2.0	2.4	ns
212	A6NDG6	PGP Phosphoglycolate phosphatase	PGP	K.NNQESDC*VSK.K	1.0	0.8	0.9	2.6	2.2	1.9	2.3	2.9	2.4	ns

213	O43390	HNRNPR Heterogeneous nuclear ribonucleoprotein R	HNRNPR	K.SAFLC*GVMK.T	0.9	0.8	0.9	2.7	2.8	1.7	1.2	3.5	2.4	ns
214	Q15019	SEPT2 Septin-2	2-Sep	R.LTVVDTPGYGDAINC*R.D	0.9	0.8	0.8	2.4	2.5	2.2	2.6	2.1	2.4	ns
215	Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multif	AIMP2	K.FSIQTMC*PIEGEGNIAR.F	0.8	0.9	0.9	2.3	2.0	2.6	2.9	1.9	2.3	ns
216	P0CW22	RPS17L 40S ribosomal protein S17-like	RPS17L	R.VC*EEIAIIPSK.K	1.0	0.8	0.9	2.4	2.5	2.1	2.7	2.0	2.3	ns
217	P46782	RPS5 40S ribosomal protein S5	RPS5	R.VNQAIWLLC*TGAR.E	0.9	0.8	0.9	2.4	2.5	2.6	2.3	1.8	2.3	ns
218	Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multif	AIMP2	R.SC*ENLAPFNTALK.L	0.7	0.7	0.7	2.4	2.2	2.4	2.5	2.1	2.3	ns
219	Q92879	CELF1 CUGBP Elav-like family member 1	CELF1	R.GC*AFVTFTTR.A	1.1	0.9	1.0	1.8	2.4	2.6	2.6	2.2	2.3	ns
220	P21964	COMT Catechol O-methyltransferase	COMT	R.GSSC*FECTHYQSFLEYR.E	0.9	0.9	0.9	3.3	2.4	1.9	2.1	1.7	2.3	ns
221	P61158	ACTR3 Actin-related protein 3	ACTR3	K.LGYAGNTEPQFIIPSC*IAIK.E	0.7	0.8	0.7	1.0	2.3	2.7	3.1	2.3	2.3	ns
222	Q96CD2	PPCDC Phosphopantothenoylcysteine decarboxylase	PPCDC	K.ASC*PAAAPLMER.K	1.0	1.0	1.0	3.0	2.2	2.1	2.2	1.8	2.3	ns
223	P23921	RRM1 Ribonucleoside-diphosphate reductase large subunit	RRM1	K.IIDINYYPVPEAC*LSNK.R	0.9	0.9	0.9	2.5	2.3	2.1	2.4	2.0	2.3	ns
224	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	K.VDENFDC*VEADDVEGK.I	0.9	1.0	0.9	3.5	2.0	1.8	1.9	2.1	2.2	ns
225	Q7L8W6	ATPBD4 ATP-binding domain-containing protein 4	ATPBD4	K.C*EGDEVEDLYELLK.L	1.0	0.8	0.9	1.8	2.6	1.8	2.7	2.3	2.2	ns
226	O43684	BUB3 Mitotic checkpoint protein BUB3	BUB3	R.TPC*NAGTFSQPEK.V	0.9	0.8	0.8	1.0	2.5	2.9	2.9	2.0	2.2	ns
227	Q9UPN9	TRIM33 E3 ubiquitin-protein ligase TRIM33	TRIM33	R.C*DPVPAANGAIR.F	0.8	0.8	0.8	2.4	0.9	2.1	4.7	1.0	2.2	ns
228	O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	R.ANSSVVSVNC*K.G	0.9	0.8	0.9	2.4	2.3	2.0	2.7	1.8	2.2	ns
229	P55060	CSE1L Exportin-2	CSE1L	K.LSTAC*PGR.V	0.7	0.8	0.8	2.1	1.9	2.2	3.0	2.0	2.2	ns
230	P62714	PPP2CB Serine/threonine-protein phosphatase 2A catalytic	PPP2CB	R.NVVTIFSAPNYC*YR.C	0.7	0.8	0.8	1.6	2.3	2.8	2.5	1.8	2.2	ns
231	P22314	UBA1 Ubiquitin-like modifier-activating enzyme 1	UBA1	K.YFLVGAGAIGC*ELLK.N	0.6	0.8	0.7	1.0	1.7	5.2	1.7	1.4	2.2	ns
232	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	K.C*EFQDAYVLLSEK.K	0.9	0.9	0.9	2.3	2.2	2.3	2.3	1.8	2.2	ns
233	P51946	CCNH Cyclin-H	CCNH	R.TC*LSQLLDIMK.S	1.0	0.9	1.0	2.4	2.3	2.1	2.4	1.7	2.2	ns
234	P23396	RPS3 40S ribosomal protein S3	RPS3	R.GLC*AIAQAESLR.Y	0.9	0.9	0.9	2.3	2.3	2.2	2.1	2.0	2.2	ns
235	P51812	RPS6KA3 Ribosomal protein S6 kinase alpha-3	RPS6KA3	R.AENGLLMTPC*YTANFVAPEVLK.R	1.0	0.9	0.9	2.5	2.0	2.6	2.0	1.8	2.2	ns
236	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.DLNYC*FSGMSDHR.Y	0.9	0.9	0.9	2.1	2.2	2.1	2.4	2.0	2.2	ns
237	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	R.QLC*DNAGFDATNILNK.L	0.9	0.7	0.8	2.6	1.9	2.5	2.2	1.5	2.1	ns
238	P57678	GEMIN4 Gem-associated protein 4	GEMIN4	R.SDPDAC*PTMPLLAMLLR.G	0.5	0.6	0.5	2.4	2.2	2.3	2.1	1.7	2.1	ns
239	P52597	HNRNPF Heterogeneous nuclear ribonucleoprotein F	HNRNPF	R.DLSYC*LSGMYDHR.Y	0.8	0.9	0.9	2.2	2.1	2.3	2.1	2.0	2.1	ns
240	P48047	ATP5O ATP synthase subunit O, mitochondrial	ATP5O	R.GEVPC*TVTSASPLEEATLSELK.T	0.9	0.7	0.8	2.5	1.9	2.1	2.2	2.0	2.1	ns
241	O15355	PPM1G Protein phosphatase 1G	PPM1G	K.C*SGDGVGAPR.L	0.6	0.8	0.7	2.1	2.1	2.2	2.2	2.0	2.1	ns

242	Q96RS6	NUDCD1 NudC domain-containing protein 1	NUDCD1	R.DSAQC*AAIAER.L	0.9	1.0	0.9	3.2	2.1	1.9	1.9	1.5	2.1	ns
243	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	K.EGTDSSQGIPQLVSNISAC*QVIAEAVR.T	0.9	0.8	0.9	2.3	2.5	1.9	2.1	1.8	2.1	ns
244	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.VC*VETVESGAMTK.D	0.8	0.8	0.8	2.1	2.2	2.1	2.4	1.7	2.1	ns
245	P49327	FASN Fatty acid synthase	FASN	R.DPETLVGYSMVGC*QR.A	0.9	0.9	0.9	2.1	2.4	2.0	1.9	2.1	2.1	ns
246	Q99798	ACO2 Aconitate hydratase, mitochondrial	ACO2	R.DLGGIVLANAC*GPCIGQWDR.K	0.9	0.9	0.9	2.3	2.0	1.7	2.5	1.8	2.1	ns
247	P49327	FASN Fatty acid synthase	FASN	K.ADEASELAC*PTPK.E	0.9	1.0	0.9	2.5	2.2	1.6	2.4	1.6	2.1	ns
248	Q04760	GLO1 Lactoylglutathione lyase	GLO1	K.C*DFPIMK.F	0.9	0.8	0.8	1.8	2.0	2.2	2.1	2.0	2.0	ns
249	E9PPU0	EPPK1 Epiplakin	EPPK1	R.YLC*GLGAVGGVR.L	0.9	0.9	0.9	1.9	2.3	1.8	2.0	2.0	2.0	ns
250	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	R.ISASC*QHPTAFEEAIPK.S	0.8	0.9	0.8	2.4	2.2	2.2	1.7	1.5	2.0	ns
251	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	R.NDTPC*GTTIGPILASR.L	0.5	0.7	0.6	1.4	2.2	2.3	2.6	1.5	2.0	ns
252	O95671	ASMTL N-acetylserotonin O-methyltransferase-like protein	ASMTL	K.VDASAC*GMER.L	0.9	0.9	0.9	1.1	1.6	2.7	2.6	2.0	2.0	ns
253	Q00765	REEP5 Receptor expression-enhancing protein 5	REEP5	K.NC*MTDLLAK.L	0.9	1.0	0.9	2.1	2.0	1.9	2.1	1.9	2.0	ns
254	P49721	PSMB2 Proteasome subunit beta type-2	PSMB2	R.NLADC*LR.S	0.9	0.9	0.9	1.3	1.9	1.9	3.1	1.8	2.0	ns
255	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.HSMNPFC*EIAVEEAVR.L	1.1	0.9	1.0	2.0	2.1	2.0	2.0	1.8	2.0	ns
256	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVGVEVPDVELEC*PDAK.L	1.0	0.9	0.9	2.6	2.1	1.6	1.9	1.7	2.0	ns
257	P13639	EEF2 Elongation factor 2	EEF2	R.YVEPIEDVPC*GNIVGLVGVDQFLVK.T	0.6	0.8	0.7	1.3	2.2	2.2	2.6	1.6	2.0	ns
258	Q9UNE7	STUB1 E3 ubiquitin-protein ligase CHIP	STUB1	R.AQQAC*IEAK.H	1.3	1.7	1.5	2.3	2.1	2.1	1.5	1.8	1.9	ns
259	P46782	RPS5 40S ribosomal protein S5	RPS5	K.AQC*PIVER.L	0.9	0.8	0.8	2.0	2.2	1.7	1.9	2.0	1.9	ns
260	P13639	EEF2 Elongation factor 2	EEF2	K.IWC*FGPDGTGPNILTDITK.G	0.9	1.0	0.9	1.2	2.2	2.1	2.1	2.0	1.9	ns
261	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	R.GQPC*SQNYR.L	1.2	1.2	1.2	1.9	2.2	1.9	2.3	1.5	1.9	ns
262	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.LVVPATQC*GSLIGK.G	0.9	0.8	0.9	2.3	2.0	1.9	1.9	1.6	1.9	ns
263	P33991	MCM4 DNA replication licensing factor MCM4	MCM4	K.AGIIC*QLNAR.T	1.0	0.9	0.9	1.2	2.0	2.4	2.3	1.7	1.9	ns
264	P78347	GTF2I General transcription factor II-I	GTF2I	R.SILSPGGSC*GPIK.V	0.9	0.9	0.9	2.3	2.2	1.6	1.9	1.6	1.9	ns
265	Q969T9	WBP2 WW domain-binding protein 2	WBP2	K.DC*EIKQPVFGANYIK.G	1.0	0.9	0.9	2.0	2.0	2.1	1.8	1.8	1.9	ns
266	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	R.DC*GGAAAVLGAFR.A	0.6	0.7	0.7	1.2	1.9	2.2	2.7	1.6	1.9	ns
267	Q14247	CTTN Src substrate cortactin	CTTN	K.HC*SQVDSVR.G	0.8	0.7	0.8	2.5	2.1	1.7	1.9	1.4	1.9	ns
268	Q14247	CTTN Src substrate cortactin	CTTN	K.C*ALGWDHQEK.L	0.9	0.9	0.9	2.2	2.0	1.8	2.0	1.5	1.9	ns
269	P37235	HPCAL1 Hippocalcin-like protein 1	HPCAL1	R.LLQC*DPSSASQF.-	0.9	0.9	0.9	2.3	1.9	1.7	1.9	1.6	1.9	ns
270	P14678	SNRPB Small nuclear ribonucleoprotein-associated protein	SNRPB	R.C*ILQDGR.I	0.8	0.8	0.8	1.6	1.9	2.1	2.2	1.7	1.9	ns
271	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	K.NVGC*LQEALQLATSFAQLR.L	0.8	0.7	0.7	1.9	1.9	1.9	1.9	1.9	1.9	ns

272	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.NMITGTSQADC*AVLIVAAGVGEFEAGISK.N	0.9	0.8	0.8	1.4	1.8	2.1	2.1	2.0	1.9	ns
273	P00966	ASS1 Argininosuccinate synthase	ASS1	R.FELSC*YSLAPQIK.V	0.8	0.9	0.8	1.5	2.2	1.9	2.0	1.8	1.9	ns
274	P60900	PSMA6 Proteasome subunit alpha type-6	PSMA6	K.C*DPAGYYCGFK.A	0.8	0.7	0.7	1.0	2.0	2.2	2.3	1.9	1.9	ns
275	P11498	PC Pyruvate carboxylase, mitochondrial	PC	R.FLYEC*PWR.R	1.0	0.8	0.9	2.0	2.3	1.7	1.3	2.2	1.9	ns
276	P60981	DSTN Destrin	DSTN	K.C*STPEEIK.K	0.9	0.9	0.9	2.5	1.7	1.7	2.0	1.4	1.8	ns
277	Q5VWZ2	LYPLAL1 Lysophospholipase-like protein 1	LYPLAL1	R.C*IVSPAGR.H	0.7	0.9	0.8	2.1	1.6	1.8	1.9	1.8	1.8	ns
278	P15924	DSP Desmoplakin	DSP	K.AC*GSEIMQK.K	1.1	0.8	0.9	2.1	2.0	2.0	1.6	1.5	1.8	ns
279	P52895	AKR1C2 Aldo-keto reductase family 1 member C2	AKR1C2	R.EEPWVDPNSPVLLEDPVLC*ALAK.K	0.9	0.9	0.9	1.8	2.0	1.9	2.0	1.4	1.8	ns
280	Q7L5D6	GET4 Golgi to ER traffic protein 4 homolog	GET4	K.EQNYC*ESR.Y	0.8	0.7	0.8	2.4	1.9	1.9	1.6	1.5	1.8	ns
281	P13639	EEF2 Elongation factor 2	EEF2	R.VTDGALVVVDCVSGVC*VQTETVLR.Q	0.7	1.1	0.9	2.0	1.7	1.8	1.6	2.0	1.8	ns
282	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.SQETEC*TYFSTPLLLGK.K	0.7	0.8	0.8	1.8	1.8	2.0	1.8	1.7	1.8	ns
283	P28074	PSMB5 Proteasome subunit beta type-5	PSMB5	K.KVIEINPYLLGTMAGGAADC*SFWER.L	0.8	0.8	0.8	1.0	1.7	2.2	2.3	1.7	1.8	ns
284	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.GPFVEAEVPDVDLEC*PDAK.L	0.9	0.9	0.9	1.9	2.0	1.8	1.7	1.6	1.8	ns
285	P61158	ACTR3 Actin-related protein 3	ACTR3	R.YSYVC*PDLVK.E	0.9	0.8	0.8	0.9	2.4	1.8	2.0	1.8	1.8	ns
286	P51858	HDGF Hepatoma-derived growth factor	HDGF	K.C*GDLVFAK.M	1.0	0.7	0.9	1.6	1.6	2.3	1.5	1.9	1.8	ns
287	Q9UI30	TRMT112 tRNA methyltransferase 112 homolog	TRMT112	R.IC*PVEFNPNFVAR.M	0.9	0.9	0.9	1.8	1.9	1.8	1.8	1.6	1.8	ns
288	O95571	ETHE1 Protein ETHE1, mitochondrial	ETHE1	R.TDFQQGC*AK.T	0.9	0.9	0.9	2.6	1.8	1.5	1.4	1.5	1.8	ns
289	P18669	PGAM1 Phosphoglycerate mutase 1	PGAM1	R.YADLTEDQLPSC*ESLK.D	0.5	0.8	0.7	1.0	1.9	1.7	2.6	1.6	1.7	ns
290	Q9Y277	VDAC3 Voltage-dependent anion-selective channel protein	VDAC3	K.VC*NYGLTFTQK.W	0.9	0.9	0.9	1.9	1.9	1.8	1.5	1.6	1.7	ns
291	P15924	DSP Desmoplakin	DSP	K.NQC*TQVVQER.E	0.8	1.3	1.1	1.9	1.7	1.7	1.7	1.7	1.7	ns
292	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitoch	MCCC2	K.MVAAVAC*AQVPK.I	0.9	0.8	0.8	1.2	1.6	1.9	2.4	1.5	1.7	ns
293	Q9Y2Q3	GSTK1 Glutathione S-transferase kappa 1	GSTK1	K.ETTEAAC*R.Y	1.0	0.9	0.9	1.8	1.7	1.9	1.6	1.7	1.7	ns
294	P51659	HSD17B4 Peroxisomal multifunctional enzyme type 2	HSD17B4	K.IC*DFENASKPQSIQESTGSIIEVLSK.I	1.0	1.0	1.0	2.1	1.7	1.6	1.8	1.3	1.7	ns
295	Q15181	PPA1 Inorganic pyrophosphatase	PPA1	K.GISC*MNTTLSESPFK.C	1.1	1.4	1.2	2.5	1.9	1.5	1.5	1.3	1.7	ns
296	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.INISEGNC*PER.I	1.0	0.9	1.0	2.0	1.7	1.5	1.9	1.4	1.7	ns
297	O14561	NDUFAB1 Acyl carrier protein, mitochondrial	NDUFAB1	K.LMC*PQEIVDYIADKK.D	0.8	0.8	0.8	1.9	0.8	3.8	1.0	0.9	1.7	ns
298	Q8WW01	TSEN15 tRNA-splicing endonuclease subunit Sen15	TSEN15	R.GDSEPTPGC*SGLGPGGVR.G	0.9	1.0	1.0	1.9	1.6	1.8	1.8	1.5	1.7	ns
299	P34896	SHMT1 Serine hydroxymethyltransferase, cytosolic	SHMT1	K.NTC*PGDR.S	0.7	0.9	0.8	0.8	2.1	1.8	2.3	1.5	1.7	ns

300	Q9NY27	PPP4R2 Serine/threonine-protein phosphatase 4 regulatory	PPP4R2	K.EVC*PVLDQFLCHVAK.T	1.0	0.9	0.9	1.6	1.7	1.4	2.0	1.7	1.7	ns
301	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	K.SC*AHDWVYE.-	0.9	0.9	0.9	1.2	1.6	1.9	2.0	1.7	1.7	ns
302	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.GSDFDC*ELR.L	0.6	1.0	0.8	1.6	1.8	1.6	1.8	1.5	1.7	ns
303	Q2TAA2	IAH1 Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	R.VILITPTPLC*ETAWEEQCIIQGCK.L	1.0	0.9	0.9	1.8	1.7	1.6	1.9	1.4	1.7	ns
304	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVDVEVPDVELEC*PDAK.L	1.1	1.1	1.1	2.1	1.8	1.5	1.5	1.3	1.7	ns
305	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	K.QEPLGSDSEGVNC*LAYDEAIMAQQDR.I	0.9	1.0	0.9	2.1	1.6	1.7	1.6	1.4	1.7	ns
306	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	R.LFC*VGFTK.K	0.9	0.8	0.8	1.9	1.6	1.8	1.6	1.4	1.7	ns
307	P50151	GNG10 Guanine nucleotide-binding protein G(I)/G(S)/G(O)	GNG10	K.VSQAAAELQQYCMQNAC*K.D	1.0	1.1	1.0	1.9	1.2	1.6	2.2	1.4	1.7	ns
308	O75153	KIAA0664 Clustered mitochondria protein homolog	KIAA0664	K.C*LTQQAVALQR.T	0.9	0.8	0.9	1.8	1.4	1.5	1.8	1.7	1.7	ns
309	Q9UJU6	DBNL Drebrin-like protein	DBNL	R.AEEDVEPEC*IMEK.V	1.3	0.9	1.1	1.7	1.4	1.8	1.4	1.9	1.6	ns
310	Q9BWD1	ACAT2 Acetyl-CoA acetyltransferase, cytosolic	ACAT2	R.ATVAPEDVSEVIFGHVLAAGC*GQNPVR.Q	0.8	0.8	0.8	1.3	1.8	1.6	1.9	1.5	1.6	ns
311	P13639	EEF2 Elongation factor 2	EEF2	R.TFC*QLILDPIFK.V	0.6	0.7	0.7	1.4	1.7	1.7	1.9	1.4	1.6	ns
312	Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.AVTNHSVYC*STK.G	0.9	0.8	0.8	2.0	1.6	1.5	1.6	1.4	1.6	ns
313	Q96EY5	FAM125A Multivesicular body subunit 12A	FAM125A	K.SC*SPLAFSAFGDLTIK.S	0.8	0.8	0.8	1.9	1.9	1.7	1.3	1.4	1.6	ns
314	Q15370	TCEB2 Transcription elongation factor B polypeptide 2	TCEB2	R.ADDTFEALC*IEPFSSPPELPDVMKPQDSGSSANEQAVQ.-	0.9	0.9	0.9	2.1	1.5	1.6	1.5	1.4	1.6	ns
315	Q86YH6	PDSS2 Decaprenyl-diphosphate synthase subunit 2	PDSS2	R.C*LLSDELSNIAMQVR.K	1.0	0.9	0.9	1.6	1.7	1.5	1.8	1.6	1.6	ns
316	Q9UBT2	UBA2 SUMO-activating enzyme subunit 2	UBA2	R.VLVVGAGGIGC*ELLK.N	0.9	0.8	0.8	1.1	1.8	1.8	1.8	1.6	1.6	ns
317	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	K.C*CSGAIIVLTK.S	0.9	0.9	0.9	1.6	1.9	1.5	1.7	1.3	1.6	ns
318	Q9P1F3	ABRACL Costars family protein ABRACL	ABRACL	K.C*ANLFEALVGTLK.A	1.0	0.8	0.9	1.8	1.6	1.7	1.5	1.5	1.6	ns
319	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	R.VPTANVSVVDLTC*R.L	0.6	0.8	0.7	0.7	1.6	2.1	2.2	1.4	1.6	ns
320	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.LVVPASQC*GSLIGK.G	0.9	0.9	0.9	1.9	1.6	1.6	1.5	1.4	1.6	ns
321	P49327	FASN Fatty acid synthase	FASN	K.AINC*ATSGVVGLVNCLR.R	0.9	0.9	0.9	2.3	1.5	1.4	1.5	1.3	1.6	ns
322	Q9NRF9	POLE3 DNA polymerase epsilon subunit 3	POLE3	R.AASVFVLYATSC*ANNFAMK.G	0.9	0.9	0.9	2.9	1.4	1.3	1.4	1.0	1.6	ns
323	Q96EY8	MMAB Cob(I)yrinic acid a,c-diamide adenosyltransferase,	MMAB	K.IQCTLQDVGSALATPC*SSAR.E	1.0	0.9	0.9	2.0	1.5	1.3	1.6	1.4	1.6	ns
324	O75940	SMNDC1 Survival of motor neuron-related-splicing factor 3	SMNDC1	K.VGVGTC*GIADKPMTQYQDTSK.Y	1.0	0.8	0.9	1.9	1.6	1.7	1.4	1.4	1.6	ns
325	Q9C0C9	UBE2O Ubiquitin-conjugating enzyme E2 O	UBE2O	R.C*YNEMALIR.V	0.7	0.9	0.8	1.9	1.3	1.8	1.5	1.3	1.6	ns

326	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	K.EGC*TEVSLLR.V	1.0	0.9	0.9	1.8	1.5	1.4	1.6	1.5	1.6	ns
327	P21964	COMT Catechol O-methyltransferase	COMT	K.IVDAVIQEHQPSVLLELGAYC*GYSAVR.M	0.9	0.9	0.9	2.1	1.8	1.4	1.4	1.1	1.5	ns
328	P11413	G6PD Glucose-6-phosphate 1-dehydrogenase	G6PD	R.TQVC*GILR.E	0.9	0.9	0.9	1.8	1.6	1.4	1.6	1.3	1.5	ns
329	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	R.GQAGGGGPGTGPGLGEAGSLATC*ELPLAK.S	1.0	0.9	0.9	2.1	1.7	1.2	1.5	1.2	1.5	ns
330	Q96P48	ARAP1 Arf-GAP with Rho-GAP domain, ANK repeat and PH dom	ARAP1	R.AVFPEGPC*EEPLQLR.K	0.9	0.7	0.8	1.9	1.8	1.2	1.3	1.5	1.5	ns
331	Q9NQC3	RTN4 Reticulon-4	RTN4	K.YSNSALGHVNC*TIK.E	0.8	0.8	0.8	1.7	1.4	1.7	1.5	1.4	1.5	ns
332	O95336	PGLS 6-phosphogluconolactonase	PGLS	R.AAC*CLAGAR.A	1.0	0.8	0.9	1.3	1.5	1.6	1.7	1.6	1.5	ns
333	O00233	PSMD9 26S proteasome non-ATPase regulatory subunit 9	PSMD9	K.GIGMNEPLVDC*EGYPR.S	0.8	1.0	0.9	1.7	1.4	1.5	1.8	1.2	1.5	ns
334	Q7L2H7	EIF3M Eukaryotic translation initiation factor 3 subunit	EIF3M	K.VAASC*GAIQYIPTELDQVR.K	0.8	0.9	0.9	1.4	1.6	1.4	1.7	1.4	1.5	ns
335	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.LFQEC*CPHSTDR.V	0.9	0.7	0.8	1.7	1.4	1.5	1.6	1.4	1.5	ns
336	P21333	FLNA Filamin-A	FLNA	K.VGTEC*GNQK.V	0.8	0.7	0.8	1.4	1.6	1.5	1.5	1.5	1.5	ns
337	Q9NZZ3	CHMP5 Charged multivesicular body protein 5	CHMP5	K.APPPSLTDC*IGTVDSR.A	0.9	1.0	1.0	1.7	1.5	1.5	1.4	1.3	1.5	ns
338	P00338	LDHA L-lactate dehydrogenase A chain	LDHA	R.VIGSGC*NLDSAR.F	0.9	0.9	0.9	1.0	1.9	1.4	1.8	1.4	1.5	ns
339	Q9BV86	NTMT1 N-terminal Xaa-Pro-Lys N-methyltransferase 1	NTMT1	R.IIC*SAGLSLLAEER.Q	1.0	0.9	0.9	1.9	1.4	1.4	1.4	1.3	1.5	ns
340	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK.G	1.0	0.9	0.9	1.8	1.5	1.3	1.5	1.2	1.5	ns
341	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	R.ALANSLAC*QGK.Y	0.5	0.8	0.6	0.9	1.5	1.7	2.2	1.0	1.5	ns
342	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	R.VFIMDSC*DELIPEYLNFIR.G	0.9	0.9	0.9	1.5	1.5	1.4	1.5	1.3	1.5	ns
343	Q16854	DGUOK Deoxyguanosine kinase, mitochondrial	DGUOK	K.AC*TAQSLGNLLDMMYR.E	0.9	0.9	0.9	1.8	1.3	1.3	1.5	1.5	1.5	ns
344	P55795	HNRNPH2 Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	R.GLPFGC*SK.E	1.0	0.9	0.9	1.4	1.5	1.5	1.4	1.4	1.4	ns
345	Q9HAV7	GRPEL1 GrpE protein homolog 1, mitochondrial	GRPEL1	K.LYGIQAFC*K.D	0.8	1.0	0.9	1.6	1.5	1.4	1.3	1.4	1.4	ns
346	Q93009	USP7 Ubiquitin carboxyl-terminal hydrolase 7	USP7	K.GTC*VEGTIPK.L	1.0	0.8	0.9	1.8	1.6	1.4	1.3	1.2	1.4	ns
347	P53602	MVD Diphosphomevalonate decarboxylase	MVD	R.DGDPLPSSLSC*K.V	0.9	1.0	0.9	1.6	1.5	1.2	1.4	1.5	1.4	ns
348	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	R.YASIC*QQNGIVPIVEPEILPDGDHDLK.R	0.5	0.8	0.6	0.9	1.4	1.6	2.0	1.2	1.4	ns
349	P26641	EEF1G Elongation factor 1-gamma	EEF1G	K.AAAPAPEEEMDEC*EQALAAEPK.A	1.0	1.0	1.0	1.7	1.4	1.3	1.5	1.1	1.4	ns
350	P84085	ARF5 ADP-ribosylation factor 5	ARF5	K.NIC*FTVWDVGGQDK.I	0.9	0.9	0.9	1.4	1.1	1.4	1.8	1.4	1.4	ns
351	P33240	CSTF2 Cleavage stimulation factor subunit 2	CSTF2	K.LC*VQNSPQEAR.N	0.9	0.9	0.9	1.4	1.5	1.4	1.5	1.4	1.4	ns

352	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	R.LQEALDAEMLEDEAGGGGAGPGGAC*K.A	1.1	0.8	0.9	1.4	1.3	1.5	1.4	1.5	1.4	ns
353	Q53T59	HS1BP3 HCLS1-binding protein 3	HS1BP3	K.LFDDPDLGGAIPLGDSLLLPAAC*ESGGPTPSLSHR.D	0.9	0.9	0.9	1.9	1.4	1.4	1.3	1.1	1.4	ns
354	Q7L1Q6	BZW1 Basic leucine zipper and W2 domain-containing prot	BZW1	R.FDPTQFQDC*IIQGLTETGTDLEAVAK.F	1.0	1.1	1.0	1.7	1.3	1.4	1.3	1.3	1.4	ns
355	P25398	RPS12 40S ribosomal protein S12	RPS12	K.LVEALC*AEHQINLIK.V	1.0	1.0	1.0	1.5	1.4	1.5	1.3	1.2	1.4	ns
356	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	K.C*LSVMEAK.V	0.8	0.9	0.8	1.6	1.3	1.5	1.4	1.2	1.4	ns
357	Q9UJW0	DCTN4 Dynactin subunit 4	DCTN4	R.LLQPDFQPVC*ASQLYPR.H	1.0	0.7	0.9	1.6	1.4	1.2	1.6	1.2	1.4	ns
358	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	R.IVDTPC*NEMNTDTFLEEINK.V	0.8	0.9	0.8	2.0	1.3	1.3	1.1	1.3	1.4	ns
359	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	R.LDFVC*SFLQK.N	0.7	0.8	0.8	1.7	1.3	1.3	1.4	1.2	1.4	ns
360	Q9Y224	C14orf166 UPF0568 protein C14orf166	C14orf166	K.LTALDYHNPAGFNC*K.D	0.9	0.9	0.9	1.4	1.4	1.3	1.5	1.2	1.4	ns
361	P60981	DSTN Destrin	DSTN	K.LGGSLIVAFEGC*PV.-	0.9	0.8	0.8	1.7	1.3	1.4	1.4	1.1	1.4	ns
362	O00204	SULT2B1 Sulfotransferase family cytosolic 2B member 1	SULT2B1	R.APWC*ETIVGAFSLPDQYSPR.L	0.9	1.0	1.0	1.3	1.3	1.5	1.3	1.4	1.4	ns
363	O75131	CPNE3 Copine-3	CPNE3	K.NC*LNPQFSK.T	1.0	0.8	0.9	1.6	1.4	1.4	1.4	1.1	1.4	ns
364	P14649	MYL6B Myosin light chain 6B	MYL6B	K.ILYSQC*GDVMR.A	0.8	0.8	0.8	1.1	1.0	1.2	2.4	1.1	1.4	ns
365	P30086	PEBP1 Phosphatidylethanolamine-binding protein 1	PEBP1	R.APVAGTC*YQAEWDDYVPK.L	0.8	0.8	0.8	1.3	1.4	1.5	1.3	1.1	1.3	ns
366	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.LSSC*DSFTSTINELNHCLSLR.T	1.0	0.8	0.9	1.5	1.2	1.5	1.5	1.1	1.3	ns
367	P62826	RAN GTP-binding nuclear protein Ran	RAN	R.VC*ENIPIVLCGNK.V	0.7	0.8	0.7	1.1	1.3	1.4	1.6	1.2	1.3	ns
368	P31939	ATIC Bifunctional purine biosynthesis protein PURH	ATIC	K.VC*MVYDLYK.T	0.7	0.8	0.7	0.7	0.9	1.8	2.3	0.9	1.3	ns
369	P53396	ACLY ATP-citrate synthase	ACLY	K.FIC*TTSAIQNR.F	0.9	0.9	0.9	1.6	1.3	1.2	1.2	1.2	1.3	ns
370	A0AVT1	UBA6 Ubiquitin-like modifier-activating enzyme 6	UBA6	R.KPNVGC*QQDSEELLK.L	0.9	0.8	0.8	1.4	1.2	1.3	1.3	1.2	1.3	ns
371	P49458	SRP9 Signal recognition particle 9 kDa protein	SRP9	K.VTDDLVC*LVYK.T	0.9	0.8	0.8	1.5	1.3	1.2	1.3	1.2	1.3	ns
372	P31947	SFN 14-3-3 protein sigma	SFN	K.GAVEKGEELSC*EER.N	0.9	0.9	0.9	1.5	1.2	1.4	1.3	1.0	1.3	ns
373	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.SSGGFVWAC*K.N	0.8	0.8	0.8	1.8	1.5	1.1	1.2	0.9	1.3	ns
374	O14964	HGS Hepatocyte growth factor-regulated tyrosine kinase	HGS	R.ACGQIFC*GK.C	0.7	0.9	0.8	2.3	1.1	1.2	0.9	1.1	1.3	ns
375	Q9H0C8	ILKAP Integrin-linked kinase-associated serine/threonine	ILKAP	R.FILLAC*DGLFK.V	1.4	0.8	1.1	1.6	1.0	1.5	1.2	1.3	1.3	ns
376	E9PPU0	EPPK1 Epiplakin	EPPK1	R.YLEGTSC*IAGVLVPAK.D	0.7	0.8	0.7	0.9	1.7	1.3	1.5	1.0	1.3	ns
377	P00492	HPRT1 Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	K.SYC*NDQSTGDIK.V	0.9	0.8	0.9	1.6	1.1	1.2	1.4	1.2	1.3	ns
378	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	K.HLNEIDLFHC*IDPNDSK.H	0.9	0.9	0.9	1.5	1.3	1.2	1.2	1.1	1.3	ns
379	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.EGVVEC*SFVK.S	0.7	0.9	0.8	1.2	0.9	1.5	1.3	1.4	1.3	ns

380	Q9UL46	PSME2 Proteasome activator complex subunit 2	PSME2	K.C*GFLPGNEK.V	0.9	0.9	0.9	1.6	1.3	1.1	1.3	1.1	1.3	ns
381	P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	K.YLEC*SALTQR.G	0.8	0.8	0.8	1.0	0.9	1.1	2.3	1.0	1.3	ns
382	P62306	SNRPF Small nuclear ribonucleoprotein F	SNRPF	R.C*NNVLYIR.G	0.9	0.9	0.9	1.4	1.2	1.3	1.3	1.1	1.3	ns
383	P62993	GRB2 Growth factor receptor-bound protein 2	GRB2	K.VLNEEC*DQNWYK.A	0.8	0.7	0.8	1.4	1.3	1.1	1.3	1.2	1.3	ns
384	O43865	AHCYL1 Putative adenosylhomocysteinase 2	AHCYL1	K.LC*VPAMNVNDSVTK.Q	0.8	1.0	0.9	1.4	1.2	1.2	1.2	1.4	1.3	ns
385	P51610	HCFC1 Host cell factor 1	HCFC1	K.LVIYGGMSGC*R.L	0.7	1.0	0.8	1.4	1.3	1.2	1.3	1.1	1.3	ns
386	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	K.ASVGFGGSC*FQK.D	0.8	0.8	0.8	1.6	1.0	1.3	1.5	0.9	1.3	ns
387	P13798	APEH Acylamino-acid-releasing enzyme	APEH	R.QPALSAAC*LGPEVTTQYGGQYR.T	0.9	1.0	0.9	1.2	1.0	1.3	1.5	1.1	1.2	ns
388	P07900	HSP90AA1 Heat shock protein HSP 90-alpha	HSP90AA1	R.VFIMDNC*EELIPEYLNFIR.G	0.9	1.0	1.0	1.4	1.2	1.3	1.2	1.1	1.2	ns
389	O15382	BCAT2 Branched-chain-amino-acid aminotransferase, mitoch	BCAT2	R.EVFGSGTAC*QVCPVHR.I	0.6	1.0	0.8	1.3	1.5	1.1	1.1	1.1	1.2	ns
390	O14980	XPO1 Exportin-1	XPO1	K.LDINLLDNVVNC*LYHGEGAQQR.M	1.0	0.9	0.9	1.5	1.1	1.2	1.3	1.1	1.2	ns
391	P07741	APRT Adenine phosphoribosyltransferase	APRT	R.VVVVDDLLATGGTMNAAC*ELLGR.L	0.7	0.7	0.7	1.1	1.2	1.4	1.3	1.1	1.2	ns
392	P36969	GPX4 Phospholipid hydroperoxide glutathione peroxidase,	GPX4	R.YAEC*GLR.I	0.9	0.9	0.9	1.5	1.2	1.2	1.3	1.1	1.2	ns
393	Q9Y365	STARD10 PCTP-like protein	STARD10	R.MEC*CDVPAETLYDVLHDIEYR.K	0.9	1.0	0.9	1.6	1.0	1.3	1.2	1.1	1.2	ns
394	P36507	MAP2K2 Dual specificity mitogen-activated protein kinase	MAP2K2	K.LC*DFGVSGQLIDSMANSFVGTR.S	0.8	0.7	0.7	1.4	1.0	1.2	1.3	1.1	1.2	ns
395	P21333	FLNA Filamin-A	FLNA	K.AHVVPC*FDASK.V	0.9	0.9	0.9	1.4	1.2	1.2	1.2	1.1	1.2	ns
396	Q9NYL2	MLTK Mitogen-activated protein kinase kinase kinase MLT	MLTK	K.IC*DFGASR.F	0.7	0.8	0.7	1.5	1.2	1.1	1.1	1.1	1.2	ns
397	Q99873	PRMT1 Protein arginine N-methyltransferase 1	PRMT1	K.VIGIEC*SSISDYAVK.I	0.8	0.8	0.8	1.3	1.2	1.2	1.2	1.1	1.2	ns
398	O43795	MYO1B Unconventional myosin-Ib	MYO1B	K.LVMSYVAAVC*GK.G	1.0	0.8	0.9	1.5	1.1	1.2	1.1	1.1	1.2	ns
399	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.YLAEVAC*GDDR.K	1.0	0.8	0.9	1.6	1.2	1.2	1.0	1.1	1.2	ns
400	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.AITIAGVPQSVTEC*VK.Q	0.9	0.9	0.9	1.3	1.1	1.3	1.2	1.0	1.2	ns
401	Q96AT9	RPE Ribulose-phosphate 3-epimerase	RPE	K.IGPSILNSDLANLGAEC*LR.M	0.7	0.7	0.7	2.2	0.7	1.0	1.1	0.9	1.2	ns
402	Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	K.LAAQSC*ALSLVR.Q	0.7	0.6	0.7	1.3	1.2	1.4	1.0	1.1	1.2	ns
403	Q9BW61	DDA1 DET1- and DDB1-associated protein 1	DDA1	R.FHADSVC*K.A	1.0	0.9	0.9	1.1	1.2	1.4	1.2	1.0	1.2	ns
404	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	K.YAGLSTC*FR.Q	1.0	0.9	0.9	1.3	1.0	1.2	1.3	1.1	1.2	ns
405	Q8N987	NECAB1 N-terminal EF-hand calcium-binding protein 1	NECAB1	K.ETLNQLQSLQNSLEC*AMETTEEQTR.Q	1.3	1.1	1.2	1.4	1.0	1.0	1.4	1.1	1.2	ns
406	Q86SX6	GLRX5 Glutaredoxin-related protein 5, mitochondrial	GLRX5	K.GTPEQPQC*GFSNAVVQILR.L	0.9	0.9	0.9	1.4	1.1	1.1	1.2	1.0	1.2	ns
407	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	K.TGQATVASGIPAGWMGLDC*GPESSK.K	0.6	0.8	0.7	0.8	1.0	1.1	1.9	1.0	1.2	ns
408	P14868	DARS Aspartate--tRNA ligase, cytoplasmic	DARS	R.LEYC*EALAMLR.E	0.9	0.8	0.8	1.4	1.1	1.2	1.1	0.9	1.1	ns

409	P52209	PGD 6-phosphogluconate dehydrogenase, decarboxylating	PGD	R.C*LSSLKDER.I	0.5	0.8	0.7	1.1	0.9	1.3	1.2	1.1	1.1	ns
410	Q96EI5	TCEAL4 Transcription elongation factor A protein-like 4	TCEAL4	R.KPEVTC*TLEDK.K	1.1	0.8	1.0	1.2	1.1	1.1	1.0	1.3	1.1	ns
411	P21291	CSRP1 Cysteine and glycine-rich protein 1	CSRP1	K.SC*FLCMVCK.K	0.9	0.9	0.9	1.2	1.0	1.0	1.5	1.0	1.1	ns
412	P30153	PPP2R1A Serine/threonine-protein phosphatase 2A 65 kDa reg	PPP2R1A	R.LNIISNLDC*VNEVIGIR.Q	0.8	0.8	0.8	1.5	1.1	1.1	1.3	0.6	1.1	ns
413	O95372	LYPLA2 Acyl-protein thioesterase 2	LYPLA2	K.TYPGVMHSSC*PQEMAAVK.E	0.8	0.8	0.8	1.1	1.0	1.2	1.4	0.9	1.1	ns
414	P37802	TAGLN2 Transgelin-2	TAGLN2	K.NMAC*VQR.T	0.9	1.0	0.9	1.3	1.1	1.1	1.2	1.0	1.1	ns
415	P60174	TPI1 Triosephosphate isomerase	TPI1	R.IIYGGSVTGATC*K.E	0.7	0.8	0.8	0.9	1.0	1.2	1.4	1.0	1.1	ns
416	Q02790	FKBP4 Peptidyl-prolyl cis-trans isomerase FKBP4	FKBP4	K.TQLAVC*QQR.I	0.8	0.8	0.8	1.1	1.0	1.1	1.2	1.0	1.1	ns
417	P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	K.GFGFVC*FSSPEEATK.A	1.0	1.1	1.0	1.1	1.0	1.1	1.2	1.0	1.1	ns
418	P23528	CFL1 Cofilin-1	CFL1	K.HELQANC*YEEVK.D	0.9	0.9	0.9	1.3	1.0	1.0	1.1	1.0	1.1	ns
419	Q9NZA1	CLIC5 Chloride intracellular channel protein 5	CLIC5	K.AGIDGESIGNC*PFSQR.L	0.9	0.8	0.8	1.1	0.9	1.3	1.0	1.1	1.1	ns
420	P23528	CFL1 Cofilin-1	CFL1	K.AVLFC*LSEDK.K	0.8	0.8	0.8	0.8	1.0	1.5	0.9	1.1	1.1	ns
421	P12004	PCNA Proliferating cell nuclear antigen	PCNA	K.C*AGNEDIITLR.A	0.6	0.8	0.7	1.2	1.0	1.1	1.2	0.9	1.1	ns
422	Q9BSH4	TACO1 Translational activator of cytochrome c oxidase 1	TACO1	K.KLDSLGLCSVSC*ALEFIPNSK.V	1.0	0.8	0.9	1.4	0.9	1.0	1.0	1.0	1.1	ns
423	P11142	HSPA8 Heat shock cognate 71 kDa protein	HSPA8	K.VC*NPIITK.L	1.0	0.9	1.0	0.8	0.9	1.1	1.5	1.0	1.1	ns
424	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	K.LNEDMAC*SVAGITSDANVLTNELR.L	1.0	0.8	0.9	0.8	1.1	1.2	1.1	1.1	1.1	ns
425	Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	R.AITIAGIPQSIIEC*VK.Q	0.9	0.9	0.9	1.2	1.0	1.2	0.9	1.0	1.1	ns
426	P61970	NUTF2 Nuclear transport factor 2	NUTF2	K.NINDAWVC*TNDMFR.L	0.6	0.7	0.7	0.9	1.0	1.2	1.2	1.0	1.1	ns
427	P25398	RPS12 40S ribosomal protein S12	RPS12	R.QAHLC*VLASNCDEPMYVK.L	0.9	1.0	1.0	1.3	1.1	1.0	0.9	1.0	1.1	ns
428	P50990	CCT8 T-complex protein 1 subunit theta	CCT8	K.IAVYSC*PFDGMITETK.G	0.9	0.9	0.9	1.2	1.0	1.1	1.1	0.9	1.0	ns
429	P37802	TAGLN2 Transgelin-2	TAGLN2	K.DGTVLC*ELINALYPEGQAPVK.K	0.8	0.9	0.9	1.0	1.0	1.2	1.0	1.0	1.0	ns
430	Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	R.VGLGIC*YDMR.F	0.9	0.9	0.9	1.2	1.0	1.0	1.0	1.0	1.0	ns
431	O75533	SF3B1 Splicing factor 3B subunit 1	SF3B1	K.VQENC*IDLVGR.I	1.1	0.9	1.0	0.2	0.8	1.1	0.9	2.1	1.0	ns
432	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	K.ATC*IGNNSAAAVSMLK.Q	0.8	0.8	0.8	0.7	1.0	1.3	1.2	0.8	1.0	ns
433	Q9BT78	COPS4 COP9 signalosome complex subunit 4	COPS4	K.QIQSLC*FQVNNLLEK.I	0.7	0.9	0.8	1.1	0.6	1.4	1.2	0.8	1.0	ns
434	P52788	SMS Spermine synthase	SMS	R.LYC*PVEFSK.E	1.0	1.0	1.0	1.0	1.0	1.3	1.0	0.8	1.0	ns
435	P31949	S100A11 Protein S100-A11	S100A11	K.ISSPTETERC*IESLIAVFQK.Y	0.8	0.8	0.8	0.9	0.6	1.4	0.8	1.3	1.0	ns
436	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	R.FC*PFAER.T	0.9	0.8	0.9	1.1	1.1	0.9	1.0	1.0	1.0	ns
437	Q04917	YWHAH 14-3-3 protein eta	YWHAH	K.NC*NDFQYESK.V	0.7	1.0	0.9	1.2	0.9	1.0	1.0	0.9	1.0	ns
438	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	K.AGSDGAKIGNC*PFSQR.L	0.9	0.9	0.9	1.0	0.9	1.0	1.0	1.0	1.0	ns

439	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	R.EEFASTC*PDDEEIELAYEQVAK.A	0.7	0.9	0.8	0.9	1.0	1.0	1.2	0.8	1.0	ns
440	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	R.LVSSPC*CIVTSTYGWTANMER.I	1.0	0.8	0.9	1.0	0.8	1.0	1.1	0.9	1.0	ns
441	P50395	GDI2 Rab GDP dissociation inhibitor beta	GDI2	R.TDDYLDQPC*YETINR.I	0.7	0.8	0.7	1.0	1.0	1.0	1.0	0.9	1.0	ns
442	P22061	PCMT1 Protein-L-isoaspartate(D-aspartate) O-methyltransf	PCMT1	K.ALDVGSGSGILTAC*FAR.M	0.8	0.9	0.8	1.0	1.0	1.1	1.0	0.9	1.0	ns
443	P62258	YWHAE 14-3-3 protein epsilon	YWHAE	K.LIC*CDILDVLDK.H	0.9	0.8	0.9	1.0	0.9	1.1	1.0	1.0	1.0	ns
444	P41250	GARS Glycine--tRNA ligase	GARS	R.SC*YDLSCHAR.A	0.7	0.8	0.7	0.9	1.1	1.2	0.7	0.9	1.0	ns
445	P30044	PRDX5 Peroxiredoxin-5, mitochondrial	PRDX5	K.ALNVEPDGTGLTC*SLAPNIISQL.-	1.0	1.0	1.0	1.1	0.9	0.9	0.9	0.9	1.0	ns
446	Q9Y696	CLIC4 Chloride intracellular channel protein 4	CLIC4	K.AGSDGESIGNC*PFSQR.L	1.0	0.8	0.9	1.0	0.9	1.0	0.9	0.9	1.0	ns
447	Q9UNH7	SNX6 Sorting nexin-6	SNX6	R.IGSSLYALGTQDSTDIC*K.F	0.9	0.8	0.9	1.1	0.7	0.9	1.1	0.9	0.9	ns
448	P60174	TPI1 Triosephosphate isomerase	TPI1	K.VPADTEVVC*APPTAYIDFAR.Q	0.6	0.8	0.7	0.8	0.8	1.0	1.3	0.8	0.9	ns
449	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	R.YLLQYQEPIPC*EQLVTALCDIK.Q	0.9	0.9	0.9	0.8	0.8	1.2	1.0	0.8	0.9	ns
450	P07737	PFN1 Profilin-1	PFN1	K.C*YEMASHLR.R	0.7	0.9	0.8	0.8	0.9	1.1	1.0	0.8	0.9	ns
451	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	K.IAAYLQSDQFC*K.M	0.8	0.8	0.8	1.0	1.0	0.8	1.0	0.7	0.9	ns
452	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	K.FLDGNELTLADC*NLLPK.L	0.6	0.8	0.7	0.8	0.9	1.1	1.0	0.8	0.9	ns
453	Q9UHX1	PUF60 Poly(U)-binding-splicing factor PUF60	PUF60	R.ALAIMC*R.V	0.9	0.8	0.8	0.9	0.8	1.1	0.9	0.8	0.9	ns
454	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	K.LNEC*VDHTPK.L	0.8	0.8	0.8	1.0	0.8	1.0	0.8	0.9	0.9	ns
455	P22234	PAICS Multifunctional protein ADE2	PAICS	K.ITSC*IFQLLQEAGIK.T	0.8	0.7	0.8	0.9	0.8	1.0	0.9	0.9	0.9	ns
456	P60174	TPI1 Triosephosphate isomerase	TPI1	K.IAVAAQNC*YK.V	0.6	0.7	0.7	0.7	0.7	1.1	1.2	0.8	0.9	ns
457	P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	K.ALYDTFSAFGNILSC*K.V	0.9	1.2	1.0	0.9	0.8	1.1	0.8	0.9	0.9	ns
458	P00390	GSR Glutathione reductase, mitochondrial	GSR	K.LGGTC*VNVGCVPK.K	0.8	0.9	0.9	1.0	0.8	0.9	0.9	0.8	0.9	ns
459	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	K.ILSC*GEVIHVK.I	0.7	0.8	0.7	1.0	0.8	0.9	0.8	0.9	0.9	ns
460	Q12849	GRSF1 G-rich sequence factor 1	GRSF1	R.YIELFLNSC*PK.G	0.8	0.9	0.9	1.1	0.7	0.8	0.8	0.7	0.8	ns
461	P34896	SHMT1 Serine hydroxymethyltransferase, cytosolic	SHMT1	R.AVLEALGSC*LNNK.Y	0.6	0.8	0.7	0.5	1.1	0.9	1.0	0.7	0.8	ns
462	P10768	ESD S-formylglutathione hydrolase	ESD	K.AETGKC*PALYWLSGLTCTEQNFISK.S	0.9	0.9	0.9	0.9	0.8	0.8	0.8	0.9	0.8	ns
463	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit 2	PSMD2	K.GTLTLC*PYHSDR.Q	0.8	0.8	0.8	0.7	0.9	0.8	0.9	0.8	0.8	ns
464	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	K.IETELRDIC*NDVLSLLEK.F	0.8	0.8	0.8	0.7	0.7	1.0	0.8	0.9	0.8	ns
465	O75874	IDH1 Isocitrate dehydrogenase	IDH1	K.SEGGFIWAC*K.N	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	ns
466	P30041	PRDX6 Peroxiredoxin-6	PRDX6	R.DFTPVC*TTELGR.A	0.5	0.6	0.6	0.4	0.9	0.9	1.1	0.7	0.8	ns
467	F5H284	PPIAL4D Peptidyl-prolyl cis-trans isomerase	PPIAL4D	R.IIPGFMC*QGGDFTR.H	0.7	0.8	0.8	0.7	0.7	0.9	0.9	0.8	0.8	ns
468	P14174	MIF Macrophage migration inhibitory factor	MIF	K.LLC*GLLAER.L	0.8	0.9	0.9	0.8	0.7	0.9	0.7	0.8	0.8	ns

469	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.SIC*TTVLELLDK.Y	0.9	0.9	0.9	0.8	0.7	0.9	0.8	0.7	0.8	ns
470	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	K.LTFSC*LGGSDNFK.H	0.8	0.7	0.8	0.7	0.8	0.9	0.7	0.8	0.8	ns
471	P52907	CAPZA1 F-actin-capping protein subunit alpha-1	CAPZA1	K.TIDGQQTIIAC*IESHQFQPK.N	0.8	0.9	0.8	0.8	0.6	1.0	0.7	0.8	0.8	ns
472	P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	K.KITIADC*GQLE.-	0.7	0.8	0.8	0.7	0.6	0.9	0.8	0.7	0.7	ns
473	P19367	HK1 Hexokinase-1	HK1	R.AAQLC*GAGMAAVVDK.I	0.9	1.4	1.2	0.7	0.6	0.9	0.7	0.8	0.7	ns
474	P04632	CAPNS1 Calpain small subunit 1	CAPNS1	R.YSDESGNMDFDNFISC*LVR.L	0.8	0.8	0.8	0.7	0.5	0.8	0.8	0.8	0.7	ns
475	P21964	COMT Catechol O-methyltransferase	COMT	R.YLPDTLLLEEC*GLLR.K	0.9	0.8	0.9	0.5	0.5	0.9	0.7	0.8	0.7	ns
476	P31350	RRM2 Ribonucleoside-diphosphate reductase subunit M2	RRM2	K.LIGMNC*TLMK.Q	0.8	0.9	0.8	0.7	0.4	0.8	0.8	0.8	0.7	ns
477	P09467	FBP1 Fructose-1,6-bisphosphatase 1	FBP1	R.GTGELTQLLNSLC*TAVK.A	0.9	0.7	0.8	0.7	0.6	0.8	0.7	0.8	0.7	ns

Table 3A-3. R-values from transnitrosation experiment at 90 µM Trx-SNO. A list of all identified peptides (* denotes labeled cysteine) is presented together with calculated Heavy:Light Ratios (R-values) in untreated (0 µM) (n=2) versus Trx-SNO-treated (90 µM) (n=5) MS analysis. Date were sorted by their average R-values of Trx-SNO-treated experiments and numbered as "Peptide #".

Peptide #	Uniprot #	Description	Symbol	Sequence	Heavy : Light Ratio								significance
					0 µM Trx-SNO			90 µM Trx-SNO					
					1	2	average	1	2	3	4	5	average	
1	P31749	AKT1 RAC-alpha serine/threonine-protein kinase	AKT1	K.TFC*GTPEYLAPEVLEDNDYGR.A	1.0	1.0	1.0	19.2	20.0	20.0	18.7	20.0	19.6	***
2	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	R.C*MALSTAVLVGEAK.K	1.1	1.0	1.1	14.5	17.2	12.7	14.9	0.0	14.8	***
3	P17858	PFKL 6-phosphofructokinase, liver type	PFKL	K.C*HDYYTTEFLYNLYSSEGK.G	1.1	0.9	1.0	13.3	12.3	17.5	0.0	0.0	14.4	***
4	Q96BF6	NACC2 Nucleus accumbens-associated protein 2	NACC2	R.NTLANSC*GTGIR.S	1.1	0.8	1.0	10.2	18.4	12.0	0.0	0.0	13.5	***
5	Q01813	PFKP 6-phosphofructokinase type C	PFKP	R.LPLMEC*VQMTQDVQK.A	1.1	1.0	1.0	13.6	12.3	12.6	13.0	0.0	12.9	***
6	Q92947	GCDH Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	K.GYGC*AGVSSVAYGLLAR.E	1.0	0.9	0.9	8.7	14.4	13.7	9.1	12.8	11.7	***
7	P07858	CTSB Cathepsin B	CTSB	R.GQDHC*GIESEVVAGIPR.T	1.0	1.0	1.0	9.7	10.0	13.9	12.5	11.5	11.5	***
8	E9PPU0	EPPK1 Epiplakin	EPPK1	R.YLQGTGC*IAGLLLPGSQER.L	0.9	0.9	0.9	8.3	9.6	9.3	10.6	13.4	10.2	***
9	Q15005	SPCS2 Signal peptidase complex subunit 2	SPCS2	R.SGGSGGC*SGAGGASNCGTGSGR.S	1.0	0.9	0.9	8.3	9.7	11.2	7.4	11.6	9.6	***
10	P17858	PFKL 6-phosphofructokinase, liver type	PFKL	R.VFANAPDSAC*VIGLK.K	1.0	0.9	0.9	7.9	8.3	10.2	10.7	10.2	9.5	***
11	P27635	RPL10 60S ribosomal protein L10	RPL10	K.MLSC*AGADR.L	1.1	1.0	1.0	7.6	7.6	11.9	10.1	10.1	9.4	***

12	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	R.AVHQC*DR.G	1.0	1.0	1.0	9.1	9.3	10.4	8.4	0.0	9.3	***
13	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.AYHEQLSVAEITNAC*FEPANQMVK.C	1.1	1.0	1.0	8.1	8.2	10.9	8.6	8.9	8.9	***
14	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.PMC*VESFSDYPPLGR.F	1.0	1.0	1.0	7.9	7.9	9.6	9.4	7.9	8.6	***
15	P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	R.TIYAGNALC*TVK.C	1.0	1.0	1.0	6.7	7.7	11.5	7.3	9.6	8.5	***
16	P26440	IVD Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	K.AC*DEGHCTAK.D	1.1	1.0	1.0	7.3	8.9	8.5	8.0	0.0	8.1	***
17	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	R.GNHEC*ASINR.I	0.9	1.0	1.0	7.0	7.9	8.8	8.0	8.7	8.1	***
18	E9PPU0	EPPK1 Epiplakin	EPPK1	R.YLC*GLGAVGGVR.L	1.1	0.9	1.0	6.9	6.8	11.4	7.5	7.4	8.0	***
19	Q92616	GCN1L1 Translational activator GCN1	GCN1L1	R.C*GLALALNK.L	0.9	0.9	0.9	7.0	8.4	8.0	7.2	8.1	7.7	***
20	P49327	FASN Fatty acid synthase	FASN	R.LGMLSPEGTC*K.A	1.1	0.9	1.0	6.3	7.6	7.4	8.2	0.0	7.4	***
21	Q4ZG55	GREB1 Protein GREB1	GREB1	R.LINSSC*LVR.T	0.9	1.0	1.0	7.2	7.2	6.1	7.4	8.4	7.2	***
22	P60709	ACTB Actin, cytoplasmic 1	ACTB	K.EKLC*YVALDFEQEMATAASSSSLEK.S	1.0	0.9	1.0	6.7	5.9	8.4	7.5	6.9	7.1	***
23	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	R.LC*PNSTGAEIR.S	1.0	1.0	1.0	5.5	6.3	8.6	7.9	0.0	7.1	***
24	E9PPU0	EPPK1 Epiplakin	EPPK1	R.LLDAQLATGGLVC*PAR.R	1.0	0.9	1.0	6.3	6.0	8.3	7.2	6.6	6.9	***
25	P07339	CTSD Cathepsin D	CTSD	K.AIGAVPLIQGEYMIPC*EK.V	0.8	0.8	0.8	5.3	6.2	7.8	6.5	7.7	6.7	***
26	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.KLGNNC*VFAPADVTSEK.D	1.0	0.9	1.0	5.6	5.9	7.8	6.1	7.6	6.6	***
27	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	R.YVAAAFPSAC*GK.T	1.1	1.0	1.0	6.4	6.8	8.1	6.3	5.3	6.6	***
28	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	R.AVC*MLSNTTAIAEAWAR.L	1.0	1.0	1.0	6.9	6.6	7.2	6.2	6.0	6.6	***
29	O95757	HSPA4L Heat shock 70 kDa protein 4L	HSPA4L	R.GC*ALQCAILSPAFK.V	1.0	0.9	0.9	5.9	6.8	6.5	7.2	6.2	6.5	***
30	P36578	RPL4 60S ribosomal protein L4	RPL4	R.SGQGAFGNMC*R.G	1.1	0.9	1.0	5.0	5.6	7.7	6.6	7.0	6.4	***
31	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	R.AVASQLDC*NFLK.V	1.0	0.9	0.9	4.9	5.8	8.8	6.6	5.8	6.4	***
32	P50213	IDH3A Isocitrate dehydrogenase	IDH3A	K.TFDLYANVRPC*VSIEGYK.T	0.9	1.1	1.0	4.5	8.4	7.0	5.8	6.1	6.3	***
33	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.DLAGC*IHGLSNVK.L	0.9	0.9	0.9	5.2	5.9	7.3	6.2	7.1	6.3	***
34	I3L2F9	Uncharacterized protein	Uncharacterized	K.NMMAAC*DPR.H	1.0	1.0	1.0	5.5	5.9	7.6	6.5	6.2	6.3	***
35	P62280	RPS11 40S ribosomal protein S11	RPS11	K.C*PFTGNVSIR.G	1.1	0.8	0.9	5.8	5.7	7.3	6.3	6.2	6.3	***
36	P62249	RPS16 40S ribosomal protein S16	RPS16	K.TATAVAHC*K.R	1.0	0.9	0.9	5.2	5.4	7.6	6.0	6.1	6.0	***
37	P42677	RPS27 40S ribosomal protein S27	RPS27	K.ARLTEGC*SFR.R	1.0	1.0	1.0	5.2	5.9	6.3	6.6	0.0	6.0	***
38	P62753	RPS6 40S ribosomal protein S6	RPS6	K.LNISFPATGC*QK.L	1.0	0.9	1.0	4.8	5.2	6.7	5.6	5.6	5.6	***
39	P62829	RPL23 60S ribosomal protein L23	RPL23	R.ISLGLPVGAVINC*ADNTGAK.N	1.0	0.9	1.0	4.9	4.9	7.5	5.1	5.4	5.6	***
40	I3L2F9	Uncharacterized protein	Uncharacterized	K.TAVC*DIPPR.G	1.1	1.0	1.0	4.9	4.9	6.5	5.5	5.4	5.5	***

41	Q8N163	KIAA1967 DBIRD complex subunit KIAA1967	KIAA1967	R.VVTQNIC*QYR.S	1.1	1.0	1.1	6.7	5.4	4.3	5.5	5.1	5.4	***
42	P23396	RPS3 40S ribosomal protein S3	RPS3	R.AC*YGVLR.F	1.0	0.9	1.0	4.4	4.6	6.8	5.2	6.1	5.4	***
43	Q13748	TUBA3D Tubulin alpha-3C/D chain	TUBA3D	R.TIQFVDWC*PTGFK.V	1.0	1.0	1.0	4.7	4.9	6.4	5.7	5.3	5.4	***
44	P46782	RPS5 40S ribosomal protein S5	RPS5	K.AQC*PIVER.L	1.0	0.9	1.0	4.8	4.9	6.0	6.0	5.2	5.4	***
45	O95747	OXSR1 Serine/threonine-protein kinase OSR1	OXSR1	K.TFVGTPC*WMAPEVMEQVR.G	1.0	0.9	0.9	5.8	4.6	5.4	5.0	5.9	5.3	***
46	P18085	ARF4 ADP-ribosylation factor 4	ARF4	K.NIC*FTVWDVGGQDR.I	1.2	1.1	1.1	7.2	5.6	4.9	3.9	5.0	5.3	***
47	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	R.AGGIETIANEFSDRC*TPSVISFGSK.N	1.0	0.9	1.0	5.2	5.0	6.1	4.7	5.5	5.3	***
48	Q9NUU7	DDX19A ATP-dependent RNA helicase DDX19A	DDX19A	K.VLVTTNVC*AR.G	1.0	1.0	1.0	4.4	4.8	6.4	4.9	5.7	5.2	***
49	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	R.AC*ALQVLSAILEGSK.Q	1.0	1.0	1.0	4.4	4.8	6.2	5.2	5.5	5.2	***
50	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	R.SIQFVDWC*PTGFK.V	1.0	1.0	1.0	4.5	4.7	6.2	5.2	5.3	5.2	***
51	P00966	ASS1 Argininosuccinate synthase	ASS1	R.FELSC*YSLAPQIK.V	1.0	1.0	1.0	5.1	4.7	5.7	4.6	5.5	5.1	***
52	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.FGRVDVAVNC*AGIAVASK.T	1.0	1.1	1.0	3.3	6.6	3.6	5.5	6.7	5.1	***
53	P50914	RPL14 60S ribosomal protein L14	RPL14	K.C*MQLTDFILK.F	1.0	0.9	0.9	4.0	4.2	6.0	5.1	5.6	5.0	***
54	O94979	SEC31A Protein transport protein Sec31A	SEC31A	K.SC*ATFSSSHR.Y	1.4	1.1	1.3	4.9	5.6	4.8	4.1	0.0	4.8	***
55	P50914	RPL14 60S ribosomal protein L14	RPL14	R.ALVDGPC*TQVR.R	1.0	1.0	1.0	4.1	4.7	5.6	4.7	5.0	4.8	***
56	P46782	RPS5 40S ribosomal protein S5	RPS5	K.TIAEC*LADELINAAK.G	1.1	1.0	1.0	3.9	4.8	5.6	4.7	5.0	4.8	***
57	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	R.LC*ALRPDDSSSAR.T	1.0	0.9	0.9	3.6	5.0	7.0	4.2	3.9	4.7	***
58	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	K.ITGC*ASPGK.T	1.0	0.9	0.9	2.8	4.7	5.8	5.5	3.9	4.5	***
59	P60866	RPS20 40S ribosomal protein S20	RPS20	K.TPC*GEGSK.T	1.2	0.9	1.1	3.9	4.0	5.7	3.9	4.7	4.5	***
60	P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	R.LIGPNC*PGVINPGECK.I	0.9	0.7	0.8	4.1	4.9	5.7	3.1	4.5	4.5	***
61	P54136	RARS Arginine--tRNA ligase, cytoplasmic	RARS	K.NC*GCLGASPNLEQLQEENLK.L	0.9	1.0	1.0	3.6	4.0	5.5	4.4	4.7	4.4	***
62	P07437	TUBB Tubulin beta chain	TUBB	K.LTTPTYGDLNHLVSATMSGVTTC*LR.F	1.1	1.0	1.0	4.2	4.1	5.4	3.5	4.9	4.4	***
63	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	K.AEMDAAIASC*K.R	0.9	0.7	0.8	3.1	4.1	4.8	4.6	5.3	4.4	***
64	P15924	DSP Desmoplakin	DSP	R.DANSENC*NK.N	1.1	1.0	1.1	3.6	4.8	5.0	3.8	4.8	4.4	***
65	P46782	RPS5 40S ribosomal protein S5	RPS5	R.VNQAIWLLC*TGAR.E	1.0	0.8	0.9	3.8	3.7	5.3	3.5	5.6	4.4	***
66	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	K.KLVIVGDGAC*GK.T	0.8	0.8	0.8	3.7	3.7	6.7	3.6	4.2	4.4	***
67	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	K.IISNASC*TTNCLAPLAK.V	1.0	1.0	1.0	3.5	3.7	4.9	5.1	4.3	4.3	***
68	P55060	CSE1L Exportin-2	CSE1L	K.IC*AVGITK.L	1.0	1.0	1.0	3.5	4.1	5.7	4.0	4.3	4.3	***
69	P82912	MRPS11 28S ribosomal protein S11, mitochondrial	MRPS11	K.ASHNNTQIQVVSASNEPLAFASC*GTEGFR.N	0.9	0.8	0.9	3.7	3.9	4.9	4.3	4.2	4.2	***
70	Q96CM8	ACSF2 Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	R.MVSTPIGGLSYVQGC*TK.K	1.1	1.1	1.1	3.6	3.5	5.4	3.9	4.3	4.1	***

71	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.YMAC*CLLYR.G	1.0	1.0	1.0	3.6	3.7	4.9	3.9	4.0	4.0	***
72	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	R.QAVLGAGLPISTPC*TTINK.V	1.0	1.0	1.0	3.5	4.1	4.4	4.0	4.0	4.0	***
73	Q9BRA2	TXNDC17 Thioredoxin domain-containing protein 17	TXNDC17	K.DAGGKSWC*PDCVQAEPVVR.E	1.1	1.0	1.0	3.4	3.1	4.8	4.4	4.0	4.0	***
74	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	R.GDEC*GLALGR.L	1.0	0.9	1.0	3.3	3.4	4.6	4.1	3.9	3.9	***
75	O95833	CLIC3 Chloride intracellular channel protein 3	CLIC3	K.ASEDGESVGHC*PSCQR.L	1.1	0.9	1.0	3.2	3.0	4.8	4.4	3.8	3.8	***
76	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	R.NVC*TEAGMFAIR.A	1.0	0.9	0.9	2.7	4.1	3.9	4.3	3.9	3.8	***
77	P13639	EEF2 Elongation factor 2	EEF2	K.DLEEDHAC*IPIK.K	1.1	0.8	1.0	3.1	3.6	4.1	3.8	4.2	3.8	***
78	P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	K.IIC*QGFTGK.Q	1.0	1.0	1.0	3.3	3.4	4.6	3.6	3.9	3.8	***
79	Q15796	SMAD2 Mothers against decapentaplegic homolog 2	SMAD2	K.AITTQNC*NTK.C	0.9	1.0	0.9	3.3	4.5	3.2	4.0	0.0	3.7	***
80	Q9UNH7	SNX6 Sorting nexin-6	SNX6	R.IGSSLYALGTQDSTDIC*K.F	0.9	0.9	0.9	3.8	3.8	3.4	3.9	3.7	3.7	***
81	P45880	VDAC2 Voltage-dependent anion-selective channel protein	VDAC2	R.PMC*IPPSYADLGK.A	1.4	1.1	1.3	2.8	4.0	4.1	4.1	3.5	3.7	***
82	Q9BV86	NTMT1 N-terminal Xaa-Pro-Lys N-methyltransferase 1	NTMT1	R.IIC*SAGLSLLAEER.Q	1.1	0.9	1.0	3.0	2.9	4.3	4.1	3.6	3.6	***
83	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.DLNYC*FSGMSDHR.Y	1.1	1.0	1.0	2.9	3.3	4.2	3.6	3.3	3.5	***
84	P28838	LAP3 Cytosol aminopeptidase	LAP3	R.SAGAC*TAAAFLK.E	1.0	0.9	1.0	3.5	3.3	3.9	3.5	3.1	3.4	***
85	P23396	RPS3 40S ribosomal protein S3	RPS3	R.GLC*AIAQAESLR.Y	1.1	1.0	1.0	3.0	3.2	4.1	3.3	3.5	3.4	***
86	Q9BTE3	MCMBP Mini-chromosome maintenance complex-binding protei	MCMBP	R.DASALLDPMEC*TDTAEEQR.V	1.1	0.8	1.0	2.2	4.7	4.0	3.4	2.6	3.4	***
87	Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multif	AIMP2	R.SC*ENLAPFNTALK.L	0.9	0.8	0.9	2.8	2.7	3.7	3.5	4.0	3.3	***
88	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.QGEYGLASIC*NGGGGASAMLIQK.L	1.0	1.0	1.0	3.3	3.1	3.9	3.2	3.2	3.3	***
89	O14976	GAK Cyclin-G-associated kinase	GAK	R.AIIQEVC*FMK.K	1.0	0.9	1.0	2.7	3.0	3.8	3.4	3.7	3.3	***
90	Q27J81	INF2 Inverted formin-2	INF2	R.AVLLASDAQEC*TLEEVVER.L	0.9	0.9	0.9	2.6	2.5	3.9	3.6	3.4	3.2	***
91	Q16186	ADRM1 Proteasomal ubiquitin receptor ADRM1	ADRM1	R.VPQC*PSGR.V	1.3	0.9	1.1	2.9	2.7	3.5	3.4	3.3	3.1	**
92	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	K.C*FIVGADNVGSK.Q	1.0	1.0	1.0	2.4	3.1	3.6	3.0	3.3	3.1	**
93	P15924	DSP Desmoplakin	DSP	K.YC*YLQNEVFGLFQK.L	1.0	1.1	1.1	2.9	2.8	3.6	3.1	2.9	3.1	**
94	Q13636	RAB31 Ras-related protein Rab-31	RAB31	K.VC*LLGDTGVGK.S	1.0	0.7	0.9	1.9	2.7	4.5	2.5	3.7	3.1	**
95	O15075	DCLK1 Serine/threonine-protein kinase DCLK1	DCLK1	R.YQDDFLLDESEC*R.V	1.3	1.0	1.2	2.8	2.7	3.5	3.1	3.2	3.0	*
96	P55769	NHP2L1 NHP2-like protein 1	NHP2L1	K.KLLDLVQQSC*NYK.Q	1.1	0.9	1.0	2.4	2.9	3.8	3.2	2.9	3.0	**
97	P49207	RPL34 60S ribosomal protein L34	RPL34	R.AYGGSMC*AK.C	1.0	1.1	1.0	2.8	2.6	3.3	3.6	2.8	3.0	**
98	P62195	PSMC5 26S protease regulatory subunit 8	PSMC5	K.GVC*TEAGMYALR.E	1.0	0.8	0.9	2.4	2.6	3.5	3.1	3.6	3.0	**

99	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.LGVENC*YFPMFVSQSALEK.E	1.1	0.9	1.0	2.6	2.6	3.5	3.1	3.2	3.0	**
100	Q9Y3E2	BOLA1 BolA-like protein 1	BOLA1	R.VC*LCQGSAGSGAIGPVEAAIR.T	1.0	0.9	1.0	2.5	3.2	3.7	2.3	3.3	3.0	**
101	P21333	FLNA Filamin-A	FLNA	R.VTYC*PTEPGNYIINIK.F	0.8	1.0	0.9	2.3	1.9	4.4	2.6	3.4	2.9	**
102	P84085	ARF5 ADP-ribosylation factor 5	ARF5	K.NIC*FTVWDVGGQDK.I	1.2	0.9	1.0	2.9	2.6	3.0	3.2	0.0	2.9	*
103	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitoch	MCCC2	K.MVAAVAC*AQVPK.I	1.1	0.8	1.0	2.3	2.6	3.7	3.1	2.8	2.9	*
104	P15924	DSP Desmoplakin	DSP	K.YQAEC*SQFK.A	0.9	0.8	0.8	2.5	2.6	2.7	2.8	3.8	2.9	**
105	B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	K.IFVGNVSAAC*TSQELR.S	1.0	1.0	1.0	2.3	3.0	3.2	2.6	3.2	2.8	*
106	Q9NZB2	FAM120A Constitutive coactivator of PPAR-gamma-like protei	FAM120A	R.GFAGVC*GFGGPYGETVATGPYR.A	1.2	0.9	1.0	3.2	2.5	2.6	2.9	3.0	2.8	ns
107	P53618	COPB1 Coatomer subunit beta	COPB1	K.ALSGYC*GFMAANLYAR.S	1.0	1.0	1.0	2.4	2.6	3.5	2.6	3.0	2.8	*
108	P08559	PDHA1 Pyruvate dehydrogenase E1 component subunit alpha,	PDHA1	R.FAAAYC*R.S	1.0	0.8	0.9	2.1	2.4	2.9	3.2	3.5	2.8	*
109	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	R.FSPNSSNPIIVSC*GWDK.L	1.0	0.9	0.9	2.6	2.5	3.1	2.9	2.9	2.8	*
110	Q9ULV4	CORO1C Coronin-1C	CORO1C	K.C*DLISIPK.K	1.1	1.0	1.0	2.3	2.8	3.4	2.9	2.4	2.8	ns
111	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	R.HIIEDPC*TLR.H	1.0	1.0	1.0	1.9	2.7	3.4	2.4	3.4	2.8	ns
112	Q07020	RPL18 60S ribosomal protein L18	RPL18	K.GC*GTVLLSGPR.K	1.0	1.1	1.0	2.1	2.3	3.6	2.8	2.9	2.7	ns
113	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	R.ADHQPLTEASYVNLPTIALC*NTDSPLR.Y	0.9	0.8	0.8	2.3	2.6	3.4	2.3	3.2	2.7	*
114	Q9H479	FN3K Fructosamine-3-kinase	FN3K	R.AFGGPGAGC*ISEGR.A	1.1	1.2	1.1	2.3	2.0	2.8	4.3	2.2	2.7	ns
115	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	K.VQYPQSQAC*K.M	1.2	1.1	1.2	3.3	2.1	2.5	2.3	3.1	2.7	ns
116	Q8IXH7	TH1L Negative elongation factor C/D	TH1L	R.AC*QALGAMLSK.G	0.9	1.1	1.0	2.6	2.3	3.0	2.5	3.0	2.7	ns
117	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.HSMNPFC*EIAVEEAVR.L	1.0	0.9	1.0	2.3	2.9	2.9	2.4	2.8	2.7	ns
118	O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	R.ANSSVVSVNC*K.G	1.1	1.0	1.0	1.9	2.4	3.7	2.5	2.7	2.7	ns
119	Q9UBT2	UBA2 SUMO-activating enzyme subunit 2	UBA2	R.VLVVGAGGIGC*ELLK.N	1.1	0.9	1.0	2.0	2.2	3.3	2.5	3.2	2.7	ns
120	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.SVHYC*PATK.K	1.2	0.9	1.1	2.3	2.5	3.3	2.5	2.6	2.6	ns
121	P62244	RPS15A 40S ribosomal protein S15a	RPS15A	K.C*GVISPR.F	0.9	0.7	0.8	2.3	1.7	3.6	2.8	2.8	2.6	*
122	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.EVIAVSCGPAQC*QETIR.T	1.0	0.9	1.0	2.3	2.2	3.1	2.9	2.5	2.6	ns
123	O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	K.SFVQWLGC*R.S	1.0	0.9	1.0	2.4	2.3	3.2	2.3	2.7	2.6	ns
124	Q96CD2	PPCDC Phosphopantothenoylcysteine decarboxylase	PPCDC	K.ASC*PAAAPLMER.K	1.1	1.1	1.1	1.9	2.2	3.6	2.6	2.6	2.6	ns
125	Q08AM6	VAC14 Protein VAC14 homolog	VAC14	K.GLEC*SPSTPTMNSYFYK.F	0.9	1.1	1.0	2.5	2.7	2.6	2.6	2.4	2.6	ns
126	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.IHMGSC*AENTAK.K	1.1	1.0	1.0	2.3	2.4	3.1	2.7	2.4	2.5	ns
127	Q9UPN9	TRIM33 E3 ubiquitin-protein ligase TRIM33	TRIM33	R.C*DPVPAANGAIR.F	1.1	1.1	1.1	3.1	3.4	3.7	1.3	1.3	2.5	ns

128	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	R.IVDTPC*NEMNTDTFLEEINK.V	1.0	1.1	1.0	1.9	2.5	3.9	2.4	2.0	2.5	ns
129	Q5TFE4	NT5DC1 5-nucleotidase domain-containing protein 1	NT5DC1	K.HFLSDTGMAC*R.S	1.1	1.0	1.0	2.4	2.2	2.9	2.5	2.6	2.5	ns
130	O95671	ASMTL N-acetylserotonin O-methyltransferase-like protein	ASMTL	K.VDASAC*GMER.L	1.0	1.2	1.1	2.6	1.7	2.9	2.5	2.8	2.5	ns
131	Q15631	TSN Translin	TSN	K.ETAAAC*VEK.-	1.0	1.1	1.1	1.9	2.3	3.0	2.2	3.1	2.5	ns
132	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	R.AGAIAPC*EVTVPAQNTGLGPEK.T	0.9	0.8	0.9	2.1	2.4	2.9	2.5	2.4	2.5	ns
133	Q15813	TBCE Tubulin-specific chaperone E	TBCE	R.NCAVSC*AGEK.G	1.0	0.8	0.9	2.1	2.2	2.7	2.5	2.8	2.5	ns
134	Q9NQT5	EXOSC3 Exosome complex component RRP40	EXOSC3	K.LLAPDC*EIIQEVGK.L	1.1	0.8	1.0	2.0	2.3	3.2	2.3	2.5	2.4	ns
135	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	R.ISAFGYLEC*SAK.T	0.8	0.8	0.8	1.7	2.6	3.3	3.0	1.5	2.4	ns
136	P63220	RPS21 40S ribosomal protein S21	RPS21	K.TYAIC*GAIR.R	1.3	1.0	1.1	2.2	2.3	2.4	2.6	2.6	2.4	ns
137	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.YVLC*TAPR.A	1.0	0.9	0.9	2.0	2.3	2.9	2.2	2.6	2.4	ns
138	P46379	BAG6 Large proline-rich protein BAG6	BAG6	R.C*NLACTPPR.H	0.8	1.0	0.9	2.1	1.6	2.5	3.1	2.6	2.4	ns
139	Q13185	CBX3 Chromobox protein homolog 3	CBX3	R.LTWHSC*PEDEAQ.-	1.0	1.1	1.0	2.3	2.0	2.4	2.6	2.6	2.4	ns
140	P49327	FASN Fatty acid synthase	FASN	R.LSIPTYGLQC*TR.A	1.0	0.9	1.0	1.8	2.1	3.0	2.3	2.7	2.4	ns
141	Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.GVPGAIVNVSSQC*SQR.A	1.0	1.0	1.0	2.1	2.1	2.9	2.3	2.4	2.4	ns
142	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	R.AQC*ETLSPDGLPEEQPQTTK.L	1.1	1.1	1.1	1.7	1.8	3.6	2.4	2.3	2.4	ns
143	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	K.VDENFDC*VEADDVEGK.I	1.0	1.1	1.0	2.1	2.2	2.5	2.4	2.2	2.3	ns
144	P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	K.ARDC*LIPMGITSENVAER.F	1.1	0.8	0.9	1.8	1.9	2.7	2.1	2.9	2.3	ns
145	P62857	RPS28 40S ribosomal protein S28	RPS28	R.TGSQGQC*TQVR.V	1.1	1.0	1.1	1.9	2.3	2.9	2.0	2.3	2.3	ns
146	Q8NBF2	NHLRC2 NHL repeat-containing protein 2	NHLRC2	K.AILFSQPLQITDTQQGC*IAPVELR.Y	1.1	1.0	1.0	1.9	2.2	2.6	2.3	2.4	2.3	ns
147	P00338	LDHA L-lactate dehydrogenase A chain	LDHA	R.VIGSGC*NLDSAR.F	1.1	1.0	1.0	1.8	1.8	2.7	2.6	2.4	2.2	ns
148	Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	R.NPVSQC*MR.G	1.1	1.0	1.1	2.0	2.1	2.1	2.5	2.6	2.2	ns
149	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.LVVPASQC*GSLIGK.G	0.9	0.9	0.9	2.0	2.2	2.5	2.3	2.2	2.2	ns
150	Q5MNZ6	WDR45L WD repeat domain phosphoinositide-interacting prot	WDR45L	R.C*NYLALVGGGK.K	1.0	1.0	1.0	1.9	2.2	2.4	2.4	2.2	2.2	ns
151	Q7Z2W4	ZC3HAV1 Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	K.NSNVDSSYLESLYQSC*PR.G	1.0	1.1	1.0	2.1	2.5	2.7	1.8	1.9	2.2	ns
152	O75153	KIAA0664 Clustered mitochondria protein homolog	KIAA0664	K.C*LTQQAVALQR.T	1.0	1.4	1.2	1.6	1.8	3.3	1.8	2.3	2.2	ns
153	H3BQZ7	Uncharacterized protein	Uncharacterized	R.NFILDQC*NVYNSGQR.R	1.1	0.9	1.0	1.7	1.9	2.7	2.2	2.2	2.2	ns
154	Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.AVTNHSVYC*STK.G	1.0	0.9	0.9	1.9	2.1	2.4	1.9	2.4	2.1	ns
155	Q9NR33	POLE4 DNA polymerase epsilon subunit 4	POLE4	K.DAYC*CAQQGK.R	0.8	0.9	0.8	3.6	1.8	1.6	1.4	2.2	2.1	ns

156	Q9BSU1	C16orf70 UPF0183 protein C16orf70	C16orf70	R.LLAAGC*GPGLLADAK.M	1.0	0.9	1.0	1.8	2.0	2.8	1.8	2.1	2.1	ns
157	Q15208	STK38 Serine/threonine-protein kinase 38	STK38	K.LSDFGLC*TGLK.K	1.1	0.8	1.0	2.0	2.1	2.5	1.9	1.9	2.1	ns
158	P55263	ADK Adenosine kinase	ADK	R.SLIANLAAANC*YK.K	1.0	0.9	0.9	1.8	1.7	3.0	2.1	1.7	2.1	ns
159	Q96SW2	CRBN Protein cereblon	CRBN	K.VQILPEC*VLPSTMSAVQLESLNK.C	0.9	1.2	1.0	2.0	1.8	2.6	1.9	2.1	2.1	ns
160	Q96P48	ARAP1 Arf-GAP with Rho-GAP domain, ANK repeat and PH dom	ARAP1	R.AVFPEGPC*EEPLQLR.K	1.0	0.9	0.9	1.7	1.9	2.6	2.1	2.0	2.1	ns
161	Q8N2W9	PIAS4 E3 SUMO-protein ligase PIAS4	PIAS4	R.VSLIC*PLVK.M	0.9	0.9	0.9	2.0	1.9	1.8	2.4	2.1	2.1	ns
162	O15294	OGT UDP-N-acetylglucosamine--peptide N-acetylglucosami	OGT	K.VMAEANHFIDLSQIPC*NGK.A	1.1	1.1	1.1	1.6	1.9	2.5	2.1	2.1	2.1	ns
163	P23528	CFL1 Cofilin-1	CFL1	K.HELQANC*YEEVK.D	1.1	1.1	1.1	1.7	1.9	2.5	2.2	1.9	2.0	ns
164	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.TLTSC*FLSCVVCVEGIVTK.C	1.2	0.9	1.0	2.2	1.6	2.7	2.2	1.5	2.0	ns
165	B5ME19	EIF3CL Eukaryotic translation initiation factor 3 subunit	EIF3CL	R.GC*ILTLVER.M	1.0	1.0	1.0	2.0	2.1	2.8	2.3	1.0	2.0	ns
166	P30281	CCND3 G1/S-specific cyclin-D3	CCND3	R.ASYFQC*VQR.E	1.1	1.0	1.0	1.8	1.9	2.4	2.2	1.9	2.0	ns
167	Q14318	FKBP8 Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8	K.C*LNNLAASQLK.L	1.1	1.0	1.0	1.9	1.8	2.3	1.7	2.4	2.0	ns
168	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	K.LEVDAIVNAANSSLLGGGGVDGC*IHR.A	1.1	0.9	1.0	1.8	1.9	2.3	2.1	2.1	2.0	ns
169	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	R.LFC*VGFTK.K	0.9	0.9	0.9	1.7	1.6	2.3	2.2	2.3	2.0	ns
170	P41250	GARS Glycine--tRNA ligase	GARS	R.SC*YDLSCHAR.A	1.1	0.9	1.0	1.8	2.3	2.9	1.5	1.6	2.0	ns
171	Q9Y6C9	MTCH2 Mitochondrial carrier homolog 2	MTCH2	K.YC*GLCDSIITIYR.E	0.9	0.8	0.8	2.0	2.0	2.6	1.8	1.5	2.0	ns
172	Q86YH6	PDSS2 Decaprenyl-diphosphate synthase subunit 2	PDSS2	R.C*LLSDELSNIAMQVR.K	1.2	1.1	1.2	2.1	1.9	2.1	2.0	1.8	2.0	ns
173	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	K.LQGATC*NNNK.L	1.0	0.9	0.9	1.4	2.3	2.3	1.1	2.8	2.0	ns
174	P45984	MAPK9 Mitogen-activated protein kinase 9	MAPK9	R.TAC*TNFMMTPYVVTR.Y	1.1	1.0	1.0	1.9	1.8	2.3	1.9	2.0	2.0	ns
175	O00233	PSMD9 26S proteasome non-ATPase regulatory subunit 9	PSMD9	K.GIGMNEPLVDC*EGYPR.S	1.5	0.8	1.2	1.8	1.8	2.1	1.9	2.2	1.9	ns
176	P45880	VDAC2 Voltage-dependent anion-selective channel protein	VDAC2	K.SC*SGVEFSTSGSSNTDTGK.V	1.0	1.0	1.0	1.9	2.1	1.8	1.9	2.0	1.9	ns
177	O15355	PPM1G Protein phosphatase 1G	PPM1G	R.GTEAGQVGEPGIPTGEAGPSC*SSASDK.L	1.1	0.8	1.0	1.6	1.9	2.3	1.8	2.1	1.9	ns
178	Q9HA64	FN3KRP Ketosamine-3-kinase	FN3KRP	R.ATGHSGGGC*ISQGR.S	1.0	0.9	1.0	1.6	1.9	2.1	1.6	2.3	1.9	ns
179	Q99873	PRMT1 Protein arginine N-methyltransferase 1	PRMT1	K.VIGIEC*SSISDYAVK.I	1.0	0.9	1.0	1.7	1.7	2.3	1.8	1.9	1.9	ns
180	P26599	PTBP1 Polypyrimidine tract-binding protein 1	PTBP1	K.LSLDGQNIYNAC*CTLR.I	1.1	1.0	1.1	1.4	1.3	3.7	1.5	1.6	1.9	ns
181	Q9UHD8	SEPT9 Septin-9	40794	R.SQEATEAAPSC*VGDMADTPR.D	1.1	1.2	1.1	1.6	1.6	2.5	1.7	2.1	1.9	ns
182	Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	R.LSTLC*PSAVLQR.L	1.0	0.9	1.0	1.7	1.6	3.0	0.9	2.4	1.9	ns
183	Q9NZZ3	CHMP5 Charged multivesicular body protein 5	CHMP5	K.APPPSLTDC*IGTVDSR.A	1.1	1.0	1.0	1.7	1.6	2.3	1.9	1.9	1.9	ns

184	Q9NY27	PPP4R2 Serine/threonine-protein phosphatase 4 regulatory	PPP4R2	K.EVC*PVLDQFLCHVAK.T	1.1	1.0	1.0	1.6	1.4	2.5	1.5	2.3	1.9	ns
185	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.TIIPLISQC*TPK.V	0.9	0.9	0.9	1.8	1.7	2.2	1.6	2.0	1.9	ns
186	P60981	DSTN Destrin	DSTN	K.C*STPEEIKK.R	1.1	1.0	1.0	1.5	1.6	2.1	1.8	2.1	1.8	ns
187	P13639	EEF2 Elongation factor 2	EEF2	K.STLTDSLVC*K.A	1.2	1.0	1.1	1.5	1.5	2.5	1.7	1.9	1.8	ns
188	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.INISEGNC*PER.I	1.0	1.0	1.0	1.4	1.7	2.3	1.8	1.8	1.8	ns
189	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	R.ISASC*QHPTAFEEAIPK.S	1.0	1.0	1.0	1.7	1.7	2.3	1.7	1.7	1.8	ns
190	P60981	DSTN Destrin	DSTN	K.LGGSLIVAFEGC*PV.-	1.1	0.9	1.0	1.5	1.7	2.2	1.7	1.9	1.8	ns
191	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	R.NDTPC*GTTIGPILASR.L	1.0	1.3	1.1	1.5	1.8	2.2	1.5	2.1	1.8	ns
192	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.GLPFGC*SK.E	1.1	1.1	1.1	1.5	1.5	1.6	2.2	2.1	1.8	ns
193	P37235	HPCAL1 Hippocalcin-like protein 1	HPCAL1	R.LLQC*DPSSASQF.-	1.1	1.0	1.0	1.5	1.6	1.7	2.3	1.7	1.8	ns
194	Q00610	CLTC Clathrin heavy chain 1	CLTC	R.IHEGC*EEPATHNALAK.I	1.0	1.2	1.1	1.6	1.7	1.8	1.9	1.8	1.8	ns
195	P49327	FASN Fatty acid synthase	FASN	K.LTPGC*EAEAETEAICFFVQQFTDMEHNR.V	1.1	1.1	1.1	1.4	1.5	2.5	1.9	1.6	1.8	ns
196	Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	K.NC*IGDFLK.T	1.0	1.0	1.0	1.4	1.6	2.3	1.9	1.7	1.8	ns
197	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.SQETEC*TYFSTPLLLGK.K	0.9	1.1	1.0	1.6	1.5	2.2	1.6	1.9	1.8	ns
198	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK.G	1.1	1.0	1.1	1.6	1.6	2.0	1.8	1.8	1.8	ns
199	Q7L5D6	GET4 Golgi to ER traffic protein 4 homolog	GET4	K.EQNYC*ESR.Y	1.1	1.0	1.0	1.5	1.7	2.0	1.7	1.8	1.8	ns
200	Q9H1B7	IRF2BPL Interferon regulatory factor 2-binding protein-lik	IRF2BPL	R.AHGC*FQDGR.S	1.1	1.0	1.0	1.7	1.7	1.9	1.5	1.9	1.7	ns
201	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.LVVPATQC*GSLIGK.G	1.0	1.0	1.0	1.5	1.7	2.1	1.8	1.7	1.7	ns
202	Q9Y296	TRAPPC4 Trafficking protein particle complex subunit 4	TRAPPC4	R.C*ELFDQNLK.L	1.2	0.9	1.1	1.6	1.8	2.0	1.8	1.4	1.7	ns
203	O94906	PRPF6 Pre-mRNA-processing factor 6	PRPF6	R.AAQDLC*EEALR.H	1.0	1.1	1.1	1.4	1.6	2.0	0.0	0.0	1.7	ns
204	Q68CP9	ARID2 AT-rich interactive domain-containing protein 2	ARID2	R.SC*SNAAFALK.Q	0.9	1.1	1.0	1.4	1.6	1.8	1.8	1.8	1.7	ns
205	Q9UI30	TRMT112 tRNA methyltransferase 112 homolog	TRMT112	R.IC*PVEFNPNFVAR.M	1.0	0.9	1.0	1.3	1.4	2.0	1.7	2.0	1.7	ns
206	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	R.GQAGGGGPGTGPGLGEAGSLATC*ELPLAK.S	1.1	1.0	1.1	1.5	1.5	2.0	1.8	1.6	1.7	ns
207	P16455	MGMT Methylated-DNA--protein-cysteine methyltransferase	MGMT	R.VVC*SSGAVGNYSGGLAVK.E	0.9	0.9	0.9	1.6	1.6	1.9	1.7	1.6	1.7	ns
208	O43684	BUB3 Mitotic checkpoint protein BUB3	BUB3	R.TPC*NAGTFSQPEK.V	1.0	1.0	1.0	1.3	1.4	1.9	1.8	2.0	1.7	ns
209	P62826	RAN GTP-binding nuclear protein Ran	RAN	R.VC*ENIPIVLCGNK.V	0.8	0.8	0.8	1.3	1.6	2.0	1.6	2.0	1.7	ns

210	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.LSSC*DSFTSTINELNHCLSLR.T	0.9	1.1	1.0	1.4	1.5	1.8	1.5	2.1	1.7	ns
211	P49721	PSMB2 Proteasome subunit beta type-2	PSMB2	R.NLADC*LR.S	1.0	0.9	1.0	1.5	1.5	2.0	1.6	1.7	1.7	ns
212	Q9Y277	VDAC3 Voltage-dependent anion-selective channel protein	VDAC3	K.VC*NYGLTFTQK.W	1.0	1.0	1.0	1.3	1.7	2.0	1.5	1.8	1.6	ns
213	Q9P258	RCC2 Protein RCC2	RCC2	K.AVQDLC*GWR.I	1.1	1.0	1.1	1.3	1.5	2.2	1.6	1.7	1.6	ns
214	P49327	FASN Fatty acid synthase	FASN	K.ADEASELAC*PTPK.E	1.0	1.1	1.1	1.3	1.8	2.0	1.8	1.4	1.6	ns
215	P36507	MAP2K2 Dual specificity mitogen-activated protein kinase	MAP2K2	K.LC*DFGVSGQLIDSMANSFVGTR.S	0.9	0.9	0.9	1.5	1.5	2.0	1.5	1.8	1.6	ns
216	Q9Y3P9	RABGAP1 Rab GTPase-activating protein 1	RABGAP1	K.LTYLGC*ASVNAPR.S	1.0	0.9	0.9	1.3	1.6	2.0	1.9	1.4	1.6	ns
217	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVDVEVPDVELEC*PDAK.L	1.4	0.9	1.2	1.4	1.5	1.9	1.6	1.8	1.6	ns
218	Q06203	PPAT Amidophosphoribosyltransferase	PPAT	K.C*ELENCQPFVVETLHGK.I	1.1	0.9	1.0	1.4	1.5	1.9	1.7	1.6	1.6	ns
219	P07741	APRT Adenine phosphoribosyltransferase	APRT	R.VVVVDDLLATGGTMNAAC*ELLGR.L	0.9	0.9	0.9	1.5	1.4	2.2	1.6	1.5	1.6	ns
220	Q15120	PDK3	PDK3	K.HIGSIDPTC*NVADVVK.D	0.9	0.9	0.9	1.5	1.5	1.9	1.5	1.6	1.6	ns
221	H3BQZ7	Uncharacterized protein	Uncharacterized	K.EGC*TEVSLLR.V	1.0	1.0	1.0	1.4	1.5	2.0	1.6	1.7	1.6	ns
222	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.ALNALC*DGLIDELNQALK.T	1.0	1.0	1.0	1.5	1.5	2.0	1.5	1.6	1.6	ns
223	Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	R.AITIAGIPQSIIEC*VK.Q	0.9	0.9	0.9	1.5	1.4	1.9	1.5	1.8	1.6	ns
224	P60604	UBE2G2 Ubiquitin-conjugating enzyme E2 G2	UBE2G2	R.VC*ISILHAPGDDPMGYESSAER.W	1.1	0.8	1.0	1.4	1.3	2.3	1.5	1.6	1.6	ns
225	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	K.AAREEC*PVFTPPGGETLDQVK.M	1.0	1.1	1.1	1.3	1.4	1.8	1.7	1.8	1.6	ns
226	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.LFQEC*CPHSTDR.V	0.9	0.9	0.9	1.3	1.4	2.1	1.5	1.6	1.6	ns
227	P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	R.GC*AVVEFK.M	1.1	1.0	1.0	1.4	1.3	2.2	1.5	1.6	1.6	ns
228	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	K.YAGLSTC*FR.Q	1.6	1.0	1.3	1.3	1.9	1.9	1.4	1.5	1.6	ns
229	P62306	SNRPF Small nuclear ribonucleoprotein F	SNRPF	R.C*NNVLYIR.G	1.0	1.0	1.0	1.4	1.5	1.9	1.5	1.6	1.6	ns
230	P21291	CSRP1 Cysteine and glycine-rich protein 1	CSRP1	K.SCFLCMVC*K.K	0.8	1.0	0.9	1.3	1.5	2.1	1.4	1.6	1.6	ns
231	P51858	HDGF Hepatoma-derived growth factor	HDGF	K.C*GDLVFAK.M	1.0	1.0	1.0	1.4	1.3	2.2	1.4	1.6	1.6	ns
232	P30519	HMOX2 Heme oxygenase 2	HMOX2	K.CPFYAAEQDKGALEGSSC*PFR.T	1.3	1.0	1.1	1.1	1.9	2.0	1.2	1.7	1.6	ns
233	Q96Q11	TRNT1 CCA tRNA nucleotidyltransferase 1, mitochondrial	TRNT1	K.YQGEHC*LLK.E	1.0	1.0	1.0	1.3	1.4	1.9	1.4	1.9	1.6	ns
234	P49458	SRP9 Signal recognition particle 9 kDa protein	SRP9	K.VTDDLVC*LVYK.T	0.8	1.0	0.9	1.5	1.3	1.9	1.4	1.7	1.6	ns
235	Q6P1X6	C8orf82 UPF0598 protein C8orf82	C8orf82	R.YEAAFPFLSPC*GR.E	1.1	1.0	1.1	1.4	1.4	1.8	1.7	1.5	1.6	ns
236	A6NDG6	PGP Phosphoglycolate phosphatase	PGP	K.NNQESDC*VSK.K	1.4	0.9	1.1	1.5	1.4	1.8	1.6	1.6	1.6	ns

237	Q15019	SEPT2 Septin-2	40787	R.LTVVDTPGYGDAINC*R.D	1.0	1.0	1.0	1.3	1.4	2.1	1.6	1.4	1.6	ns
238	Q04760	GLO1 Lactoylglutathione lyase	GLO1	K.C*DFPIMK.F	0.9	1.2	1.0	1.4	1.3	1.9	1.5	1.6	1.6	ns
239	O14980	XPO1 Exportin-1	XPO1	K.LDINLLDNVVNC*LYHGEGAQQR.M	1.1	1.0	1.1	1.4	1.5	1.8	1.6	1.5	1.5	ns
240	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVGVEVPDVELEC*PDAK.L	0.9	1.1	1.0	1.6	1.4	1.8	1.5	1.5	1.5	ns
241	Q6QNY0	BLOC1S3 Biogenesis of lysosome-related organelles complex	BLOC1S3	R.GDLC*ALAER.L	0.7	0.9	0.8	1.6	1.1	1.8	1.4	1.8	1.5	ns
242	P51610	HCFC1 Host cell factor 1	HCFC1	K.LVIYGGMSGC*R.L	1.1	1.0	1.0	1.3	1.4	2.0	1.5	1.5	1.5	ns
243	F5H284	PPIAL4D Peptidyl-prolyl cis-trans isomerase	PPIAL4D	R.IIPGFMC*QGGDFTR.H	0.8	1.1	0.9	1.0	1.1	1.4	3.1	1.2	1.5	ns
244	O43795	MYO1B Unconventional myosin-Ib	MYO1B	K.LVMSYVAAVC*GK.G	1.0	0.8	0.9	1.4	1.1	1.9	1.6	1.7	1.5	ns
245	Q96I99	SUCLG2 Succinyl-CoA ligase	SUCLG2	R.SC*NGPVLVGSPQGGVDIEEVAASNPELIFK.E	0.8	0.9	0.8	1.4	1.4	1.4	1.9	1.7	1.5	ns
246	P49915	GMPS GMP synthase	GMPS	K.AC*TTEEDQEK.L	1.0	1.1	1.0	1.2	1.3	2.1	1.6	1.5	1.5	ns
247	P11413	G6PD Glucose-6-phosphate 1-dehydrogenase	G6PD	R.TQVC*GILR.E	1.0	0.9	0.9	1.3	1.2	1.8	1.7	1.6	1.5	ns
248	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	R.VFIMDSC*DELIPEYLNFIR.G	1.1	0.9	1.0	1.4	1.5	1.7	1.5	1.5	1.5	ns
249	P07737	PFN1 Profilin-1	PFN1	K.C*YEMASHLR.R	0.9	0.9	0.9	1.4	1.2	1.8	1.3	1.9	1.5	ns
250	P47756	CAPZB F-actin-capping protein subunit beta	CAPZB	R.QMEKDETVSDC*SPHIANIGR.L	1.1	1.1	1.1	1.3	1.2	2.0	1.5	1.6	1.5	ns
251	Q9C0C9	UBE2O Ubiquitin-conjugating enzyme E2 O	UBE2O	R.C*YNEMALIR.V	1.1	1.1	1.1	1.5	1.2	1.8	1.6	1.5	1.5	ns
252	A0AVT1	UBA6 Ubiquitin-like modifier-activating enzyme 6	UBA6	R.KPNVGC*QQDSEELLK.L	1.0	0.9	1.0	1.4	1.4	1.8	1.5	1.5	1.5	ns
253	P49189	ALDH9A1 4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	K.GALMANFLTQGQVC*CNGTR.V	1.0	0.8	0.9	1.6	1.4	1.8	1.2	1.5	1.5	ns
254	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	K.C*PTSGR.L	1.0	0.9	1.0	1.3	1.4	1.8	1.4	1.5	1.5	ns
255	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	K.HLNEIDLFHC*IDPNDSK.H	1.1	1.0	1.0	1.3	1.4	1.8	1.6	1.5	1.5	ns
256	Q9UPM8	AP4E1 AP-4 complex subunit epsilon-1	AP4E1	R.SSC*STLPDYLLYQCQK.V	0.9	0.6	0.8	1.4	1.5	1.8	1.3	1.5	1.5	ns
257	P35270	SPR Sepiapterin reductase	SPR	R.TVVNISSLC*ALQPFK.G	1.0	0.9	0.9	1.3	1.3	1.9	1.6	1.5	1.5	ns
258	Q6IA69	NADSYN1 Glutamine-dependent NAD(+) synthetase	NADSYN1	K.NSSQETC*TR.A	1.0	0.9	1.0	1.3	1.3	1.7	1.5	1.6	1.5	ns
259	O75874	IDH1 Isocitrate dehydrogenase	IDH1	K.SEGGFIWAC*K.N	1.1	1.0	1.1	1.4	1.5	1.6	1.4	1.5	1.5	ns
260	P53396	ACLY ATP-citrate synthase	ACLY	K.FIC*TTSAIQNR.F	1.1	1.2	1.1	1.4	1.4	1.7	1.5	1.4	1.5	ns
261	P30153	PPP2R1A Serine/threonine-protein phosphatase 2A 65 kDa reg	PPP2R1A	R.LNIISNLDC*VNEVIGIR.Q	1.0	0.9	1.0	1.6	1.4	1.5	1.4	1.6	1.5	ns
262	P26641	EEF1G Elongation factor 1-gamma	EEF1G	K.AAAPAPEEEMDEC*EQALAAEPK.A	1.2	1.1	1.1	1.4	1.3	1.8	1.5	1.5	1.5	ns
263	P49327	FASN Fatty acid synthase	FASN	K.AINC*ATSGVVGLVNCLR.R	1.0	0.9	0.9	1.3	1.4	1.8	1.5	1.5	1.5	ns
264	P60763	RAC3 Ras-related C3 botulinum toxin substrate 3	RAC3	R.AVLC*PPPVK.K	1.1	1.0	1.0	1.3	1.3	1.9	1.5	1.4	1.5	ns
265	P13639	EEF2 Elongation factor 2	EEF2	K.IWC*FGPDGTGPNILTDITK.G	1.0	1.0	1.0	1.3	1.4	1.6	1.4	1.7	1.5	ns

266	Q9NZL4	HSPBP1 Hsp70-binding protein 1	HSPBP1	R.LLDRDAC*DTVR.V	1.1	0.9	1.0	1.3	1.2	2.0	1.5	1.4	1.5	ns
267	P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	K.LC*FSTAQHAS.-	0.8	1.0	0.9	1.3	1.7	1.3	1.5	1.6	1.5	ns
268	Q9NQC3	RTN4 Reticulon-4	RTN4	K.YSNSALGHVNC*TIK.E	1.1	1.1	1.1	1.3	1.5	1.9	1.3	1.4	1.5	ns
269	P04632	CAPNS1 Calpain small subunit 1	CAPNS1	R.YSDESGNMDFDNFISC*LVR.L	1.0	1.0	1.0	1.4	1.4	1.8	1.4	1.5	1.5	ns
270	Q93052	LPP Lipoma-preferred partner	LPP	K.TYITDPVSAPC*APPLQPK.G	1.1	1.0	1.1	1.2	1.4	1.7	1.5	1.5	1.5	ns
271	Q96RS6	NUDCD1 NudC domain-containing protein 1	NUDCD1	R.DSAQC*AAIAER.L	1.2	0.9	1.0	1.2	1.4	1.9	1.4	1.5	1.5	ns
272	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	R.LDFVC*SFLQK.N	1.0	0.8	0.9	1.2	1.2	1.7	1.6	1.7	1.5	ns
273	Q9H3U1	UNC45A Protein unc-45 homolog A	UNC45A	R.AIQTVSC*LLQGPCDAGNR.A	0.9	1.1	1.0	1.4	1.3	1.7	1.3	1.6	1.5	ns
274	P13489	RNH1 Ribonuclease inhibitor	RNH1	R.ELDLSNNC*LGDAGILQLVESVR.Q	1.4	0.8	1.1	1.3	1.5	1.6	1.4	1.5	1.5	ns
275	P22626	HNRNPA2B1 Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	K.LTDC*VVMRDPASK.R	1.1	0.9	1.0	1.3	1.3	1.6	1.5	1.6	1.5	ns
276	P53602	MVD Diphosphomevalonate decarboxylase	MVD	R.DGDPLPSSLSC*K.V	1.2	1.1	1.2	1.7	1.2	1.6	1.4	1.4	1.5	ns
277	O14964	HGS Hepatocyte growth factor-regulated tyrosine kinase	HGS	R.AC*GQIFCGK.C	1.1	1.0	1.1	1.6	1.2	1.8	1.5	1.2	1.5	ns
278	P78347	GTF2I General transcription factor II-I	GTF2I	R.SILSPGGSC*GPIK.V	1.0	1.0	1.0	1.3	1.6	1.7	1.4	1.4	1.5	ns
279	Q9NYL2	MLTK Mitogen-activated protein kinase kinase kinase MLT	MLTK	K.IC*DFGASR.F	1.0	1.0	1.0	1.6	1.1	1.8	1.2	1.6	1.5	ns
280	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	R.GQPC*SQNYR.L	1.1	1.1	1.1	1.2	1.2	1.7	1.5	1.6	1.4	ns
281	P52895	AKR1C2 Aldo-keto reductase family 1 member C2	AKR1C2	R.EEPWVDPNSPVLLEDPVLC*ALAK.K	0.9	1.1	1.0	1.3	1.4	1.6	1.5	1.5	1.4	ns
282	Q15459	SF3A1 Splicing factor 3A subunit 1	SF3A1	R.EVLDQVC*YR.V	0.9	1.1	1.0	1.3	1.1	1.6	2.0	1.3	1.4	ns
283	Q8NFR3	SPTSSB Serine palmitoyltransferase small subunit B	SPTSSB	K.IC*GYHSTISN.-	1.1	1.0	1.0	1.4	1.4	1.7	1.3	1.4	1.4	ns
284	P60981	DSTN Destrin	DSTN	K.HEC*QANGPEDLNR.A	0.9	0.9	0.9	1.3	1.2	1.5	1.4	1.8	1.4	ns
285	P04183	TK1 Thymidine kinase, cytosolic	TK1	R.NTMEALPAC*LLR.D	1.0	0.8	0.9	1.5	1.1	1.9	1.2	0.0	1.4	ns
286	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.AITIAGVPQSVTEC*VK.Q	1.0	0.8	0.9	1.3	1.2	1.9	1.2	1.6	1.4	ns
287	O15355	PPM1G Protein phosphatase 1G	PPM1G	K.C*SGDGVGAPR.L	0.9	0.9	0.9	1.2	1.3	1.8	1.5	1.5	1.4	ns
288	P21333	FLNA Filamin-A	FLNA	K.AHVVPC*FDASK.V	1.1	1.1	1.1	1.2	1.3	1.8	1.3	1.5	1.4	ns
289	Q7L2H7	EIF3M Eukaryotic translation initiation factor 3 subunit	EIF3M	K.VAASC*GAIQYIPTELDQVR.K	1.1	1.0	1.0	1.1	1.5	1.6	1.4	1.5	1.4	ns
290	O95861	BPNT1 3(2),5-bisphosphate nucleotidase 1	BPNT1	K.TC*ATDLQTK.A	1.0	0.9	0.9	1.2	1.4	1.8	1.3	1.3	1.4	ns
291	Q96EY8	MMAB Cob(I)yrinic acid a,c-diamide adenosyltransferase,	MMAB	K.IQCTLQDVGSALATPC*SSAR.E	1.1	1.0	1.0	1.1	1.4	1.7	1.5	1.4	1.4	ns
292	P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	K.GFGFVC*FSSPEEATK.A	1.1	1.0	1.0	1.2	1.3	1.7	1.2	1.6	1.4	ns
293	Q92879	CELF1 CUGBP Elav-like family member 1	CELF1	R.GC*AFVTFTTR.A	1.0	1.0	1.0	1.3	1.4	1.6	1.5	1.3	1.4	ns

294	P13639	EEF2 Elongation factor 2	EEF2	R.TFC*QLILDPIFK.V	0.9	0.8	0.9	1.1	1.3	1.9	1.2	1.5	1.4	ns
295	O43765	SGTA Small glutamine-rich tetratricopeptide repeat-cont	SGTA	R.AIC*IDPAYSK.A	0.9	1.1	1.0	1.4	1.3	1.4	1.5	1.3	1.4	ns
296	P38646	HSPA9 Stress-70 protein, mitochondrial	HSPA9	K.AKC*ELSSSVQTDINLPYLTMDSSGPK.H	1.2	1.1	1.2	1.1	1.3	1.6	1.5	1.5	1.4	ns
297	Q9Y508	RNF114 RING finger protein 114	RNF114	R.DC*GGAAQLAGPAAEADPLGR.F	1.0	1.0	1.0	1.2	1.4	1.7	1.4	1.3	1.4	ns
298	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.YLAEVAC*GDDR.K	0.9	1.0	0.9	1.3	1.0	1.4	1.6	1.7	1.4	ns
299	P22061	PCMT1 Protein-L-isoaspartate(D-aspartate) O-methyltransf	PCMT1	K.ALDVGSGSGILTAC*FAR.M	0.9	1.0	0.9	1.7	1.2	1.6	1.1	1.4	1.4	ns
300	Q7L1Q6	BZW1 Basic leucine zipper and W2 domain-containing prot	BZW1	K.ERFDPTQFQDC*IIQGLTETGTDLEAVAK.F	1.3	1.0	1.2	1.3	1.3	1.6	1.3	1.4	1.4	ns
301	P20073	ANXA7 Annexin A7	ANXA7	R.LGTDESC*FNMILATR.S	1.0	1.0	1.0	1.2	1.4	1.5	1.4	1.4	1.4	ns
302	P00390	GSR Glutathione reductase, mitochondrial	GSR	K.LGGTC*VNVGCVPK.K	1.0	1.0	1.0	1.2	1.3	1.5	1.4	1.4	1.4	ns
303	O43390	HNRNPR Heterogeneous nuclear ribonucleoprotein R	HNRNPR	K.SAFLC*GVMK.T	1.0	0.8	0.9	1.2	1.2	1.4	1.4	1.6	1.4	ns
304	P10768	ESD S-formylglutathione hydrolase	ESD	K.AETGKCPALYWLSGLTC*TEQNFISK.S	0.9	0.9	0.9	1.1	1.2	1.5	1.5	1.5	1.4	ns
305	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	K.FIC*EQDHQNFLR.L	1.1	0.9	1.0	1.2	1.2	1.5	1.5	1.4	1.4	ns
306	Q9Y3D0	FAM96B Mitotic spindle-associated MMXD complex subunit MI	FAM96B	R.VAAALENTHLLEVVNQC*LSAR.S	0.9	0.9	0.9	1.3	1.5	1.3	1.3	1.5	1.4	ns
307	P55212	CASP6 Caspase-6	CASP6	R.GTC*ADRDNLTR.R	1.4	0.9	1.1	1.1	1.2	1.5	1.6	1.5	1.4	ns
308	O75131	CPNE3 Copine-3	CPNE3	K.NC*LNPQFSK.T	1.1	1.0	1.0	1.2	1.3	1.7	1.3	1.4	1.4	ns
309	P55735	SEC13 Protein SEC13 homolog	SEC13	R.FASGGC*DNLIK.L	0.9	1.0	1.0	1.2	1.1	1.6	1.7	1.3	1.4	ns
310	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	R.YASIC*QQNGIVPIVEPEILPDGDHDLK.R	0.8	1.0	0.9	1.1	1.1	1.8	1.0	1.7	1.4	ns
311	P31947	SFN 14-3-3 protein sigma	SFN	K.GAVEKGEELSC*EER.N	1.1	1.0	1.0	1.1	1.2	1.5	1.4	1.4	1.3	ns
312	P62258	YWHAE 14-3-3 protein epsilon	YWHAE	K.LIC*CDILDVLDK.H	0.9	1.0	0.9	1.5	1.3	1.9	1.1	1.0	1.3	ns
313	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	K.LNEC*VDHTPK.L	1.0	1.2	1.1	1.3	1.1	1.7	1.3	1.3	1.3	ns
314	P31948	STIP1 Stress-induced-phosphoprotein 1	STIP1	K.ALDLDSSC*K.E	0.9	1.1	1.0	1.0	1.3	1.8	1.6	1.0	1.3	ns
315	Q9NXG2	THUMPD1 THUMP domain-containing protein 1	THUMPD1	R.C*DAGGPR.Q	1.0	1.1	1.1	1.1	1.3	1.6	1.4	1.3	1.3	ns
316	Q9Y365	STARD10 PCTP-like protein	STARD10	R.MEC*CDVPAETLYDVLHDIEYR.K	1.1	1.1	1.1	1.1	1.2	1.7	1.2	1.4	1.3	ns
317	Q9Y3A3	MOB4 MOB-like protein phocein	MOB4	R.HTLDGAAC*LLNSNK.Y	1.0	0.9	0.9	1.2	1.3	1.5	1.4	1.3	1.3	ns
318	P22314	UBA1 Ubiquitin-like modifier-activating enzyme 1	UBA1	K.SIPIC*TLK.N	1.0	1.0	1.0	1.2	1.3	1.5	1.4	1.3	1.3	ns
319	P30086	PEBP1 Phosphatidylethanolamine-binding protein 1	PEBP1	R.APVAGTC*YQAEWDDYVPK.L	0.8	0.7	0.7	1.1	1.1	1.5	1.1	1.7	1.3	ns
320	P35270	SPR Sepiapterin reductase	SPR	R.AVC*LLTGASR.G	1.0	0.8	0.9	1.2	1.2	1.5	1.3	1.4	1.3	ns
321	P55263	ADK Adenosine kinase	ADK	R.TGC*TFPEKPDFH.-	1.1	0.9	1.0	1.2	1.3	1.5	1.3	1.3	1.3	ns

322	Q86SX6	GLRX5 Glutaredoxin-related protein 5, mitochondrial	GLRX5	K.GTPEQPQC*GFSNAVVQILR.L	1.1	1.0	1.0	1.2	1.3	1.5	1.3	1.3	1.3	ns
323	Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	R.VGLGIC*YDMR.F	1.0	0.9	1.0	1.2	1.2	1.5	1.3	1.3	1.3	ns
324	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	K.C*LSVMEAK.V	1.1	1.9	1.5	1.2	1.3	1.7	1.1	1.3	1.3	ns
325	Q9Y490	TLN1 Talin-1	TLN1	K.VVAPTISSPVC*QEQLVEAGR.L	0.7	1.1	0.9	1.2	1.3	1.2	1.4	1.3	1.3	ns
326	Q9UL25	RAB21 Ras-related protein Rab-21	RAB21	K.VVLLGEGC*VGK.T	1.0	1.1	1.0	1.1	1.3	1.5	1.2	1.4	1.3	ns
327	O14966	RAB7L1 Ras-related protein Rab-7L1	RAB7L1	K.C*DLSPWAVSR.D	1.1	1.1	1.1	1.1	1.5	1.3	1.2	0.0	1.3	ns
328	Q96EY5	FAM125A Multivesicular body subunit 12A	FAM125A	K.SC*SPLAFSAFGDLTIK.S	1.1	1.1	1.1	1.1	1.1	1.6	1.2	1.4	1.3	ns
329	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	K.C*CSGAIIVLTK.S	1.1	1.0	1.0	1.1	1.1	1.6	1.2	1.3	1.3	ns
330	P14174	MIF Macrophage migration inhibitory factor	MIF	K.LLC*GLLAER.L	0.9	1.1	1.0	1.2	1.2	1.4	1.2	1.4	1.3	ns
331	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	R.GC*ITIIGGGDTATCCAK.W	1.1	0.9	1.0	1.3	1.2	1.4	1.3	1.1	1.3	ns
332	Q12765	SCRN1 Secernin-1	SCRN1	K.TQSPC*FGDDDPAKKEPR.F	0.9	0.9	0.9	1.0	1.2	1.5	1.3	1.3	1.3	ns
333	Q9Y2S2	CRYL1 Lambda-crystallin homolog	CRYL1	R.VILSSSTSC*LMPSK.L	1.2	1.1	1.2	1.2	1.1	1.5	1.3	1.2	1.3	ns
334	Q13630	TSTA3 GDP-L-fucose synthase	TSTA3	K.VVSCLSTC*IFPDK.T	0.8	0.6	0.7	1.6	1.1	1.6	0.9	1.1	1.3	ns
335	Q13526	PIN1 Peptidyl-prolyl cis-trans isomerase NIMA-interacti	PIN1	K.IKSGEEDFESLASQFSDC*SSAK.A	1.1	1.0	1.1	1.2	1.2	1.4	1.3	1.3	1.3	ns
336	O95336	PGLS 6-phosphogluconolactonase	PGLS	R.AAC*CLAGAR.A	1.0	0.9	1.0	1.2	1.2	1.4	1.2	1.2	1.2	ns
337	Q9BW61	DDA1 DET1- and DDB1-associated protein 1	DDA1	R.FHADSVC*K.A	1.0	0.9	1.0	1.1	1.3	1.5	1.1	1.2	1.2	ns
338	P60174	TPI1 Triosephosphate isomerase	TPI1	R.IIYGGSVTGATC*K.E	0.9	1.0	0.9	1.2	1.2	1.4	1.2	1.3	1.2	ns
339	P61970	NUTF2 Nuclear transport factor 2	NUTF2	K.NINDAWVC*TNDMFR.L	0.9	1.0	0.9	1.1	1.4	1.4	1.2	1.2	1.2	ns
340	P00492	HPRT1 Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	K.SYC*NDQSTGDIK.V	1.0	1.1	1.1	1.2	1.2	1.4	1.1	1.3	1.2	ns
341	P49753	ACOT2 Acyl-coenzyme A thioesterase 2, mitochondrial	ACOT2	K.SEFYANEAC*KR.L	1.1	1.1	1.1	1.2	1.2	1.3	1.1	1.4	1.2	ns
342	P51649	ALDH5A1 Succinate-semialdehyde dehydrogenase, mitochondria	ALDH5A1	R.NTGQTC*VCSNQFLVQR.G	1.0	1.0	1.0	1.1	1.2	1.5	1.0	1.2	1.2	ns
343	P50552	VASP Vasodilator-stimulated phosphoprotein	VASP	K.MQPDQQVVINC*AIVR.G	1.0	0.9	0.9	1.0	1.3	1.4	1.1	1.3	1.2	ns
344	Q9Y696	CLIC4 Chloride intracellular channel protein 4	CLIC4	K.AGSDGESIGNC*PFSQR.L	1.0	1.1	1.1	1.5	1.1	1.3	1.2	1.1	1.2	ns
345	Q04917	YWHAH 14-3-3 protein eta	YWHAH	K.ELETVC*NDVLSLLDK.F	1.2	0.6	0.9	1.1	0.9	2.0	1.1	1.1	1.2	ns
346	P11142	HSPA8 Heat shock cognate 71 kDa protein	HSPA8	K.VC*NPIITK.L	0.9	1.1	1.0	1.0	1.0	1.6	0.9	1.4	1.2	ns
347	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.IC*PVETLVEEAIQCAEK.I	1.2	0.9	1.1	1.2	1.2	1.4	1.1	1.2	1.2	ns
348	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	K.IETELRDIC*NDVLSLLEK.F	0.9	1.1	1.0	1.1	1.3	1.4	0.9	1.4	1.2	ns
349	P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	K.KITIADC*GQLE.-	0.8	1.0	0.9	1.1	1.0	1.5	1.0	1.5	1.2	ns
350	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	R.ALANSLAC*QGK.Y	0.9	1.0	1.0	1.0	1.0	1.4	1.2	1.4	1.2	ns
351	P37802	TAGLN2 Transgelin-2	TAGLN2	K.NMAC*VQR.T	1.0	1.0	1.0	1.1	1.2	1.5	1.2	1.1	1.2	ns

352	P53582	METAP1 Methionine aminopeptidase 1	METAP1	R.VCETDGC*SSEAK.L	1.0	1.0	1.0	1.4	1.1	1.2	1.2	1.2	1.2	ns
353	P25398	RPS12 40S ribosomal protein S12	RPS12	R.QAHLC*VLASNCDEPMYVK.L	1.0	1.2	1.1	1.0	1.2	1.4	1.2	1.2	1.2	ns
354	H3BU86	STX16-NPEPL1 Protein STX16-NPEPL1	STX16-NPEPL1	R.AC*SEQEGR.L	1.1	1.0	1.1	1.0	1.4	1.5	1.2	0.9	1.2	ns
355	P60174	TPI1 Triosephosphate isomerase	TPI1	K.IAVAAQNC*YK.V	0.9	1.1	1.0	1.1	1.1	1.5	1.0	1.2	1.2	ns
356	P09467	FBP1 Fructose-1,6-bisphosphatase 1	FBP1	R.GTGELTQLLNSLC*TAVK.A	0.9	1.0	1.0	1.2	1.1	1.5	0.9	1.2	1.2	ns
357	P37802	TAGLN2 Transgelin-2	TAGLN2	K.DGTVLC*ELINALYPEGQAPVK.K	0.9	1.0	1.0	1.1	1.2	1.3	1.0	1.2	1.2	ns
358	Q01518	CAP1 Adenylyl cyclase-associated protein 1	CAP1	R.ALLVTASQC*QQPAENK.L	0.8	1.1	0.9	1.1	1.1	1.4	1.1	1.1	1.2	ns
359	Q9Y224	C14orf166 UPF0568 protein C14orf166	C14orf166	K.LTALDYHNPAGFNC*K.D	1.0	0.9	1.0	1.0	1.1	1.4	1.2	1.2	1.2	ns
360	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	R.FC*PFAER.T	1.0	0.9	1.0	1.1	1.1	1.3	1.2	1.1	1.2	ns
361	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	R.LVSSPC*CIVTSTYGWTANMER.I	1.0	1.0	1.0	1.0	1.1	1.5	1.1	1.1	1.2	ns
362	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	K.AGSDGAKIGNC*PFSQR.L	1.1	0.9	1.0	1.1	1.1	1.3	1.1	1.2	1.2	ns
363	Q02790	FKBP4 Peptidyl-prolyl cis-trans isomerase FKBP4	FKBP4	K.TQLAVC*QQR.I	0.9	1.0	1.0	1.0	0.9	1.4	1.1	1.2	1.1	ns
364	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.NTGIIC*TIGPASR.S	0.8	0.9	0.9	0.9	1.0	1.3	1.0	1.3	1.1	ns
365	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	K.TGQATVASGIPAGWMGLDC*GPESSKK.Y	1.0	1.0	1.0	1.2	1.0	1.3	1.0	1.1	1.1	ns
366	P60174	TPI1 Triosephosphate isomerase	TPI1	K.VPADTEVVC*APPTAYIDFAR.Q	0.8	1.0	0.9	1.0	1.1	1.4	1.0	1.1	1.1	ns
367	Q04917	YWHAH 14-3-3 protein eta	YWHAH	K.NC*NDFQYESK.V	1.2	0.9	1.1	1.0	1.0	1.2	1.2	1.2	1.1	ns
368	Q9UL46	PSME2 Proteasome activator complex subunit 2	PSME2	K.C*GFLPGNEK.V	1.0	0.9	1.0	0.9	1.1	1.3	1.1	1.1	1.1	ns
369	P23528	CFL1 Cofilin-1	CFL1	K.AVLFC*LSEDKK.N	0.9	1.1	1.0	1.1	1.0	1.4	0.7	1.2	1.1	ns
370	P53582	METAP1 Methionine aminopeptidase 1	METAP1	K.LGIQGSYFCSQEC*FK.G	1.2	1.0	1.1	0.9	0.9	1.5	1.0	1.0	1.1	ns
371	P31949	S100A11 Protein S100-A11	S100A11	K.ISSPTETERC*IESLIAVFQK.Y	0.7	0.9	0.8	0.9	1.1	1.4	0.9	0.9	1.0	ns
372	Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	K.LAAQSC*ALSLVR.Q	0.8	1.1	0.9	1.0	1.2	1.0	1.1	0.9	1.0	ns
373	Q8TAQ2	SMARCC2 SWI/SNF complex subunit SMARCC2	SMARCC2	R.NLAGDVC*AIMR.V	1.0	0.9	1.0	0.9	0.9	1.2	0.9	1.0	1.0	ns
374	P30044	PRDX5 Peroxiredoxin-5, mitochondrial	PRDX5	K.ALNVEPDGTGLTC*SLAPNIISQL.-	1.1	1.1	1.1	0.8	0.9	1.2	0.9	1.0	1.0	ns
375	P33240	CSTF2 Cleavage stimulation factor subunit 2	CSTF2	K.LC*VQNSPQEAR.N	0.9	1.0	1.0	0.8	0.7	1.1	1.0	0.9	0.9	ns
376	Q14914	PTGR1 Prostaglandin reductase 1	PTGR1	R.IAIC*GAISTYNR.T	1.0	1.0	1.0	0.8	0.8	1.1	0.8	1.0	0.9	ns
377	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	K.LTFSC*LGGSDNFK.H	0.8	1.0	0.9	0.9	0.8	1.1	0.8	0.9	0.9	ns
378	P10599	TXN Thioredoxin	TXN	K.LVVVDFSATWC*GPCK.M	1.0	0.8	0.9	0.6	0.6	0.9	0.9	0.8	0.8	ns
379	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	R.VPTANVSVVDLTC*R.L	0.9	1.0	1.0	0.4	0.4	0.6	0.4	0.5	0.5	ns

Table 3A-4. R-values of cysteines (* denotes labeled cysteine) identified from transnitrosation experiments at 500 μM GSNO, 500 μM CoA-SNO, and 90 μM Trx-SNO. 756 cysteine residues identified in all transnitrosation donor-treated samples are presented together with calculated Heavy:Light ratios (R-values). Five replicates of each donor-treated experiments were performed. Each cysteine's sensitivity to GSNO, CoA-SNO and Trx-SNO were ranked by their average R-values respectively and listed in the sub-columns under " sensitivity rank". Date was sorted by the average of GSNO-treated experiments.

sensitivity rank			Uniprot #	Description	Symbol	Sequence
NO donor						
Trx-SNO	CoA-SNO	GSNO				
138	24	1	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	K.IISNASC*TTNCLAPLAK.V
468	358	2	O94906	PRPF6 Pre-mRNA-processing factor 6	PRPF6	R.AAQDLC*EEALR.H
57	25	3	P07339	CTSD Cathepsin D	CTSD	K.AIGAVPLIQGEYMIPC*EK.V
6	3	4	Q01813	PFKP 6-phosphofructokinase type C	PFKP	R.LPLMEC*VQMTQDVQK.A
7	4	5	Q92947	GCDH Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	K.GYGC*AGVSSVAYGLLAR.E
125	48	6	P07437	TUBB Tubulin beta chain	TUBB	K.LTTPTYGDLNHLVSATMSGVTTC*LR.F
349	32	7	P29590	PML Protein PML	PML	R.LQDLSSC*ITQGK.D
44	15	8	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.VMTIPYQPMPASSPVIC*AGGQDR.C
60	17	9	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.KLGNNC*VFAPADVTSEK.D
12	34	10	P28290	SSFA2 Sperm-specific antigen 2	SSFA2	R.VC*SVNPPSAIEMQLR.R
2	22	11	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	R.C*MALSTAVLVGEAK.K
361	56	12	Q04726	TLE3 Transducin-like enhancer protein 3	TLE3	K.SPISQLDC*LNR.D
254	107	13	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	R.QC*PIMDPAWEAPEGVPIDAIIFGGR.R
30	33	14	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.AYHEQLSVAEITNAC*FEPANQMVK.C
20	85	15	P62241	RPS8 40S ribosomal protein S8	RPS8	K.NC*IVLIDSTPYR.Q
250	275	16	Q02543	RPL18A 60S ribosomal protein L18a	RPL18A	R.DLTTAGAVTQC*YR.D
93	98	17	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	K.TSAPITC*ELLNK.Q
1	1	18	P31749	AKT1 RAC-alpha serine/threonine-protein kinase	AKT1	K.TFC*GTPEYLAPEVLEDNDYGR.A
203	43	19	Q9Y3E2	BOLA1 BolA-like protein 1	BOLA1	R.VC*LCQGSAGSGAIGPVEAAIR.T
41	45	20	P26440	IVD Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	K.AC*DEGHCTAK.D
33	29	21	P36578	RPL4 60S ribosomal protein L4	RPL4	R.YAIC*SALAASALPALVMSK.G
62	71	22	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	R.AVC*MLSNTTAIAEAWAR.L
666	11	23	P04183	TK1 Thymidine kinase, cytosolic	TK1	R.NTMEALPAC*LLR.D
34	113	24	Q9H9P8	L2HGDH L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	K.AC*FLGATVK.Y
264	106	25	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.GC*DVVVIPAGVPR.K
74	94	26	P50213	IDH3A Isocitrate dehydrogenase	IDH3A	R.IEAAC*FATIK.D
88	10	27	Q8TCU6	PREX1 Phosphatidylinositol 3,4,5-trisphosphate-dependent	PREX1	R.LC*VLNEILGTER.D
526	180	28	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	R.VGAFTMVC*K.D
55	28	29	P04183	TK1 Thymidine kinase, cytosolic	TK1	R.YSSSFC*THDR.N
26	66	30	O14733	MAP2K7 Dual specificity mitogen-activated protein kinase	MAP2K7	R.SAGC*AAYMAPER.I
265	263	31	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	K.YTVQDESHSEWVSC*VR.F
47	46	32	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.NMITGTAPLDGC*ILVVAANDGPMPQTR.E

Heavy : Light Ratio																		
500 µM GSNO							500 µM CoA-SNO						90 µM Trx-SNO					
1	2	3	4	5	average	1	2	3	4	5	average	1	2	3	4	5	average
5.4	4.4	4.2	5.2	5.1	4.9	6.3	5.3	6.7	7.3	6.4	6.4	3.7	3.7	4.8	4.6	4.3	4.2
4.0	5.3	3.0	4.7	4.4	4.3	5.5	1.5	1.1	0.4	1.5	2.0	1.4	0.0	0.0	1.4	2.0	1.6
3.7	3.2	4.2	4.7	3.7	3.9	8.1	6.2	5.7	7.0	4.5	6.3	5.3	7.2	7.8	6.3	7.7	6.9
4.0	3.5	3.4	4.0	3.7	3.7	11.4	10.6	9.4	10.7	9.2	10.3	13.6	12.3	12.6	13.2	12.9	12.9
4.0	3.5	3.4	4.0	3.7	3.7	11.4	10.6	9.4	10.7	9.2	10.3	13.6	12.3	12.6	13.2	12.9	12.9
3.8	3.5	3.5	4.0	3.6	3.7	5.3	5.5	5.2	5.2	4.8	5.2	4.2	4.1	5.4	4.7	4.6	4.6
1.6	3.3	3.9	0.0	5.2	3.5	3.6	4.6	0.0	9.4	0.0	5.9	1.6	0.0	0.0	1.4	2.8	1.9
3.2	3.2	3.4	4.0	3.4	3.4	0.0	7.1	7.3	8.6	6.4	7.4	6.5	7.8	9.4	0.0	7.9	7.9
3.6	3.4	3.2	3.8	3.1	3.4	5.1	7.7	7.5	7.7	7.6	7.1	5.6	5.9	7.8	6.1	7.6	6.6
0.0	3.4	3.1	3.0	3.8	3.4	5.1	5.9	5.9	6.3	5.3	5.7	12.1	11.8	0.0	11.0	0.0	11.6
3.0	3.2	2.8	4.2	3.4	3.3	7.2	6.2	7.1	6.9	5.5	6.6	14.7	17.4	0.0	13.0	15.0	15.0
4.6	3.1	2.2	3.3	3.5	3.3	5.3	0.0	4.5	6.1	4.1	5.0	1.8	1.6	2.2	2.0	1.9	1.9
3.5	3.1	3.1	3.7	3.2	3.3	4.7	3.7	3.7	3.8	3.8	4.0	2.2	2.5	2.7	2.9	2.4	2.6
3.4	3.0	3.2	3.6	3.3	3.3	6.4	5.9	5.6	6.3	5.1	5.9	8.1	8.2	10.9	8.6	8.9	8.9
2.7	3.2	3.2	3.7	3.5	3.3	4.2	4.5	4.5	4.7	4.0	4.4	7.7	10.7	11.2	9.8	9.7	9.8
3.8	3.5	2.4	4.0	2.1	3.2	2.8	2.3	3.2	2.8	1.4	2.5	1.7	0.0	2.9	2.8	3.1	2.6
3.5	3.3	2.4	3.3	3.3	3.1	5.1	4.2	5.3	1.3	5.3	4.2	4.0	4.3	0.0	5.2	8.8	5.6
3.6	2.9	2.9	3.2	2.9	3.1	8.8	11.6	14.6	11.7	8.0	10.9	18.5	18.5	18.7	19.3	18.7	18.7
2.5	3.1	3.2	3.4	3.1	3.1	5.6	5.6	4.8	5.6	4.9	5.3	2.5	3.2	3.7	2.3	3.6	3.1
3.6	2.5	2.9	2.9	3.3	3.1	0.0	5.2	4.7	0.0	5.9	5.3	7.1	8.9	0.0	8.0	0.0	8.0
0.0	2.9	2.7	3.1	3.5	3.0	7.5	6.4	5.5	5.7	5.8	6.2	6.9	0.0	9.3	0.0	9.9	8.7
3.0	2.9	2.8	3.3	3.1	3.0	4.8	4.8	4.7	4.6	4.3	4.6	5.9	6.5	7.6	6.7	6.2	6.6
3.0	2.4	3.1	3.7	2.8	3.0	7.0	8.5	8.5	7.0	8.2	7.9	1.5	1.1	1.9	0.6	1.2	1.3
2.9	4.0	2.5	2.9	2.6	3.0	3.7	3.7	3.8	4.8	3.4	3.9	7.2	7.7	0.0	7.7	11.9	8.6
3.3	2.3	3.3	3.6	2.6	3.0	3.8	4.3	3.1	3.9	5.0	4.0	1.9	2.1	4.0	0.0	2.1	2.5
4.0	2.3	2.6	2.8	2.9	2.9	4.2	4.5	4.6	4.9	3.2	4.3	6.3	9.3	2.4	7.4	0.0	6.4
2.8	2.4	2.4	3.2	3.8	2.9	9.0	8.3	4.9	8.1	9.8	8.0	5.1	4.3	7.5	6.1	0.0	5.7
3.0	2.8	2.8	3.1	2.8	2.9	3.2	2.8	2.7	3.0	3.5	3.0	1.2	1.9	1.4	1.4	1.6	1.5
2.8	2.6	2.8	3.0	3.1	2.9	0.0	7.9	6.4	5.4	5.2	6.2	5.2	7.1	8.3	8.5	6.9	7.2
2.9	2.8	2.1	2.3	4.2	2.9	4.5	3.4	3.0	7.6	4.7	4.7	4.7	0.0	0.0	14.1	9.7	9.5
2.8	2.8	2.8	3.3	2.4	2.8	3.1	2.8	2.8	1.8	2.2	2.5	2.1	2.4	2.7	2.6	2.8	2.5
2.7	2.7	2.5	3.0	3.2	2.8	5.5	4.6	5.3	5.5	5.3	5.3	6.7	7.8	9.3	6.8	7.9	7.7

3	18	33	P17858	PFKL 6-phosphofructokinase, liver type	PFKL	K.C*HDYYTTEFLYNLYSSEGK.G
76	73	34	P07437	TUBB Tubulin beta chain	TUBB	K.NMMAAC*DPR.H
9	61	35	P62280	RPS11 40S ribosomal protein S11	RPS11	R.DVQIGDIVTVGEC*RPLSK.T
23	37	36	P17858	PFKL 6-phosphofructokinase, liver type	PFKL	R.VFANAPDSAC*VIGLK.K
35	54	37	P49327	FASN Fatty acid synthase	FASN	R.LGMLSPEGTC*K.A
92	31	38	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.FGRVDVAVNC*AGIAVASK.T
80	44	39	P42677	RPS27 40S ribosomal protein S27	RPS27	K.ARLTEGC*SFR.R
18	165	40	Q9Y5M8	SRPRB Signal recognition particle receptor subunit beta	SRPRB	K.NTPSFLIAC*NK.Q
8	16	41	P07858	CTSB Cathepsin B	CTSB	R.GQDHC*GIESEVVAGIPR.T
96	67	42	P07437	TUBB Tubulin beta chain	TUBB	K.TAVC*DIPPR.G
50	88	43	P60709	ACTB Actin, cytoplasmic 1	ACTB	K.C*DVDIRK.D
4	52	44	P35250	RFC2 Replication factor C subunit 2	RFC2	K.TTSILC*LAR.A
11	104	45	P23396	RPS3 40S ribosomal protein S3	RPS3	K.GC*EVVVSGK.L
45	81	46	Q92616	GCN1L1 Translational activator GCN1	GCN1L1	R.C*GLALALNK.L
116	105	47	Q92797	SYMPK Symplekin	SYMPK	K.AVAC*SGAAQVR.I
239	77	48	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	K.LWNTLGVC*K.Y
141	93	49	P83731	RPL24 60S ribosomal protein L24	RPL24	K.VELC*SFSGYK.I
240	151	50	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	K.VQYPQSQAC*K.M
514	290	51	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	K.C*PTSGR.L
37	210	52	P50213	IDH3A Isocitrate dehydrogenase	IDH3A	K.TFDLYANVRPC*VSIEGYK.T
106	30	53	P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB2	K.AC*GDSTLTQITAGLDPVGR.I
36	95	54	LLGL2	LLGL2 Lethal(2) giant larvae protein homolog 2	LLGL2	R.SLVPYGPFPC*K.A
110	110	55	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.RSIQFVDWC*PTGFK.V
227	84	56	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	R.FSPNSSNPIIVSC*GWDK.L
186	51	57	P22102	GART Trifunctional purine biosynthetic protein adenosin	GART	R.SAGVQC*FGPTAEAAQLESSK.R
208	129	58	P49207	RPL34 60S ribosomal protein L34	RPL34	R.AYGGSMC*AK.C
223	155	59	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	K.VVVVQAISALC*QK.Y
376	148	60	P31948	STIP1 Stress-induced-phosphoprotein 1	STIP1	K.ALDLDSSC*K.E
124	244	61	P49327	FASN Fatty acid synthase	FASN	R.LLSAAC*R.L
27	76	62	P27635	RPL10 60S ribosomal protein L10	RPL10	K.MLSC*AGADR.L
161	62	63	O95833	CLIC3 Chloride intracellular channel protein 3	CLIC3	K.ASEDGESVGHC*PSC*QR.L
10	39	64	P35250	RFC2 Replication factor C subunit 2	RFC2	R.FALAC*NASDK.I
205	350	65	Q13045	FLII Protein flightless-1 homolog	FLII	R.NQLTSLPSAIC*K.L
134	192	66	O43264	ZW10 Centromere/kinetochore protein zw10 homolog	ZW10	R.LAPILC*DGTATFVDLVPGFR.R

3.0	2.7	2.5	3.0	2.8	2.8	7.7	7.8	5.9	6.7	6.6	6.9	13.3	12.3	17.5	0.0	0.0	14.4
3.0	2.6	2.6	3.0	2.8	2.8	5.1	4.8	4.5	4.5	4.2	4.6	5.5	5.9	7.6	6.5	6.2	6.3
2.9	2.5	2.6	3.1	2.7	2.8	4.9	4.8	4.4	5.1	4.2	4.7	10.9	12.7	0.0	11.4	12.9	12.0
2.8	2.6	2.8	3.2	2.4	2.8	5.6	5.9	5.6	5.5	5.2	5.6	8.3	9.6	10.2	9.8	10.3	9.6
2.7	2.6	2.7	3.0	2.7	2.7	3.9	5.8	5.1	5.4	5.1	5.0	7.3	7.7	8.4	10.1	9.0	8.5
3.3	2.4	2.7	2.8	2.5	2.7	4.7	5.5	5.7	6.8	7.1	5.9	3.6	6.6	5.5	6.7	5.6	5.6
2.8	2.6	2.6	3.2	2.4	2.7	5.8	5.8	5.0	5.0	4.8	5.3	5.2	5.9	6.3	6.6	6.0	6.0
2.6	1.4	2.7	3.4	3.3	2.7	3.7	3.5	3.5	2.0	3.1	3.2	10.3	8.6	12.2	9.9	8.8	10.0
2.9	3.1	2.4	2.5	2.5	2.7	5.4	6.7	8.1	7.8	8.6	7.3	0.0	9.9	16.0	12.5	11.5	12.5
2.7	2.6	2.5	2.9	2.7	2.7	5.0	4.7	4.3	5.2	4.1	4.7	4.9	5.0	6.5	5.4	5.4	5.4
2.5	2.6	2.6	2.9	2.6	2.7	3.8	3.9	5.0	4.9	4.2	4.4	6.1	7.4	8.8	7.3	8.0	7.5
2.5	3.4	2.2	2.6	2.5	2.6	5.1	5.8	4.4	0.0	4.9	5.1	14.8	15.4	0.0	12.6	0.0	14.3
2.3	3.1	2.9	2.2	2.7	2.6	3.9	4.8	3.0	4.3	4.6	4.1	11.8	11.4	0.0	9.6	14.2	11.8
3.2	2.1	2.3	3.1	2.5	2.6	4.1	5.2	4.9	3.9	4.2	4.4	7.0	8.4	8.0	7.2	8.1	7.7
0.0	2.5	3.1	0.0	2.3	2.6	0.0	5.3	4.5	0.0	2.5	4.1	3.1	4.8	0.0	6.6	0.0	4.8
2.9	2.1	2.7	2.8	2.6	2.6	3.7	4.8	4.8	5.2	4.4	4.6	2.2	2.3	3.1	3.0	2.8	2.7
2.7	2.5	2.1	2.6	3.2	2.6	5.2	4.2	4.0	0.0	3.8	4.3	4.2	0.0	4.5	4.1	3.8	4.1
1.9	2.3	2.7	3.6	2.6	2.6	3.9	3.6	2.8	3.1	3.1	3.3	3.3	2.1	2.5	2.3	3.1	2.7
2.6	2.5	2.5	2.6	2.8	2.6	2.2	2.6	2.5	2.4	2.3	2.4	1.3	1.4	1.8	1.4	1.5	1.5
2.7	2.1	2.4	3.0	2.8	2.6	3.9	2.8	2.8	2.4	2.4	2.9	6.2	8.4	9.3	9.8	8.7	8.5
2.6	2.2	2.7	2.8	2.6	2.6	5.0	6.7	5.7	6.7	5.9	6.0	4.4	5.9	0.0	5.3	0.0	5.2
3.0	2.4	1.8	3.0	2.5	2.5	5.1	0.0	4.7	3.4	3.7	4.3	7.6	0.0	9.5	8.8	8.1	8.5
2.5	2.4	2.4	2.9	2.5	2.5	4.4	4.1	3.8	3.9	3.5	3.9	4.6	4.8	5.2	5.2	5.3	5.0
2.6	2.3	2.5	2.8	2.4	2.5	3.5	5.1	4.5	4.9	3.9	4.4	2.6	2.5	3.1	2.9	3.0	2.8
2.6	1.5	3.0	2.6	2.9	2.5	5.3	0.0	0.0	4.6	5.4	5.1	3.8	4.6	2.8	2.1	3.3	3.3
2.5	2.3	2.5	2.9	2.3	2.5	4.1	3.4	3.2	4.1	3.2	3.6	2.8	2.6	3.3	3.6	2.8	3.0
2.6	2.6	2.1	2.9	2.4	2.5	2.9	3.2	3.7	3.2	3.3	3.3	2.3	2.6	3.9	2.5	3.1	2.9
3.2	1.9	2.5	2.4	2.4	2.5	3.8	3.1	4.2	2.8	2.9	3.3	3.8	1.3	1.8	1.3	1.0	1.8
2.6	0.0	2.5	2.6	2.3	2.5	1.9	3.0	3.0	2.9	2.7	2.7	4.1	0.0	5.3	4.4	4.7	4.6
2.4	2.2	2.5	2.9	2.5	2.5	5.6	4.8	4.4	4.2	4.1	4.6	7.6	7.6	11.9	10.1	10.1	9.4
2.4	1.8	3.6	2.4	2.2	2.5	6.3	5.3	1.8	5.4	4.6	4.7	3.2	3.0	4.8	4.2	3.6	3.7
2.7	2.8	0.0	2.8	1.7	2.5	6.9	5.2	5.7	4.7	4.8	5.5	8.2	15.4	0.0	10.6	13.4	11.9
2.2	2.4	2.4	2.9	2.5	2.5	1.9	2.5	0.0	2.0	1.8	2.0	2.2	0.0	3.5	3.3	3.2	3.0
2.5	3.7	2.1	2.1	1.9	2.5	2.8	3.6	3.0	2.8	2.5	3.0	4.1	3.5	5.9	3.9	4.5	4.4

15	57	67	P35250	RFC2 Replication factor C subunit 2	RFC2	K.VC*DEPHPLLVK.E
86	118	68	Q13748	TUBA3D Tubulin alpha-3C/D chain	TUBA3D	R.TIQFVDWC*PTGFK.V
51	75	69	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	R.LC*PNSTGAEIR.S
63	40	70	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	R.YVAAAFPSAC*GK.T
71	69	71	P36578	RPL4 60S ribosomal protein L4	RPL4	R.SGQGAFGNMC*R.G
266	131	72	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.IC*DDELILIK.N
53	72	73	Q4ZG55	GREB1 Protein GREB1	GREB1	R.LINSSC*LVR.T
68	92	74	Q8N8R5	C2orf69 UPF0565 protein C2orf69	C2orf69	R.C*SLSAEVR.R
167	242	75	P11586	MTHFD1 C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	R.GDLNDCFIPC*TPK.G
146	158	76	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.YMAC*CLLYR.G
291	26	77	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.SLHDALC*VVK.R
109	144	78	P50914	RPL14 60S ribosomal protein L14	RPL14	K.C*MQLTDFILK.F
16	9	79	P25398	RPS12 40S ribosomal protein S12	RPS12	K.KLGEWVGLC*K.I
696	154	80	P53582	METAP1 Methionine aminopeptidase 1	METAP1	R.VCETDGC*SSEAK.L
159	50	81	P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	K.IIC*QGFTGK.Q
143	178	82	P16278	GLB1 Beta-galactosidase	GLB1	K.TVGAALDILC*PSGPIK.S
117	161	83	P50914	RPL14 60S ribosomal protein L14	RPL14	R.ALVDGPC*TQVR.R
49	214	84	P11586	MTHFD1 C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	K.C*THWAEGGK.G
215	211	85	Q7RTV0	PHF5A PHD finger-like domain-containing protein 5A	PHF5A	R.ICDEC*NYGSYQGR.C
153	207	86	Q96CW1	AP2M1 AP-2 complex subunit mu	AP2M1	K.MC*DVMAAYFGK.I
24	41	87	P33992	MCM5 DNA replication licensing factor MCM5	MCM5	R.C*SVLAAANSVFGR.W
77	222	88	Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	K.SSVNC*PFSSQDMK.Y
29	271	89	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	K.TFTDC*FNC*LPIAAIVDEK.I
48	220	90	P58107	EPPK1 Epiplakin	EPPK1	R.LLDAQLATGGLVC*PAR.R
718	8	91	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	K.FC*LDNGAK.S
66	163	92	P62280	RPS11 40S ribosomal protein S11	RPS11	K.C*PFTGNVSIR.G
427	53	93	Q68CP9	ARID2 AT-rich interactive domain-containing protein 2	ARID2	R.SC*SNAAFALK.Q
253	453	94	Q08AM6	VAC14 Protein VAC14 homolog	VAC14	K.GLEC*SPSTPTMNSYFYK.F
164	101	95	P45880	VDAC2 Voltage-dependent anion-selective channel protein	VDAC2	R.PMC*IPPSYADLGK.A
177	201	96	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit 2	PSMD2	R.C*ALGVFR.K
17	171	97	P58107	EPPK1 Epiplakin	EPPK1	R.YLQGTGC*IAGLLLPGSQER.L
52	123	98	P60709	ACTB Actin, cytoplasmic 1	ACTB	K.EKLC*YVALDFEQEMATAASSSSLEK.S
226	153	99	P53618	COPB1 Coatomer subunit beta	COPB1	K.ALSGYC*GFMAANLYAR.S
303	753	100	Q99439	CNN2 Calponin-2	CNN2	K.C*ASQVGMTAPGTR.R

2.2	2.8	2.1	2.7	2.4	2.4	4.7	4.6	6.5	4.8	4.3	5.0	10.8	0.0	0.0	10.3	10.2	10.4
2.4	2.4	2.3	2.7	2.5	2.4	4.2	3.8	3.5	3.8	3.5	3.8	5.0	5.0	6.0	6.3	6.4	5.7
2.6	2.4	2.3	2.4	2.4	2.4	4.7	4.1	4.9	4.6	4.6	4.6	5.4	6.3	10.3	7.9	7.5	7.5
2.8	2.1	2.3	2.6	2.4	2.4	5.6	6.3	5.3	4.4	5.6	5.4	6.4	6.8	8.1	6.3	5.3	6.6
2.6	2.1	2.2	2.6	2.5	2.4	5.0	5.2	4.9	4.2	4.0	4.6	5.0	5.6	7.7	6.6	7.0	6.4
0.0	2.3	2.4	2.6	2.4	2.4	3.6	4.0	3.7	3.1	3.7	3.6	1.9	0.0	3.8	1.9	0.0	2.5
3.1	0.6	2.5	3.5	2.3	2.4	3.8	5.4	4.1	4.0	5.8	4.6	7.2	7.2	6.1	7.4	8.4	7.2
2.5	2.2	2.0	2.9	0.0	2.4	4.1	4.7	4.5	0.0	4.0	4.3	6.0	0.0	5.7	6.4	7.6	6.4
2.1	2.2	2.6	3.2	2.1	2.4	2.5	2.5	1.8	2.1	4.5	2.7	3.3	2.4	5.2	0.0	0.0	3.6
2.5	2.3	2.3	2.6	2.4	2.4	3.4	3.3	3.3	3.2	3.0	3.2	3.6	3.7	4.9	3.8	4.0	4.0
1.9	2.0	2.5	3.3	2.3	2.4	5.5	7.5	6.3	6.2	6.1	6.3	2.2	2.7	2.9	1.5	0.0	2.3
2.5	2.3	2.2	2.5	2.4	2.4	3.3	3.7	3.2	3.4	3.2	3.4	4.2	4.2	6.0	5.4	5.6	5.1
2.0	2.4	2.3	2.9	2.3	2.4	7.8	7.5	9.3	10.5	6.4	8.3	10.0	8.8	13.1	0.0	9.4	10.3
2.3	2.6	1.6	2.8	2.5	2.4	0.0	5.8	2.6	2.9	1.9	3.3	1.4	1.1	1.2	1.2	1.2	1.2
2.0	2.3	2.4	2.6	2.5	2.4	4.4	5.5	5.6	4.7	5.6	5.2	3.3	3.4	4.6	3.6	3.9	3.8
2.4	2.3	2.3	2.6	2.1	2.3	4.4	2.7	2.9	3.0	2.3	3.1	4.9	3.6	0.0	3.8	0.0	4.1
2.5	2.1	2.1	2.7	2.3	2.3	3.2	3.5	3.1	3.2	3.1	3.2	4.1	4.7	5.6	4.6	5.0	4.8
1.4	2.8	2.8	2.5	2.1	2.3	1.7	2.1	4.1	3.9	2.3	2.8	7.1	7.3	6.9	8.7	0.0	7.5
2.2	2.4	2.1	2.1	2.7	2.3	2.8	2.7	2.7	3.1	3.1	2.9	2.2	0.0	4.6	2.2	2.9	3.0
2.3	2.3	2.2	2.5	2.3	2.3	0.0	2.9	3.2	2.5	3.0	2.9	3.6	0.0	0.0	4.0	4.2	3.9
2.2	2.8	1.9	2.8	1.9	2.3	4.9	6.8	4.9	5.1	5.6	5.4	8.2	9.6	0.0	0.0	11.0	9.6
2.5	2.7	2.0	2.4	2.0	2.3	2.8	2.3	3.4	0.0	2.8	2.8	5.2	7.4	5.2	8.1	5.3	6.2
0.0	2.0	2.4	2.4	2.4	2.3	2.7	2.8	2.1	2.7	2.0	2.5	8.1	6.7	11.3	8.3	10.6	9.0
2.5	2.1	2.4	2.2	2.3	2.3	3.0	4.0	2.7	2.5	2.0	2.8	7.8	6.1	8.3	7.2	8.9	7.6
0.8	2.6	2.4	3.1	2.5	2.3	6.8	9.9	8.6	0.0	8.6	8.5	0.0	1.1	0.0	0.9	1.3	1.1
2.3	2.2	1.9	2.4	2.5	2.3	3.2	3.5	3.2	3.2	2.9	3.2	6.0	6.7	7.3	6.3	6.2	6.5
2.2	1.9	2.9	1.9	2.5	2.3	5.0	5.3	5.6	4.9	4.5	5.1	1.4	1.6	1.8	1.8	1.8	1.7
2.3	1.8	2.7	2.2	0.0	2.2	1.9	1.5	1.6	1.8	0.0	1.7	2.5	2.7	2.6	2.6	2.4	2.6
1.9	1.7	2.7	2.8	2.1	2.2	4.3	4.3	4.4	0.0	3.6	4.1	2.8	4.0	4.1	4.1	3.6	3.7
2.2	0.0	2.3	2.4	2.0	2.2	4.3	0.0	2.9	1.8	2.8	2.9	3.1	2.9	4.1	3.8	3.2	3.4
2.1	2.4	0.0	2.6	1.7	2.2	4.5	2.8	2.5	3.2	2.6	3.1	8.2	9.6	9.3	10.6	13.4	10.2
2.2	2.0	2.2	2.4	2.2	2.2	3.1	3.8	4.0	4.0	3.7	3.7	6.3	7.8	8.4	7.5	7.2	7.4
2.1	2.1	2.1	2.5	2.3	2.2	3.1	3.7	3.6	2.9	3.3	3.3	2.4	2.6	3.4	2.6	3.0	2.8
3.6	1.4	1.9	1.9	0.0	2.2	0.7	0.5	0.9	0.6	0.6	0.7	2.0	0.0	2.4	0.0	2.1	2.2

40	251	101	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	R.GNHEC*ASINR.I
229	203	102	P08559	PDHA1 Pyruvate dehydrogenase E1 component subunit alpha,	PDHA1	R.FAAAYC*R.S
19	13	103	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	K.C*EYPAAC*NALETLLIHR.D
87	70	104	P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	R.LGGEVSC*LVAGTK.C
69	141	105	P26641	EEF1G Elongation factor 1-gamma	EEF1G	R.FPEELTQTFMSC*NLITGMFQR.L
443	35	106	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.ALNALC*DGLIDELNQALK.T
13	74	107	P26440	IVD Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	R.GSNTC*ELIFEDC*KIPAANILGHENK.G
155	177	108	Q5UIP0	RIF1 Telomere-associated protein RIF1	RIF1	K.SLIDNFALNPDILC*SAK.R
598	130	109	O43815	STRN Striatin	STRN	K.C*YIASAGADALAK.V
84	149	110	Q8N163	KIAA1967 DBIRD complex subunit KIAA1967	KIAA1967	R.VVTQNIC*QYR.S
196	36	111	P15924	DSP Desmoplakin	DSP	K.YC*YLQNEVFGLFQK.L
108	133	112	P62829	RPL23 60S ribosomal protein L23	RPL23	R.ISLGLPVGAVINC*ADNTGAK.N
94	5	113	Q9NZB2	FAM120A Constitutive coactivator of PPAR-gamma-like protei	FAM120A	R.VAAASGHC*GAFSGSDSSR.T
56	65	114	P62249	RPS16 40S ribosomal protein S16	RPS16	K.TATAVAHC*K.R
31	63	115	P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	R.TIYAGNALC*TVK.C
189	189	116	Q14152	EIF3A Eukaryotic translation initiation factor 3 subunit	EIF3A	K.NIC*QQVNIK.S
166	314	117	P62714	PPP2CB Serine/threonine-protein phosphatase 2A catalytic	PPP2CB	R.NVVTIFSAPNYC*YR.C
554	379	118	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	R.GQPC*SQNYR.L
32	111	119	P24468	NR2F2 COUP transcription factor 2	NR2F2	R.FGSQC*MQPNNIMGIENICELAAR.M
43	6	120	P62888	RPL30 60S ribosomal protein L30	RPL30	R.VC*TLAIIDPGDSDIIR.S
299	339	121	Q8WXH0	SYNE2 Nesprin-2	SYNE2	K.NLAGEC*QNINK.Q
73	181	122	P62753	RPS6 40S ribosomal protein S6	RPS6	K.LNISFPATGC*QK.L
100	115	123	O95747	OXSR1 Serine/threonine-protein kinase OSR1	OXSR1	K.TFVGTPC*WMAPEVMEQVR.G
113	14	124	P15924	DSP Desmoplakin	DSP	R.GVITDQNSDGYC*QTGTMSR.H
334	132	125	Q14318	FKBP8 Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8	K.C*LNNLAASQLK.L
22	143	126	P49327	FASN Fatty acid synthase	FASN	K.AFDTAGNGYC*R.S
89	307	127	O75150	RNF40 E3 ubiquitin-protein ligase BRE1B	RNF40	R.LTCPC*CNTR.K
157	21	128	P13639	EEF2 Elongation factor 2	EEF2	K.DLEEDHAC*IPIK.K
190	157	129	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	R.MLSAVSQQVQC*IQEALR.E
90	108	130	Q86Y56	HEATR2 HEAT repeat-containing protein 2	HEATR2	R.RPPEAC*EELR.L
99	194	131	O60716	CTNND1 Catenin delta-1	CTNND1	K.TPAILEASAGAIQNLC*AGR.W
104	137	132	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	R.AC*ALQVLSAILEGSK.Q
200	184	133	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	K.C*FIVGADNVGSK.Q
144	229	134	P46776	RPL27A 60S ribosomal protein L27a	RPL27A	K.RNQSFC*PTVNLDK.L

2.2	2.0	2.2	2.4	2.2	2.2	3.2	2.6	2.6	2.5	2.3	2.6	7.0	7.9	8.8	8.0	8.7	8.1
0.0	1.9	2.2	2.4	0.0	2.2	3.6	2.9	2.9	2.6	2.6	2.9	2.1	2.4	2.9	3.2	3.5	2.8
2.3	2.1	2.0	2.0	2.5	2.2	6.8	8.0	7.2	7.2	8.5	7.5	11.5	15.6	7.8	4.9	0.0	9.9
2.3	1.9	2.2	2.4	2.0	2.2	3.8	4.9	4.5	5.4	4.6	4.6	6.1	6.0	0.0	5.4	5.5	5.7
2.1	2.1	0.0	2.3	0.0	2.2	3.0	3.5	3.6	0.0	3.6	3.4	5.5	5.9	7.5	6.2	7.0	6.4
2.3	2.1	2.1	2.3	2.1	2.2	6.3	5.4	5.4	5.9	5.0	5.6	1.5	1.5	2.0	1.6	1.6	1.6
2.1	2.1	2.1	2.6	2.0	2.2	5.1	4.8	3.3	5.8	4.0	4.6	9.6	8.7	13.6	11.4	0.0	10.8
0.0	1.7	1.9	3.3	1.7	2.2	3.0	3.4	2.9	0.0	3.0	3.1	3.2	4.2	0.0	4.2	0.0	3.9
1.5	2.1	2.2	2.6	2.3	2.2	4.2	3.4	5.5	2.1	2.8	3.6	1.4	1.4	1.5	1.5	1.3	1.4
1.8	2.2	1.9	2.4	2.5	2.1	3.6	3.4	3.6	3.4	2.7	3.3	6.9	5.4	5.5	5.8	5.4	5.8
2.5	1.7	2.1	2.1	2.3	2.1	6.0	5.5	5.3	5.5	5.8	5.6	3.3	2.8	3.6	3.1	2.9	3.1
2.2	1.9	2.0	2.3	2.2	2.1	4.0	3.8	3.4	3.3	3.3	3.5	4.4	4.9	5.8	5.1	5.4	5.1
2.3	1.7	2.0	2.5	2.0	2.1	12.1	8.7	11.2	8.8	7.5	9.7	4.6	6.1	5.0	6.2	5.8	5.5
2.0	1.9	2.3	2.3	1.9	2.1	3.9	5.6	5.1	4.2	4.6	4.7	7.2	7.1	7.7	6.3	7.0	7.0
1.9	2.1	2.0	2.2	2.0	2.0	5.1	4.6	4.4	5.2	4.1	4.7	7.5	7.5	11.4	9.0	8.6	8.8
2.3	1.7	2.0	2.2	2.0	2.0	3.0	3.3	3.2	2.8	2.7	3.0	3.6	0.0	3.3	0.0	2.9	3.3
2.3	1.8	2.2	2.0	1.9	2.0	1.6	2.3	2.8	2.6	1.8	2.2	2.8	4.7	0.0	3.8	3.4	3.6
1.6	1.7	2.5	2.1	2.2	2.0	1.9	2.2	1.9	2.3	1.5	1.9	1.2	1.2	1.7	1.5	1.6	1.4
2.2	2.1	2.2	1.7	1.9	2.0	4.9	3.5	3.3	5.3	2.6	3.9	9.1	8.4	7.2	8.7	10.1	8.7
2.1	1.9	1.8	2.2	2.0	2.0	9.9	8.2	8.4	8.7	8.2	8.7	6.2	6.6	0.0	8.8	10.2	7.9
2.5	1.5	2.2	1.8	0.0	2.0	2.2	0.0	2.8	0.0	1.3	2.1	1.9	2.2	0.0	2.5	2.3	2.2
2.0	1.8	1.9	2.2	2.0	2.0	3.0	3.0	2.7	2.8	3.7	3.0	7.7	6.4	6.7	5.4	5.7	6.4
1.8	2.0	1.7	2.5	2.0	2.0	2.7	4.6	4.0	3.8	3.8	3.8	5.8	4.6	5.4	5.0	5.9	5.3
2.1	2.0	1.5	2.5	1.9	2.0	7.0	7.1	0.0	0.0	8.5	7.5	4.1	0.0	5.0	6.5	4.1	4.9
1.8	1.8	2.2	2.3	1.9	2.0	3.2	4.1	3.5	3.2	3.9	3.6	1.9	1.8	2.3	1.7	2.4	2.0
2.1	1.9	1.9	2.1	1.9	2.0	3.6	4.1	3.2	3.1	2.9	3.4	5.7	0.0	0.0	9.5	14.0	9.7
2.4	0.0	1.7	2.0	1.8	2.0	2.7	2.3	1.5	0.0	2.5	2.3	5.1	5.2	7.8	4.9	5.6	5.7
2.0	1.8	1.9	2.4	1.8	2.0	5.8	8.2	0.0	7.2	5.4	6.6	3.1	3.6	4.1	3.8	4.2	3.8
2.1	2.0	1.8	2.3	1.6	2.0	4.6	2.5	3.3	3.6	2.2	3.3	2.7	2.7	0.0	3.8	4.0	3.3
2.0	1.9	0.0	2.0	0.0	2.0	0.0	4.0	3.3	4.7	3.9	4.0	5.7	4.5	8.4	5.6	4.2	5.7
0.0	0.0	2.0	2.2	1.7	2.0	2.8	0.0	3.2	3.0	2.8	3.0	0.0	0.0	4.9	3.8	7.4	5.4
2.3	1.5	2.0	2.3	1.7	2.0	4.4	3.5	3.3	3.1	3.1	3.5	4.4	4.8	6.2	5.2	5.5	5.2
1.9	1.8	1.9	2.1	2.0	1.9	3.6	3.0	2.8	3.0	2.6	3.0	2.4	3.1	3.6	3.0	3.3	3.1
2.3	1.8	1.8	2.0	1.7	1.9	2.8	2.6	3.1	3.0	2.4	2.8	4.2	4.0	0.0	0.0	4.2	4.1

256	7	135	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.AFAAGADIKEMQNLSFQDC*YSSK.F
581	343	136	P62701	RPS4X 40S ribosomal protein S4, X isoform	RPS4X	K.FDTGNLC*MVTGGANLGR.I
130	202	137	P55060	CSE1L Exportin-2	CSE1L	K.IC*AVGITK.L
224	119	138	B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	K.IFVGNVSAAC*TSQELR.S
28	49	139	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	R.AVHQC*DR.G
353	384	140	Q9Y5L0	TNPO3 Transportin-3	TNPO3	K.GLC*EKPLASAAAK.A
230	200	141	Q07020	RPL18 60S ribosomal protein L18	RPL18	K.GC*GTVLLSGPR.K
14	239	142	P04183	TK1 Thymidine kinase, cytosolic	TK1	K.LTAVC*MECFR.E
156	135	143	O95782	AP2A1 AP-2 complex subunit alpha-1	AP2A1	K.TVFEALQAPAC*HENMVK.V
58	198	144	Q9BTZ2	DHRS4 Dehydrogenase/reductase SDR family member 4	DHRS4	R.VNC*LAPGLIK.T
21	336	145	P07384	CAPN1 Calpain-1 catalytic subunit	CAPN1	R.LEIC*NLTPDALK.S
38	257	146	Q9Y2R9	MRPS7 28S ribosomal protein S7, mitochondrial	MRPS7	K.NC*EPMIGLVPILK.G
119	190	147	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	R.LC*ALRPDDSSSAR.T
233	89	148	Q16576	RBBP7 Histone-binding protein RBBP7	RBBP7	R.VHIPNDDAQFDASHC*DSDKGEFGGFGSVTGK.I
61	103	149	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.KGDEC*ELLGHSK.N
285	311	150	Q9NQT5	EXOSC3 Exosome complex component RRP40	EXOSC3	K.LLAPDC*EIIQEVGK.L
59	205	151	P62330	ARF6 ADP-ribosylation factor 6	ARF6	R.DRNWYVQPSC*ATSGDGLYEGLTWLTSNYK.S
421	152	152	Q9H1B7	IRF2BPL Interferon regulatory factor 2-binding protein-lik	IRF2BPL	R.AHGC*FQDGR.S
326	352	153	O15294	OGT UDP-N-acetylglucosamine--peptide N-acetylglucosami	OGT	K.VMAEANHFIDLSQIPC*NGK.A
219	140	154	P31689	DNAJA1 DnaJ homolog subfamily A member 1	DNAJA1	K.GAVEC*CPNCR.G
371	206	155	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.TIIPLISQC*TPK.V
231	276	156	O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	K.SFVQWLGC*R.S
242	305	157	O76039	CDKL5 Cyclin-dependent kinase-like 5	CDKL5	K.LC*DFGFAR.N
306	265	158	O14980	XPO1 Exportin-1	XPO1	K.DLLGLC*EQKR.G
168	378	159	Reverse_Q86V97	KBTBD6 Kelch repeat and BTB domain-containing protein 6	KBTBD6	R.RALFSAC*AER.V
139	120	160	P82912	MRPS11 28S ribosomal protein S11, mitochondrial	MRPS11	K.ASHNNTQIQVVSASNEPLAFASC*GTEGFR.N
129	182	161	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	K.KLVIVGDGAC*GK.T
222	20	162	P15924	DSP Desmoplakin	DSP	K.YQAEC*SQFK.A
311	160	163	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	R.NFILDQC*NVYNSGQR.R
105	405	164	P00966	ASS1 Argininosuccinate synthase	ASS1	K.GNDQVRFELSC*YSLAPQIK.V
308	326	165	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	K.C*AMTALSSK.L
270	169	166	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	R.AGAIAPC*EVTVPAQNTGLGPEK.T
238	218	167	P62244	RPS15A 40S ribosomal protein S15a	RPS15A	K.C*GVISPR.F
322	382	168	Q9UL40	ZNF346 Zinc finger protein 346	ZNF346	K.NQC*LFTNTQCK.V

2.0	1.9	1.8	2.0	1.9	1.9	8.8	8.2	8.1	10.0	8.3	8.6	2.2	2.2	3.5	2.0	2.9	2.5
2.0	1.7	2.0	2.2	1.7	1.9	2.1	2.3	2.2	1.8	2.1	2.1	1.4	1.8	0.0	1.4	1.2	1.4
1.9	2.1	1.7	2.0	1.9	1.9	3.1	3.4	3.4	1.9	2.8	2.9	3.5	4.1	6.3	4.0	4.2	4.4
1.8	1.8	2.0	2.1	1.8	1.9	4.5	4.0	2.9	4.2	3.0	3.7	2.3	3.0	3.2	2.6	3.2	2.8
2.0	1.8	1.7	2.2	1.7	1.9	0.0	6.0	5.1	4.9	4.8	5.2	9.1	9.3	10.4	8.4	0.0	9.3
1.8	1.4	2.9	1.6	0.0	1.9	2.0	2.0	1.8	2.0	0.0	1.9	0.0	2.0	2.4	1.9	1.4	1.9
1.9	1.7	1.8	2.0	2.0	1.9	3.0	3.3	2.7	2.8	3.0	2.9	2.1	2.3	3.6	3.0	2.9	2.8
1.1	1.6	1.4	3.1	2.3	1.9	2.6	2.4	3.1	3.8	1.5	2.7	6.8	12.9	6.8	10.7	16.0	10.6
2.0	1.5	2.0	1.7	2.2	1.9	0.0	3.6	0.0	3.1	3.8	3.5	2.6	5.1	4.7	3.0	0.0	3.8
2.1	1.8	1.8	1.9	1.7	1.9	2.4	3.3	3.0	2.9	3.2	3.0	7.1	0.0	7.4	5.7	7.0	6.8
1.9	1.7	1.9	2.4	1.5	1.9	2.6	2.4	1.9	2.1	1.5	2.1	7.5	7.3	11.8	9.9	12.3	9.7
2.0	1.8	1.8	1.9	1.9	1.9	2.6	2.6	2.7	2.5	2.5	2.6	6.4	0.0	7.8	10.5	8.2	8.2
2.0	1.5	1.8	2.0	1.9	1.8	3.4	3.4	2.7	3.2	2.3	3.0	3.6	5.0	7.0	4.2	3.9	4.7
1.7	1.6	1.4	1.9	2.6	1.8	4.7	4.5	4.1	4.6	3.8	4.4	2.3	2.6	3.4	2.8	0.0	2.8
1.8	1.8	1.7	2.1	1.8	1.8	3.7	5.0	3.9	4.3	3.8	4.1	5.3	5.6	7.7	6.2	8.3	6.6
1.8	1.7	0.0	1.7	2.2	1.8	2.6	2.3	2.2	2.2	1.9	2.2	1.9	2.3	3.0	2.3	2.2	2.3
2.1	1.6	1.9	1.9	1.6	1.8	3.3	0.0	3.0	3.0	2.4	2.9	5.5	6.7	7.7	7.5	5.7	6.6
0.0	1.5	0.0	2.8	1.2	1.8	0.0	4.6	2.8	3.4	2.4	3.3	1.7	1.6	1.9	1.5	1.9	1.7
1.8	0.0	1.6	1.9	1.9	1.8	3.2	2.1	1.5	0.0	1.4	2.0	1.6	1.9	2.5	2.1	2.1	2.1
2.2	1.8	1.5	1.6	2.0	1.8	4.1	0.0	4.2	0.0	2.1	3.4	2.8	3.0	0.0	2.9	0.0	2.9
1.7	1.8	1.9	1.9	1.9	1.8	2.7	3.0	3.2	3.1	2.6	2.9	1.8	1.7	2.2	1.6	2.0	1.8
1.7	1.6	1.8	1.8	2.1	1.8	2.4	2.4	2.9	2.3	2.3	2.5	2.8	2.9	3.0	2.3	2.9	2.8
1.7	0.0	2.2	1.5	0.0	1.8	2.9	2.1	0.0	0.0	1.9	2.3	2.3	2.5	2.8	2.6	3.2	2.7
1.8	1.8	1.8	1.8	1.9	1.8	3.2	2.4	2.2	3.0	1.9	2.5	2.0	2.0	2.7	1.7	2.4	2.2
1.7	1.8	1.8	2.0	1.7	1.8	3.0	2.0	2.2	0.8	1.7	1.9	2.5	3.4	0.0	0.0	4.9	3.6
2.0	1.3	1.8	2.2	1.5	1.8	4.3	5.1	3.2	3.2	2.9	3.7	3.7	3.9	4.9	4.3	4.2	4.2
2.3	1.6	1.6	1.8	1.6	1.8	3.1	3.1	3.1	3.4	2.5	3.0	3.7	4.3	6.7	3.6	4.2	4.5
1.8	1.7	1.6	2.1	1.7	1.8	7.4	9.9	6.7	4.6	5.1	6.7	2.5	2.6	2.7	2.8	3.8	2.9
1.6	1.5	1.7	2.2	1.8	1.8	3.4	3.8	2.8	3.4	2.8	3.2	1.7	1.9	2.7	2.2	2.2	2.2
2.1	1.7	1.6	1.6	1.8	1.8	1.5	2.2	1.9	2.0	1.8	1.9	5.5	4.7	5.7	4.6	5.5	5.2
1.8	2.4	1.5	1.7	1.4	1.8	2.2	2.0	2.6	2.4	1.7	2.2	1.9	2.2	2.6	1.8	2.3	2.2
1.7	1.6	1.7	2.0	1.8	1.8	3.3	3.3	3.0	3.5	2.6	3.1	2.1	2.4	2.9	2.6	2.5	2.5
1.7	1.8	1.7	1.8	1.7	1.8	3.6	2.8	2.7	2.6	2.5	2.8	2.3	1.7	3.6	3.3	2.7	2.7
2.0	0.0	1.3	1.3	2.4	1.8	1.9	2.3	1.6	0.0	2.1	1.9	1.7	1.6	3.5	2.1	1.4	2.1

310	256	169	Q7Z406	MYH14 Myosin-14	MYH14	K.ADLLLEPC*SHYR.F
136	96	170	Q96CM8	ACSF2 Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	R.MVSTPIGGLSYVQGC*TK.K
491	293	171	Q15019	SEPT2 Septin-2	42249	R.LTVVDTPGYGDAINC*R.D
178	327	172	P23396	RPS3 40S ribosomal protein S3	RPS3	R.GLC*AIAQAESLR.Y
70	212	173	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	R.AVASQLDC*NFLK.V
236	60	174	Q9H479	FN3K Fructosamine-3-kinase	FN3K	R.AFGGPGAGC*ISEGR.A
172	297	175	Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multif	AIMP2	K.FSIQTMC*PIEGEGNIAR.F
132	252	176	P53618	COPB1 Coatomer subunit beta	COPB1	K.VLSECSPLMNDIFNKEC*R.Q
486	319	177	P30519	HMOX2 Heme oxygenase 2	HMOX2	K.CPFYAAEQDKGALEGSSC*PFR.T
195	224	178	P23919	DTYMK Thymidylate kinase	DTYMK	K.LVEALC*AAGHR.A
171	168	179	Q6ZRV2	FAM83H Protein FAM83H	FAM83H	R.TVAGPTYYC*R.T
478	269	180	P49321	NASP Nuclear autoantigenic sperm protein	NASP	R.KPTDGASSSNC*VTDISHLVR.K
165	164	181	P55060	CSE1L Exportin-2	CSE1L	K.NLFEDQNTLTSIC*EK.V
85	126	182	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	K.SGDAAIVEMVPGKPMC*VESFSQYPPLGR.F
374	273	183	P21333	FLNA Filamin-A	FLNA	K.THEAEIVEGENHTYC*IR.F
377	642	184	Q6IA86	ELP2 Elongator complex protein 2	ELP2	K.TLLASAC*K.A
280	215	185	P62910	RPL32 60S ribosomal protein L32	RPL32	K.SYC*AEIAHNVSSK.N
160	232	186	Q8WTW3	COG1 Conserved oligomeric Golgi complex subunit 1	COG1	K.AQAISPC*VQNFCSALDSK.L
490	291	187	A6NDG6	PGP Phosphoglycolate phosphatase	PGP	K.NNQESDC*VSK.K
359	577	188	P33992	MCM5 DNA replication licensing factor MCM5	MCM5	K.C*SPIGVYTSGK.G
475	437	189	O95571	ETHE1 Protein ETHE1, mitochondrial	ETHE1	R.TDFQQGC*AK.T
115	270	190	Q8WXG6	MADD MAP kinase-activating death domain protein	MADD	K.LINMTYC*PK.T
126	79	191	P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	R.LIGPNC*PGVINPGEC*K.I
678	179	192	P53621	COPA Coatomer subunit alpha	COPA	R.TTYQALPC*LPSMYGYPNR.N
188	236	193	P15880	RPS2 40S ribosomal protein S2	RPS2	R.GC*TATLGNFAK.A
626	315	194	P55060	CSE1L Exportin-2	CSE1L	K.LSTAC*PGR.V
158	341	195	P57678	GEMIN4 Gem-associated protein 4	GEMIN4	R.SDPDAC*PTMPLLAMLLR.G
65	86	196	O95757	HSPA4L Heat shock 70 kDa protein 4L	HSPA4L	R.GC*ALQCAILSPAFK.V
112	240	197	P46782	RPS5 40S ribosomal protein S5	RPS5	K.TIAEC*LADELINAAK.G
162	351	198	Q15796	SMAD2 Mothers against decapentaplegic homolog 2	SMAD2	K.AITTQNC*NTK.C
95	68	199	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	R.AGGIETIANEFSDRC*TPSVISFGSK.N
179	145	200	Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	K.AVVVC*PK.D
198	246	201	Q969Z0	TBRG4 Protein TBRG4	TBRG4	R.LATDLLSLMPSLTSGEVAHC*AK.S
237	259	202	P53618	COPB1 Coatomer subunit beta	COPB1	K.VLSEC*SPLMNDIFNK.E

1.7	1.8	1.6	1.9	1.8	1.7	2.7	2.4	3.1	0.0	2.2	2.6	1.9	2.3	2.6	2.1	1.9	2.2
1.8	1.8	1.6	1.8	1.7	1.7	4.3	5.6	3.5	4.9	3.1	4.2	3.6	3.5	5.4	3.9	4.8	4.3
1.8	1.6	1.6	1.9	1.8	1.7	2.4	2.5	2.2	2.6	2.1	2.4	1.3	1.4	2.1	1.6	1.4	1.6
1.8	1.7	1.6	1.8	1.8	1.7	2.3	2.3	2.2	2.1	2.0	2.2	3.0	3.2	4.1	3.3	3.4	3.4
1.7	1.8	1.7	1.8	1.7	1.7	2.9	3.2	2.8	2.7	2.6	2.8	4.9	5.8	8.8	6.8	5.8	6.4
1.6	1.4	2.0	1.8	1.8	1.7	9.5	0.5	4.7	4.1	4.7	4.7	2.3	2.0	2.8	4.3	2.2	2.7
1.6	1.6	1.8	2.0	1.6	1.7	2.3	2.0	2.6	2.9	1.9	2.3	3.1	2.5	4.5	3.9	3.6	3.5
1.5	0.0	1.6	1.7	2.1	1.7	2.3	3.5	2.0	1.7	3.5	2.6	3.4	4.8	4.6	4.6	4.5	4.4
1.7	1.7	1.6	1.8	1.9	1.7	2.6	1.6	2.4	0.0	0.0	2.2	1.1	1.9	2.0	1.2	1.7	1.6
1.4	1.8	0.0	0.0	2.0	1.7	1.8	3.2	0.0	3.2	2.9	2.8	3.2	2.8	0.0	0.0	3.5	3.2
1.7	0.0	1.7	1.8	0.0	1.7	1.8	3.5	3.1	3.8	3.6	3.2	3.6	3.4	3.5	3.8	3.3	3.5
0.0	1.3	1.7	2.1	1.7	1.7	3.4	1.5	1.6	3.5	2.5	2.5	1.1	1.1	2.2	2.0	1.5	1.6
2.2	1.3	1.6	2.1	1.4	1.7	2.0	2.9	4.4	3.5	3.1	3.2	3.2	4.2	3.7	0.0	3.7	3.7
1.6	1.6	1.8	1.9	1.6	1.7	2.2	4.1	4.0	4.7	3.2	3.7	5.7	5.0	6.3	0.0	6.0	5.8
1.6	1.6	1.6	2.3	1.4	1.7	2.8	0.0	2.8	2.5	1.7	2.5	0.0	1.7	2.4	1.5	0.0	1.8
2.2	0.0	1.2	2.3	1.2	1.7	1.2	0.0	1.1	0.0	1.1	1.1	1.3	2.1	0.0	2.2	0.0	1.8
1.6	1.7	1.7	1.7	1.8	1.7	2.8	2.5	2.9	3.6	2.4	2.8	2.4	1.8	3.5	2.6	1.7	2.4
1.6	1.7	1.6	2.0	1.5	1.7	3.2	0.0	2.6	0.0	2.3	2.7	2.1	3.7	4.4	4.0	4.5	3.8
1.7	1.7	1.6	1.8	1.8	1.7	2.6	2.2	1.9	2.3	2.9	2.4	1.5	1.4	1.8	1.6	1.6	1.6
2.1	1.7	1.2	2.2	1.3	1.7	1.6	1.2	1.2	0.0	1.2	1.3	1.3	0.0	0.0	2.1	2.4	1.9
0.0	1.6	1.7	1.6	1.9	1.7	2.6	1.8	1.5	1.4	1.5	1.8	1.3	1.3	1.9	1.8	1.6	1.6
1.7	1.7	1.6	1.7	1.7	1.7	2.9	2.8	1.7	2.7	2.3	2.5	4.8	0.0	6.5	4.6	3.7	4.9
1.7	1.7	1.6	1.7	1.8	1.7	5.7	4.6	3.5	4.2	4.5	4.5	4.1	4.9	5.4	4.0	4.5	4.6
1.3	1.6	1.5	2.2	1.8	1.7	0.0	3.5	3.2	3.6	2.0	3.1	0.9	1.0	1.8	0.0	1.2	1.2
1.7	1.7	1.6	1.7	1.6	1.7	3.2	2.8	2.5	2.7	2.3	2.7	2.8	2.8	3.7	3.4	3.7	3.3
1.9	1.5	1.6	1.8	1.6	1.7	2.1	1.9	2.2	3.0	2.0	2.2	1.1	0.0	1.6	1.3	1.3	1.3
1.8	0.0	1.4	1.8	0.0	1.7	2.4	2.2	2.2	2.1	1.5	2.1	3.3	4.5	3.7	3.6	3.7	3.8
1.8	1.7	1.5	1.5	1.7	1.7	4.4	4.2	4.4	4.5	4.4	4.4	5.9	6.8	6.5	7.2	6.2	6.5
1.7	1.6	1.6	1.8	1.7	1.7	3.3	2.8	2.5	2.5	2.3	2.7	4.0	4.8	5.6	4.7	5.8	5.0
2.2	2.1	1.4	1.4	1.3	1.7	2.0	1.4	1.8	3.0	2.0	2.0	3.3	4.5	3.2	4.0	3.7	3.7
1.6	1.6	1.6	1.9	1.6	1.7	3.9	5.3	4.7	5.5	3.9	4.7	5.2	5.0	7.3	4.7	5.5	5.5
1.8	0.8	1.8	1.9	1.9	1.7	3.4	3.8	3.5	3.2	3.1	3.4	2.9	2.9	4.4	3.4	3.4	3.4
1.5	1.5	1.6	1.9	1.7	1.7	0.0	2.6	2.9	2.5	2.6	2.7	3.2	2.1	3.8	0.0	3.3	3.1
0.0	1.7	1.4	1.7	1.8	1.7	2.4	2.5	2.4	0.0	3.0	2.6	3.1	3.0	1.5	3.0	2.9	2.7

375	386	203	P33991	MCM4 DNA replication licensing factor MCM4	MCM4	K.AGIIC*QLNAR.T
595	267	204	Q9Y508	RNF114 RING finger protein 114	RNF114	R.DC*GGAAQLAGPAAEADPLGR.F
217	548	205	P21333	FLNA Filamin-A	FLNA	R.VTYC*PTEPGNYIINIK.F
128	112	206	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	K.AEMDAAIASC*K.R
756	172	207	P10599	TXN Thioredoxin	TXN	K.C*MPTFQFFK.K
409	185	208	P13639	EEF2 Elongation factor 2	EEF2	K.EGALC*EENMR.G
83	217	209	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.C*ATITPDEAR.V
210	237	210	P62195	PSMC5 26S protease regulatory subunit 8	PSMC5	K.GVC*TEAGMYALR.E
131	47	211	P15924	DSP Desmoplakin	DSP	R.DANSENC*NK.N
493	396	212	Q0PNE2	ELP6 Elongator complex protein 6	ELP6	R.AEGLATGFC*R.D
67	134	213	Q99836	MYD88 Myeloid differentiation primary response protein M	MYD88	R.FITVCDYTNPC*TK.S
260	174	214	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	R.ISAFGYLEC*SAK.T
98	335	215	P23396	RPS3 40S ribosomal protein S3	RPS3	R.AC*YGVLR.F
91	354	216	Q8TEW0	PARD3 Partitioning defective 3 homolog	PARD3	K.VTVC*FGR.T
347	428	217	P45880	VDAC2 Voltage-dependent anion-selective channel protein	VDAC2	K.SC*SGVEFSTSGSSNTDTGK.V
449	87	218	Q06203	PPAT Amidophosphoribosyltransferase	PPAT	K.C*ELENCQPFVVETLHGK.I
276	395	219	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.YVLC*TAPR.A
416	59	220	P16455	MGMT Methylated-DNA--protein-cysteine methyltransferase	MGMT	R.VVC*SSGAVGNYSGGLAVK.E
244	454	221	Q9UBT2	UBA2 SUMO-activating enzyme subunit 2	UBA2	R.VLVVGAGGIGC*ELLK.N
151	150	222	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	K.LGSAVVTRGDEC*GLALGR.L
357	159	223	Q9Y6D5	ARFGEF2 Brefeldin A-inhibited guanine nucleotide-exchange	ARFGEF2	K.ANFIEADKYFLPFELAC*QSK.S
140	260	224	Q29RF7	PDS5A Sister chromatid cohesion protein PDS5 homolog A	PDS5A	R.ELLDLHKQPTSEANC*SAMFGK.L
318	221	225	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	K.LQGATC*NNNK.L
455	400	226	Q92797	SYMPK Symplekin	SYMPK	K.ATNLC*FAER.N
351	183	227	P45984	MAPK9 Mitogen-activated protein kinase 9	MAPK9	R.TAC*TNFMMTPYVVTR.Y
133	300	228	P46782	RPS5 40S ribosomal protein S5	RPS5	R.VNQAIWLLC*TGAR.E
747	42	229	P10599	TXN Thioredoxin	TXN	K.LVVVDFSATWC*GPC*K.M
589	302	230	Q92879	CELF1 CUGBP Elav-like family member 1	CELF1	R.GC*AFVTFTTR.A
176	253	231	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	K.ITGC*ASPGK.T
175	156	232	Q9Y5Q8	GTF3C5 General transcription factor 3C polypeptide 5	GTF3C5	R.VC*TNPVDR.K
259	294	233	O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	R.ANSSVVSVNC*K.G
262	287	234	Q96CD2	PPCDC Phosphopantothenoylcysteine decarboxylase	PPCDC	K.ASC*PAAAPLMER.K
331	439	235	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.TLTSC*FLSCVVCVEGIVTK.C
330	367	236	B5ME19	EIF3CL Eukaryotic translation initiation factor 3 subunit	EIF3CL	R.GC*ILTLVER.M

2.1	1.2	0.0	0.0	1.7	1.6	1.2	2.0	2.4	2.3	1.7	1.9	1.6	0.0	2.1	0.0	1.9	1.8
1.6	1.8	1.5	1.6	1.7	1.6	3.1	2.3	2.3	3.1	1.9	2.5	1.2	1.4	1.7	1.4	1.4	1.4
1.8	1.6	1.4	1.9	1.5	1.6	0.0	0.0	1.5	1.6	1.1	1.4	2.3	1.9	4.4	2.6	3.4	2.9
1.7	1.6	1.6	1.9	1.5	1.6	3.5	4.0	4.4	3.7	4.0	3.9	3.2	4.6	4.8	4.6	5.3	4.5
1.4	1.2	2.4	1.7	1.5	1.6	3.8	3.6	3.1	3.0	2.2	3.1	0.2	0.2	0.3	0.2	0.2	0.2
0.0	1.1	2.6	0.0	1.3	1.6	1.0	3.2	3.5	3.4	3.9	3.0	1.6	0.0	1.6	1.5	2.3	1.8
1.5	1.5	1.7	1.8	1.6	1.6	2.7	2.6	3.3	2.8	2.8	2.8	4.7	5.8	7.0	4.5	7.1	5.8
1.6	1.6	1.5	1.9	1.6	1.6	2.3	2.7	3.4	2.5	2.6	2.7	2.4	2.6	3.5	3.1	3.6	3.0
1.2	1.6	1.8	2.1	1.4	1.6	5.2	6.8	5.4	4.4	4.4	5.2	3.6	4.8	5.0	3.8	4.8	4.4
0.0	0.0	1.5	1.8	1.6	1.6	2.2	1.5	1.9	1.9	2.1	1.9	2.0	1.3	1.9	1.2	1.5	1.6
1.9	1.4	1.7	1.6	1.5	1.6	3.7	3.1	3.3	4.9	2.7	3.5	5.6	7.1	0.0	6.6	0.0	6.4
1.9	1.2	1.8	1.8	1.5	1.6	2.7	3.2	3.0	3.8	2.8	3.1	1.7	2.6	3.3	3.5	1.6	2.5
1.7	1.7	1.5	1.7	1.6	1.6	2.4	1.9	2.3	0.0	1.9	2.1	4.4	4.6	6.8	5.2	6.1	5.4
1.7	1.7	1.5	1.7	1.6	1.6	0.0	1.9	2.3	2.1	1.9	2.0	4.4	0.0	6.9	5.2	6.1	5.6
1.8	1.4	1.6	0.0	0.0	1.6	1.5	1.6	0.0	0.0	2.3	1.8	1.9	2.1	1.8	1.9	2.0	1.9
1.6	1.3	1.4	1.7	2.1	1.6	4.7	3.9	5.1	3.5	4.7	4.4	1.4	1.5	1.9	1.7	1.6	1.6
1.6	1.5	1.6	1.6	1.6	1.6	2.0	2.0	2.1	0.0	1.6	1.9	2.0	2.3	2.9	2.2	2.6	2.4
1.7	1.6	1.4	1.6	1.7	1.6	6.1	5.2	3.3	4.1	5.0	4.7	1.6	1.7	1.9	1.8	1.7	1.7
1.6	1.5	1.6	1.7	1.5	1.6	1.4	1.8	1.7	1.8	1.8	1.7	2.0	2.2	3.3	2.5	3.2	2.7
1.7	1.5	1.5	1.7	1.6	1.6	2.8	3.6	3.3	3.7	3.2	3.3	3.7	3.4	4.6	4.1	3.9	3.9
0.0	0.0	1.7	1.6	1.6	1.6	4.6	3.3	2.8	3.2	2.2	3.2	1.5	1.9	2.2	2.0	2.0	1.9
1.3	1.5	1.4	1.5	2.3	1.6	2.9	2.3	3.0	2.6	1.9	2.6	3.7	3.8	4.9	3.8	4.6	4.2
1.8	1.9	1.5	1.5	1.2	1.6	1.9	3.6	3.0	3.4	2.2	2.8	1.4	2.1	2.3	2.0	2.8	2.1
0.0	1.5	1.5	1.8	1.6	1.6	2.1	1.5	1.9	1.9	2.1	1.9	2.0	1.3	1.9	1.2	1.8	1.6
1.6	1.4	1.6	1.6	1.7	1.6	3.0	3.6	2.9	2.8	2.8	3.0	1.8	1.8	2.3	1.9	2.0	1.9
1.6	1.5	0.0	0.0	1.6	1.6	2.4	2.5	2.6	2.3	1.8	2.3	3.8	3.7	5.3	3.5	5.6	4.4
1.5	1.2	2.1	1.7	1.4	1.6	6.0	7.7	3.3	5.2	4.4	5.3	0.6	0.6	0.9	0.9	0.8	0.8
1.8	1.5	1.5	1.5	1.7	1.6	1.8	2.4	2.6	2.6	2.2	2.3	1.2	1.4	1.6	1.5	1.3	1.4
1.6	1.4	1.7	1.7	1.5	1.6	3.0	3.1	2.2	2.3	2.5	2.6	2.1	4.7	3.9	3.5	2.8	3.4
1.6	1.1	1.7	2.0	1.5	1.6	4.0	0.0	3.4	3.1	2.6	3.3	2.6	3.9	0.0	3.9	3.2	3.4
1.7	1.4	1.6	1.8	1.5	1.6	2.4	2.3	2.2	2.7	2.2	2.4	2.0	2.4	3.0	2.5	2.7	2.5
1.4	1.5	1.7	1.8	1.6	1.6	3.0	2.2	2.1	2.2	2.5	2.4	1.9	2.5	3.0	2.6	2.6	2.5
2.4	1.4	1.1	1.6	1.4	1.6	0.0	1.9	1.7	2.0	1.6	1.8	2.2	1.6	2.7	2.2	1.5	2.0
1.6	0.0	1.7	1.1	2.0	1.6	2.0	1.9	2.0	0.0	2.0	2.0	2.0	2.1	2.8	2.3	1.0	2.0

120	128	237	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	K.HLC*QQLQAEQAAAEK.R
97	370	238	P46782	RPS5 40S ribosomal protein S5	RPS5	K.AQC*PIVER.L
639	366	239	Q00765	REEP5 Receptor expression-enhancing protein 5	REEP5	K.NC*MTDLLAK.L
452	401	240	P14678	SNRPB Small nuclear ribonucleoprotein-associated protein	SNRPB	R.C*ILQDGR.I
212	281	241	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.LGVENC*YFPMFVSQSALEK.E
501	204	242	Q96I99	SUCLG2 Succinyl-CoA ligase	SUCLG2	R.SC*NGPVLVGSPQGGVDIEEVAASNPELIFK.E
302	230	243	Q7Z2W4	ZC3HAV1 Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	K.NSNVDSSYLESLYQSC*PR.G
148	261	244	Q9Y285	FARSA Phenylalanine--tRNA ligase alpha subunit	FARSA	K.VNLQMVYDSPLC*R.L
123	284	245	P60866	RPS20 40S ribosomal protein S20	RPS20	K.TPC*GEGSK.T
122	344	246	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.VC*VETVESGAMTK.D
422	398	247	P41240	CSK Tyrosine-protein kinase CSK	CSK	R.SVLGGDC*LLK.F
338	289	248	P38606	ATP6V1A V-type proton ATPase catalytic subunit A	ATP6V1A	R.VLDALFPCVQGGTTAIPGAFGC*GK.T
569	321	249	P60981	DSTN Destrin	DSTN	K.HEC*QANGPEDLNR.A
570	324	250	Q6XZF7	DNMBP Dynamin-binding protein	DNMBP	R.SLDQTSPC*PLVLVR.I
135	109	251	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	R.GNVC*GDSK.S
369	416	252	O75439	PMPCB Mitochondrial-processing peptidase subunit beta	PMPCB	R.LC*TSVTESEVAR.A
642	325	253	P0CW22	RPS17L 40S ribosomal protein S17-like	RPS17L	R.VC*EEIAIIPSK.K
339	464	254	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	R.LFC*VGFTK.K
635	317	255	P55263	ADK Adenosine kinase	ADK	R.TGC*TFPEKPDFH.-
647	478	256	Q96EY5	FAM125A Multivesicular body subunit 12A	FAM125A	K.SC*SPLAFSAFGDLTIK.S
246	58	257	P19838	NFKB1 Nuclear factor NF-kappa-B p105 subunit	NFKB1	R.YVC*EGPSHGGLPGASSEK.N
79	264	258	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	K.GC*LLYGPPGTGK.T
42	376	259	P58107	EPPK1 Epiplakin	EPPK1	R.YLC*GLGAVGGVR.L
221	365	260	Q9P2R7	SUCLA2 Succinyl-CoA ligase	SUCLA2	R.IC*NQVLVCER.K
111	262	261	P35914	HMGCL Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	K.LLEAGNFIC*QALNR.K
372	166	262	Q9BUL9	RPP25 Ribonuclease P protein subunit p25	RPP25	R.SEEAPAGC*GAEGGGPGSGPFADLAPGAVHMR.V
75	279	263	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.DLAGC*IHGLSNVK.L
211	286	264	P62191	PSMC1 26S protease regulatory subunit 4	PSMC1	K.AIC*TEAGLMALR.E
107	147	265	Q13418	ILK Integrin-linked protein kinase	ILK	K.FSFQC*PGR.M
539	225	266	Q93052	LPP Lipoma-preferred partner	LPP	K.TYITDPVSAPC*APPLQPK.G
182	301	267	Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multif	AIMP2	R.SC*ENLAPFNTALK.L
333	357	268	Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	K.DC*EVVMMIGLPGAGK.T
396	504	269	Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	R.LSTLC*PSAVLQR.L
652	489	270	O95747	OXSR1 Serine/threonine-protein kinase OSR1	OXSR1	K.C*QTSMDELLK.E

1.7	0.9	1.6	1.6	1.9	1.6	0.0	4.1	3.7	2.8	3.9	3.6	4.0	5.0	5.4	0.0	4.5	4.7
1.6	1.6	1.3	1.7	1.6	1.6	2.0	2.3	1.7	2.0	1.9	2.0	5.1	5.1	6.0	5.9	5.1	5.4
0.0	1.5	1.3	2.1	1.4	1.6	2.1	2.0	1.9	2.1	1.9	2.0	1.2	1.3	0.0	1.3	1.4	1.3
1.6	0.0	1.4	1.7	1.5	1.6	1.6	1.9	2.1	2.2	1.7	1.9	1.3	2.0	1.6	1.7	0.0	1.6
0.0	1.3	1.3	1.8	1.8	1.5	2.6	2.8	2.4	2.3	2.2	2.4	2.6	2.6	3.5	3.1	3.2	3.0
1.6	1.4	1.4	1.7	1.6	1.5	3.0	2.9	2.8	3.0	2.9	2.9	1.4	1.4	1.4	1.9	1.7	1.5
1.2	1.3	1.6	1.9	1.7	1.5	3.8	2.5	2.3	2.9	2.3	2.8	2.1	2.5	2.7	1.8	1.9	2.2
1.1	1.5	1.6	2.0	1.6	1.5	2.9	3.0	2.5	2.4	2.0	2.5	4.6	3.0	4.4	0.0	3.9	4.0
1.6	1.5	1.5	1.7	1.5	1.5	2.6	2.6	2.4	2.3	2.2	2.4	3.9	4.0	5.7	4.7	4.7	4.6
1.4	1.4	1.4	2.0	1.5	1.5	2.1	2.1	2.1	2.4	1.7	2.1	3.5	5.0	4.4	5.2	5.3	4.7
0.0	1.4	1.4	1.6	1.7	1.5	2.5	1.8	1.8	0.0	1.5	1.9	1.6	1.7	0.0	1.8	1.7	1.7
1.6	1.5	1.4	1.6	1.6	1.5	2.2	2.9	2.4	2.4	2.0	2.4	1.7	1.9	2.3	0.0	2.1	2.0
1.5	1.4	1.7	1.6	1.5	1.5	1.9	2.3	2.4	2.6	1.9	2.2	1.3	1.2	1.5	1.4	1.8	1.4
1.2	2.0	1.4	1.5	1.5	1.5	0.0	2.6	1.2	2.9	2.0	2.2	1.6	1.2	0.0	1.6	1.4	1.4
1.5	1.6	1.4	1.8	1.3	1.5	0.0	3.5	4.2	3.5	4.6	4.0	3.8	4.0	5.2	4.1	4.3	4.3
2.0	1.6	1.4	1.3	1.3	1.5	1.5	2.1	1.9	0.0	0.0	1.8	1.7	0.0	0.0	2.1	1.7	1.9
1.5	1.4	1.6	1.7	1.5	1.5	2.3	2.3	2.3	2.1	2.0	2.2	1.2	1.4	1.3	1.3	1.4	1.3
1.6	1.6	1.6	1.2	1.6	1.5	1.9	1.8	1.7	1.4	1.5	1.7	1.7	1.6	2.3	2.2	2.3	2.0
1.4	1.4	1.4	1.8	1.5	1.5	0.0	2.1	2.6	2.3	1.8	2.2	1.2	1.3	1.5	1.3	1.3	1.3
1.1	1.5	1.5	2.1	1.4	1.5	1.9	1.9	1.7	1.3	1.4	1.6	1.1	1.1	1.6	1.2	1.4	1.3
1.5	1.5	1.5	1.6	1.5	1.5	5.1	5.1	3.5	0.0	5.2	4.7	2.5	2.4	3.2	2.7	2.4	2.6
1.5	1.8	0.7	1.8	1.7	1.5	2.1	3.0	0.9	3.0	3.6	2.5	7.1	5.5	5.2	0.0	6.6	6.1
1.4	1.6	1.3	1.5	1.6	1.5	1.9	2.1	1.8	2.0	2.0	2.0	6.9	6.8	11.4	7.5	7.4	8.0
1.7	1.1	1.8	0.0	1.4	1.5	2.2	1.8	2.1	1.9	1.9	2.0	0.0	3.9	3.3	2.4	1.9	2.9
1.4	1.3	1.6	1.7	1.5	1.5	2.4	2.5	2.6	2.7	2.5	2.5	5.0	4.3	0.0	0.0	5.7	5.0
1.4	1.5	1.5	1.5	1.5	1.5	3.5	3.3	3.2	3.6	2.3	3.2	1.6	0.0	2.2	1.8	1.9	1.8
1.5	1.4	1.5	1.7	1.5	1.5	2.7	2.8	1.8	2.7	2.3	2.5	5.2	5.9	7.3	6.3	7.1	6.3
1.5	1.4	1.6	1.6	1.4	1.5	2.3	2.5	2.6	2.5	2.1	2.4	0.0	2.5	3.2	2.9	3.5	3.0
1.5	1.3	1.5	1.5	1.6	1.5	4.5	3.6	2.8	3.5	2.4	3.4	4.8	5.3	0.0	4.3	6.3	5.2
1.4	1.4	1.4	1.7	1.5	1.5	3.6	3.4	2.5	2.7	1.8	2.8	1.2	1.4	1.7	1.5	1.5	1.5
1.0	1.7	1.4	1.7	1.6	1.5	2.4	2.2	2.4	2.5	2.1	2.3	2.8	2.7	3.7	3.5	4.0	3.3
2.1	1.6	1.3	1.3	1.1	1.5	2.8	1.8	1.9	1.8	1.7	2.0	1.6	2.5	2.0	1.8	2.2	2.0
1.0	1.8	2.0	1.3	1.2	1.5	1.9	1.1	1.4	2.5	0.8	1.5	1.7	1.6	2.4	0.9	2.4	1.8
1.4	1.0	2.0	1.3	1.6	1.5	1.2	2.4	1.0	1.0	2.5	1.6	1.1	0.0	1.4	1.3	1.4	1.3

384	508	271	P11413	G6PD Glucose-6-phosphate 1-dehydrogenase	G6PD	R.TQVC*GILR.E
193	372	272	O00148	DDX39A ATP-dependent RNA helicase DDX39A	DDX39A	R.AIVDC*GFEHPSEVQHECIPQAILGMDVLCQAK.S
400	383	273	Q5T4S7	UBR4 E3 ubiquitin-protein ligase UBR4	UBR4	K.AVQC*LNTSSK.E
232	312	274	Q13636	RAB31 Ras-related protein Rab-31	RAB31	K.VC*LLGDTGVGK.S
101	406	275	P11498	PC Pyruvate carboxylase, mitochondrial	PC	R.FLYEC*PWR.R
81	91	276	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	K.ERVC*NLIDSGTK.E
184	195	277	O14976	GAK Cyclin-G-associated kinase	GAK	R.AIIQEVC*FMK.K
645	268	278	Q9UL25	RAB21 Ras-related protein Rab-21	RAB21	K.VVLLGEGC*VGK.T
573	333	279	O15355	PPM1G Protein phosphatase 1G	PPM1G	K.C*SGDGVGAPR.L
436	424	280	Q9Y277	VDAC3 Voltage-dependent anion-selective channel protein	VDAC3	K.VC*NYGLTFTQK.W
46	363	281	P09429	HMGB1 High mobility group protein B1	HMGB1	K.MSSYAFFVQTC*R.E
147	337	282	P62241	RPS8 40S ribosomal protein S8	RPS8	R.LDVGNFSWGSEC*CTR.K
332	175	283	P30281	CCND3 G1/S-specific cyclin-D3	CCND3	R.ASYFQC*VQR.E
315	440	284	Q9NY27	PPP4R2 Serine/threonine-protein phosphatase 4 regulatory	PPP4R2	K.EVC*PVLDQFLCHVAK.T
154	142	285	P51153	RAB13 Ras-related protein Rab-13	RAB13	R.LLLGNKC*DMEAK.R
373	255	286	Q06330	RBPJ Recombining binding protein suppressor of hairless	RBPJ	R.IIQFQATPC*PK.E
268	122	287	P46013	MKI67 Antigen KI-67	MKI67	R.KADVEGELLAC*R.N
185	254	288	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.QGEYGLASIC*NGGGGASAMLIQK.L
288	443	289	Q9Y2Q3	GSTK1 Glutathione S-transferase kappa 1	GSTK1	K.ETTEAAC*R.Y
397	450	290	Q00610	CLTC Clathrin heavy chain 1	CLTC	R.IHEGC*EEPATHNALAK.I
417	407	291	P50570	DNM2 Dynamin-2	DNM2	K.LQDAFSSIGQSC*HLDLPQIAVVGGQSAGK.S
574	616	292	P21333	FLNA Filamin-A	FLNA	K.AHVVPC*FDASK.V
248	274	293	Q14C86	GAPVD1 GTPase-activating protein and VPS9 domain-containi	GAPVD1	R.FSLC*SDNLEGISEGPSNR.S
616	473	294	Q9UJU6	DBNL Drebrin-like protein	DBNL	R.AEEDVEPEC*IMEK.V
142	377	295	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.TVLIAC*NVK.Q
631	19	296	Q9Y3A3	MOB4 MOB-like protein phocein	MOB4	R.HTLDGAAC*LLNSNK.Y
287	622	297	Q969H4	CNKSR1 Connector enhancer of kinase suppressor of ras 1	CNKSR1	K.NLLQLC*PQSLEALAVR.S
234	313	298	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	R.HIIEDPC*TLR.H
194	162	299	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	R.ADHQPLTEASYVNLPTIALC*NTDSPLR.Y
442	360	300	P49327	FASN Fatty acid synthase	FASN	K.ADEASELAC*PTPK.E
329	409	301	Q6P996	PDXDC1 Pyridoxal-dependent decarboxylase domain-containin	PDXDC1	R.HSC*DALNR.W
191	191	302	Q27J81	INF2 Inverted formin-2	INF2	R.AVLLASDAQEC*TLEEVVER.L
319	296	303	Q15208	STK38 Serine/threonine-protein kinase 38	STK38	K.LSDFGLC*TGLK.K
582	331	304	Q9H1B7	IRF2BPL Interferon regulatory factor 2-binding protein-lik	IRF2BPL	K.EGVPGADMLPQPYLDASC*PMLPTALVSLSR.A
150	97	305	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	R.QAVLGAGLPISTPC*TTINK.V

1.4	1.3	1.5	1.7	1.4	1.5	1.8	1.6	1.5	1.6	1.3	1.5	2.8	1.2	1.7	1.7	1.6	1.8
1.5	0.0	1.3	1.6	1.5	1.5	2.0	2.1	1.9	2.1	1.8	2.0	2.9	2.6	4.1	0.0	3.3	3.2
2.0	1.2	1.3	1.4	1.3	1.5	1.1	2.2	2.0	2.2	2.2	1.9	1.5	1.5	3.0	1.2	1.6	1.8
1.6	1.3	1.5	1.5	1.4	1.5	1.9	2.7	2.2	2.3	2.1	2.2	1.9	2.7	3.7	2.8	2.8	2.8
1.5	1.5	1.4	1.4	1.6	1.5	2.0	2.3	1.7	1.3	2.2	1.9	4.4	0.0	5.7	5.2	6.0	5.3
1.5	1.4	1.4	1.7	1.3	1.5	3.4	5.2	3.9	4.5	4.7	4.3	4.7	4.1	7.8	7.7	5.8	6.0
0.0	1.5	1.5	1.5	1.3	1.5	4.6	2.9	2.1	3.2	1.9	3.0	2.7	3.0	3.8	3.4	3.7	3.3
1.4	1.4	1.4	1.6	1.5	1.4	2.9	2.6	2.3	2.4	2.3	2.5	1.1	1.3	1.5	1.2	1.4	1.3
1.3	1.5	1.5	1.5	1.5	1.4	2.3	2.1	1.9	2.6	1.8	2.1	1.2	1.3	1.8	1.5	1.5	1.4
0.0	1.3	1.9	1.6	1.0	1.4	1.9	1.9	2.1	1.5	1.6	1.8	1.3	1.7	2.0	1.5	1.8	1.6
1.4	1.7	1.4	1.4	1.4	1.4	0.6	0.0	1.1	4.1	2.2	2.0	5.0	0.0	11.2	0.0	7.0	7.7
0.0	1.3	1.5	1.6	1.4	1.4	2.4	0.0	2.1	0.0	1.8	2.1	3.4	3.4	5.6	0.0	3.6	4.0
1.5	1.4	1.3	1.5	1.5	1.4	3.6	3.3	3.2	2.9	2.5	3.1	1.8	1.9	2.4	2.2	1.9	2.0
1.4	1.3	1.3	1.4	1.8	1.4	1.6	1.7	1.7	2.0	1.8	1.8	2.7	1.4	2.5	1.8	2.2	2.1
1.4	1.4	1.4	1.6	0.0	1.4	4.2	0.0	3.8	2.6	3.0	3.4	2.7	3.0	3.5	7.1	3.2	3.9
1.1	2.0	1.0	0.0	1.7	1.4	2.6	2.6	2.2	3.3	2.3	2.6	0.0	1.5	2.5	1.5	0.0	1.8
0.0	1.3	1.3	2.2	1.0	1.4	0.0	4.4	3.5	0.0	3.3	3.7	2.3	0.0	0.0	2.4	2.8	2.5
0.0	1.7	1.2	1.5	1.3	1.4	2.9	2.8	2.4	2.5	2.5	2.6	3.3	3.1	3.9	3.1	3.2	3.3
0.0	1.1	1.2	1.9	1.5	1.4	1.8	1.7	1.9	1.6	1.7	1.7	0.0	2.2	2.3	2.4	0.0	2.3
1.6	1.1	1.4	1.6	1.5	1.4	2.6	1.6	1.4	1.3	1.6	1.7	1.6	1.7	1.8	1.9	1.8	1.8
1.6	1.4	1.3	0.0	1.5	1.4	0.0	2.2	0.0	1.9	1.6	1.9	1.2	0.0	2.0	0.0	2.0	1.7
0.0	1.2	1.9	0.0	1.2	1.4	1.4	1.2	1.2	1.2	1.1	1.2	1.3	1.3	1.8	1.3	1.5	1.4
1.2	1.8	1.1	1.5	0.0	1.4	2.6	2.9	2.5	2.5	2.0	2.5	2.2	2.9	2.7	0.0	0.0	2.6
1.1	1.1	1.5	1.7	1.6	1.4	1.7	1.4	1.8	1.4	1.9	1.6	1.0	1.5	1.7	0.0	1.3	1.4
1.4	1.7	1.2	1.3	1.5	1.4	1.4	2.0	2.3	2.0	2.1	2.0	4.8	0.0	0.0	3.6	4.1	4.1
1.4	1.4	1.4	1.5	1.4	1.4	6.5	7.6	6.4	7.7	6.0	6.9	1.2	1.3	1.5	1.4	1.3	1.3
0.0	1.1	1.4	1.7	1.5	1.4	0.0	1.3	1.2	1.3	1.1	1.2	2.2	0.0	2.7	0.0	2.0	2.3
1.6	1.2	1.3	1.6	1.4	1.4	3.0	2.3	2.1	2.0	1.9	2.2	1.9	2.7	3.4	2.4	3.4	2.8
1.4	1.3	1.5	1.7	1.3	1.4	3.8	3.1	2.9	2.9	3.2	3.2	2.3	3.3	3.4	3.9	3.2	3.2
1.3	1.3	1.3	1.8	1.4	1.4	2.2	2.2	1.6	2.4	1.6	2.0	1.3	1.8	2.0	1.8	1.4	1.6
1.2	1.6	0.0	1.4	1.4	1.4	0.0	1.4	1.5	2.6	0.0	1.9	0.0	1.5	2.7	2.0	0.0	2.0
1.5	1.0	1.5	2.0	1.1	1.4	3.3	3.2	2.2	3.1	3.1	3.0	2.6	2.5	3.9	3.6	3.5	3.2
1.6	1.6	1.3	1.2	1.3	1.4	3.4	2.1	2.1	0.0	1.8	2.3	2.0	2.1	2.5	1.9	1.9	2.1
1.6	0.0	1.0	1.6	0.0	1.4	0.0	2.4	2.2	2.6	1.5	2.2	1.2	1.5	1.5	0.0	1.5	1.4
1.3	1.4	1.4	1.4	1.4	1.4	4.3	4.9	3.7	4.4	3.9	4.2	3.5	4.1	4.4	3.8	4.0	4.0

296	231	306	Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	R.NPVSQC*MR.G
403	322	307	Q05655	PRKCD Protein kinase C delta type	PRKCD	K.VLMSVQYFLEDVDC*K.Q
381	587	308	Q8N1F7	NUP93 Nuclear pore complex protein Nup93	NUP93	K.SSGQSAQLLSHEPGDPPC*LR.R
402	472	309	Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	K.NC*IGDFLK.T
25	233	310	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.PMC*VESFSDYPPLGR.F
519	570	311	A0AVT1	UBA6 Ubiquitin-like modifier-activating enzyme 6	UBA6	R.KPNVGC*QQDSEELLK.L
218	538	312	P84085	ARF5 ADP-ribosylation factor 5	ARF5	K.NIC*FTVWDVGGQDK.I
214	272	313	P62316	SNRPD2 Small nuclear ribonucleoprotein Sm D2	SNRPD2	K.NNTQVLINC*R.N
152	332	314	P18085	ARF4 ADP-ribosylation factor 4	ARF4	K.NIC*FTVWDVGGQDR.I
365	492	315	Q6P2E9	EDC4 Enhancer of mRNA-decapping protein 4	EDC4	K.SC*QAMFQQINDSFR.L
354	389	316	Q96EB1	ELP4 Elongator complex protein 4	ELP4	K.VEPC*SLTPGYTK.L
673	288	317	P22102	GART Trifunctional purine biosynthetic protein adenosin	GART	K.QVLVAPGNAGTAC*SEK.I
432	299	318	O43684	BUB3 Mitotic checkpoint protein BUB3	BUB3	R.TPC*NAGTFSQPEK.V
228	116	319	Q9ULV4	CORO1C Coronin-1C	CORO1C	K.C*DLISIPK.K
274	234	320	P63220	RPS21 40S ribosomal protein S21	RPS21	K.TYAIC*GAIR.R
360	578	321	Q9BXJ9	NAA15 N-alpha-acetyltransferase 15, NatA auxiliary subun	NAA15	R.LFNTAVC*ESK.D
627	491	322	P22314	UBA1 Ubiquitin-like modifier-activating enzyme 1	UBA1	K.SIPIC*TLK.N
281	258	323	P49327	FASN Fatty acid synthase	FASN	R.LSIPTYGLQC*TR.A
257	241	324	Q9UN37	VPS4A Vacuolar protein sorting-associated protein 4A	VPS4A	K.LLEPVVC*MSDMLR.S
261	345	325	Q15813	TBCE Tubulin-specific chaperone E	TBCE	R.NCAVSC*AGEK.G
414	298	326	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	K.C*NTNTAIELK.L
448	420	327	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.SQETEC*TYFSTPLLLGK.K
395	369	328	P49368	CCT3 T-complex protein 1 subunit gamma	CCT3	R.TLIQNC*GASTIR.L
54	99	329	P48556	PSMD8 26S proteasome non-ATPase regulatory subunit 8	PSMD8	K.C*GEELGR.L
202	280	330	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	R.YVDIAIPC*NNK.G
279	285	331	P67936	TPM4 Tropomyosin alpha-4 chain	TPM4	K.EENVGLHQTLDQTLNELNC*I.-
286	385	332	P20073	ANXA7 Annexin A7	ANXA7	R.LGTDESC*FNMILATR.S
64	12	333	Q9GZZ9	UBA5 Ubiquitin-like modifier-activating enzyme 5	UBA5	R.EGVC*AASLPTTMGVVAGILVQNVLK.F
458	399	334	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	K.YC*SGTGWPSFSEAHGTSGSDESHTGILR.R
440	124	335	P12532	CKMT1B Creatine kinase U-type, mitochondrial	CKMT1B	R.LGYILTC*PSNLGTGLR.A
102	243	336	Q9NP73	ALG13 UDP-N-acetylglucosamine transferase subunit ALG13	ALG13	K.ADLVISHAGAGSC*LETLEK.G
368	637	337	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.FFSDC*K.I
460	482	338	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	R.DQSAQC*TASK.S
255	170	339	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.DGLTDVYNKIHMGSC*AENTAK.K

1.5	1.3	1.3	1.5	1.4	1.4	2.9	3.5	2.6	2.5	2.2	2.7	2.0	2.1	2.1	2.5	2.6	2.2
0.0	1.2	1.5	0.0	1.5	1.4	0.0	1.7	2.0	3.2	1.9	2.2	0.0	1.6	0.0	1.6	2.1	1.8
1.6	0.0	1.3	0.0	1.3	1.4	1.3	1.4	0.0	1.3	1.1	1.3	1.5	0.0	2.0	0.0	2.0	1.8
0.0	1.5	1.2	1.5	1.4	1.4	1.7	1.7	1.8	0.0	1.4	1.6	1.4	1.6	2.3	1.9	1.7	1.8
1.4	1.3	1.4	1.5	1.4	1.4	3.0	3.0	2.5	3.0	2.2	2.7	10.2	7.5	10.0	11.5	8.8	9.6
1.5	1.6	1.2	1.2	1.4	1.4	1.4	1.2	1.3	1.3	1.2	1.3	1.4	1.4	1.8	1.4	1.5	1.5
1.5	1.5	1.3	1.4	1.3	1.4	1.4	1.1	1.4	1.8	1.4	1.4	2.9	2.6	3.0	3.2	2.9	2.9
1.4	0.0	1.3	1.7	1.1	1.4	1.8	2.8	2.8	2.9	2.0	2.5	2.2	2.8	3.1	2.6	4.3	3.0
1.4	1.2	1.3	1.5	1.5	1.4	2.5	1.9	2.2	2.4	1.6	2.1	3.3	4.3	4.9	3.9	3.3	3.9
1.3	0.0	1.5	1.4	1.4	1.4	2.1	1.3	1.4	0.0	1.6	1.6	1.6	0.0	1.9	2.0	2.1	1.9
1.1	1.3	1.4	1.6	1.5	1.4	2.1	2.1	1.6	0.0	1.9	1.9	1.5	0.0	0.0	1.9	2.3	1.9
0.0	1.2	1.3	1.6	1.4	1.4	2.9	0.0	2.3	2.6	1.9	2.4	0.9	1.3	0.0	0.0	1.5	1.2
1.2	1.5	1.3	1.6	1.2	1.4	1.4	2.5	2.9	2.9	2.0	2.3	1.3	1.4	1.9	1.8	2.0	1.7
1.4	1.3	1.3	1.5	1.4	1.4	4.2	4.5	3.3	3.3	3.6	3.8	2.3	2.8	3.4	2.9	2.6	2.8
1.2	1.7	1.2	1.2	1.5	1.4	3.4	3.1	2.4	2.4	2.3	2.7	2.3	2.3	2.6	2.6	2.5	2.4
1.3	1.7	1.2	1.3	1.3	1.4	1.6	1.2	1.2	0.0	1.2	1.3	1.3	0.0	0.0	2.1	2.4	1.9
1.3	1.4	1.4	1.4	1.4	1.4	1.9	1.7	1.5	0.0	1.3	1.6	1.2	1.3	1.5	1.4	1.3	1.3
1.2	1.5	1.4	1.3	1.4	1.4	2.4	3.0	2.5	2.6	2.3	2.6	1.8	2.1	3.0	2.3	2.7	2.4
0.0	1.3	1.1	1.7	1.3	1.4	2.9	3.2	2.8	2.4	2.1	2.7	2.1	2.3	2.8	2.8	2.7	2.5
1.2	1.1	1.5	1.1	1.8	1.4	1.7	2.1	2.2	2.6	1.8	2.1	2.1	2.5	2.7	2.5	2.8	2.5
1.7	1.0	1.6	1.3	1.1	1.4	2.3	3.0	1.8	0.0	2.3	2.3	1.3	1.7	0.0	1.8	2.1	1.7
1.3	1.3	1.4	1.4	1.4	1.4	1.8	1.8	2.0	1.8	1.7	1.8	1.6	1.5	1.8	1.5	1.9	1.6
0.0	0.0	1.2	1.5	1.3	1.4	0.0	2.2	1.9	0.0	1.8	2.0	1.3	2.1	0.0	1.9	0.0	1.8
2.3	1.4	1.0	1.0	1.1	1.3	3.6	4.2	4.1	4.4	4.5	4.2	5.3	0.0	8.9	5.1	9.6	7.2
1.4	1.2	1.4	1.5	1.3	1.3	1.8	3.0	2.8	2.0	2.7	2.5	2.6	3.0	0.0	3.0	3.8	3.1
1.5	1.0	1.4	1.6	1.3	1.3	3.6	2.2	1.7	2.7	1.8	2.4	2.3	0.0	2.3	2.6	2.3	2.4
1.5	1.3	1.2	1.4	1.4	1.3	2.5	1.1	2.3	0.0	1.9	1.9	2.0	3.2	2.5	1.7	2.3	2.3
1.4	1.3	1.3	1.3	1.4	1.3	0.0	0.0	8.0	8.3	6.8	7.7	5.5	0.0	8.3	0.0	5.7	6.5
1.7	1.3	1.1	1.2	1.4	1.3	1.8	2.6	1.7	1.6	1.6	1.9	1.4	1.4	2.0	1.7	0.0	1.6
1.3	1.3	0.0	0.0	1.4	1.3	0.0	4.3	3.2	3.9	3.5	3.7	1.4	1.4	2.1	0.0	1.6	1.6
1.3	1.3	1.3	1.5	1.3	1.3	3.1	3.3	2.6	2.3	2.1	2.7	4.7	5.0	0.0	5.4	5.8	5.2
1.4	1.2	1.5	1.3	1.3	1.3	1.4	1.1	1.0	0.0	1.0	1.1	1.6	1.6	0.0	2.0	2.3	1.9
1.1	1.6	1.3	1.3	1.3	1.3	0.0	1.4	1.8	1.8	1.5	1.6	0.0	1.1	1.9	0.0	1.9	1.6
1.4	1.2	1.3	1.4	1.4	1.3	3.3	3.4	2.7	3.2	3.0	3.1	2.3	2.4	3.1	2.7	2.4	2.6

513	417	340	P49189	ALDH9A1 4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	K.GALMANFLTQGQVC*CNGTR.V
511	500	341	Q9C0C9	UBE2O Ubiquitin-conjugating enzyme E2 O	UBE2O	R.C*YNEMALIR.V
103	266	342	Q9NUU7	DDX19A ATP-dependent RNA helicase DDX19A	DDX19A	K.VLVTTNVC*AR.G
509	445	343	Q14139	UBE4A Ubiquitin conjugation factor E4 A	UBE4A	R.SQQEIC*EQLNINHMIQR.I
180	355	344	Q9BTE3	MCMBP Mini-chromosome maintenance complex-binding protei	MCMBP	R.DASALLDPMEC*TDTAEEQR.V
617	746	345	P19367	HK1 Hexokinase-1	HK1	R.AAQLC*GAGMAAVVDK.I
435	447	346	P15924	DSP Desmoplakin	DSP	K.NQC*TQVVQER.E
269	197	347	P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	R.AALEALGSC*LNNK.Y
401	304	348	E7EQ34	GOSR2 Golgi SNAP receptor complex member 2	GOSR2	K.QVHEIQSC*MGR.L
387	397	349	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	R.ISASC*QHPTAFEEAIPK.S
453	502	350	H3BQZ7	Uncharacterized protein	Uncharacterized	K.EGC*TEVSLLR.V
549	497	351	P49327	FASN Fatty acid synthase	FASN	K.AINC*ATSGVVGLVNCLR.R
701	503	352	P49915	GMPS GMP synthase	GMPS	R.VICAEEPYIC*K.D
343	404	353	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.NMITGTSQADC*AVLIVAAGVGEFEAGISK.N
653	467	354	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	K.C*C*SGAIIVLTK.S
362	277	355	Q9UHD8	SEPT9 Septin-9	42256	R.SQEATEAAPSC*VGDMADTPR.D
292	348	356	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	K.VDENFDC*VEADDVEGK.I
82	573	357	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.SSGGFVWAC*K.N
352	374	358	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	K.AC*QSIYPLHDVFVR.K
405	392	359	P15924	DSP Desmoplakin	DSP	K.AC*GSEIMQK.K
325	249	360	Q86XN7	PROSER1 Proline and serine-rich protein 1	PROSER1	K.DGEEC*TNEGK.G
411	393	361	P33316	DUT Deoxyuridine 5-triphosphate nucleotidohydrolase,	DUT	R.IAQLIC*ER.I
420	514	362	Q9Y296	TRAPPC4 Trafficking protein particle complex subunit 4	TRAPPC4	R.C*ELFDQNLK.L
385	121	363	P13639	EEF2 Elongation factor 2	EEF2	K.STLTDSLVC*K.A
169	318	364	P21964	COMT Catechol O-methyltransferase	COMT	R.GSSC*FECTHYQSFLEYR.E
267	364	365	P62633	CNBP Cellular nucleic acid-binding protein	CNBP	R.C*GESGHLAR.E
206	226	366	P55769	NHP2L1 NHP2-like protein 1	NHP2L1	K.KLLDLVQQSC*NYK.Q
284	138	367	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	R.AAVEEGIVLGGGC*ALLR.C
201	167	368	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitoch	MCCC2	K.AATGEEVSAEDLGGADLHC*R.K
447	419	369	Q06323	PSME1 Proteasome activator complex subunit 1	PSME1	K.VDVFREDLC*TK.T
464	488	370	Q9P1F3	ABRACL Costars family protein ABRACL	ABRACL	K.C*ANLFEALVGTLK.A
163	512	371	Q13330	MTA1 Metastasis-associated protein MTA1	MTA1	R.ALDC*SSSVR.Q
204	90	372	O15075	DCLK1 Serine/threonine-protein kinase DCLK1	DCLK1	R.YQDDFLLDESEC*R.V
532	493	373	Q9NZL4	HSPBP1 Hsp70-binding protein 1	HSPBP1	R.LLDRDAC*DTVR.V

1.6	1.4	0.0	0.0	1.0	1.3	2.6	1.7	1.5	1.6	1.7	1.8	1.6	1.4	1.8	1.2	1.5	1.5
1.2	1.3	1.2	1.5	1.5	1.3	1.9	1.3	1.8	1.5	1.3	1.6	1.5	1.2	1.8	1.6	1.5	1.5
1.4	1.3	1.3	1.3	1.3	1.3	2.8	2.7	2.7	2.4	2.2	2.5	4.4	4.8	6.4	4.9	5.7	5.2
1.4	0.0	1.4	1.3	1.3	1.3	2.1	0.0	1.5	0.0	1.5	1.7	1.4	0.0	1.7	0.0	1.4	1.5
1.4	1.1	1.5	0.0	0.0	1.3	2.0	2.0	0.0	2.3	1.8	2.0	2.2	4.7	4.0	3.4	2.6	3.4
2.0	1.5	1.2	0.9	1.1	1.3	0.7	0.6	0.9	0.7	0.8	0.7	1.1	0.0	2.0	1.1	1.2	1.4
1.1	1.4	1.3	1.3	1.4	1.3	1.9	1.7	1.7	1.6	1.7	1.7	1.5	1.7	0.0	1.7	1.7	1.7
0.0	1.3	1.3	1.6	1.1	1.3	1.3	4.3	3.7	2.2	3.2	3.0	2.1	2.2	0.0	2.9	2.8	2.5
1.2	1.4	1.3	1.3	1.4	1.3	2.3	1.5	1.4	0.0	3.9	2.3	1.6	1.6	2.1	1.6	1.8	1.8
1.3	1.3	1.3	1.4	1.4	1.3	2.4	1.9	1.9	1.8	1.5	1.9	1.7	1.7	2.3	1.7	1.7	1.8
1.3	1.5	1.2	1.2	1.4	1.3	1.8	1.5	1.4	1.6	1.4	1.6	1.5	1.5	2.0	1.5	1.6	1.6
1.3	1.4	1.3	1.5	1.1	1.3	2.3	1.5	1.4	1.5	1.2	1.6	1.3	1.4	1.8	1.3	1.5	1.5
1.2	1.4	1.4	1.3	1.3	1.3	1.7	1.4	1.5	1.7	1.4	1.5	1.0	1.3	0.0	1.3	1.1	1.2
1.3	1.4	1.4	1.3	1.3	1.3	1.4	1.8	2.1	2.1	2.0	1.9	1.8	0.0	2.1	1.8	2.2	2.0
1.2	1.5	1.3	1.3	1.2	1.3	1.6	1.9	1.5	1.9	1.4	1.7	1.1	1.1	1.6	1.3	1.3	1.3
1.2	1.3	1.3	1.6	1.2	1.3	3.3	2.4	1.9	2.5	2.1	2.5	1.6	1.6	2.5	1.7	2.1	1.9
1.3	1.1	1.3	1.5	1.3	1.3	2.9	1.9	1.7	1.8	1.9	2.0	2.1	2.2	2.5	2.4	2.2	2.3
1.4	1.3	1.2	1.3	1.4	1.3	1.8	1.4	1.1	1.2	1.0	1.3	5.1	5.3	7.4	6.1	5.7	5.9
1.2	1.6	1.3	1.4	1.1	1.3	2.8	1.8	1.8	1.8	1.6	2.0	1.2	2.5	2.1	0.0	1.9	1.9
1.5	1.3	1.2	1.2	1.2	1.3	2.4	2.0	2.0	1.6	1.5	1.9	1.5	1.6	2.1	1.8	0.0	1.8
1.4	1.2	1.2	0.0	0.0	1.3	0.0	3.5	2.4	2.6	2.1	2.6	1.5	2.4	0.0	0.0	2.3	2.1
1.4	1.1	1.3	1.3	1.3	1.3	2.5	1.4	2.0	1.9	1.7	1.9	1.5	0.0	1.7	1.8	2.0	1.8
1.5	1.1	1.3	1.3	1.3	1.3	2.1	1.4	1.3	1.6	1.2	1.5	1.6	0.0	2.0	1.8	1.4	1.7
1.3	1.1	1.2	1.3	1.5	1.3	4.4	3.9	3.6	3.4	3.4	3.7	1.5	1.6	2.4	1.7	1.8	1.8
1.4	1.2	1.2	1.3	1.3	1.3	3.4	2.5	1.8	1.8	1.6	2.2	3.6	3.5	0.0	3.7	0.0	3.6
1.1	1.2	1.4	1.4	1.4	1.3	2.3	1.4	2.1	1.9	2.3	2.0	2.2	2.8	2.9	3.1	1.6	2.5
1.3	1.3	1.2	1.3	1.3	1.3	3.2	3.2	2.5	2.9	2.1	2.8	2.4	2.9	3.6	3.4	2.9	3.0
1.3	1.2	1.3	1.3	1.3	1.3	4.1	3.6	3.2	3.7	2.6	3.4	2.6	2.1	0.0	2.4	2.3	2.3
1.4	1.3	1.1	1.3	1.4	1.3	4.0	0.0	2.6	2.8	3.3	3.2	3.1	2.4	3.7	3.2	0.0	3.1
1.2	1.2	1.3	1.5	1.3	1.3	2.0	1.8	1.8	0.0	1.7	1.8	1.4	0.0	0.0	1.9	1.5	1.6
1.1	1.3	1.3	1.4	1.3	1.3	1.8	1.6	1.7	1.5	1.5	1.6	1.3	0.0	2.0	0.0	1.5	1.6
0.0	0.0	1.2	1.6	1.0	1.3	1.0	1.7	0.0	2.1	1.2	1.5	1.4	1.1	6.2	6.3	0.0	3.7
1.3	1.2	1.3	1.4	1.3	1.3	5.6	4.9	4.8	0.0	2.1	4.3	2.8	2.7	3.5	3.1	3.2	3.0
1.2	1.2	1.4	1.3	1.3	1.3	1.8	1.7	1.6	1.6	1.3	1.6	1.3	1.2	2.0	1.5	1.4	1.5

525	495	374	Q9NQC3	RTN4 Reticulon-4	RTN4	K.YSNSALGHVNC*TIK.E
388	442	375	Q9NSD9	FARSB Phenylalanine--tRNA ligase beta subunit	FARSB	K.EYTAC*ELMNIYK.T
561	543	376	Q15459	SF3A1 Splicing factor 3A subunit 1	SF3A1	R.EVLDQVC*YR.V
290	127	377	Q86YS7	KIAA0528 Uncharacterized protein KIAA0528	KIAA0528	R.SAPPC*ANSTVGVVK.M
410	412	378	Q7L5D6	GET4 Golgi to ER traffic protein 4 homolog	GET4	K.EQNYC*ESR.Y
197	308	379	P23921	RRM1 Ribonucleoside-diphosphate reductase large subunit	RRM1	K.IIDINYYPVPEAC*LSNK.R
390	483	380	Q13045	FLII Protein flightless-1 homolog	FLII	R.TGLC*YLPEELAALQK.L
355	38	381	Q9HA64	FN3KRP Ketosamine-3-kinase	FN3KRP	R.ATGHSGGGC*ISQGR.S
312	509	382	Q96P48	ARAP1 Arf-GAP with Rho-GAP domain, ANK repeat and PH dom	ARAP1	R.AVFPEGPC*EEPLQLR.K
419	146	383	Q06587	RING1 E3 ubiquitin-protein ligase RING1	RING1	R.FC*SDCIVTALR.S
199	481	384	P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	K.C*VVVGDGAVGK.T
313	477	385	Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.AVTNHSVYC*STK.G
546	388	386	P60763	RAC3 Ras-related C3 botulinum toxin substrate 3	RAC3	R.AVLC*PPPVK.K
225	451	387	Q9Y2S7	POLDIP2 Polymerase delta-interacting protein 2	POLDIP2	R.DC*PHISQR.S
438	320	388	Q9P258	RCC2 Protein RCC2	RCC2	K.AVQDLC*GWR.I
366	527	389	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.GLPFGC*SK.E
737	555	390	Q15257	PPP2R4 Serine/threonine-protein phosphatase 2A activator	PPP2R4	R.IDYGTGHEAAFAAFLC*C*LC*K.I
566	342	391	Q8IWX8	CHERP Calcium homeostasis endoplasmic reticulum protein	CHERP	K.LALEQQQLIC*K.Q
121	589	392	O43865	AHCYL1 Putative adenosylhomocysteinase 2	AHCYL1	K.LC*VPAMNVNDSVTK.Q
610	209	393	O43390	HNRNPR Heterogeneous nuclear ribonucleoprotein R	HNRNPR	K.SAFLC*GVMK.T
294	114	394	Q8NBF2	NHLRC2 NHL repeat-containing protein 2	NHLRC2	K.AILFSQPLQITDTQQGC*IAPVELR.Y
412	353	395	P49721	PSMB2 Proteasome subunit beta type-2	PSMB2	R.NLADC*LR.S
516	534	396	Q9UPM8	AP4E1 AP-4 complex subunit epsilon-1	AP4E1	R.SSC*STLPDYLLYQCQK.V
700	690	397	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	K.AGSDGAKIGNC*PFSQR.L
346	468	398	O75153	KIAA0664 Clustered mitochondria protein homolog	KIAA0664	K.C*LTQQAVALQR.T
241	524	399	Q8IXH7	TH1L Negative elongation factor C/D	TH1L	R.AC*QALGAMLSK.G
406	469	400	Q9H0W8	SMG9 Protein SMG9	SMG9	R.REDFC*PR.K
545	595	401	P13489	RNH1 Ribonuclease inhibitor	RNH1	R.ELDLSNNC*LGDAGILQLVESVR.Q
459	238	402	Q8NFG4	FLCN Folliculin	FLCN	K.VFEAEQFGC*PQR.A
39	102	403	Q3MIP1	ITPRIPL2 Inositol 1,4,5-trisphosphate receptor-interacting	ITPRIPL2	R.DC*KPFADAFCVDVRGRRHLSATLVLRWFQSHLQR.S
534	519	404	Q6IA69	NADSYN1 Glutamine-dependent NAD(+) synthetase	NADSYN1	K.NSSQETC*TR.A
391	27	405	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.IC*PVETLVEEAIQC*AEK.I
601	506	406	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	K.EADQKEQFSQGSPSNC*LETSLAEIFPLGK.N
423	425	407	P28074	PSMB5 Proteasome subunit beta type-5	PSMB5	K.KVIEINPYLLGTMAGGAADC*SFWER.L

1.1	1.5	1.0	1.3	1.5	1.3	1.8	1.4	1.8	1.5	1.4	1.6	1.3	1.5	1.9	1.3	1.5	1.5
1.3	1.3	1.2	1.4	0.0	1.3	2.4	0.0	2.0	1.1	1.4	1.7	0.0	1.8	2.0	1.7	0.0	1.8
0.0	1.2	0.9	1.6	1.5	1.3	1.5	1.6	1.4	1.3	1.2	1.4	1.3	1.1	1.6	2.0	1.3	1.4
1.1	0.0	1.1	1.6	1.4	1.3	4.5	3.3	3.3	0.0	3.4	3.6	1.6	2.2	2.8	2.1	2.8	2.3
0.0	0.0	1.3	1.1	1.4	1.3	2.4	1.9	1.9	1.6	1.5	1.8	1.5	1.7	2.0	1.7	1.8	1.8
1.4	1.2	1.2	1.3	1.3	1.3	2.5	2.3	2.1	2.4	2.0	2.3	2.7	2.6	4.0	3.3	3.1	3.1
1.2	1.1	1.3	1.4	1.3	1.3	1.9	1.6	1.8	0.0	1.3	1.6	1.4	1.7	0.0	1.9	2.2	1.8
1.2	1.3	1.2	0.0	1.4	1.3	0.0	5.0	6.9	6.3	4.0	5.6	1.6	1.9	2.1	1.6	2.3	1.9
0.0	1.3	1.3	1.4	1.1	1.3	1.9	1.8	1.2	1.3	1.5	1.5	2.1	1.9	2.6	2.1	2.0	2.1
0.9	1.7	1.2	1.3	1.3	1.3	3.5	2.9	2.9	4.0	3.7	3.4	1.9	1.1	2.5	1.5	1.6	1.7
1.2	1.3	1.5	1.1	1.3	1.3	1.9	1.4	1.7	0.0	1.5	1.6	4.6	2.4	0.0	2.3	0.0	3.1
1.3	1.5	1.3	1.2	1.1	1.3	2.0	1.6	1.5	1.6	1.4	1.6	1.9	2.1	2.4	1.9	2.4	2.1
1.1	1.3	0.0	0.0	1.4	1.3	0.0	1.9	1.9	2.1	1.9	1.9	1.3	1.3	1.8	1.5	1.4	1.5
1.6	1.1	1.0	0.0	1.3	1.3	0.0	1.8	0.0	1.6	1.7	1.7	2.1	0.0	4.0	2.4	2.8	2.8
1.3	1.1	1.3	1.4	1.3	1.3	2.2	2.1	1.8	3.3	1.6	2.2	1.3	1.5	2.2	1.6	1.7	1.6
1.5	1.2	1.2	1.3	1.1	1.3	1.5	1.5	1.5	1.4	1.4	1.5	1.5	0.0	1.6	2.2	2.1	1.9
1.2	0.0	1.3	0.8	1.7	1.3	0.7	1.2	1.9	2.0	1.0	1.4	1.3	0.8	1.2	0.8	0.9	1.0
1.1	1.3	1.3	1.2	1.4	1.3	2.5	2.3	1.9	0.0	1.6	2.1	1.3	1.5	0.0	1.4	1.6	1.4
1.2	1.0	1.4	1.2	1.4	1.3	1.4	1.2	1.2	1.2	1.4	1.3	3.9	4.1	6.3	5.0	4.2	4.7
1.4	1.1	1.3	1.3	1.2	1.3	2.7	2.8	3.9	1.6	3.5	2.9	1.2	1.2	1.4	1.4	1.6	1.4
1.3	1.2	1.3	1.3	1.2	1.3	4.0	4.4	3.1	4.8	2.9	3.8	1.9	2.2	2.6	2.3	2.4	2.3
1.3	1.3	1.2	1.2	1.3	1.3	1.9	1.9	1.9	2.8	1.8	2.0	1.7	1.5	2.2	1.6	1.7	1.7
1.3	1.1	1.3	1.3	1.3	1.3	1.7	1.3	1.5	0.0	1.2	1.4	1.4	1.5	1.8	1.3	1.5	1.5
1.3	1.2	1.2	1.3	1.3	1.3	1.0	0.9	1.0	1.0	1.0	1.0	1.1	1.1	1.3	1.1	1.2	1.2
1.3	1.2	1.2	1.3	1.3	1.3	1.8	1.4	1.5	1.8	1.7	1.7	1.6	1.8	2.2	1.8	2.3	2.0
0.7	1.4	1.3	1.3	1.7	1.3	0.8	2.0	1.8	0.0	1.2	1.5	2.6	2.3	3.0	2.5	3.0	2.7
1.4	0.0	1.1	1.2	1.4	1.2	1.7	1.2	1.7	2.2	1.4	1.6	2.2	2.0	1.1	0.0	0.0	1.8
0.0	1.2	1.2	1.3	1.3	1.2	0.0	1.3	1.1	1.4	1.3	1.3	1.3	1.5	1.6	1.4	1.5	1.5
0.0	1.4	0.0	1.1	1.3	1.2	2.3	2.7	3.0	3.5	2.0	2.7	2.1	2.1	0.0	0.7	1.5	1.6
1.3	1.2	1.2	1.5	1.1	1.2	3.0	4.4	5.3	4.2	3.7	4.1	7.1	0.0	0.0	8.6	8.8	8.2
1.1	1.1	1.0	1.8	1.1	1.2	0.0	1.2	1.3	2.4	1.2	1.5	1.3	1.3	1.7	1.5	1.6	1.5
1.2	1.2	1.3	1.4	1.2	1.2	0.0	0.0	6.5	6.1	6.1	6.2	1.7	0.0	1.8	0.0	1.9	1.8
1.4	1.4	1.2	1.0	1.2	1.2	1.8	0.0	1.4	1.5	0.0	1.5	1.1	1.2	1.6	1.7	0.0	1.4
1.2	1.3	1.4	1.2	1.2	1.2	1.0	1.7	2.2	2.2	1.7	1.8	1.5	0.0	1.9	0.0	1.7	1.7

556	742	408	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	R.LC*YSSDHEK.L
273	329	409	Q9UL15	BAG5 BAG family molecular chaperone regulator 5	BAG5	K.TELQGLIGQLDEVSLEKNPC*IR.E
393	402	410	P37235	HPCAL1 Hippocalcin-like protein 1	HPCAL1	R.LLQC*DPSSASQF.-
503	347	411	Q99798	ACO2 Aconitate hydratase, mitochondrial	ACO2	R.DLGGIVLANAC*GPCIGQWDR.K
607	517	412	Q7L2H7	EIF3M Eukaryotic translation initiation factor 3 subunit	EIF3M	K.VAASC*GAIQYIPTELDQVR.K
295	490	413	O14561	NDUFAB1 Acyl carrier protein, mitochondrial	NDUFAB1	K.LMC*PQEIVDYIADKK.D
277	125	414	Q13185	CBX3 Chromobox protein homolog 3	CBX3	R.LTWHSC*PEDEAQ.-
258	338	415	Q9BYG5	PARD6B Partitioning defective 6 homolog beta	PARD6B	R.HGAGSGC*LGTMEVK.S
479	528	416	Q96TA1	FAM129B Niban-like protein 1	FAM129B	K.GPTKEELC*K.S
472	531	417	Q93009	USP7 Ubiquitin carboxyl-terminal hydrolase 7	USP7	K.GTC*VEGTIPK.L
498	536	418	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	R.VFIMDSC*DELIPEYLNFIR.G
492	208	419	Q6P1X6	C8orf82 UPF0598 protein C8orf82	C8orf82	R.YEAAFPFLSPC*GR.E
173	328	420	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.DLNYC*FSGMSDHR.Y
307	436	421	P49840	GSK3A Glycogen synthase kinase-3 alpha	GSK3A	K.LC*DFGSAK.Q
398	501	422	P49327	FASN Fatty acid synthase	FASN	K.LTPGC*EAEAETEAICFFVQQFTDMEHNR.V
350	515	423	O00233	PSMD9 26S proteasome non-ATPase regulatory subunit 9	PSMD9	K.GIGMNEPLVDC*EGYPR.S
340	187	424	O75934	BCAS2 Pre-mRNA-splicing factor SPF27	BCAS2	R.IENLELMSQHGC*NAWK.V
304	186	425	P63220	RPS21 40S ribosomal protein S21	RPS21	K.C*SASNR.I
278	223	426	Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.GVPGAIVNVSSQC*SQR.A
114	323	427	P78406	RAE1 mRNA export factor	RAE1	K.VFTASC*DK.T
392	295	428	Q15233	NONO Non-POU domain-containing octamer-binding protein	NONO	R.C*SEGSFLLTTFPR.P
174	394	429	Q9UPN9	TRIM33 E3 ubiquitin-protein ligase TRIM33	TRIM33	R.C*DPVPAANGAIR.F
713	705	430	Q9P107	GMIP GEM-interacting protein	GMIP	R.LC*QAFENGR.A
378	643	431	O95059	RPP14 Ribonuclease P protein subunit p14	RPP14	R.IC*SSGLVK.L
341	292	432	P55263	ADK Adenosine kinase	ADK	R.SLIANLAAANC*YK.K
540	340	433	Q96RS6	NUDCD1 NudC domain-containing protein 1	NUDCD1	R.DSAQC*AAIAER.L
456	434	434	O75390	CS Citrate synthase, mitochondrial	CS	K.LPC*VAAK.I
209	448	435	O94885	SASH1 SAM and SH3 domain-containing protein 1	SASH1	R.C*GIPEALVQR.Y
473	458	436	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.GSDFDC*ELR.L
578	516	437	Q9NYL2	MLTK Mitogen-activated protein kinase kinase kinase MLT	MLTK	K.FDDLQFFENC*GGGSFGSVYR.A
657	507	438	O95336	PGLS 6-phosphogluconolactonase	PGLS	R.AAC*CLAGAR.A
591	525	439	Q7L1Q6	BZW1 Basic leucine zipper and W2 domain-containing prot	BZW1	R.FDPTQFQDC*IIQGLTETGTDLEAVAK.F
457	547	440	Q9UJW0	DCTN4 Dynactin subunit 4	DCTN4	R.LLQPDFQPVC*ASQLYPR.H
480	627	441	O43795	MYO1B Unconventional myosin-Ib	MYO1B	K.LVMSYVAAVC*GK.G

1.2	1.4	1.1	1.3	1.3	1.2	1.0	0.5	0.7	0.0	0.8	0.7	1.3	0.8	2.2	1.5	0.0	1.4
1.2	1.3	1.1	1.4	1.3	1.2	3.0	1.9	1.8	2.2	2.0	2.2	2.0	0.0	2.8	2.6	0.0	2.5
0.0	1.2	1.3	1.3	1.3	1.2	2.3	1.9	1.7	1.9	1.6	1.9	1.5	1.6	1.7	2.3	1.7	1.8
1.0	1.3	1.1	1.4	1.4	1.2	2.3	2.0	1.7	2.5	1.8	2.1	0.0	1.5	1.6	0.0	1.5	1.5
1.5	1.1	1.2	1.2	1.2	1.2	1.4	1.6	1.4	1.7	1.4	1.5	1.1	1.2	1.6	1.5	1.5	1.4
1.2	1.3	1.3	1.3	1.2	1.2	1.9	0.8	2.8	1.0	1.4	1.6	2.4	2.0	3.0	1.1	2.8	2.2
1.3	1.2	1.2	1.3	1.3	1.2	4.1	4.1	2.9	4.2	3.2	3.7	2.3	2.0	2.4	2.6	2.6	2.4
1.1	1.5	1.1	1.3	1.1	1.2	3.0	1.9	1.9	2.3	1.4	2.1	1.9	0.0	3.3	2.4	2.6	2.5
1.0	1.1	1.2	1.3	1.5	1.2	1.8	1.6	0.0	1.3	1.2	1.5	1.5	1.3	1.9	1.6	1.7	1.6
1.0	1.1	1.2	1.3	1.5	1.2	1.8	1.6	1.4	1.3	1.2	1.4	1.5	1.4	1.9	1.6	1.7	1.6
1.1	1.4	1.2	1.2	1.3	1.2	1.4	1.5	1.4	1.5	1.2	1.4	1.4	1.5	1.8	1.5	1.6	1.5
1.3	1.1	1.2	1.3	1.2	1.2	2.8	3.2	2.8	3.1	2.6	2.9	1.4	1.4	1.8	1.7	1.5	1.6
1.3	1.2	1.2	1.3	1.3	1.2	2.1	2.2	2.1	2.4	2.0	2.2	2.9	3.3	4.2	3.6	3.3	3.5
1.0	1.2	1.0	1.8	1.2	1.2	2.3	1.7	1.7	1.6	1.5	1.8	2.1	2.0	2.7	2.1	1.9	2.2
1.2	1.2	1.1	1.4	1.3	1.2	2.0	0.0	1.4	1.5	1.4	1.6	1.4	1.5	2.5	1.9	1.6	1.8
1.3	1.2	1.2	1.3	1.1	1.2	1.7	1.4	1.5	1.8	1.2	1.5	1.8	1.7	2.1	1.9	2.2	1.9
1.3	1.0	1.2	1.4	1.2	1.2	4.0	0.0	3.1	2.2	2.7	3.0	1.7	0.0	2.8	1.7	1.8	2.0
1.2	0.0	1.2	1.3	1.2	1.2	3.2	3.2	2.9	0.0	2.7	3.0	2.1	2.1	0.0	2.4	2.1	2.2
1.3	1.2	1.1	1.3	1.3	1.2	2.5	3.2	2.8	2.9	2.6	2.8	2.1	2.2	2.9	2.3	2.4	2.4
0.7	0.9	1.2	2.2	1.1	1.2	1.7	3.0	2.3	0.0	1.8	2.2	3.0	4.3	8.6	5.5	3.1	4.9
1.1	1.0	1.4	1.3	1.4	1.2	2.7	2.7	1.9	0.0	2.1	2.4	0.0	1.9	1.8	0.0	1.7	1.8
0.9	1.5	1.0	1.9	0.9	1.2	2.4	2.0	2.1	2.0	1.0	1.9	3.7	3.4	3.0	3.8	3.3	3.5
0.0	1.1	1.2	1.2	1.4	1.2	1.0	1.0	0.0	0.7	1.0	0.9	1.0	1.3	1.3	1.3	0.9	1.1
1.3	0.0	1.2	1.2	1.2	1.2	1.2	1.1	1.1	0.0	1.1	1.1	1.3	2.1	0.0	2.2	0.0	1.8
1.0	1.4	1.2	1.3	1.1	1.2	1.8	1.9	2.4	3.9	1.8	2.4	1.8	1.7	2.6	2.1	1.7	2.0
1.2	1.4	1.0	1.3	1.2	1.2	2.8	2.1	1.9	1.9	1.7	2.1	1.2	1.4	1.9	1.4	1.5	1.5
1.2	1.0	1.2	1.3	1.4	1.2	1.3	2.0	2.0	0.0	1.8	1.8	1.5	0.0	2.0	1.4	1.6	1.6
0.0	0.0	1.1	1.3	1.3	1.2	1.4	2.0	1.7	0.0	1.7	1.7	0.0	2.9	0.0	3.2	2.9	3.0
1.1	1.3	1.3	1.2	1.3	1.2	1.6	1.8	1.6	1.8	1.5	1.7	1.3	1.4	1.9	1.6	1.8	1.6
1.2	1.0	1.1	1.5	1.4	1.2	2.2	1.7	1.2	1.4	1.1	1.5	1.4	0.0	1.5	1.4	0.0	1.4
1.2	1.2	1.1	1.3	1.3	1.2	1.3	1.6	1.6	1.7	1.5	1.5	1.2	1.2	1.5	1.2	1.2	1.3
1.4	1.1	1.2	1.2	1.2	1.2	2.1	1.3	1.4	1.3	1.3	1.5	1.4	1.3	1.6	1.3	1.5	1.4
1.3	1.4	1.0	1.0	1.4	1.2	1.6	1.4	1.2	1.6	1.2	1.4	1.2	1.7	1.7	2.0	1.4	1.6
1.4	1.1	1.1	1.2	1.2	1.2	1.6	1.1	1.2	1.1	0.9	1.2	1.4	1.3	1.9	1.6	1.7	1.6

344	459	442	Q9NVU0	POLR3E DNA-directed RNA polymerase III subunit RPC5	POLR3E	R.AAGTDSFNGHPPQGC*ASTPVAR.E
559	245	443	P62195	PSMC5 26S protease regulatory subunit 8	PSMC5	K.FVVDVDKNIDINDVTPNC*R.V
597	479	444	Q15370	TCEB2 Transcription elongation factor B polypeptide 2	TCEB2	R.ADDTFEALC*IEPFSSPPELPDVMKPQDSGSSANEQAVQ.-
632	661	445	Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	R.VGLGIC*YDMR.F
271	188	446	Q15631	TSN Translin	TSN	K.ETAAAC*VEK.-
445	461	447	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVDVEVPDVELEC*PDAK.L
450	470	448	Q2TAA2	IAH1 Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	R.VILITPTPLC*ETAWEEQCIIQGCK.L
517	414	449	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	R.KENQWC*EEK.-
693	456	450	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	K.SC*AHDWVYE.-
643	695	451	O43765	SGTA Small glutamine-rich tetratricopeptide repeat-cont	SGTA	K.AIELNPANAVYFC*NR.A
213	330	452	P51812	RPS6KA3 Ribosomal protein S6 kinase alpha-3	RPS6KA3	R.AENGLLMTPC*YTANFVAPEVLK.R
497	373	453	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVGVEVPDVELEC*PDAK.L
542	647	454	Q9H3U1	UNC45A Protein unc-45 homolog A	UNC45A	R.AIQTVSC*LLQGPCDAGNR.A
145	729	455	Q12849	GRSF1 G-rich sequence factor 1	GRSF1	R.YIELFLNSC*PK.G
321	247	456	O15355	PPM1G Protein phosphatase 1G	PPM1G	R.GTEAGQVGEPGIPTGEAGPSC*SSASDK.L
466	518	457	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.LFQEC*CPHSTDR.V
434	615	458	O15382	BCAT2 Branched-chain-amino-acid aminotransferase, mitoch	BCAT2	R.EVFGSGTAC*QVCPVHR.I
487	632	459	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	K.YAGLSTC*FR.Q
425	452	460	Q8WW01	TSEN15 tRNA-splicing endonuclease subunit Sen15	TSEN15	R.GDSEPTPGC*SGLGPGGVR.G
628	545	461	Q16630	CPSF6 Cleavage and polyadenylation specificity factor su	CPSF6	R.ELHGQNPVVTPC*NK.Q
289	432	462	P17844	DDX5 Probable ATP-dependent RNA helicase DDX5	DDX5	R.LIDFLEC*GK.T
243	371	463	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.HSMNPFC*EIAVEEAVR.L
275	23	464	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.VC*NFLASQVPFPSR.L
638	444	465	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	K.TRPDGNC*FYR.A
746	540	466	P33240	CSTF2 Cleavage stimulation factor subunit 2	CSTF2	K.LC*VQNSPQEAR.N
537	597	467	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	K.HLNEIDLFHC*IDPNDSK.H
78	139	468	Q6YN16	HSDL2 Hydroxysteroid dehydrogenase-like protein 2	HSDL2	K.TAIHTAAMDMLGGPGIESQC*R.K
470	585	469	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.EGVVEC*SFVK.S
669	176	470	Q13526	PIN1 Peptidyl-prolyl cis-trans isomerase NIMA-interacti	PIN1	K.IKSGEEDFESLASQFSDC*SSAK.A
508	462	471	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	K.QEPLGSDSEGVNC*LAYDEAIMAQQDR.I
118	544	472	O14966	RAB7L1 Ras-related protein Rab-7L1	RAB7L1	K.C*DLSPWAVSR.D
272	80	473	Q9UQ35	SRRM2 Serine/arginine repetitive matrix protein 2	SRRM2	R.SVSPC*SNVESR.L
611	346	474	P13639	EEF2 Elongation factor 2	EEF2	R.YVEPIEDVPC*GNIVGLVGVDQFLVK.T
496	605	475	O14980	XPO1 Exportin-1	XPO1	K.LDINLLDNVVNC*LYHGEGAQQR.M

1.4	1.4	0.9	0.0	0.0	1.2	0.0	1.8	1.4	2.0	1.4	1.7	1.9	1.5	2.5	0.0	2.1	2.0
1.0	1.0	1.4	1.4	1.2	1.2	0.0	2.9	2.5	0.0	2.5	2.7	1.5	1.1	0.0	0.0	1.8	1.4
0.0	1.2	1.1	1.4	1.1	1.2	2.1	1.5	1.6	1.5	1.4	1.6	1.0	0.0	1.5	1.6	1.4	1.4
1.4	1.1	1.0	1.2	1.3	1.2	1.3	1.1	1.1	1.0	1.0	1.1	1.2	1.2	1.6	1.4	1.3	1.3
1.2	1.2	1.0	1.4	1.2	1.2	3.4	2.8	3.0	3.4	2.3	3.0	1.9	2.3	3.0	2.2	3.1	2.5
1.1	1.1	1.1	1.4	1.2	1.2	2.1	1.8	1.5	1.5	1.3	1.7	1.4	1.5	1.9	1.6	1.8	1.6
1.2	1.1	1.1	1.3	1.3	1.2	1.8	1.7	1.6	1.8	1.4	1.6	1.3	1.5	1.9	0.0	1.8	1.6
1.2	1.2	1.2	1.2	1.2	1.2	2.2	1.8	1.8	1.8	1.6	1.8	1.5	1.5	0.0	1.5	1.5	1.5
1.4	1.4	1.0	1.0	1.2	1.2	1.2	1.6	1.9	2.0	1.7	1.7	1.2	1.2	0.0	1.2	1.3	1.2
0.8	1.0	1.6	1.0	1.6	1.2	0.7	0.0	1.4	0.0	0.8	1.0	1.2	1.2	1.4	0.0	1.4	1.3
0.0	1.1	1.3	1.1	1.2	1.2	2.5	2.0	2.6	2.0	1.8	2.2	3.2	2.5	3.2	3.0	0.0	3.0
1.1	1.1	1.2	1.5	1.1	1.2	2.6	2.1	1.6	1.9	1.7	2.0	1.6	1.4	1.8	1.5	1.5	1.5
1.3	0.0	1.2	1.1	0.0	1.2	1.4	1.0	0.0	0.0	0.9	1.1	1.4	1.3	1.7	1.3	1.6	1.5
1.1	1.4	1.2	1.0	0.0	1.2	1.1	0.7	0.8	0.8	0.7	0.8	0.0	3.4	4.5	3.5	4.6	4.0
1.2	1.1	1.2	1.3	1.2	1.2	3.1	3.0	2.6	2.5	2.0	2.6	1.8	1.9	2.3	2.3	2.1	2.1
1.2	1.1	1.3	1.3	1.2	1.2	1.7	1.4	1.5	1.6	1.4	1.5	1.3	1.4	2.1	1.5	1.6	1.6
1.1	1.2	1.1	1.1	1.4	1.2	1.4	1.4	1.1	1.1	1.1	1.2	1.6	1.6	1.9	1.6	0.0	1.7
1.3	1.1	1.1	1.3	1.2	1.2	1.3	1.0	1.2	1.2	1.1	1.2	1.3	1.9	1.9	1.4	1.5	1.6
1.2	1.1	1.1	1.1	1.3	1.2	1.9	1.6	1.8	1.8	1.5	1.7	1.6	1.7	0.0	1.8	0.0	1.7
1.1	0.0	1.2	1.1	1.3	1.2	1.5	1.3	1.4	1.3	1.4	1.4	0.0	1.1	1.4	1.5	0.0	1.3
1.2	1.1	1.2	1.2	1.1	1.2	2.5	2.1	1.7	0.8	1.6	1.8	2.0	2.5	0.0	2.4	0.0	2.3
1.1	1.0	1.3	1.3	1.2	1.2	2.0	2.1	2.0	2.0	1.8	2.0	2.3	3.0	2.9	2.3	2.8	2.7
0.0	1.1	1.5	0.0	1.0	1.2	0.0	5.9	6.6	6.8	0.0	6.4	2.0	2.6	2.6	0.0	2.5	2.4
1.3	1.2	0.0	0.0	1.0	1.2	1.5	1.9	1.7	2.0	1.6	1.7	1.2	1.2	1.5	1.3	1.3	1.3
1.2	1.1	1.2	1.2	1.2	1.2	1.4	1.5	1.4	1.5	1.4	1.4	0.8	0.7	1.1	1.0	0.9	0.9
1.2	1.1	1.1	1.2	1.2	1.2	1.5	1.3	1.2	1.2	1.1	1.3	1.3	1.4	1.7	1.5	1.4	1.5
0.9	1.2	1.1	1.5	1.1	1.2	2.8	3.6	2.7	4.7	0.0	3.4	2.1	8.0	8.6	0.0	0.0	6.2
0.0	1.2	1.2	1.1	1.2	1.2	1.2	0.9	1.5	1.3	1.4	1.3	1.6	1.3	1.9	0.0	1.7	1.6
1.1	1.1	1.1	1.3	1.2	1.2	3.4	3.1	2.5	3.7	2.9	3.1	1.2	1.2	1.4	1.3	1.3	1.3
1.3	1.0	1.1	1.3	1.2	1.2	2.1	1.6	1.7	1.6	1.4	1.7	1.0	0.0	1.9	0.0	1.7	1.5
1.3	0.0	1.2	1.1	1.1	1.2	1.0	1.2	1.7	2.1	1.0	1.4	1.1	1.5	1.3	1.2	0.0	1.3
1.1	1.1	1.1	1.5	1.1	1.2	0.0	5.1	4.2	4.8	3.8	4.5	1.9	2.3	4.2	1.9	2.3	2.5
1.0	1.1	1.2	1.1	1.4	1.2	1.8	2.2	2.2	2.6	1.6	2.1	1.2	1.3	2.2	0.8	1.4	1.4
1.2	1.1	1.2	1.2	1.2	1.2	1.5	1.2	1.1	1.3	1.1	1.2	1.4	1.5	1.8	1.6	1.5	1.5

149	2	476	Q9BRA2	TXNDC17 Thioredoxin domain-containing protein 17	TXNDC17	K.DAGGKSWC*PDCVQAEPVVR.E
245	216	477	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.QAIDDDC*NQTGQMTAGFLDWPQGTFASQVTLEGDKLK.V
672	529	478	Q16854	DGUOK Deoxyguanosine kinase, mitochondrial	DGUOK	K.AC*TAQSLGNLLDMMYR.E
495	612	479	Q9UK41	VPS28 Vacuolar protein sorting-associated protein 28 hom	VPS28	R.LDC*PLAMER.I
656	659	480	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	R.TIC*AILENYQTEK.G
187	173	481	P28838	LAP3 Cytosol aminopeptidase	LAP3	R.SAGAC*TAAAFLK.E
382	381	482	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.LVVPATQC*GSLIGK.G
463	601	483	P62306	SNRPF Small nuclear ribonucleoprotein F	SNRPF	R.C*NNVLYIR.G
593	609	484	P38646	HSPA9 Stress-70 protein, mitochondrial	HSPA9	K.AKC*ELSSSVQTDINLPYLTMDSSGPK.H
5	100	485	Q96BF6	NACC2 Nucleus accumbens-associated protein 2	NACC2	R.NTLANSC*GTGIR.S
655	610	486	P07900	HSP90AA1 Heat shock protein HSP 90-alpha	HSP90AA1	R.VFIMDNC*EELIPEYLNFIR.G
504	599	487	P49915	GMPS GMP synthase	GMPS	K.AC*TTEEDQEK.L
220	422	488	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitoch	MCCC2	K.MVAAVAC*AQVPK.I
624	496	489	O43765	SGTA Small glutamine-rich tetratricopeptide repeat-cont	SGTA	R.AIC*IDPAYSK.A
485	410	490	Q52LJ0	FAM98B Protein FAM98B	FAM98B	R.EKTAC*AINK.V
309	368	491	P56381	ATP5E ATP synthase subunit epsilon, mitochondrial	ATP5E	R.YSQIC*AK.A
137	521	492	Q9BV86	NTMT1 N-terminal Xaa-Pro-Lys N-methyltransferase 1	NTMT1	R.IIC*SAGLSLLAEER.Q
216	415	493	Q9UNE7	STUB1 E3 ubiquitin-protein ligase CHIP	STUB1	R.AQQAC*IEAK.H
444	607	494	P07741	APRT Adenine phosphoribosyltransferase	APRT	R.VVVVDDLLATGGTMNAAC*ELLGR.L
317	475	495	Q9BSU1	C16orf70 UPF0183 protein C16orf70	C16orf70	R.LLAAGC*GPGLLADAK.M
739	471	496	P43897	TSFM Elongation factor Ts, mitochondrial	TSFM	R.FEC*GEGEEAAETE.-
636	630	497	Q86SX6	GLRX5 Glutaredoxin-related protein 5, mitochondrial	GLRX5	K.GTPEQPQC*GFSNAVVQILR.L
324	375	498	O60547	GMDS GDP-mannose 4,6 dehydratase	GMDS	K.YYRPTEVDFLQGDC*TK.A
594	513	499	O43747	AP1G1 AP-1 complex subunit gamma-1	AP1G1	R.FTC*TVNR.I
300	55	500	Q5MNZ6	WDR45L WD repeat domain phosphoinositide-interacting prot	WDR45L	R.C*NYLALVGGGK.K
394	136	501	Q9BV79	MECR Trans-2-enoyl-CoA reductase, mitochondrial	MECR	R.LALNC*VGGK.S
623	499	502	O75940	SMNDC1 Survival of motor neuron-related-splicing factor 3	SMNDC1	K.VGVGTC*GIADKPMTQYQDTSK.Y
676	698	503	Q9Y696	CLIC4 Chloride intracellular channel protein 4	CLIC4	K.AGSDGESIGNC*PFSQR.L
323	463	504	P60981	DSTN Destrin	DSTN	K.C*STPEEIK.K
170	614	505	Q9Y5X2	SNX8 Sorting nexin-8	SNX8	K.ESAQCVGDEFLNC*K.L
680	721	506	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	K.IAAYLQSDQFC*K.M
588	652	507	P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	K.GFGFVC*FSSPEEATK.A
523	539	508	P26641	EEF1G Elongation factor 1-gamma	EEF1G	K.AAAPAPEEEMDEC*EQALAAEPK.A
599	535	509	Q8N6M0	OTUD6B OTU domain-containing protein 6B	OTUD6B	K.DC*ALTVVALR.S

1.2	1.1	1.1	1.3	1.2	1.2	10.6	14.0	7.2	11.6	11.0	10.9	3.4	3.1	4.8	4.4	4.0	4.0
0.0	1.0	1.1	1.3	1.2	1.2	2.4	2.8	3.3	2.9	0.0	2.8	2.0	0.0	3.1	2.6	2.9	2.6
1.1	1.1	1.1	1.4	1.2	1.2	1.8	1.3	1.3	1.5	1.5	1.5	1.2	1.3	1.6	1.1	1.1	1.2
1.1	1.2	1.1	1.3	1.2	1.2	0.0	1.1	1.4	0.0	1.1	1.2	1.5	1.6	0.0	1.4	1.7	1.5
1.2	1.2	1.1	1.2	1.2	1.2	1.2	0.9	1.2	0.0	1.0	1.1	1.1	1.3	0.0	1.3	1.3	1.3
1.1	1.0	1.2	1.4	1.2	1.2	2.8	3.7	3.0	3.1	3.0	3.1	3.0	3.3	3.6	3.7	2.9	3.3
1.2	1.1	1.2	1.2	1.2	1.2	2.3	2.0	1.9	1.9	1.6	1.9	1.9	1.9	2.1	1.8	1.6	1.8
1.2	1.1	1.1	1.2	1.2	1.2	1.4	1.2	1.3	1.3	1.1	1.3	1.4	1.5	2.0	1.5	1.6	1.6
1.1	1.0	1.1	1.4	1.1	1.2	1.4	1.2	1.4	1.1	1.1	1.2	1.1	1.3	1.6	1.5	1.5	1.4
1.2	1.6	0.7	0.0	1.2	1.2	5.1	1.5	4.8	4.7	4.7	4.1	10.2	0.0	19.2	0.0	12.0	13.8
1.2	1.1	1.2	1.3	1.1	1.2	1.4	1.2	1.3	1.2	1.0	1.2	1.2	0.0	0.0	1.3	1.4	1.3
1.3	1.0	1.1	1.2	0.0	1.2	0.0	1.4	1.3	1.1	1.2	1.3	1.2	1.3	2.1	1.6	1.5	1.5
1.2	1.1	1.2	1.2	1.1	1.2	1.2	2.0	1.9	2.4	1.5	1.8	2.3	2.6	3.7	3.1	2.8	2.9
1.5	0.9	1.1	1.2	1.1	1.2	2.1	1.5	1.4	0.0	1.4	1.6	1.2	1.3	1.4	1.5	1.3	1.3
0.0	0.0	1.1	1.1	1.2	1.2	2.8	1.7	1.5	0.0	1.4	1.9	1.4	1.6	0.0	1.6	1.7	1.6
0.0	1.1	1.2	1.3	1.1	1.2	2.3	2.1	1.8	1.8	1.9	2.0	1.8	0.0	2.4	0.0	2.3	2.2
1.2	1.2	1.0	1.2	1.1	1.2	1.9	1.4	1.4	1.4	1.3	1.5	3.9	4.0	4.0	4.5	4.7	4.2
1.1	1.3	1.0	1.2	1.0	1.1	1.9	2.1	2.1	1.5	1.6	1.8	2.2	2.6	3.7	3.3	2.8	2.9
1.0	1.3	1.1	1.2	1.1	1.1	1.1	1.2	1.4	1.3	1.1	1.2	1.5	1.4	2.2	1.6	1.5	1.6
1.1	1.2	1.0	1.1	1.3	1.1	2.2	1.5	1.5	1.7	1.3	1.6	1.8	2.0	2.8	1.8	2.1	2.1
0.8	0.0	1.2	1.3	1.3	1.1	0.7	1.5	2.1	0.0	2.3	1.6	0.8	0.0	1.1	0.0	1.1	1.0
1.2	1.1	1.1	1.2	1.2	1.1	1.4	1.1	1.1	1.2	1.0	1.2	1.2	1.3	1.5	1.3	1.3	1.3
1.2	1.1	1.1	1.3	1.1	1.1	2.3	2.0	1.7	2.1	1.7	2.0	1.5	2.1	2.5	2.1	0.0	2.1
1.2	0.0	1.1	1.2	1.2	1.1	1.8	1.5	1.4	0.0	1.4	1.5	1.3	1.3	0.0	1.4	1.6	1.4
1.1	1.2	1.0	1.1	1.2	1.1	4.5	5.0	4.6	6.3	4.7	5.0	1.9	2.2	2.4	2.4	2.2	2.2
1.3	1.0	1.0	1.1	1.3	1.1	3.1	4.2	3.7	0.0	3.0	3.5	1.5	1.5	0.0	1.7	2.4	1.8
1.0	1.4	1.0	1.2	1.1	1.1	1.9	1.6	1.7	1.4	1.4	1.6	0.0	1.3	1.3	1.4	0.0	1.3
1.1	1.2	1.0	1.2	1.1	1.1	1.0	0.9	1.0	0.9	0.9	1.0	1.5	1.2	1.3	1.1	1.1	1.2
1.1	1.2	1.0	1.2	1.2	1.1	1.5	1.7	1.5	2.3	1.4	1.7	1.5	1.8	2.7	1.8	2.5	2.1
1.0	0.0	1.3	1.1	1.1	1.1	1.3	1.2	1.0	0.0	1.3	1.2	2.5	3.0	3.9	3.7	4.8	3.6
1.2	1.1	1.1	1.2	1.2	1.1	1.0	1.2	0.8	0.5	0.7	0.9	1.1	1.1	1.5	1.2	1.2	1.2
1.0	1.2	1.3	1.2	1.0	1.1	1.1	1.1	1.1	1.2	1.0	1.1	1.2	1.3	1.7	1.2	1.6	1.4
1.2	1.1	1.2	1.1	1.1	1.1	1.7	1.4	1.3	1.5	1.1	1.4	1.4	1.4	1.8	1.5	1.5	1.5
1.1	1.1	1.0	1.2	1.2	1.1	2.0	1.3	1.2	0.0	1.3	1.4	1.3	0.0	0.0	1.6	1.2	1.4

550	349	510	P78347	GTF2I General transcription factor II-I	GTF2I	R.SILSPGGSC*GPIK.V
584	532	511	P53602	MVD Diphosphomevalonate decarboxylase	MVD	R.DGDPLPSSLSC*K.V
736	431	512	P49915	GMPS GMP synthase	GMPS	K.TVGVQGDC*R.S
356	618	513	Q99873	PRMT1 Protein arginine N-methyltransferase 1	PRMT1	K.VIGIEC*SSISDYAVK.I
755	303	514	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	K.AVYTQDC*PLAAAK.A
327	429	515	Q96SW2	CRBN Protein cereblon	CRBN	K.VQILPEC*VLPSTMSAVQLESLNK.C
565	460	516	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	R.GCITIIGGGDTATC*C*AK.W
663	117	517	Q9Y2S2	CRYL1 Lambda-crystallin homolog	CRYL1	R.VILSSSTSC*LMPSK.L
428	433	518	Q9UI30	TRMT112 tRNA methyltransferase 112 homolog	TRMT112	R.IC*PVEFNPNFVAR.M
183	611	519	Q9UNH7	SNX6 Sorting nexin-6	SNX6	R.IGSSLYALGTQDSTDIC*K.F
348	421	520	P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	K.AC*QIFVR.N
709	553	521	Q9Y224	C14orf166 UPF0568 protein C14orf166	C14orf166	K.LTALDYHNPAGFNC*K.D
536	568	522	P53396	ACLY ATP-citrate synthase	ACLY	K.FIC*TTSAIQNR.F
521	719	523	P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	R.GLELIASENFC*SR.A
614	679	524	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	K.FIC*EQDHQNFLR.L
380	283	525	P35270	SPR Sepiapterin reductase	SPR	K.GKLVDC*K.V
558	411	526	P52895	AKR1C2 Aldo-keto reductase family 1 member C2	AKR1C2	R.EEPWVDPNSPVLLEDPVLC*ALAK.K
579	613	527	Q9Y365	STARD10 PCTP-like protein	STARD10	R.MEC*CDVPAETLYDVLHDIEYR.K
469	361	528	Q8N335	GPD1L Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	R.IC*DEITGR.V
413	590	529	P49327	FASN Fatty acid synthase	FASN	R.AAPLDSIHSLAAYYIDC*IR.Q
557	602	530	Q52LJ0	FAM98B Protein FAM98B	FAM98B	K.SLC*NLEESITSAGR.D
714	606	531	Q9H0C8	ILKAP Integrin-linked kinase-associated serine/threonine phosphatase 2C	ILKAP	R.FILLAC*DGLFK.V
336	635	532	P14868	DARS Aspartate--tRNA ligase, cytoplasmic	DARS	R.LEYC*EALAMLR.E
477	664	533	P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	K.LC*FSTAQHAS.-
192	83	534	P45985	MAP2K4 Dual specificity mitogen-activated protein kinase	MAP2K4	K.LC*DFGISGQLVDSIAK.T
207	449	535	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitoch	MCCC2	K.NIAQIAVVMGSC*TAGGAYVPAMADENIIVR.K
367	466	536	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.INISEGNC*PER.I
580	559	537	Q9BW61	DDA1 DET1- and DDB1-associated protein 1	DDA1	R.FHADSVC*K.A
698	571	538	Q9NTK5	OLA1 Obg-like ATPase 1	OLA1	K.STFFNVLTNSQASAENFPFC*TIDPNESR.V
754	423	539	Q15181	PPA1 Inorganic pyrophosphatase	PPA1	K.GISC*MNTTLSESPFK.C
535	565	540	P36405	ARL3 ADP-ribosylation factor-like protein 3	ARL3	K.LSC*VPVLIFANK.Q
407	465	541	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	K.GLLDVTC*K.T
297	520	542	P00338	LDHA L-lactate dehydrogenase A chain	LDHA	R.VIGSGC*NLDSAR.F
717	658	543	Q02790	FKBP4 Peptidyl-prolyl cis-trans isomerase FKBP4	FKBP4	K.TQLAVC*QQR.I

1.1	1.0	1.1	1.2	1.2	1.1	2.3	2.2	2.2	1.9	1.6	2.0	1.3	1.6	1.7	1.4	1.4	1.5
1.1	1.1	1.1	1.2	1.1	1.1	1.6	1.5	1.2	1.4	1.5	1.4	1.7	1.2	1.6	1.2	1.4	1.4
1.3	0.7	1.1	1.3	1.4	1.1	2.2	1.8	1.6	1.8	1.5	1.8	1.2	0.9	0.0	0.0	1.0	1.0
1.1	1.1	1.0	1.2	1.2	1.1	1.3	1.2	1.2	1.2	1.1	1.2	1.8	1.7	2.3	1.8	1.9	1.9
1.1	0.0	0.9	1.3	1.2	1.1	2.3	2.5	2.5	2.0	2.1	2.3	0.4	0.4	0.5	0.4	0.3	0.4
0.9	0.0	0.0	1.4	1.1	1.1	2.1	1.7	1.7	1.7	1.7	1.8	2.0	1.8	2.6	1.9	2.1	2.1
1.1	1.0	1.2	0.0	1.1	1.1	0.0	1.4	0.0	2.0	1.6	1.7	1.4	0.0	1.8	0.0	1.1	1.4
0.0	1.2	1.0	1.2	1.2	1.1	3.8	0.0	3.7	0.0	3.8	3.8	1.2	1.1	1.5	1.3	1.2	1.3
0.9	1.2	1.2	1.2	1.2	1.1	1.8	1.9	1.8	1.8	1.6	1.8	1.3	1.4	2.0	1.7	2.0	1.7
1.1	1.0	1.1	1.2	1.2	1.1	1.7	0.9	1.3	1.1	1.1	1.2	2.8	3.8	3.4	2.9	3.8	3.3
1.2	1.1	1.1	1.0	1.2	1.1	1.9	1.9	1.7	0.0	1.8	1.8	2.0	1.7	2.2	1.8	2.1	1.9
1.1	1.1	1.1	1.2	1.1	1.1	1.4	1.4	1.3	1.5	1.2	1.4	1.0	1.1	1.4	1.2	1.2	1.2
1.3	1.0	1.0	1.2	1.2	1.1	1.6	1.3	1.2	1.2	1.2	1.3	1.4	1.4	1.6	1.5	1.4	1.5
0.0	1.2	0.9	0.0	1.2	1.1	0.8	0.9	0.0	0.0	0.9	0.9	1.3	0.0	1.7	1.3	1.6	1.5
1.0	1.0	1.1	1.3	1.2	1.1	1.1	0.0	1.0	0.0	1.0	1.0	1.2	1.2	1.5	1.5	1.4	1.4
1.2	1.1	1.2	1.1	1.1	1.1	2.5	2.8	2.1	0.0	2.3	2.4	2.4	2.0	2.0	1.4	1.4	1.8
0.0	1.1	1.1	1.3	1.0	1.1	1.8	2.0	1.9	2.0	1.4	1.8	1.3	1.4	1.6	1.5	1.5	1.4
1.1	1.0	1.3	1.1	1.0	1.1	1.6	1.0	1.3	1.2	1.1	1.2	1.2	1.8	1.7	1.2	1.3	1.4
0.0	1.0	1.1	1.2	1.1	1.1	1.6	1.6	3.7	0.0	1.1	2.0	1.4	1.7	0.0	1.7	0.0	1.6
1.1	1.1	1.0	0.0	1.2	1.1	1.1	1.1	1.4	1.5	1.2	1.3	1.6	0.0	2.2	1.5	0.0	1.7
1.2	0.8	1.2	1.2	1.2	1.1	1.6	1.3	1.1	0.0	1.1	1.2	1.2	1.3	0.0	0.0	1.8	1.4
1.0	1.0	1.4	1.2	0.9	1.1	1.6	1.0	1.3	1.2	1.2	1.2	1.5	0.8	1.2	1.1	1.1	1.1
1.1	1.2	1.1	1.0	1.1	1.1	1.4	1.1	1.2	1.1	0.9	1.1	1.9	2.1	0.0	2.1	0.0	2.0
1.2	1.2	1.0	1.1	1.1	1.1	1.2	1.0	1.2	1.0	1.0	1.1	1.4	1.7	1.3	1.5	2.1	1.6
1.2	1.2	0.9	1.3	1.1	1.1	4.7	4.7	4.3	0.0	4.0	4.4	3.2	3.0	3.1	4.7	2.2	3.2
1.3	1.1	1.0	1.0	1.1	1.1	2.0	0.0	2.0	1.4	1.5	1.7	3.4	0.0	0.0	2.6	3.1	3.0
1.1	1.0	1.1	1.2	1.1	1.1	2.0	1.7	1.5	1.7	1.4	1.7	1.6	1.7	2.3	1.8	1.9	1.9
1.1	1.2	1.2	1.0	1.1	1.1	1.8	1.2	1.4	1.2	1.1	1.3	1.1	1.3	2.4	1.1	1.2	1.4
1.2	1.1	0.9	1.1	1.3	1.1	1.5	1.3	1.2	1.5	1.1	1.3	1.2	1.1	0.0	1.3	1.2	1.2
1.2	1.0	1.2	1.1	1.1	1.1	2.5	1.9	1.5	1.5	1.6	1.8	0.4	0.4	0.6	0.4	0.4	0.4
0.0	1.1	1.3	1.0	1.1	1.1	1.6	0.0	1.1	1.2	0.0	1.3	1.0	0.0	2.3	0.0	1.2	1.5
1.1	1.1	1.1	1.1	1.1	1.1	2.1	1.4	1.7	1.7	1.3	1.7	1.4	1.5	2.1	1.8	1.9	1.8
1.1	1.1	1.2	1.1	1.1	1.1	1.0	1.9	1.4	1.8	1.4	1.5	1.8	1.8	2.7	2.5	2.3	2.2
0.8	1.1	1.0	1.4	1.2	1.1	1.1	1.0	1.1	1.2	1.0	1.1	1.0	0.9	1.4	1.1	1.2	1.1

252	334	544	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.EVIAVSC*GPAQCQETIR.T
316	608	545	P36969	GPX4 Phospholipid hydroperoxide glutathione peroxidase,	GPX4	R.YAEC*GLR.I
691	600	546	Q99460	PSMD1 26S proteasome non-ATPase regulatory subunit 1	PSMD1	K.VLTMPETC*R.Y
551	617	547	Q9NYL2	MLTK Mitogen-activated protein kinase kinase kinase MLT	MLTK	K.IC*DFGASR.F
515	554	548	Q5JRX3	PITRM1 Presequence protease, mitochondrial	PITRM1	R.SQQSKPQDASC*LPALK.V
251	505	549	Q5TFE4	NT5DC1 5-nucleotidase domain-containing protein 1	NT5DC1	K.HFLSDTGMAC*R.S
467	413	550	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	K.AAREEC*PVFTPPGGETLDQVK.M
505	603	551	P78347	GTF2I General transcription factor II-I	GTF2I	K.ITINPGC*VVVDGMPPGVSFK.A
298	487	552	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.LVVPASQC*GSLIGK.G
282	430	553	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	R.AQC*ETLSPDGLPEEQPQTTK.L
429	561	554	P62826	RAN GTP-binding nuclear protein Ran	RAN	R.VC*ENIPIVLCGNK.V
681	588	555	Q15149	PLEC Plectin	PLEC	K.AFC*GFEDPR.T
441	657	556	Q9Y4P1	ATG4B Cysteine protease ATG4B	ATG4B	K.NFPAIGGTGPTSDTGWGC*MLR.C
547	575	557	Q9NVG8	TBC1D13 TBC1 domain family member 13	TBC1D13	R.LLQDYPITDVC*QILQK.A
650	696	558	P62258	YWHAE 14-3-3 protein epsilon	YWHAE	K.LIC*C*DILDVLDK.H
247	310	559	Q8TB45	DEPTOR DEP domain-containing mTOR-interacting protein	DEPTOR	K.SPSSQETHDSPFC*LR.K
358	408	560	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	R.VTEELWQAALSTLNPNPTDSCPLYLNYATVAALPC*R.V
541	552	561	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	R.LDFVC*SFLQK.N
424	619	562	P36507	MAP2K2 Dual specificity mitogen-activated protein kinase	MAP2K2	K.LC*DFGVSGQLIDSMANSFVGTR.S
731	196	563	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.AEGSDVANAVLDGADC*IMLSGETAK.G
408	523	564	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK.G
585	418	565	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.GPFVEAEVPDVDLEC*PDAK.L
533	380	566	P13639	EEF2 Elongation factor 2	EEF2	K.IWC*FGPDGTGPNILTDITK.G
489	566	567	P49458	SRP9 Signal recognition particle 9 kDa protein	SRP9	K.VTDDLVC*LVYK.T
710	687	568	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	R.FC*PFAER.T
608	441	569	Q8N201	INTS1 Integrator complex subunit 1	INTS1	R.SQDGDTAAC*SLIQAR.L
476	665	570	P55786	NPEPPS Puromycin-sensitive aminopeptidase	NPEPPS	R.SKDGVC*VR.V
738	591	571	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	K.ASVGFGGSC*FQK.D
646	674	572	P50990	CCT8 T-complex protein 1 subunit theta	CCT8	K.IAVYSC*PFDGMITETK.G
418	702	573	P60900	PSMA6 Proteasome subunit alpha type-6	PSMA6	R.GKDC*AVIVTQK.K
649	677	574	P55735	SEC13 Protein SEC13 homolog	SEC13	R.FASGGC*DNLIK.L
305	446	575	P51659	HSD17B4 Peroxisomal multifunctional enzyme type 2	HSD17B4	K.IC*DFENASKPQSIQESTGSIIEVLSK.I
563	624	576	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.AITIAGVPQSVTEC*VK.Q
293	78	577	P62857	RPS28 40S ribosomal protein S28	RPS28	R.TGSQGQC*TQVR.V

1.1	0.0	1.1	1.3	1.0	1.1	2.2	2.2	2.4	0.0	1.8	2.1	2.1	2.2	3.1	2.9	2.5	2.6
1.1	1.0	1.1	1.2	1.2	1.1	1.5	1.2	1.2	1.3	1.1	1.2	2.0	2.1	0.0	2.2	2.2	2.1
0.0	1.2	0.7	0.0	1.3	1.1	0.9	1.2	2.0	1.6	0.8	1.3	0.0	0.0	1.3	0.9	1.4	1.2
1.0	1.2	0.9	1.2	1.2	1.1	1.5	1.2	1.1	1.1	1.1	1.2	1.6	1.1	1.8	1.2	1.6	1.5
1.2	1.0	1.0	1.4	1.0	1.1	1.5	1.4	1.3	0.0	1.3	1.4	1.0	1.6	1.7	0.0	1.7	1.5
1.2	1.1	1.0	1.1	1.1	1.1	1.6	1.6	0.0	1.6	1.4	1.5	2.6	2.2	2.9	2.6	2.7	2.6
0.0	1.3	1.0	1.1	1.1	1.1	1.9	1.8	2.0	0.0	1.6	1.8	1.3	1.4	1.8	1.7	1.8	1.6
1.1	0.0	1.1	0.0	1.1	1.1	0.0	1.3	0.0	1.2	1.3	1.2	1.3	1.4	1.7	0.0	1.8	1.5
1.1	1.1	1.1	1.1	1.1	1.1	1.9	1.6	1.6	1.5	1.4	1.6	2.0	2.2	2.6	2.3	2.2	2.2
0.0	0.0	1.1	1.1	1.0	1.1	2.0	1.8	1.9	1.7	1.6	1.8	1.7	1.8	3.6	2.4	2.3	2.4
1.0	1.0	1.3	1.0	1.1	1.1	1.1	1.3	1.4	1.6	1.2	1.3	1.3	1.6	2.0	1.6	2.0	1.7
1.1	1.1	1.0	1.2	1.1	1.1	1.5	1.3	1.2	0.0	1.1	1.3	1.2	1.2	0.0	1.3	1.2	1.2
1.0	1.1	0.0	1.2	1.2	1.1	0.0	1.2	1.2	1.0	1.0	1.1	1.4	1.6	2.1	0.0	1.5	1.6
1.1	1.0	0.9	1.4	1.1	1.1	1.7	1.2	1.2	1.3	1.1	1.3	1.3	1.5	1.6	1.6	1.3	1.5
1.2	1.0	1.1	1.1	1.1	1.1	1.0	0.8	1.1	1.0	0.9	1.0	1.3	1.3	1.9	1.1	0.9	1.3
1.0	1.2	1.2	1.0	1.0	1.1	2.3	2.6	1.9	2.6	1.9	2.3	1.7	3.4	2.6	2.5	3.0	2.6
0.9	1.0	1.2	1.2	1.1	1.1	2.6	0.0	1.7	0.0	1.3	1.9	1.7	0.0	0.0	2.3	1.7	1.9
1.2	1.1	1.0	1.1	1.1	1.1	1.7	1.3	1.3	1.4	1.2	1.4	1.2	1.2	1.7	1.6	1.7	1.5
1.1	1.0	1.1	1.0	1.2	1.1	1.5	1.0	1.2	1.3	1.1	1.2	1.6	1.4	2.0	1.7	1.8	1.7
0.0	0.9	1.2	1.1	1.0	1.1	0.8	3.2	3.8	4.2	2.8	3.0	0.7	0.0	1.1	1.0	1.4	1.0
1.1	1.0	1.1	1.1	1.1	1.1	1.8	1.5	1.3	1.5	1.2	1.5	1.6	1.6	2.0	1.8	1.8	1.8
1.0	1.2	1.1	1.1	1.0	1.1	1.9	2.0	1.8	1.8	1.6	1.8	0.9	1.1	2.0	1.7	1.4	1.4
0.0	1.1	1.1	1.0	1.1	1.1	1.2	2.2	2.1	2.1	2.0	1.9	1.3	1.4	1.6	1.4	1.7	1.5
1.1	1.0	1.1	1.1	1.1	1.1	1.5	1.3	1.3	1.3	1.2	1.3	1.5	1.3	1.9	1.4	1.7	1.6
1.1	1.0	1.1	1.2	1.1	1.1	1.1	1.1	0.9	1.0	1.0	1.0	1.1	1.1	1.3	1.2	1.1	1.2
0.0	1.0	1.1	1.2	1.1	1.1	1.5	1.1	1.4	3.0	0.0	1.7	0.0	1.3	1.3	1.5	0.0	1.4
1.2	0.9	1.2	1.1	1.0	1.1	1.3	1.0	1.2	1.0	0.9	1.1	1.4	1.4	2.2	1.3	1.7	1.6
1.2	1.0	1.3	0.8	1.1	1.1	1.6	1.0	1.3	1.5	0.9	1.3	0.8	0.9	1.2	1.1	0.9	1.0
1.1	1.0	1.0	1.2	1.1	1.1	1.2	1.0	1.1	1.1	0.9	1.0	0.0	1.3	0.0	1.3	1.2	1.3
1.1	1.2	0.9	1.2	0.0	1.1	0.0	0.0	1.2	0.8	0.9	0.9	0.0	0.8	2.9	0.8	2.4	1.7
1.1	1.1	1.0	1.1	1.1	1.1	1.2	1.0	1.0	1.0	0.9	1.0	1.1	1.2	1.6	1.3	1.3	1.3
0.9	1.0	1.3	1.1	1.1	1.1	2.1	1.7	1.6	1.8	1.3	1.7	1.8	0.0	2.3	2.1	2.5	2.2
1.0	1.2	1.1	0.9	1.1	1.1	1.3	1.1	1.3	1.1	1.0	1.2	1.2	1.2	1.9	1.3	1.6	1.4
1.0	1.1	1.1	1.1	1.1	1.1	4.7	5.1	4.2	4.7	3.6	4.5	1.9	2.3	2.9	2.0	2.3	2.3

370	511	578	Q9NZZ3	CHMP5 Charged multivesicular body protein 5	CHMP5	K.APPPSLTDC*IGTVDSR.A
404	692	579	P57081	WDR4 tRNA (guanine-N(7)-)-methyltransferase subunit WDR	WDR4	K.SGDVYSFSVLEPHGC*GR.L
675	387	580	Q969T9	WBP2 WW domain-binding protein 2	WBP2	K.DC*EIKQPVFGANYIK.G
433	510	581	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	R.GQAGGGGPGTGPGLGEAGSLATC*ELPLAK.S
695	646	582	P37802	TAGLN2 Transgelin-2	TAGLN2	K.NMAC*VQR.T
337	278	583	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	K.LEVDAIVNAANSSLLGGGGVDGC*IHR.A
606	494	584	Q9NX24	NHP2 H/ACA ribonucleoprotein complex subunit 2	NHP2	K.ADPDGPEAQAEAC*SGER.T
590	639	585	P30153	PPP2R1A Serine/threonine-protein phosphatase 2A 65 kDa reg	PPP2R1A	R.LNIISNLDC*VNEVIGIR.Q
481	596	586	Q96Q11	TRNT1 CCA tRNA nucleotidyltransferase 1, mitochondrial	TRNT1	K.YQGEHC*LLK.E
439	681	587	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	R.EEFASTC*PDDEEIELAYEQVAK.A
625	707	588	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	K.LNEC*VDHTPK.L
345	480	589	Q86YH6	PDSS2 Decaprenyl-diphosphate synthase subunit 2	PDSS2	R.C*LLSDELSNIAMQVR.K
674	711	590	Q14103	HNRNPD Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	K.FGEVVDC*TLKLDPITGR.S
383	551	591	P60981	DSTN Destrin	DSTN	K.LGGSLIVAFEGC*PV.-
527	282	592	P37837	TALDO1 Transaldolase	TALDO1	K.ALAGC*DFLTISPK.L
729	629	593	Q9BXV9	C14orf142 Uncharacterized protein C14orf142	C14orf142	R.VSC*EAPGDGDPFQGLLSGVAQMK.D
552	485	594	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	K.RYTC*GEAPDYDR.S
335	672	595	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	R.HLGYTLC*K.Q
572	526	596	Q6KB66	KRT80 Keratin, type II cytoskeletal 80	KRT80	R.C*HIDLSGIVEEVK.A
686	584	597	P52597	HNRNPF Heterogeneous nuclear ribonucleoprotein F	HNRNPF	R.GLPFGC*TK.E
518	64	598	P35270	SPR Sepiapterin reductase	SPR	R.TVVNISSLC*ALQPFK.G
484	219	599	P13639	EEF2 Elongation factor 2	EEF2	R.ETVSEESNVLC*LSK.S
494	356	600	Q04760	GLO1 Lactoylglutathione lyase	GLO1	K.C*DFPIMK.F
568	476	601	P13639	EEF2 Elongation factor 2	EEF2	R.TFC*QLILDPIFK.V
619	569	602	P31947	SFN 14-3-3 protein sigma	SFN	K.GAVEKGEELSC*EER.N
530	649	603	Q9Y5P6	GMPPB Mannose-1-phosphate guanyltransferase beta	GMPPB	R.LC*SGPGIVGNVLVDPSAR.I
640	522	604	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	K.C*LSVMEAK.V
524	579	605	P33316	DUT Deoxyuridine 5-triphosphate nucleotidohydrolase,	DUT	K.TDIQIALPSGC*YGR.V
603	620	606	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.YLAEVAC*GDDR.K
592	359	607	Q9P2T1	GMPR2 GMP reductase 2	GMPR2	K.VGIGPGSVC*TTR.K
431	250	608	P13639	EEF2 Elongation factor 2	EEF2	R.C*LYASVLTAQPR.L
721	686	609	Q01518	CAP1 Adenylyl cyclase-associated protein 1	CAP1	R.ALLVTASQC*QQPAENK.L
127	391	610	O95671	ASMTL N-acetylserotonin O-methyltransferase-like protein	ASMTL	K.LTAC*QVATAFNLSR.F
301	556	611	O00204	SULT2B1 Sulfotransferase family cytosolic 2B member 1	SULT2B1	R.APWC*ETIVGAFSLPDQYSPR.L

1.0	1.1	1.1	1.1	1.0	1.1	1.7	1.5	1.5	1.5	1.3	1.5	1.7	1.6	2.2	1.9	1.9	1.9
1.5	0.8	1.2	0.9	1.0	1.1	1.1	1.2	0.9	1.0	0.7	1.0	1.3	1.5	2.6	1.6	0.0	1.8
1.0	1.1	1.2	1.1	1.0	1.1	2.0	2.0	2.1	1.8	1.8	1.9	0.9	1.1	1.9	1.1	0.0	1.2
1.1	1.0	0.9	1.1	1.1	1.1	2.1	1.7	1.2	1.5	1.2	1.5	1.5	1.5	2.0	1.8	1.6	1.7
1.3	1.0	0.9	1.0	1.1	1.1	1.3	1.1	1.1	1.2	1.0	1.1	1.1	1.2	1.5	1.2	1.1	1.2
1.1	1.0	1.0	1.0	1.1	1.1	3.2	3.0	2.2	2.2	1.7	2.5	1.8	1.9	2.3	2.1	2.1	2.0
0.9	1.0	1.0	1.3	0.0	1.1	1.9	1.9	1.3	1.5	1.4	1.6	1.4	1.2	1.5	1.3	1.5	1.4
1.0	1.1	0.9	1.2	1.1	1.1	1.5	1.1	1.1	1.3	0.6	1.1	1.6	0.9	1.5	1.5	1.6	1.4
1.3	1.0	1.1	1.1	0.9	1.1	1.2	1.3	1.4	1.2	1.2	1.3	1.3	1.4	1.9	1.5	1.9	1.6
0.9	1.0	1.3	1.1	1.1	1.1	0.9	1.0	1.1	1.2	0.9	1.0	1.3	1.4	0.0	1.7	2.2	1.6
1.0	1.3	1.0	1.0	1.0	1.1	1.0	0.8	1.0	0.8	0.9	0.9	1.3	1.1	1.7	1.3	1.3	1.3
0.7	1.1	1.2	1.3	1.0	1.1	1.6	1.7	1.5	1.8	1.6	1.6	2.1	1.9	2.1	2.0	1.8	2.0
0.0	1.1	1.0	0.9	1.1	1.1	0.8	0.9	1.0	0.0	0.8	0.9	1.3	1.1	0.0	1.3	0.0	1.2
1.1	1.0	1.0	1.1	1.0	1.0	1.7	1.3	1.4	1.4	1.1	1.4	1.5	1.7	2.3	1.7	1.9	1.8
0.0	1.1	0.0	0.9	1.2	1.0	2.0	0.0	3.0	2.4	0.0	2.4	1.5	1.5	1.7	1.1	1.6	1.5
0.0	1.2	1.1	1.1	0.8	1.0	1.5	1.3	0.3	1.5	1.3	1.2	1.3	0.0	1.0	0.8	1.1	1.1
1.0	1.0	1.2	1.1	0.9	1.0	1.8	1.6	1.6	1.7	1.4	1.6	1.5	1.1	0.0	1.3	1.9	1.5
0.9	0.0	1.2	1.0	1.0	1.0	0.9	0.8	1.1	0.0	1.4	1.0	1.8	1.6	2.6	0.0	0.0	2.0
1.0	1.0	1.0	1.1	1.1	1.0	1.8	1.3	1.4	1.6	1.2	1.5	0.0	1.3	1.7	1.3	0.0	1.4
1.0	1.1	1.1	1.0	1.0	1.0	1.5	1.3	1.3	0.0	1.0	1.3	1.1	1.1	1.5	0.9	1.4	1.2
1.1	0.9	1.1	1.0	1.1	1.0	4.1	5.0	3.3	6.0	5.0	4.7	1.3	1.3	1.9	1.6	1.5	1.5
0.0	1.0	1.1	1.0	1.1	1.0	0.9	2.6	3.8	3.9	3.0	2.8	1.5	1.5	0.0	1.8	0.0	1.6
1.0	0.9	1.2	1.2	0.9	1.0	1.8	2.0	2.2	2.1	2.0	2.0	1.4	1.3	1.9	1.5	1.6	1.6
1.0	1.1	1.0	1.1	1.0	1.0	1.4	1.7	1.7	1.9	1.4	1.6	1.1	1.5	1.9	1.2	1.5	1.4
1.0	1.0	1.1	1.1	1.0	1.0	1.5	1.2	1.4	1.3	1.1	1.3	1.1	1.2	1.5	1.4	1.4	1.3
1.0	1.0	1.0	1.0	1.1	1.0	0.0	1.2	1.0	1.2	1.0	1.1	1.3	1.4	1.9	0.0	1.4	1.5
1.2	1.0	0.9	1.0	1.1	1.0	1.5	1.9	1.5	1.4	1.2	1.5	1.2	1.3	1.7	1.1	1.3	1.3
1.0	1.4	0.9	0.9	1.0	1.0	1.4	1.0	1.5	0.0	1.2	1.3	1.3	1.8	0.0	1.4	0.0	1.5
0.9	1.1	1.1	1.0	1.1	1.0	1.6	1.2	1.2	1.0	1.1	1.2	1.3	1.0	1.4	1.6	1.7	1.4
1.6	0.6	0.9	1.0	1.1	1.0	2.3	2.0	2.0	0.0	1.8	2.0	1.3	1.5	0.0	1.4	0.0	1.4
1.1	1.2	1.2	1.0	0.8	1.0	1.0	3.0	2.8	3.1	3.2	2.6	1.2	1.5	2.1	1.5	2.1	1.7
0.9	1.1	1.0	0.9	1.2	1.0	1.1	1.0	0.9	0.0	1.0	1.0	1.1	1.1	0.0	1.1	1.1	1.1
1.1	0.9	1.0	1.0	1.0	1.0	2.5	2.1	2.1	1.4	1.5	1.9	0.0	0.0	4.8	4.5	4.2	4.5
1.3	1.0	1.1	0.8	0.9	1.0	1.3	1.3	1.5	1.3	1.4	1.4	2.0	2.1	2.4	0.0	2.3	2.2

426	576	612	P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	K.QPAIMPGQSYGLEDGSC*SYKDFSESR.N
446	572	613	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.LSSC*DSFTSTINELNHCLSLR.T
500	594	614	P51610	HCFC1 Host cell factor 1	HCFC1	K.LVIYGGMSGC*R.L
510	546	615	P47756	CAPZB F-actin-capping protein subunit beta	CAPZB	K.DETVSDC*SPHIANIGR.L
633	537	616	Q9NXG2	THUMPD1 THUMP domain-containing protein 1	THUMPD1	R.C*DAGGPR.Q
712	670	617	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	R.LVSSPC*C*IVTSTYGWTANMER.I
660	653	618	Q12765	SCRN1 Secernin-1	SCRN1	K.TQSPC*FGDDDPAKKEPR.F
600	235	619	Q9H3P7	ACBD3 Golgi resident protein GCP60	ACBD3	K.QVLMGPYNPDTC*PEVGFFDVLGNDR.R
741	199	620	Q8TAQ2	SMARCC2 SWI/SNF complex subunit SMARCC2	SMARCC2	R.NLAGDVC*AIMR.V
671	583	621	P00492	HPRT1 Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	K.SYC*NDQSTGDIK.V
560	621	622	Q9BWJ5	SF3B5 Splicing factor 3B subunit 5	SF3B5	K.MLQPC*GPPADKPEEN.-
719	309	623	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	R.GDFC*IQVGR.N
587	498	624	Q96EY8	MMAB Cob(I)yrinic acid a,c-diamide adenosyltransferase,	MMAB	K.IQCTLQDVGSALATPC*SSAR.E
586	557	625	O75131	CPNE3 Copine-3	CPNE3	K.NC*LNPQFSK.T
634	564	626	P30086	PEBP1 Phosphatidylethanolamine-binding protein 1	PEBP1	R.APVAGTC*YQAEWDDYVPK.L
181	735	627	P30626	SRI Sorcin	SRI	R.CLTQSGIAGGYKPFNLETC*R.L
620	567	628	P31939	ATIC Bifunctional purine biosynthesis protein PURH	ATIC	K.VC*MVYDLYK.T
612	530	629	Q9HAV7	GRPEL1 GrpE protein homolog 1, mitochondrial	GRPEL1	K.LYGIQAFC*K.D
740	644	630	Q14914	PTGR1 Prostaglandin reductase 1	PTGR1	R.IAIC*GAISTYNR.T
454	730	631	P07237	P4HB Protein disulfide-isomerase	P4HB	K.KEEC*PAVR.L
263	549	632	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	R.IVDTPC*NEMNTDTFLEEINK.V
249	558	633	Q9GZQ3	COMMD5 COMM domain-containing protein 5	COMMD5	K.FVVSSLQGEDC*R.E
629	710	634	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	R.ISSINSISALC*EATGADVEEVATAIGMDQR.I
728	403	635	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	K.NVGC*LQEALQLATSFAQLR.L
622	213	636	P35270	SPR Sepiapterin reductase	SPR	R.AVC*LLTGASR.G
283	628	637	P26599	PTBP1 Polypyrimidine tract-binding protein 1	PTBP1	K.LSLDGQNIYNAC*CTLR.I
637	663	638	P60660	MYL6 Myosin light polypeptide 6	MYL6	K.ILYSQC*GDVMR.A
742	227	639	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.GIFPVLC*K.D
379	641	640	P21964	COMT Catechol O-methyltransferase	COMT	R.LITIEINPDC*AAITQR.M
575	727	641	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	K.ILSC*GEVIHVK.I
363	701	642	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	R.YLLQYQEPIPC*EQLVTALC*DIK.Q
605	640	643	O95372	LYPLA2 Acyl-protein thioesterase 2	LYPLA2	K.TYPGVMHSSC*PQEMAAVK.E
386	390	644	O75348	ATP6V1G1 V-type proton ATPase subunit G 1	ATP6V1G1	R.GSC*STEVEKETQEK.M
679	648	645	P49753	ACOT2 Acyl-coenzyme A thioesterase 2, mitochondrial	ACOT2	K.SEFYANEAC*KR.L

1.1	0.9	1.0	1.1	1.1	1.0	1.6	1.4	1.1	0.0	1.1	1.3	1.5	1.7	0.0	0.0	1.9	1.7
0.9	1.2	1.0	1.1	1.0	1.0	1.5	1.2	1.3	1.5	1.1	1.3	1.3	1.5	1.8	1.5	2.1	1.6
1.1	1.0	1.2	1.0	0.9	1.0	1.4	1.3	1.2	1.3	1.1	1.3	1.3	1.4	2.0	1.5	1.5	1.5
1.0	1.0	1.2	1.0	0.9	1.0	1.5	1.4	1.4	1.4	1.2	1.4	1.3	1.2	2.0	1.5	1.6	1.5
0.8	1.0	1.1	1.1	1.3	1.0	1.5	1.4	1.4	1.4	1.4	1.4	1.1	1.3	1.6	1.4	1.3	1.3
1.2	0.9	0.9	1.0	1.0	1.0	1.0	0.8	1.3	1.3	0.9	1.1	1.0	1.1	1.5	1.1	1.1	1.2
1.1	0.9	1.0	1.0	1.2	1.0	1.2	1.2	1.0	1.0	1.1	1.1	1.0	1.2	1.5	1.3	1.3	1.3
0.0	1.0	1.1	1.1	1.0	1.0	3.9	1.8	2.7	2.9	2.3	2.7	1.3	0.0	1.7	1.3	1.2	1.4
1.0	0.9	1.0	1.1	1.0	1.0	2.0	3.9	2.6	3.2	3.0	2.9	0.9	0.9	1.2	0.9	1.0	1.0
1.0	1.1	0.9	1.0	1.0	1.0	1.6	1.1	1.2	1.4	1.2	1.3	1.2	1.3	1.4	1.2	1.2	1.3
1.2	0.9	1.1	1.3	0.5	1.0	1.9	0.7	0.9	1.7	0.8	1.2	1.1	1.4	1.7	0.0	1.6	1.4
1.1	1.2	0.9	0.9	1.0	1.0	1.3	3.3	3.2	2.3	1.3	2.3	1.1	1.0	0.0	1.1	1.3	1.1
1.1	0.9	0.9	1.1	1.1	1.0	2.0	1.5	1.3	1.6	1.4	1.6	1.1	1.4	1.7	1.5	1.4	1.4
1.0	1.0	1.0	1.0	1.0	1.0	1.7	1.4	1.3	1.4	1.1	1.4	1.2	1.6	1.7	1.3	1.4	1.4
0.9	1.1	1.1	1.0	1.1	1.0	1.3	1.4	1.5	1.3	1.1	1.3	1.1	1.1	1.5	1.1	1.7	1.3
1.1	1.1	1.1	1.0	0.8	1.0	0.8	0.7	0.9	0.8	0.8	0.8	2.5	0.0	2.7	3.9	4.3	3.4
0.0	1.3	0.9	1.0	0.8	1.0	0.7	0.9	1.8	2.3	0.9	1.3	1.1	1.5	1.3	1.5	0.0	1.3
0.8	1.0	1.1	1.0	1.1	1.0	1.6	1.5	1.4	1.3	1.4	1.4	1.2	0.0	1.7	1.3	1.3	1.4
0.8	1.4	0.9	0.8	0.0	1.0	1.1	1.0	1.2	0.0	1.2	1.1	0.8	0.8	1.1	1.1	1.0	1.0
0.0	1.2	0.9	0.8	1.1	1.0	0.9	0.0	0.0	0.9	0.8	0.8	0.0	1.5	2.0	1.3	0.0	1.6
1.1	1.0	0.9	1.0	1.0	1.0	2.0	1.3	1.3	1.1	1.3	1.4	1.9	3.0	3.4	2.4	2.0	2.5
0.8	1.2	1.0	1.0	1.0	1.0	1.7	1.2	1.2	0.0	0.0	1.3	1.3	0.0	0.0	4.8	1.7	2.6
0.9	1.1	1.0	0.9	1.1	1.0	1.1	0.6	0.9	0.0	0.9	0.9	1.4	1.1	1.7	0.0	1.2	1.3
0.9	0.9	0.6	1.6	1.0	1.0	1.9	1.9	1.9	1.9	1.9	1.9	0.7	0.0	0.9	1.8	0.9	1.1
0.9	1.1	1.0	1.0	0.9	1.0	2.9	2.8	3.2	2.9	2.4	2.8	1.2	1.2	1.6	1.3	1.4	1.3
1.0	0.7	1.2	1.0	1.1	1.0	1.2	1.0	1.3	0.0	1.2	1.2	1.4	2.2	3.7	1.5	3.0	2.3
0.9	1.0	1.1	1.0	1.0	1.0	1.1	1.0	1.2	1.0	1.1	1.1	1.1	1.1	1.6	1.4	1.3	1.3
0.8	1.0	1.2	1.0	1.0	1.0	2.3	2.6	2.9	3.6	2.5	2.8	0.7	0.8	1.4	1.0	0.0	1.0
1.1	1.0	0.9	1.0	1.0	1.0	1.3	1.2	1.2	0.0	0.9	1.1	0.0	1.8	0.0	2.0	1.7	1.8
0.9	1.0	0.8	1.2	1.1	1.0	0.9	0.7	1.0	0.8	0.8	0.8	1.4	0.0	1.8	1.2	1.3	1.4
0.8	1.3	1.0	0.9	0.9	1.0	0.8	0.8	1.2	1.0	0.8	0.9	1.7	2.3	2.4	1.6	1.4	1.9
1.1	1.0	0.9	1.0	0.9	1.0	1.1	1.0	1.2	1.4	0.9	1.1	1.3	0.0	1.6	1.4	1.3	1.4
1.0	0.0	0.9	1.0	0.0	1.0	0.0	1.9	2.2	2.0	1.7	1.9	1.3	1.7	2.5	0.0	0.0	1.8
1.0	1.0	0.8	0.9	1.2	1.0	1.4	1.0	1.0	1.0	1.1	1.1	1.2	1.2	1.3	1.1	1.4	1.2

389	362	646	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	R.NDTPC*GTTIGPILASR.L
465	645	647	P60604	UBE2G2 Ubiquitin-conjugating enzyme E2 G2	UBE2G2	R.VC*ISILHAPGDDPMGYESSAER.W
488	740	648	P52907	CAPZA1 F-actin-capping protein subunit alpha-1	CAPZA1	K.TIDGQQTIIAC*IESHQFQPK.N
399	455	649	P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitocho	LRPPRC	R.IHDVLC*K.L
644	306	650	P61158	ACTR3 Actin-related protein 3	ACTR3	K.LGYAGNTEPQFIIPSC*IAIK.E
544	634	651	O14818	PSMA7 Proteasome subunit alpha type-7	PSMA7	R.VEC*QSHR.L
621	666	652	P12004	PCNA Proliferating cell nuclear antigen	PCNA	K.C*AGNEDIITLR.A
562	723	653	Q96AT9	RPE Ribulose-phosphate 3-epimerase	RPE	K.IGPSILNSDLANLGAEC*LR.M
462	667	654	Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	R.AITIAGIPQSIIEC*VK.Q
512	712	655	Q8IY67	RAVER1 Ribonucleoprotein PTB-binding 1	RAVER1	R.ALSAVHSPTFCQLAC*GQDGQLK.G
564	316	656	Q96EY5	FAM125A Multivesicular body subunit 12A	FAM125A	R.GFSAISC*TVEGAPASFGK.S
685	581	657	P63167	DYNLL1 Dynein light chain 1, cytoplasmic	DYNLL1	K.NADMSEEMQQDSVEC*ATQALEK.Y
502	592	658	P62993	GRB2 Growth factor receptor-bound protein 2	GRB2	K.VLNEEC*DQNWYK.A
727	671	659	P60981	DSTN Destrin	DSTN	K.AVIFC*LSADKK.C
667	714	660	Q96FX7	TRMT61A tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit	TRMT61A	R.FCSFSPC*IEQVQR.T
677	745	661	Q13404	UBE2V1 Ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	K.LPQPPEGQC*YSN.-
730	562	662	Q96EL3	MRPL53 39S ribosomal protein L53, mitochondrial	MRPL53	R.VQFC*PFEK.N
602	582	663	P58107	EPPK1 Epiplakin	EPPK1	R.YLEGTSC*IAGVLVPAK.D
364	668	664	Q9BSH4	TACO1 Translational activator of cytochrome c oxidase 1	TACO1	K.KLDSLGLCSVSC*ALEFIPNSK.V
451	426	665	P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	R.GC*AVVEFK.M
483	427	666	P51858	HDGF Hepatoma-derived growth factor	HDGF	K.C*GDLVFAK.M
567	580	667	O14745	SLC9A3R1 Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	R.IVEVNGVC*MEGK.Q
664	435	668	P18669	PGAM1 Phosphoglycerate mutase 1	PGAM1	R.YADLTEDQLPSC*ESLK.D
474	604	669	Q92879	CELF1 CUGBP Elav-like family member 1	CELF1	K.AMHQAQTMEGC*SSPMVVK.F
720	680	670	O43681	ASNA1 ATPase ASNA1	ASNA1	K.IDTHNIIVNQLVFPDPEKPC*K.M
723	662	671	Q04917	YWHAH 14-3-3 protein eta	YWHAH	K.NC*NDFQYESK.V
715	682	672	P08107	HSPA1B Heat shock 70 kDa protein 1A/1B	HSPA1B	R.ARFEELC*SDLFR.S
613	732	673	P10768	ESD S-formylglutathione hydrolase	ESD	K.AETGKCPALYWLSGLTC*TEQNFISK.S
609	722	674	P40925	MDH1 Malate dehydrogenase, cytoplasmic	MDH1	K.AIC*DHVR.D
543	248	675	P80404	ABAT 4-aminobutyrate aminotransferase, mitochondrial	ABAT	R.NKGVVLGGC*GDK.S
437	699	676	Q6NXG1	ESRP1 Epithelial splicing regulatory protein 1	ESRP1	R.VNYKFESGTC*SK.M
235	713	677	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit 2	PSMD2	K.GTLTLC*PYHSDR.Q
555	542	678	P17931	LGALS3 Galectin-3	LGALS3	R.VIVC*NTK.L
577	636	679	P52209	PGD 6-phosphogluconate dehydrogenase, decarboxylating	PGD	R.C*LSSLKDER.I
415	708	680	P22234	PAICS Multifunctional protein ADE2	PAICS	K.ITSC*IFQLLQEAGIK.T

1.0	0.9	1.0	1.0	0.9	1.0	1.4	2.2	2.3	2.6	1.5	2.0	1.5	1.8	2.2	1.5	2.1	1.8
0.0	0.0	1.0	1.1	0.9	1.0	1.5	1.0	1.1	0.0	0.9	1.1	1.4	1.3	2.3	1.5	1.6	1.6
0.9	1.0	1.0	1.0	1.0	1.0	0.8	0.6	1.0	0.7	0.8	0.8	1.2	1.4	2.1	0.0	0.0	1.6
1.1	0.9	1.1	0.9	0.9	1.0	2.3	1.3	1.3	1.2	2.3	1.7	1.2	3.5	1.4	1.3	1.6	1.8
0.9	1.0	1.1	0.9	1.0	1.0	1.0	2.3	2.7	3.1	2.3	2.3	1.0	1.1	1.7	0.0	1.4	1.3
0.9	0.9	1.2	1.1	0.8	1.0	0.0	1.0	1.2	1.2	0.0	1.1	1.2	0.0	1.8	1.3	1.6	1.5
0.9	1.0	1.0	1.0	0.9	1.0	1.2	1.0	1.1	1.2	0.9	1.1	1.0	1.1	1.3	1.6	1.7	1.3
0.8	1.0	1.4	0.8	0.9	1.0	0.7	0.7	1.0	1.1	0.8	0.9	1.2	1.4	1.4	1.5	1.8	1.4
1.0	1.1	1.0	0.9	1.0	1.0	1.2	1.0	1.2	0.9	1.0	1.1	1.5	1.4	1.9	1.5	1.8	1.6
1.0	0.0	0.9	1.1	0.9	1.0	1.1	0.9	0.8	0.9	0.8	0.9	1.2	0.0	1.6	1.6	1.7	1.5
0.9	1.0	0.9	1.0	0.9	1.0	2.3	0.0	2.7	0.0	1.7	2.2	1.3	0.0	1.8	1.6	1.0	1.4
0.9	1.0	0.9	0.9	1.0	1.0	0.9	1.5	0.0	1.4	1.3	1.3	0.9	0.0	1.7	0.0	1.0	1.2
0.9	1.0	1.0	1.0	1.0	1.0	1.4	1.3	1.1	1.3	1.2	1.3	1.2	1.3	2.2	1.5	1.5	1.5
1.1	1.0	1.0	0.8	0.9	1.0	0.9	1.3	1.1	1.1	0.8	1.0	0.0	0.9	1.3	1.0	1.1	1.1
1.1	0.0	0.9	0.8	1.1	1.0	1.0	1.0	0.9	0.6	0.9	0.9	1.3	1.2	0.0	1.3	0.0	1.3
0.8	1.1	1.0	0.9	1.1	1.0	0.6	0.5	1.0	0.6	1.1	0.7	0.0	1.0	1.6	1.1	1.3	1.2
0.8	0.0	0.9	0.9	1.3	1.0	0.0	1.7	1.2	0.0	1.1	1.3	1.1	0.9	0.0	1.2	0.0	1.1
0.8	0.9	1.0	1.1	0.9	1.0	0.9	1.7	1.3	1.5	1.0	1.3	0.0	1.3	1.6	1.2	1.5	1.4
0.7	1.0	1.0	1.1	0.9	1.0	1.4	0.9	1.0	1.0	1.0	1.1	1.8	0.0	2.3	1.6	0.0	1.9
0.8	1.1	1.0	1.1	0.9	1.0	1.6	1.6	2.3	1.5	1.9	1.8	1.4	1.5	2.2	1.5	1.6	1.6
0.8	1.1	1.0	1.1	0.9	1.0	1.6	1.6	2.3	1.5	1.9	1.8	1.4	1.3	2.2	1.4	1.6	1.6
0.0	0.0	1.2	0.9	0.7	1.0	1.4	1.2	1.4	1.1	0.0	1.3	1.3	1.5	0.0	0.0	1.4	1.4
1.0	0.9	1.1	0.9	0.8	1.0	1.0	1.9	1.7	2.6	1.6	1.8	1.5	0.9	1.4	1.4	1.2	1.3
0.4	1.4	1.0	0.8	1.2	1.0	1.2	1.3	1.3	1.3	1.1	1.2	1.5	0.0	2.2	1.1	0.0	1.6
1.0	1.3	0.7	0.8	0.9	1.0	1.0	0.8	1.3	1.0	0.9	1.0	0.9	0.0	1.6	1.0	1.0	1.1
0.9	1.1	0.9	0.9	1.0	0.9	1.2	0.9	1.4	1.0	0.9	1.1	1.0	1.0	1.2	1.2	1.2	1.1
0.9	1.0	1.0	0.9	1.0	0.9	0.9	0.9	1.2	1.1	1.0	1.0	1.0	1.0	1.5	0.9	1.2	1.1
1.0	0.9	0.9	1.0	0.9	0.9	0.9	0.8	0.8	0.8	0.9	0.8	1.1	1.2	1.5	1.5	1.5	1.4
0.9	1.1	1.0	0.8	1.0	0.9	0.7	0.7	1.1	1.0	0.9	0.9	1.5	0.0	1.4	1.2	0.0	1.4
0.9	0.6	0.9	1.0	1.3	0.9	2.4	2.4	3.0	0.0	2.7	2.6	1.3	1.5	0.0	1.4	1.7	1.5
0.9	0.9	0.0	1.0	0.0	0.9	1.1	0.0	0.0	0.9	0.8	0.9	1.7	1.5	1.9	0.0	1.5	1.6
1.0	0.9	1.1	0.8	0.9	0.9	0.7	0.9	1.1	0.9	0.8	0.9	2.7	1.3	3.8	1.4	4.5	2.7
0.9	1.0	1.1	0.8	0.9	0.9	0.0	1.6	1.4	1.4	1.1	1.4	1.3	1.6	1.7	1.1	1.6	1.4
0.9	1.0	0.9	0.9	1.0	0.9	1.1	0.9	1.3	1.2	1.1	1.1	1.2	1.2	1.8	1.2	1.6	1.4
1.0	0.9	0.9	0.9	1.0	0.9	0.9	0.8	1.0	0.9	0.9	0.9	1.7	0.0	2.2	1.5	1.6	1.7

665	541	681	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	R.LQEALDAEMLEDEAGGGGAGPGGAC*K.A
687	598	682	P13798	APEH Acylamino-acid-releasing enzyme	APEH	R.QPALSAAC*LGPEVTTQYGGQYR.T
735	724	683	P61981	YWHAG 14-3-3 protein gamma	YWHAG	K.NC*SETQYESK.V
615	631	684	P28838	LAP3 Cytosol aminopeptidase	LAP3	R.QVVDC*QLADVNNIGK.Y
682	688	685	O60664	PLIN3 Perilipin-3	PLIN3	R.DIAQQLQATC*TSLGSSIQGLPTNVK.D
553	623	686	O14964	HGS Hepatocyte growth factor-regulated tyrosine kinase	HGS	R.AC*GQIFCGK.C
722	675	687	P23528	CFL1 Cofilin-1	CFL1	K.AVLFC*LSEDK.K
748	563	688	Q9Y676	MRPS18B 28S ribosomal protein S18b, mitochondrial	MRPS18B	K.VVGNPC*PIC*R.D
699	651	689	P60174	TPI1 Triosephosphate isomerase	TPI1	R.IIYGGSVTGATC*K.E
703	678	690	P37802	TAGLN2 Transgelin-2	TAGLN2	K.DGTVLC*ELINALYPEGQAPVK.K
744	754	691	Q96BN8	FAM105B Protein FAM105B	FAM105B	R.VRGDNYC*ALR.A
482	638	692	P21291	CSRP1 Cysteine and glycine-rich protein 1	CSRP1	K.SC*FLC*MVC*K.K
528	715	693	Q15369	TCEB1 Transcription elongation factor B polypeptide 1	TCEB1	K.VC*MYFTYK.V
726	633	694	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	K.TGQATVASGIPAGWMGLDC*GPESSK.K
522	733	695	O75874	IDH1 Isocitrate dehydrogenase	IDH1	K.SEGGFIWAC*K.N
548	718	696	P22626	HNRNPA2B1 Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	K.LTDC*VVMRDPASK.R
661	752	697	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	R.GC*ITIIGGGDTATC*C*AK.W
328	660	698	P23528	CFL1 Cofilin-1	CFL1	K.HELQANC*YEEVK.D
538	747	699	P04632	CAPNS1 Calpain small subunit 1	CAPNS1	R.YSDESGNMDFDNFISC*LVR.L
716	193	700	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.NTGIIC*TIGPASR.S
641	716	701	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	K.FLDGNELTLADC*NLLPK.L
734	626	702	Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	K.LAAQSC*ALSLVR.Q
604	694	703	P22061	PCMT1 Protein-L-isoaspartate(D-aspartate) O-methyltransf	PCMT1	K.ALDVGSGSGILTAC*FAR.M
683	673	704	P61970	NUTF2 Nuclear transport factor 2	NUTF2	K.NINDAWVC*TNDMFR.L
596	741	705	Q96FJ2	DYNLL2 Dynein light chain 2, cytoplasmic	DYNLL2	K.NADMSEDMQQDAVDC*ATQAMEK.Y
749	486	706	P13489	RNH1 Ribonuclease inhibitor	RNH1	R.SNELGDVGVHC*VLQGLQTPSC*K.I
499	656	707	Q6QNY0	BLOC1S3 Biogenesis of lysosome-related organelles complex	BLOC1S3	R.GDLC*ALAER.L
583	684	708	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	K.ATC*IGNNSAAAVSMLK.Q
725	700	709	P60174	TPI1 Triosephosphate isomerase	TPI1	K.VPADTEVVC*APPTAYIDFAR.Q
659	669	710	P11142	HSPA8 Heat shock cognate 71 kDa protein	HSPA8	K.VC*NPIITK.L
684	689	711	Q04917	YWHAH 14-3-3 protein eta	YWHAH	K.ELETVC*NDVLSLLDK.F
658	726	712	P00491	PNP Purine nucleoside phosphorylase	PNP	R.AC*VMMQGR.F
724	586	713	Q9UL46	PSME2 Proteasome activator complex subunit 2	PSME2	K.C*GFLPGNEK.V
314	725	714	Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	K.VVFC*PVK.E

0.8	0.9	1.0	1.0	1.0	0.9	1.4	1.3	1.5	1.4	1.5	1.4	1.4	1.3	1.4	0.0	1.0	1.3
0.0	1.1	0.8	0.9	1.0	0.9	1.2	1.0	1.3	1.7	1.1	1.3	1.0	1.3	0.0	1.3	0.0	1.2
0.9	0.9	1.0	0.9	0.9	0.9	0.0	0.0	0.7	0.7	1.1	0.9	1.0	0.9	0.0	0.0	1.1	1.0
0.0	0.9	0.9	0.9	1.0	0.9	1.9	1.1	0.9	1.1	0.8	1.2	1.2	1.1	1.7	1.2	1.6	1.4
1.0	0.0	1.0	0.8	0.9	0.9	1.1	1.1	1.0	0.0	0.9	1.0	1.2	1.2	0.0	1.3	1.2	1.2
1.0	0.7	0.9	1.2	0.9	0.9	1.6	1.1	1.2	1.0	1.1	1.2	1.6	1.2	1.8	1.5	1.2	1.5
0.5	1.0	1.1	0.9	1.1	0.9	0.9	1.2	1.1	0.9	1.1	1.0	1.1	1.0	1.4	0.8	1.2	1.1
1.3	0.0	0.5	2.3	0.5	0.9	1.0	0.9	2.0	1.4	1.4	1.3	0.0	1.2	1.1	1.0	0.0	0.7
0.7	1.1	0.9	1.0	1.0	0.9	0.9	1.0	1.2	1.4	1.0	1.1	1.1	1.2	1.3	1.1	1.2	1.2
0.9	1.0	1.0	0.8	0.9	0.9	1.0	1.0	1.2	1.0	1.0	1.0	1.1	1.2	1.3	1.0	1.2	1.2
0.0	0.0	0.8	0.9	1.0	0.9	0.5	0.5	0.8	0.0	0.0	0.6	0.0	1.1	1.1	0.6	0.0	0.9
0.9	0.8	0.9	1.0	1.0	0.9	1.2	1.0	1.0	1.5	1.0	1.1	1.4	1.5	2.1	1.3	1.6	1.6
0.9	1.3	0.9	0.8	0.7	0.9	0.8	0.9	1.0	0.0	0.9	0.9	1.9	0.6	0.0	0.0	1.9	1.5
0.9	1.0	1.0	0.7	1.0	0.9	0.8	1.0	1.1	1.9	1.0	1.1	1.2	1.1	0.0	1.0	1.1	1.1
0.9	0.9	0.8	0.9	1.0	0.9	0.8	0.8	0.8	0.8	0.8	0.8	1.4	1.5	1.6	1.4	1.5	1.5
0.9	0.8	1.1	0.9	0.8	0.9	0.9	0.9	0.8	0.9	0.9	0.9	1.3	1.3	1.6	1.5	1.6	1.5
0.0	0.9	0.9	0.9	1.0	0.9	0.6	0.5	1.0	0.6	0.5	0.7	1.2	1.3	1.4	1.3	1.1	1.3
0.9	0.9	0.9	0.9	1.0	0.9	1.3	1.0	1.0	1.1	1.0	1.1	1.7	1.9	2.5	2.1	2.0	2.0
0.9	1.0	0.9	0.9	0.9	0.9	0.7	0.5	0.8	0.8	0.8	0.7	1.4	1.4	1.8	1.4	1.5	1.5
0.8	1.0	1.0	0.9	0.8	0.9	3.0	2.8	3.2	3.4	2.4	3.0	0.9	1.1	1.3	1.1	1.3	1.1
0.9	0.9	1.0	0.7	1.0	0.9	0.8	0.9	1.1	0.8	0.8	0.9	1.1	1.3	0.0	1.0	1.9	1.3
0.9	0.7	1.0	1.0	0.9	0.9	1.3	1.2	1.4	1.0	1.1	1.2	1.0	1.2	1.0	1.1	0.9	1.0
0.9	0.9	0.9	0.8	0.9	0.9	1.0	1.0	1.1	1.0	0.9	1.0	1.7	1.2	1.6	1.1	1.4	1.4
0.9	0.9	0.9	0.9	0.9	0.9	0.9	1.0	1.1	1.2	1.0	1.0	1.0	1.4	1.4	1.2	1.2	1.2
0.8	0.8	1.2	0.8	0.9	0.9	0.7	0.7	0.9	0.8	0.7	0.8	1.2	0.0	0.0	1.4	1.6	1.4
1.0	0.8	0.9	0.9	0.9	0.9	1.4	1.6	1.6	2.0	1.4	1.6	0.0	0.6	0.8	0.7	0.6	0.6
0.0	0.9	0.8	0.9	0.9	0.9	1.1	1.6	0.8	1.1	0.9	1.1	1.6	1.1	1.8	1.4	1.8	1.5
0.8	0.8	0.9	0.9	0.9	0.9	0.7	1.0	1.3	1.2	0.8	1.0	0.0	1.3	1.6	1.3	1.4	1.4
0.8	1.0	1.0	0.8	0.9	0.9	0.8	0.8	1.0	1.3	0.8	0.9	1.0	1.1	1.4	1.0	1.1	1.1
0.8	0.9	1.0	0.9	0.9	0.9	0.8	0.9	1.1	1.5	1.0	1.1	1.0	0.0	1.6	0.9	1.4	1.3
0.0	1.0	0.9	0.8	0.9	0.9	1.1	0.8	1.1	1.1	0.9	1.0	1.1	0.9	2.0	1.1	1.1	1.2
0.7	1.1	1.0	0.7	0.8	0.9	0.6	0.7	1.0	1.0	0.9	0.8	1.1	0.0	0.0	0.9	1.8	1.3
0.9	0.8	0.9	1.0	0.9	0.9	1.6	1.2	1.2	1.3	1.1	1.3	0.8	1.1	1.3	1.2	1.1	1.1
1.0	0.8	0.8	1.0	0.8	0.9	0.7	1.0	0.9	0.0	0.9	0.9	1.9	2.0	2.2	2.3	2.4	2.1

654	693	715	P50395	GDI2 Rab GDP dissociation inhibitor beta	GDI2	R.TDDYLDQPC*YETINR.I
618	533	716	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	R.YASIC*QQNGIVPIVEPEILPDGDHDLK.R
694	574	717	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	R.ALANSLAC*QGK.Y
507	704	718	P07737	PFN1 Profilin-1	PFN1	K.C*YEMASHLR.R
576	703	719	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	R.YDDMAAC*MK.S
529	709	720	Q9UHX1	PUF60 Poly(U)-binding-splicing factor PUF60	PUF60	R.ALAIMC*R.V
688	737	721	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.SIC*TTVLELLDK.Y
520	744	722	P55212	CASP6 Caspase-6	CASP6	R.GTC*ADRDNLTR.R
648	736	723	P14174	MIF Macrophage migration inhibitory factor	MIF	K.LLC*GLLAER.L
662	731	724	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	K.IETELRDIC*NDVLSLLEK.F
732	685	725	P31949	S100A11 Protein S100-A11	S100A11	K.ISSPTETERC*IESLIAVFQK.Y
690	720	726	P60174	TPI1 Triosephosphate isomerase	TPI1	K.IAVAAQNC*YK.V
745	738	727	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	K.LTFSC*LGGSDNFK.H
689	228	728	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.IC*PVETLVEEAIQC*AEK.I
531	474	729	O75663	TIPRL TIP41-like protein	TIPRL	K.VAC*AEEWQESR.T
471	625	730	P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	K.YLEC*SALTQR.G
630	706	731	P08107	HSPA1B Heat shock 70 kDa protein 1A/1B	HSPA1B	K.ELEQVC*NPIISGLYQGAGGPGPGGFGAQGPK.G
704	750	732	P09467	FBP1 Fructose-1,6-bisphosphatase 1	FBP1	R.GTGELTQLLNSLC*TAVK.A
708	691	733	P61158	ACTR3 Actin-related protein 3	ACTR3	R.LPAC*VVDC*GTGYTK.L
706	734	734	P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	R.IIPGFMC*QGGDFTR.H
668	650	735	P14625	HSP90B1 Endoplasmin	HSP90B1	R.LTESPC*ALVASQYGWSGNMER.I
430	655	736	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	R.SC*YLSSLDLLLEHR.L
571	717	737	P00390	GSR Glutathione reductase, mitochondrial	GSR	K.LGGTC*VNVGCVPK.K
692	743	738	P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	K.KITIADC*GQLE.-
702	748	739	P21964	COMT Catechol O-methyltransferase	COMT	R.YLPDTLLLEEC*GLLR.K
506	593	740	Q9BWD1	ACAT2 Acetyl-CoA acetyltransferase, cytosolic	ACAT2	R.ATVAPEDVSEVIFGHVLAAGC*GQNPVR.Q
670	484	741	Q9Y3D0	FAM96B Mitotic spindle-associated MMXD complex subunit MI	FAM96B	R.VAAALENTHLLEVVNQC*LSAR.S
707	676	742	P31150	GDI1 Rab GDP dissociation inhibitor alpha	GDI1	R.TDDYLDQPC*LETVNR.I
743	697	743	P30044	PRDX5 Peroxiredoxin-5, mitochondrial	PRDX5	K.ALNVEPDGTGLTC*SLAPNIISQL.-
751	755	744	P13489	RNH1 Ribonuclease inhibitor	RNH1	K.LSLQNC*C*LTGAGC*GVLSSTLR.T
320	82	745	P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	K.ARDC*LIPMGITSENVAER.F
342	683	746	P41250	GARS Glycine--tRNA ligase	GARS	R.SC*YDLSC*HAR.A
72	751	747	Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	K.GNGIVEC*LGPK.-
697	739	748	U2AF2	U2AF2 Splicing factor U2AF 65 kDa subunit	U2AF2	K.SIEIPRPVDGVEVPGC*GK.I
733	749	749	P60174	TPI1 Triosephosphate isomerase	TPI1	K.DC*GATWVVLGHSER.R

0.8	1.0	0.9	0.8	1.0	0.9	1.0	1.0	1.0	1.0	0.9	1.0	1.1	1.1	2.0	0.9	1.3	1.3
0.8	0.9	0.9	0.8	0.9	0.9	0.9	1.4	1.6	2.0	1.2	1.4	1.1	1.1	1.8	1.0	1.7	1.4
0.8	0.9	1.0	0.7	0.9	0.9	0.9	1.5	1.5	1.5	1.0	1.3	1.0	1.0	1.4	1.2	1.4	1.2
0.9	0.9	0.8	0.8	0.9	0.9	0.8	0.9	1.1	1.0	0.8	0.9	1.4	1.2	1.8	1.3	1.9	1.5
0.9	0.0	1.1	0.7	0.7	0.9	0.7	0.7	1.1	1.0	1.0	0.9	1.1	0.0	1.6	0.9	2.0	1.4
0.8	1.1	0.8	0.8	0.8	0.9	0.9	0.8	1.1	0.9	0.8	0.9	1.3	0.0	1.7	0.0	1.5	1.5
0.8	1.0	0.9	0.8	0.8	0.9	0.8	0.7	0.9	0.8	0.7	0.8	1.2	1.1	0.0	1.0	1.6	1.2
0.0	0.8	0.9	1.0	0.8	0.9	0.0	0.8	0.6	1.0	0.6	0.7	1.3	1.2	1.5	1.5	2.0	1.5
0.9	0.9	0.9	0.8	0.9	0.9	0.8	0.7	0.9	0.7	0.8	0.8	1.2	1.2	1.4	1.2	1.4	1.3
0.7	1.0	1.0	0.8	0.8	0.8	0.8	0.7	1.0	0.8	0.9	0.8	1.1	1.3	1.4	0.9	1.7	1.3
0.6	1.0	0.9	0.9	0.8	0.8	0.9	0.7	1.4	0.8	1.3	1.0	0.9	1.1	1.4	0.9	0.9	1.0
0.8	0.9	0.9	0.7	0.9	0.8	0.6	0.7	1.1	1.2	0.8	0.9	1.0	1.1	1.4	1.2	1.3	1.2
0.8	1.0	0.8	0.8	0.8	0.8	0.7	0.8	0.9	0.7	0.8	0.8	0.9	0.8	1.1	0.9	0.9	0.9
0.7	0.9	0.9	0.9	0.7	0.8	2.6	2.7	2.9	3.2	2.5	2.8	1.2	1.2	1.4	1.1	1.2	1.2
1.0	0.8	0.8	0.8	0.0	0.8	2.0	0.0	0.0	1.6	1.4	1.6	1.7	0.0	1.6	1.5	1.2	1.5
0.9	0.6	1.0	0.9	0.9	0.8	1.0	1.2	1.1	1.6	1.0	1.2	1.7	1.6	1.8	1.3	0.0	1.6
0.7	0.9	0.9	0.7	0.9	0.8	0.0	1.0	0.9	0.8	0.9	0.9	1.2	0.0	1.5	0.0	1.3	1.3
0.8	0.9	0.8	0.8	0.8	0.8	0.7	0.6	0.7	0.7	0.8	0.7	1.2	1.1	1.5	0.9	1.2	1.2
1.0	0.6	0.9	0.9	0.9	0.8	0.9	0.9	1.1	1.1	0.9	1.0	1.0	1.1	0.0	0.0	1.3	1.2
0.8	0.9	0.9	0.7	0.8	0.8	0.7	0.7	0.9	0.9	0.8	0.8	1.0	1.1	1.4	1.1	1.3	1.2
0.0	0.0	0.8	0.8	0.9	0.8	1.0	0.0	1.1	1.0	1.3	1.1	0.0	1.2	0.0	1.2	1.4	1.3
0.8	0.9	0.8	0.8	0.9	0.8	0.8	1.1	1.1	1.4	1.1	1.1	1.2	2.1	1.8	0.0	0.0	1.7
0.7	0.8	0.8	0.8	0.9	0.8	1.0	0.8	0.9	0.9	0.8	0.9	1.3	1.3	1.7	1.5	1.4	1.4
0.7	1.0	0.8	0.8	0.8	0.8	0.7	0.6	0.9	0.8	0.7	0.7	1.1	1.0	1.5	1.0	1.5	1.2
0.8	0.9	0.8	0.7	0.8	0.8	0.6	0.6	0.9	0.7	0.8	0.7	1.2	0.0	1.5	0.8	1.2	1.2
1.1	0.8	0.6	0.7	0.9	0.8	1.1	1.3	1.3	1.4	1.2	1.3	1.4	1.4	1.9	0.0	1.5	1.5
0.7	0.8	1.0	0.9	0.7	0.8	1.5	1.6	0.0	1.6	1.8	1.6	0.9	1.5	1.3	1.1	1.5	1.3
0.8	0.8	0.9	0.7	0.8	0.8	0.8	0.9	1.2	1.4	0.9	1.0	1.2	0.9	1.6	0.9	1.3	1.2
0.7	0.8	0.9	0.8	0.8	0.8	1.1	0.9	0.9	0.9	0.9	1.0	0.8	0.9	1.2	0.9	1.0	1.0
1.1	0.4	0.8	0.8	0.8	0.8	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.6	0.3	0.0	0.5
0.8	0.7	0.7	0.8	0.8	0.8	4.7	5.0	4.4	4.5	3.6	4.4	1.8	1.9	2.7	2.1	2.1	2.1
0.8	0.7	0.8	0.8	0.8	0.8	0.9	1.1	1.2	1.0	0.9	1.0	1.8	2.3	2.8	1.5	1.6	2.0
0.6	0.7	0.7	1.1	0.6	0.8	0.7	0.8	0.6	0.8	0.5	0.7	6.5	0.0	0.0	6.4	6.2	6.4
0.7	0.0	0.7	0.7	0.8	0.7	1.2	0.5	0.0	0.9	0.5	0.8	1.0	1.0	1.4	1.3	1.3	1.2
0.6	0.0	0.7	0.7	0.9	0.7	0.5	0.7	0.9	0.0	0.8	0.7	1.1	1.0	0.0	1.0	0.0	1.0

711	560	750	P25398	RPS12 40S ribosomal protein S12	RPS12	K.VVGC*SCVVVK.D
461	438	751	O43290	SART1 U4/U6.U5 tri-snRNP-associated protein 1	SART1	K.SLPSAVYC*IEDK.M
705	654	752	P25398	RPS12 40S ribosomal protein S12	RPS12	R.QAHLC*VLASNCDEPMYVK.L
651	550	753	P25398	RPS12 40S ribosomal protein S12	RPS12	K.LVEALC*AEHQINLIK.V
752	728	754	P30041	PRDX6 Peroxiredoxin-6	PRDX6	R.DFTPVC*TTELGR.A
753	457	755	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	R.VPTANVSVVDLTC*R.L
750	756	756	P41250	GARS Glycine--tRNA ligase	GARS	K.C*SVLPLSQNQEFMPFVK.E

0.0	0.7	0.7	0.7	0.7	0.7	1.5	0.0	0.7	1.7	1.6	1.3	1.0	1.0	1.3	1.3	1.2	1.2
0.0	0.0	0.7	0.6	0.7	0.6	2.2	0.0	1.8	0.0	1.3	1.8	1.4	1.2	0.0	0.0	2.2	1.6
0.6	0.6	0.6	0.6	0.7	0.6	1.3	1.1	1.0	1.0	1.0	1.1	1.0	1.2	1.4	1.1	1.2	1.2
0.6	0.6	0.6	0.6	0.6	0.6	1.5	1.4	1.5	1.3	1.2	1.4	1.3	1.2	1.3	1.4	1.2	1.3
1.0	0.5	0.5	0.5	0.5	0.6	0.4	0.9	0.9	1.2	0.8	0.8	0.5	0.6	0.5	0.4	0.0	0.5
0.4	0.5	0.4	0.4	0.4	0.4	0.7	2.0	2.1	2.2	1.4	1.7	0.4	0.4	0.5	0.4	0.5	0.5
0.0	0.2	0.2	0.2	0.2	0.2	0.0	0.4	0.3	0.6	0.4	0.4	0.4	0.0	0.6	0.0	0.6	0.5

Table 3A-5. PDB codes, solvent-accessible surface area (SASA) and pK_a values for 19 of the most-sensitive and insensitive cysteines to GSNO, CoA-SNO and Trx-SNO transnitrosation respectively. Data from this table are plotted in Figure 3-7.

19 GSNO-sensitive cysteines with PDB entries						
Peptide #	Uniprot #	Symbol	Sequence	PDB	SASA (Å^2)	pK_a
1	P04406	GAPDH	ISNASCTTNCL	1U8F	18.712	11.18
2	P07339	CTSD	EYMIPCEKVST	1LYW	5.256	–
3	Q01813	PFKP	LPLMECVQMTQ	4U1R	5.754	11.03
4	Q92947	GCDH	IKGYGCAGVSS	1SIQ	0.000	11.23
5	Q99714	HSD17B10	KLGNNCVFAPA	2O23	0.000	11.26
6	P31749	AKT1	TMKTFCGTPEY	4EJN	2.253	–
7	P26440	IVD	NVAKACDEGHC	1IVH	0.000	–
8	P36578	RPL4	KRYAICSALAA	4UG0	0.000	11.00
9	P04183	TK1	EALPACLLRDV	2ORV	26.727	9.37
10	P40926	MDH2	DCLKGCDVVVI	4WLV	0.000	10.61
11	Q8TCU6	PREX1	LRLRLCVLNEI	4YON	45.320	9.30
12	P04183	TK1	YSSSFCTHDRN	2ORV	64.257	8.97
13	O14733	MAP2K7	TRSAGCAAYMA	3WZU	14.636	10.59
14	P63244	GNB2L1	SEWVSCVRFSP	4AOW	3.802	9.82
15	P49327	FASN	SPEGTCKAFDT	3HHD	0.000	12.76
16	Q99714	HSD17B10	DVAVNCAGIAV	2O23	0.000	10.69
17	P07858	CTSB	RGQDHCGIESE	3PBH	3.319	11.79
18	P60709	ACTB	NSIMKCDVDIR	3J82	0.068	10.53
19	P63244	GNB2L1	NTLGVCKYTVQ	4AOW	6.423	8.80
19 GSNO-insensitive cysteines with PDB entries						
Peptide #	Uniprot #	Symbol	Sequence	PDB	SASA (Å^2)	pK_a
1	Q9UHX1	PUF60	ALAIMCRVYVG	3UWT	12.219	11.45
2	P27348	YWHAQ	ELRSICTTVLE	2BTP	0	12.52
3	P55212	CASP6	ERRGTCADRDN	4HVA	33.628	10.28
4	P14174	MIF	YSKLLCGLLAE	1MIF	13.173	10.08
5	P63104	YWHAZ	ELRDICNDVLS	2O02	0	12.47
6	P31949	S100A11	TETERCIESLI	2LUC	33.66	9.37
7	P60174	TPI1	VAAQNCYKVTN	4POD	0	11.94
8	Q15185	PTGES3	KLTFSCLGGSD	1EJF	0	10.81
9	P30084	ECHS1	LVSKICPVETL	2HW5	0.204	11.63
10	P30084	ECHS1	EEAIQCAEKIA	2HW5	16.643	9.18
11	P15153	RAC2	VKYLECSALTQ	1DS6	0.222	12.14
12	)MV9 (P0DM	HSPA1B	ELEQVCNPIIS	4PO2	0	7.44
13	P09467	FBP1	LLNSLCTAVKA	2Y5K	9.271	11.05
14	P62937	PPIA	IPGFMCQGGDF	4YUO	0	12.47
15	Q9BQ69	MACROD1	AELRSCYLSSL	2X47	0	11.23
16	P00390	GSR	KLGGTCVNVGC	3DK8	8.24	13.94
17	P62937	PPIA	ITIADCGQLE*	4YUO	1.267	11.43
18	P21964	COMT	LLLEECGLLRK	4PYK	12.471	9.93
19	Q9BWD1	ACAT2	VLAAGCGQNPV	1WL5	9.421	8.59

19 CoA-SNO-sensitive cysteines with PDB entries						
Peptide #	Uniprot #	Symbol	Sequence	PDB	SASA (Å^2)	pK_a
1	P31749	AKT1	TMKTFCGTPEY	4EJN	2.253	–
2	Q9BRA2	TXNDC17	GGKSWCPDCVQ	1WOU	4.919	–
3	Q01813	PFKP	LPLMECVQMTQ	4U1R	5.754	11.03
4	Q92947	GCDH	IKGYGCAGVSS	1SIQ	0.000	11.23
5	P30084	ECHS1	LSFQDCYSSKF	2HW5	20.113	9.64
6	P00558	PGK1	PSIKFCLDNGA	3ZOZ	0.000	12.22
7	Q8TCU6	PREX1	LRLRLCVLNEI	4YON	45.320	9.30
8	P04183	TK1	EALPACLLRDV	2ORV	26.727	9.37
9	Q9GZZ9	UBA5	KREGVCAASLP	3H8V	1.748	9.76
10	P54886	ALDH18A1	VRDSKCEYPAA	2H5G	0.529	10.94
11	P54886	ALDH18A1	EYPAACNALET	2H5G	21.058	3.40
12	P07858	CTSB	RGQDHCGIESE	3PBH	3.319	11.79
13	Q99714	HSD17B10	KLGNNCVFAPA	2O23	0.000	11.26
14	Q99714	HSD17B10	LPEKVCNFLAS	2O23	62.971	8.78
15	P04406	GAPDH	ISNASCTTNCL	1U8F	18.712	11.18
16	P07339	CTSD	EYMIPCEKVST	1LYW	5.256	–
17	P30084	ECHS1	LVSKICPVETL	2HW5	0.204	11.63
18	P30084	ECHS1	EEAIQCAEKIA	2HW5	16.643	9.18
19	P04183	TK1	YSSSFCTHDRN	2ORV	64.257	8.97
19 CoA-SNO-insensitive cysteines with PDB entries						
Peptide #	Uniprot #	Symbol	Sequence	PDB	SASA (Å^2)	pK_a
1	Q96FX7	TRMT61A	CSFSPCIEQVQ	5CCB	58.964	9.5
2	Q15369	TCEB1	VLSKVCMYFTY	1VCB	0	11.44
3	O00299	CLIC1	LTLADCNLLPK	1K0M	0	13.71
4	P00390	GSR	KLGGTCVNVGC	3DK8	8.24	13.94
5	P22626	HNRNPA2B1	GKLTDCVVMRD	1X4B	13.342	10.32
6	P34897	SHMT2	ASENFCSRAAL	3OU5	0.402	11
7	P60174	TPI1	VAAQNCYKVTN	4POD	0	11.94
8	P21266	GSTM3	QSDQFCKMPIN	3GTU	29.912	9.34
9	Q96AT9	RPE	NLGAECLRMLD	3OVP	0	11.71
10	P61981	YWHAG	YLIKNCSETQY	3UZD	4.38	10.35
11	Q9UBE0	SAE1	KKVVFCPVKEA	3KYC	0.243	10.96
12	P00491	PNP	LNGRACVMMQG	3K8Q	0	12.14
13	P30041	PRDX6	DFTPVCTTELG	1PRX	1.054	10.22
14	Q12849	GRSF1	LFLNSCPKGK*	4QU7	29.36	9.13
15	P07237	P4HB	LKKEECPAVRL	4EKZ	0	10.53
16	P63104	YWHAZ	ELRDICNDVLS	2O02	0	12.47
17	P10768	ESD	LSGLTCTEQNF	3FCX	2.991	9.98
18	O75874	IDH1	GFIWACKNYDG	1T09	6.815	11.39
19	P62937	PPIA	IPGFMCQGGDF	4YUO	0	12.47
19 Trx-SNO-sensitive cysteines with PDB entries						
Peptide #	Uniprot #	Symbol	Sequence	PDB	SASA (Å^2)	pK_a
1	P31749	AKT1	TMKTFCGTPEY	4EJN	2.253	–
2	Q01813	PFKP	LPLMECVQMTQ	4U1R	5.754	11.03

3	Q92947	GCDH	IKGYGCAGVSS	1SIQ	0.000	11.23
4	P07858	CTSB	RGQDHCGIESE	3PBH	3.319	11.79
5	P26440	IVD	RGSNTCELIFE	1IVH	0.000	11.39
6	P26440	IVD	LIFEDCKIPAA	1IVH	0.092	11.09
7	P04183	TK1	KLTAVCMECFR	2ORV	0.000	5.89
8	P54886	ALDH18A1	VRDSKCEYPAA	2H5G	0.529	10.94
9	P54886	ALDH18A1	EYPAACNALET	2H5G	21.058	3.40
10	P07384	CAPN1	TRLEICNLTPD	2ARY	11.349	11.92
11	P49327	FASN	AGNGYCRSEGV	3HHD	0.000	11.51
12	O14733	MAP2K7	TRSAGCAAYMA	3WZU	14.636	10.59
13	P36873	PPP1CC	KTFTDCFNCLP	1JK7	0.075	8.12
14	P36873	PPP1CC	TDCFNCLPIAA	1JK7	0.000	10.65
15	P13804	ETFA	AGNALCTVKCD	2A1U	27.706	9.22
16	P24468	NR2F2	RFGSQCMQPNN	3CJW	46.835	9.56
17	P36578	RPL4	KRYAICSALAA	4UG0	0.000	11.00
18	P49327	FASN	SPEGTCKAFDT	3HHD	0.000	12.76
19	P36873	PPP1CC	RGNHECASINR	1JK7	0.616	11.23

19 Trx-SNO-insensitive cysteines with PDB entries

Peptide #	Uniprot #	Symbol	Sequence	PDB	SASA (Å^2)	pK_a
1	Q04917	YWHAH	FLIKNCNDFQY	2C63	3.458	10.7
2	P60174	TPI1	DTEVVCAPPTA	4POD	0	12.29
3	P00558	PGK1	WMGLDCGPESS	3ZOZ	0	12.43
4	P60981	DSTN	KAVIFCLSADK	1AK7	0	16.74
5	P14618	PKM	LDGADCIMLSG	3BJT	0	12.84
6	P31949	S100A11	TETERCIESLI	2LUC	33.66	9.37
7	P60174	TPI1	GMIKDCGATWV	4POD	35.078	10.11
8	Q08211	DHX9	LAAQSCALSLV	3VYX	0	11.38
9	P61981	YWHAG	YLIKNCSETQY	3UZD	4.38	10.35
10	P49915	GMPS	GVQGDCRSYSY	2VXO	68.393	9.17
11	Q15257	PPP2R4	FAAFLCCLCKI	2HV6	3.653	13.15
12	Q15257	PPP2R4	AAFLCCLCKIG	2HV6	0	14.32
13	Q15257	PPP2R4	FLCCLCKIGVL	2HV6	6.782	11.86
14	O60701	UGDH	GFGGSCFQKDV	4QEJ	33.156	10.59
15	Q14914	PTGR1	GRIAICGAIST	2Y05	4.735	12.4
16	P14618	PKM	IFPVLCKDPVQ	3BJT	0	10.68
17	P30044	PRDX5	GTGLTCSLAPN	1OC3	8.158	10.03
18	Q96BN8	FAM105B	RGDNYCALRAT	3ZNV	1.18	11.03
19	Q15185	PTGES3	KLTFSCLGGSD	1EJF	0	10.81

Table 3A-6. Comparison of cysteine transnitrosatio sensitivity to cysteine reactivity. A list of all peptides (* denotes labeled cysteine) identified in the GSNO (500 μM), CoA-SNO (500 μM), Trx-C73-SNO (90 μM) analysis and a previous study of cysteine reactivity (reactivity ratio) is presented together with calculated heavy:light ratios (R-values). In the reactivity data, the ratios are presented as light:heavy, where labeling at 100 μM IA (light) was compared to 10 μM IA (heavy). A lower ratio value in the reactivity ratio column signifies increased reactivity of a cysteine.

Peptide #	Uniprot #	Description	Symbol	Sequence	Ratio			
					IA	GSNO (H/L)	CoA-SNO (H/L)	Trx-SNO (H/L)
					10/1	500 μM	500 μM	90 μM
1	P78417	GSTO1 Glutathione transferase omega-1	GSTO1	R.FC*PFAER.T	0.8	1.1	1.0	1.2
2	P49189	ALDH9A1 aldehyde dehydrogenase 9A1	ALDH9A1	K.GALMANFLTQGQVC*CNGTR.V	0.9	1.3	1.8	1.5
3	Q9BRA2	TXNDC17 Thioredoxin domain-containing protein 17 E	TXNDC17	K.DAGGKSWC*PDCVQAEPVVR.E	1.0	1.2	10.9	4.0
4	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	R.C*MALSTAVLVGEAK.K	1.1	3.3	6.6	15.0
5	P12532	CKMT1A CKMT1B Creatine kinase, ubiquitous mitochon	CKMT1A	R.LGYILTC*PSNLGTGLR.A	1.1	1.3	3.7	1.6
6	P16455	MGMT Methylated-DNA--protein-cysteine methyltransf	MGMT	R.VVC*SSGAVGNYSGGLAVK.E	1.2	1.6	4.7	1.7
7	O75874	IDH1 Isocitrate dehydrogenase [NADP] cytoplasmic E	IDH1	K.SEGGFIWAC*K.N	1.4	0.9	0.8	1.5
8	Q9Y696	CLIC4 Chloride intracellular channel protein 4 ENS	CLIC4	K.AGSDGESIGNC*PFSQR.L	1.5	1.1	1.0	1.2
9	O95336	PGLS 6-phosphogluconolactonase	PGLS	R.AAC*CLAGAR.A	1.5	1.2	1.5	1.3
10	Q9H0W8	C19orf61 59 kDa protein	C19orf61	R.REDFC*PR.K	1.5	1.2	1.6	1.8
11	P46782	RPS5 40S ribosomal protein S5	RPS5	K.AQC*PIVER.L	1.6	1.6	2.0	5.4
12	Q9BW61	C19orf58 Uncharacterized protein C19orf58	C19orf58	R.FHADSVC*K.A	1.7	1.1	1.3	1.4
13	Q8N1F7	NUP93 Nuclear pore complex protein Nup93	NUP93	K.SSGQSAQLLSHEPGDPPC*LR.R	1.8	1.4	1.3	1.8
14	Q99873	PRMT1 HMT1 hnRNP methyltransferase-like 2 isoform	PRMT1	K.VIGIEC*SSISDYAVK.I	1.9	1.1	1.2	1.9
15	O00299	DDAH2 CLIC1 Chloride intracellular channel protein	DDAH2	K.AGSDGAKIGNC*PFSQR.L	2.0	1.3	1.0	1.2
16	A0AVT1	UBE1L2 Isoform 1 of Ubiquitin-activating enzyme E1	UBE1L2	R.KPNVGC*QQDSEELLK.L	2.0	1.4	1.3	1.5
17	P07339	CTSD Cathepsin D precursor	CTSD	K.AIGAVPLIQGEYMIPC*EK.V	2.1	3.9	6.3	6.9
18	P23396	RPS3 40S ribosomal protein S3	RPS3	R.GLC*AIAQAESLR.Y	2.2	1.7	2.2	3.4
19	P07437	TUBB Tubulin beta chain	TUBB	K.LTTPTYGDLNHLVSATMSGVTTC*LR.F	2.3	3.7	5.2	4.6
20	Q9NQR4	NIT2 Nitrilase family member 2	NIT2	R.VGLGIC*YDMR.F	2.4	1.2	1.1	1.3
21	Q9BTE3	C10orf119 Uncharacterized protein C10orf119	C10orf119	R.DASALLDPMEC*TDTAEEQR.V	2.5	1.3	2.0	3.4
22	Q9NYL2	ZAK Isoform 1 of Mitogen-activated protein kinase	ZAK	K.FDDLQFFENC*GGGSFGSVYR.A	2.6	1.2	1.5	1.4
23	Q9HA64	FN3KRP Ketosamine-3-kinase	FN3KRP	R.ATGHSGGGC*ISQGR.S	2.6	1.3	5.6	1.9
24	Q13418	ILK Integrin-linked protein kinase	ILK	K.FSFQC*PGR.M	2.6	1.5	3.4	5.2
25	Q9NQC3	RTN4 Isoform 1 of Reticulon-4	RTN4	K.YSNSALGHVNC*TIK.E	2.8	1.3	1.6	1.5

26	Q8NDH3	STX16 56 kDa protein	STX16	R.VTEELWQAALSTLNPNPTDSCPLYLNYATVAALPC*R.V	2.8	1.1	1.9	1.9
27	P62249	RPS16 RPS16 protein	RPS16	K.TATAVAHC*K.R	2.8	2.1	4.7	7.0
28	Q5TFE4	NT5DC1 5-nucleotidase domain-containing protein 1	NT5DC1	K.HFLSDTGMAC*R.S	3.0	1.1	1.5	2.6
29	P62280	RPS11 40S ribosomal protein S11	RPS11	K.C*PFTGNVSIR.G	3.0	2.3	3.2	6.5
30	O15294	OGT Isoform 3 of UDP-N-acetylglucosamine--peptide	OGT	K.VMAEANHFIDLSQIPC*NGK.A	3.0	1.8	2.0	2.1
31	Q99714	HSD17B10 Isoform 1 of 3-hydroxyacyl-CoA dehydrogen	HSD17B10	K.KLGNNC*VFAPADVTSEK.D	3.1	3.4	7.1	6.6
32	P45984	MAPK9 Isoform Alpha-2 of Mitogen-activated protein	MAPK9	R.TAC*TNFMMTPYVVTR.Y	3.2	1.6	3.0	1.9
33	P28838	LAP3 Isoform 1 of Cytosol aminopeptidase	LAP3	R.SAGAC*TAAAFLK.E	3.3	1.2	3.1	3.3
34	P38117	ETFB Isoform 2 of Electron transfer flavoprotein s	ETFB	K.HSMNPFC*EIAVEEAVR.L	3.5	1.2	2.0	2.7
35	Q9ULA0	DNPEP aspartyl aminopeptidase	DNPEP	K.C*PTSGR.L	3.5	2.6	2.4	1.5
36	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.YMAC*CLLYR.G	3.6	2.4	3.2	4.0
37	Q7L1Q6	BZW1 similar to basic leucine zipper and W2 domain	BZW1	R.FDPTQFQDC*IIQGLTETGTDLEAVAK.F	3.6	1.2	1.5	1.4
38	P55735	SEC13 41 kDa protein	SEC13	R.FASGGC*DNLIK.L	3.7	1.1	1.0	1.3
39	Q7L5D6	C7orf20 Protein of unknown function DUF410 family	C7orf20	K.EQNYC*ESR.Y	3.7	1.3	1.8	1.8
40	Q96CM8	FLJ20920 hypothetical protein LOC80221	FLJ20920	R.MVSTPIGGLSYVQGC*TK.K	3.8	1.7	4.2	4.3
41	P30044	PRDX5 Isoform Mitochondrial of Peroxiredoxin-5, mi	PRDX5	K.ALNVEPDGTGLTC*SLAPNIISQL.-	3.8	0.8	1.0	1.0
42	O95571	ETHE1 ETHE1 protein, mitochondrial precursor	ETHE1	R.TDFQQGC*AK.T	3.8	1.7	1.8	1.6
43	Q9NQ88	C12orf5 Uncharacterized protein C12orf5	C12orf5	K.EADQKEQFSQGSPSNC*LETSLAEIFPLGK.N	3.8	1.2	1.5	1.4
44	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondria	IDH2	K.SSGGFVWAC*K.N	3.9	1.3	1.3	5.9
45	Q9Y3E2	BOLA1 BolA-like protein 1	BOLA1	R.VC*LCQGSAGSGAIGPVEAAIR.T	3.9	3.1	5.3	3.1
46	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.TLTSC*FLSCVVCVEGIVTK.C	4.0	1.6	1.8	2.0
47	Q5MNZ6	WDR45L WD repeat domain phosphoinositide-interacti	WDR45L	R.C*NYLALVGGGK.K	4.0	1.1	5.0	2.2
48	Q2TAA2	IAH1 Isoamyl acetate-hydrolyzing esterase 1 homolo	IAH1	R.VILITPTPLC*ETAWEEQCIIQGCK.L	4.0	1.2	1.6	1.6
49	P14618	PKM2 Uncharacterized protein PKM2	PKM2	R.AEGSDVANAVLDGADC*IMLSGETAK.G	4.0	1.1	3.0	1.0
50	O43795	MYO1B Isoform 1 of Myosin-Ib	MYO1B	K.LVMSYVAAVC*GK.G	4.1	1.2	1.2	1.6
51	P04632	CAPNS1 34 kDa protein	CAPNS1	R.YSDESGNMDFDNFISC*LVR.L	4.1	0.9	0.7	1.5
52	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit	PSMD2	K.GTLTLC*PYHSDR.Q	4.2	0.9	0.9	2.7
53	A6NDG6	LOC283871 hypothetical protein LOC283871	LOC283871	K.NNQESDC*VSK.K	4.2	1.7	2.4	1.6
54	P42677	_ Uncharacterized protein ENSP00000301828	_	K.ARLTEGC*SFR.R	4.2	2.7	5.3	6.0
55	Q9BSH4	CCDC44 Coiled-coil domain-containing protein 44 EN	CCDC44	K.KLDSLGLCSVSC*ALEFIPNSK.V	4.3	1.0	1.1	1.9
56	P31749	AKT1 RAC-alpha serine/threonine-protein kinase ENS	AKT1	K.TFC*GTPEYLAPEVLEDNDYGR.A	4.3	3.1	10.9	18.7
57	Q16822	PCK2 mitochondrial phosphoenolpyruvate carboxykina	PCK2	R.YVAAAFPSAC*GK.T	4.4	2.4	5.4	6.6
58	Q15813	TBCE Tubulin-specific chaperone E	TBCE	R.NCAVSC*AGEK.G	4.4	1.4	2.1	2.5
59	Q8NDH3	STX16 56 kDa protein	STX16	R.IVDTPC*NEMNTDTFLEEINK.V	4.4	1.0	1.4	2.5
60	O15355	PPM1G Protein phosphatase 1G	PPM1G	K.C*SGDGVGAPR.L	4.4	1.4	2.1	1.4

61	P52895	AKR1C2 Aldo-keto reductase family 1 member C2 ENSG	AKR1C2	R.EEPWVDPNSPVLLEDPVLC*ALAK.K	4.4	1.1	1.8	1.4
62	P10599	TXN Thioredoxin	TXN	K.LVVVDFSATWC*GPC*K.M	4.4	1.6	5.3	0.8
63	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.AYHEQLSVAEITNAC*FEPANQMVK.C	4.5	3.3	5.9	8.9
64	Q96EY8	MMAB Cob	MMAB	K.IQCTLQDVGSALATPC*SSAR.E	4.5	1.0	1.6	1.4
65	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.RSIQFVDWC*PTGFK.V	4.5	2.5	3.9	5.0
66	Q6KB66	KRT80 Keratin-80	KRT80	R.C*HIDLSGIVEEVK.A	4.5	1.0	1.5	1.4
67	P55060	CSE1L Isoform 1 of Exportin-2	CSE1L	K.IC*AVGITK.L	4.5	1.9	2.9	4.4
68	P15880	RPS2 40S ribosomal protein S2	RPS2	R.GC*TATLGNFAK.A	4.6	1.7	2.7	3.3
69	P31949	S100A11 Protein S100-A11	S100A11	K.ISSPTETERC*IESLIAVFQK.Y	4.6	0.8	1.0	1.0
70	P11498	PC Pyruvate carboxylase, mitochondrial precursor E	PC	R.FLYEC*PWR.R	4.6	1.5	1.9	5.3
71	Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.GVPGAIVNVSSQC*SQR.A	4.6	1.2	2.8	2.4
72	Q06330	RBPJ Isoform APCR-2 of Recombining binding protein	RBPJ	R.IIQFQATPC*PK.E	4.6	1.4	2.6	1.8
73	P55769	NHP2L1 NHP2-like protein 1	NHP2L1	K.KLLDLVQQSC*NYK.Q	4.6	1.3	2.8	3.0
74	P22314	UBE1 Ubiquitin-activating enzyme E1	UBE1	K.SIPIC*TLK.N	4.6	1.4	1.6	1.3
75	Q13526	PIN1 Peptidyl-prolyl cis-trans isomerase NIMA-inte	PIN1	K.IKSGEEDFESLASQFSDC*SSAK.A	4.6	1.2	3.1	1.3
76	Q13748	TUBA1A Tubulin alpha-1A chain	TUBA1A	R.TIQFVDWC*PTGFK.V	4.6	2.4	3.8	5.7
77	P49327	FASN Fatty acid synthase	FASN	K.LTPGC*EAEAETEAICFFVQQFTDMEHNR.V	4.7	1.2	1.6	1.8
78	Q9Y5Y2	NUBP2 Nucleotide-binding protein 2	NUBP2	R.AVHQC*DR.G	4.7	1.9	5.2	9.3
79	Q9BQ69	MACROD1 MACRO domain-containing protein 1	MACROD1	K.LEVDAIVNAANSSLLGGGGVDGC*IHR.A	4.7	1.1	2.5	2.0
80	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	K.SGDAAIVEMVPGKPMC*VESFSQYPPLGR.F	4.7	1.7	3.7	5.8
81	Q14139	UBE4A Isoform 2 of Ubiquitin conjugation factor E4	UBE4A	R.SQQEIC*EQLNINHMIQR.I	4.7	1.3	1.7	1.5
82	O75390	CS Citrate synthase, mitochondrial precursor	CS	K.LPC*VAAK.I	4.8	1.2	1.8	1.6
83	O95747	STK39 STE20/SPS1-related proline-alanine-rich prot	STK39	K.TFVGTPC*WMAPEVMEQVR.G	4.8	2.0	3.8	5.3
84	P07437	TUBB Tubulin beta chain	TUBB	K.NMMAAC*DPR.H	4.8	2.8	4.6	6.3
85	O75940	SMNDC1 Survival of motor neuron-related-splicing f	SMNDC1	K.VGVGTC*GIADKPMTQYQDTSK.Y	4.8	1.1	1.6	1.3
86	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	R.YDDMAAC*MK.S	4.8	0.9	0.9	1.4
87	P33240	CSTF2 Uncharacterized protein CSTF2	CSTF2	K.LC*VQNSPQEAR.N	4.8	1.2	1.4	0.9
88	Q7Z2W4	ZC3HAV1 Isoform 1 of Zinc finger CCCH type antivir	ZC3HAV1	K.NSNVDSSYLESLYQSC*PR.G	4.8	1.5	2.8	2.2
89	O75131	CPNE3 Copine-3	CPNE3	K.NC*LNPQFSK.T	4.9	1.0	1.4	1.4
90	Q96Q11	TRNT1 Isoform 1 of tRNA-nucleotidyltransferase 1,	TRNT1	K.YQGEHC*LLK.E	4.9	1.1	1.3	1.6
91	P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/	GNB2	K.AC*GDSTLTQITAGLDPVGR.I	4.9	2.6	6.0	5.2
92	Q9H0C8	ILKAP Integrin-linked kinase-associated serine/thr	ILKAP	R.FILLAC*DGLFK.V	4.9	1.1	1.2	1.1
93	P14174	MIF Macrophage migration inhibitory factor	MIF	K.LLC*GLLAER.L	4.9	0.9	0.8	1.3
94	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.IC*DDELILIK.N	4.9	2.4	3.6	2.5
95	Q00765	REEP5 Receptor expression-enhancing protein 5 ENSG	REEP5	K.NC*MTDLLAK.L	4.9	1.6	2.0	1.3
96	Q9NQT5	EXOSC3 Exosome complex exonuclease RRP40	EXOSC3	K.LLAPDC*EIIQEVGK.L	5.0	1.8	2.2	2.3

97	P10809	HSPD1 61 kDa protein	HSPD1	R.AAVEEGIVLGGGC*ALLR.C	5.0	1.3	3.4	2.3
98	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.NMITGTSQADC*AVLIVAAGVGEFEAGISK.N	5.0	1.3	1.9	2.0
99	Q9NXG2	THUMPD1 Putative uncharacterized protein DKFZp686C	THUMPD1	R.C*DAGGPR.Q	5.0	1.0	1.4	1.3
100	O15355	PPM1G Protein phosphatase 1G	PPM1G	R.GTEAGQVGEPGIPTGEAGPSC*SSASDK.L	5.0	1.2	2.6	2.1
101	P26641	EEF1G Elongation factor 1-gamma	EEF1G	R.FPEELTQTFMSC*NLITGMFQR.L	5.0	2.2	3.4	6.4
102	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	K.IETELRDIC*NDVLSLLEK.F	5.1	0.8	0.8	1.3
103	Q27J81	C14orf173 inverted formin 2 isoform 1	C14orf173	R.AVLLASDAQEC*TLEEVVER.L	5.1	1.4	3.0	3.2
104	O14980	XPO1 Exportin-1	XPO1	K.LDINLLDNVVNC*LYHGEGAQQR.M	5.1	1.2	1.2	1.5
105	P13639	EEF2 Elongation factor 2	EEF2	K.IWC*FGPDGTGPNILTDITK.G	5.1	1.1	1.9	1.5
106	Q99714	HSD17B10 Isoform 1 of 3-hydroxyacyl-CoA dehydrogen	HSD17B10	K.VC*NFLASQVPFPSR.L	5.1	1.2	6.4	2.4
107	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2	MSRB2	K.YC*SGTGWPSFSEAHGTSGSDESHTGILR.R	5.1	1.3	1.9	1.6
108	P49327	FASN Fatty acid synthase	FASN	K.AINC*ATSGVVGLVNCLR.R	5.2	1.3	1.6	1.5
109	P13639	EEF2 Elongation factor 2	EEF2	K.STLTDSLVC*K.A	5.2	1.3	3.7	1.8
110	P15924	DSP Isoform DPI of Desmoplakin	DSP	K.YC*YLQNEVFGLFQK.L	5.2	2.1	5.6	3.1
111	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	K.ASVGFGGSC*FQK.D	5.2	1.1	1.3	1.0
112	Q9Y4P1	LOC727737 similar to APG4 autophagy 4 homolog B is	LOC727737	K.NFPAIGGTGPTSDTGWGC*MLR.C	5.2	1.1	1.1	1.6
113	Q16822	PCK2 mitochondrial phosphoenolpyruvate carboxykina	PCK2	R.QC*PIMDPAWEAPEGVPIDAIIFGGR.R	5.2	3.3	4.0	2.6
114	Q9H2U2	PPA2 Isoform 2 of Inorganic pyrophosphatase 2, mit	PPA2	R.GQPC*SQNYR.L	5.2	2.0	1.9	1.4
115	P60174	TPI1 Isoform 1 of Triosephosphate isomerase	TPI1	K.IAVAAQNC*YK.V	5.2	0.8	0.9	1.2
116	P62888	RPL30 60S ribosomal protein L30	RPL30	R.VC*TLAIIDPGDSDIIR.S	5.3	2.0	8.7	7.9
117	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.QGEYGLASIC*NGGGGASAMLIQK.L	5.3	1.4	2.6	3.3
118	P04075	ALDOA 45 kDa protein	ALDOA	R.ALANSLAC*QGK.Y	5.3	0.9	1.3	1.2
119	P48735	IDH2 Isocitrate dehydrogenase [NADP], mitochondria	IDH2	K.DLAGC*IHGLSNVK.L	5.3	1.5	2.5	6.3
120	P57721	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.INISEGNC*PER.I	5.3	1.1	1.7	1.9
121	P62753	RPS6 40S ribosomal protein S6	RPS6	K.LNISFPATGC*QK.L	5.3	2.0	3.0	6.4
122	P62316	SNRPD2 Small nuclear ribonucleoprotein Sm D2	SNRPD2	K.NNTQVLINC*R.N	5.3	1.4	2.5	3.0
123	P07737	PFN1 Profilin-1	PFN1	K.C*YEMASHLR.R	5.3	0.9	0.9	1.5
124	P28074	PSMB5 Putative uncharacterized protein DKFZp686I01	PSMB5	K.KVIEINPYLLGTMAGGAADC*SFWER.L	5.3	1.2	1.8	1.7
125	P63220	RPS21 8.2 kDa differentiation factor	RPS21	K.C*SASNR.I	5.3	1.2	3.0	2.2
126	O00299	DDAH2 CLIC1 Chloride intracellular channel protein	DDAH2	R.EEFASTC*PDDEEIELAYEQVAK.A	5.3	1.1	1.0	1.6
127	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.DGLTDVYNKIHMGSC*AENTAK.K	5.3	1.3	3.1	2.6
128	Q52LJ0	FAM98B family with sequence similarity 98, member	FAM98B	R.EKTAC*AINK.V	5.3	1.2	1.9	1.6
129	P61978	HNRPK Isoform 2 of Heterogeneous nuclear ribonucle	HNRPK	K.IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK.G	5.4	1.1	1.5	1.8
130	P62306	SNRPF Small nuclear ribonucleoprotein F	SNRPF	R.C*NNVLYIR.G	5.4	1.2	1.3	1.6
131	P08238	HSP90AB1 85 kDa protein	HSP90AB1	R.VFIMDSC*DELIPEYLNFIR.G	5.4	1.2	1.4	1.5
132	P00390	GSR Isoform Mitochondrial of Glutathione reductase	GSR	K.LGGTC*VNVGCVPK.K	5.4	0.8	0.9	1.4

133	Q6YN16	HSDL2 Hydroxysteroid dehydrogenase-like protein 2	HSDL2	K.TAIHTAAMDMLGGPGIESQC*R.K	5.4	1.2	3.4	6.2
134	Q52LJ0	FAM98B family with sequence similarity 98, member	FAM98B	K.SLC*NLEESITSAGR.D	5.4	1.1	1.2	1.4
135	Q00610	CLTC Isoform 1 of Clathrin heavy chain 1	CLTC	R.IHEGC*EEPATHNALAK.I	5.4	1.4	1.7	1.8
136	P00338	LDHA Isoform 1 of L-lactate dehydrogenase A chain	LDHA	R.VIGSGC*NLDSAR.F	5.4	1.1	1.5	2.2
137	P49591	SARS Uncharacterized protein SARS	SARS	K.YAGLSTC*FR.Q	5.4	1.2	1.2	1.6
138	P10599	TXN Thioredoxin	TXN	K.C*MPTFQFFK.K	5.4	1.6	3.1	0.2
139	P49321	NASP nuclear autoantigenic sperm protein isoform 1	NASP	R.KPTDGASSSNC*VTDISHLVR.K	5.5	1.7	2.5	1.6
140	P07437	TUBB Tubulin beta chain	TUBB	K.TAVC*DIPPR.G	5.5	2.7	4.7	5.4
141	P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal precurs	ACAA1	K.ARDC*LIPMGITSENVAER.F	5.5	0.8	4.4	2.1
142	P14618	PKM2 Uncharacterized protein PKM2	PKM2	R.GIFPVLC*K.D	5.5	1.0	2.8	1.0
143	P07741	APRT 20 kDa protein	APRT	R.VVVVDDLLATGGTMNAAC*ELLGR.L	5.5	1.1	1.2	1.6
144	P60866	_ Uncharacterized protein ENSP00000348430	_	K.TPC*GEGSK.T	5.5	1.5	2.4	4.6
145	P55786	NPEPPS Puromycin-sensitive aminopeptidase	NPEPPS	R.SKDGVC*VR.V	5.5	1.1	1.1	1.6
146	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.VMTIPYQPMPASSPVIC*AGGQDR.C	5.5	3.4	7.4	7.9
147	P60981	DSTN Destrin	DSTN	K.HEC*QANGPEDLNR.A	5.6	1.5	2.2	1.4
148	P04183	TK1 thymidine kinase 1, soluble	TK1	R.YSSSFC*THDR.N	5.6	2.9	6.2	7.2
149	P31947	SFN Isoform 1 of 14-3-3 protein sigma	SFN	K.GAVEKGEELSC*EER.N	5.6	1.0	1.3	1.3
150	P04406	GAPDH 39 kDa protein	GAPDH	K.IISNASC*TTNCLAPLAK.V	5.6	4.9	6.4	4.2
151	Q9UHD8	SEPT9 Isoform 1 of Septin-9	9-Sep	R.SQEATEAAPSC*VGDMADTPR.D	5.6	1.3	2.5	1.9
152	Q9P258	RCC2 Protein RCC2	RCC2	K.AVQDLC*GWR.I	5.6	1.3	2.2	1.6
153	P60174	TPI1 Isoform 1 of Triosephosphate isomerase	TPI1	K.VPADTEVVC*APPTAYIDFAR.Q	5.6	0.9	0.9	1.1
154	Q9Y224	C14orf166 Protein C14orf166	C14orf166	K.LTALDYHNPAGFNC*K.D	5.6	1.1	1.4	1.2
155	Q9NZL4	HSPBP1 Isoform 1 of Hsp70-binding protein 1	HSPBP1	R.LLDRDAC*DTVR.V	5.6	1.3	1.6	1.5
156	P47756	CAPZB Capping protein	CAPZB	K.DETVSDC*SPHIANIGR.L	5.7	1.0	1.4	1.5
157	Q09666	AHNAK AHNAK nucleoprotein isoform 1	AHNAK	K.LEGDLTGPSVGVEVPDVELEC*PDAK.L	5.7	1.2	2.0	1.5
158	P52272	HNRPM Isoform 1 of Heterogeneous nuclear ribonucle	HNRPM	K.AC*QIFVR.N	5.7	1.1	1.8	1.9
159	O43264	ZW10 Centromere/kinetochore protein zw10 homolog E	ZW10	R.LAPILC*DGTATFVDLVPGFR.R	5.7	2.5	3.0	4.4
160	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.PMC*VESFSDYPPLGR.F	5.7	1.4	2.7	9.6
161	O75663	TIPRL Uncharacterized protein TIPRL	TIPRL	K.VAC*AEEWQESR.T	5.7	0.8	1.6	1.5
162	P49840	GSK3B Isoform 2 of Glycogen synthase kinase-3 beta	GSK3B	K.LC*DFGSAK.Q	5.8	1.2	1.8	2.2
163	Q86YS7	KIAA0528 KIAA0528 protein	KIAA0528	R.SAPPC*ANSTVGVVK.M	5.8	1.3	3.6	2.3
164	P53396	ACLY ATP-citrate synthase	ACLY	K.FIC*TTSAIQNR.F	5.8	1.1	1.3	1.5
165	P22234	PAICS Multifunctional protein ADE2	PAICS	K.ITSC*IFQLLQEAGIK.T	5.8	0.9	0.9	1.7
166	P11413	G6PD Isoform Long of Glucose-6-phosphate 1-dehydro	G6PD	R.TQVC*GILR.E	5.8	1.5	1.5	1.8
167	P23528	CFL1 Uncharacterized protein CFL1	CFL1	K.HELQANC*YEEVK.D	5.8	0.9	1.1	2.0
168	P36507	MAP2K2 Dual specificity mitogen-activated protein	MAP2K2	K.LC*DFGVSGQLIDSMANSFVGTR.S	5.8	1.1	1.2	1.7
169	P62993	GRB2 Isoform 1 of Growth factor receptor-bound pro	GRB2	K.VLNEEC*DQNWYK.A	5.8	1.0	1.3	1.5

170	P67936	TPM4 Isoform 2 of Tropomyosin alpha-4 chain	TPM4	K.EENVGLHQTLDQTLNELNC*I.-	5.8	1.3	2.4	2.4
171	Q9Y5P6	GMPPB AMIGO3 GDP-mannose pyrophosphorylase B isofo	GMPPB	R.LC*SGPGIVGNVLVDPSAR.I	5.9	1.0	1.1	1.5
172	Q13185	CBX3 LOC653972 Chromobox protein homolog 3	CBX3	R.LTWHSC*PEDEAQ.-	5.9	1.2	3.7	2.4
173	P78417	GSTO1 Glutathione transferase omega-1	GSTO1	K.LNEC*VDHTPK.L	5.9	1.1	0.9	1.3
174	Q86SX6	GLRX5 Glutaredoxin-related protein 5	GLRX5	K.GTPEQPQC*GFSNAVVQILR.L	5.9	1.1	1.2	1.3
175	Q9UJW0	DCTN4 Dynactin subunit 4	DCTN4	R.LLQPDFQPVC*ASQLYPR.H	5.9	1.2	1.4	1.6
176	P40926	MDH2 Malate dehydrogenase, mitochondrial precursor	MDH2	K.EGVVEC*SFVK.S	5.9	1.2	1.3	1.6
177	P49721	PSMB2 Proteasome beta 2 subunit variant (Fragment)	PSMB2	R.NLADC*LR.S	5.9	1.3	2.0	1.7
178	Q96RS6	NUDCD1 NudC domain-containing protein 1	NUDCD1	R.DSAQC*AAIAER.L	5.9	1.2	2.1	1.5
179	Q92879	CUGBP1 Isoform 4 of CUG-BP- and ETR-3-like factor	CUGBP1	R.GC*AFVTFTTR.A	5.9	1.6	2.3	1.4
180	Q9H3U1	UNC45A Isoform 1 of UNC45 homolog A	UNC45A	R.AIQTVSC*LLQGPCDAGNR.A	5.9	1.2	1.1	1.5
181	Q96EY5	FAM125A Isoform 1 of Protein FAM125A	FAM125A	K.SC*SPLAFSAFGDLTIK.S	6.0	1.5	1.6	1.3
182	P49588	AARS Uncharacterized protein AARS	AARS	K.C*LSVMEAK.V	6.0	1.0	1.5	1.3
183	Q9BV86	C9orf32 Protein of unknown function DUF858, methyl	C9orf32	R.IIC*SAGLSLLAEER.Q	6.0	1.2	1.5	4.2
184	Q9BXJ9	NARG1 Isoform 1 of NMDA receptor-regulated protein	NARG1	R.LFNTAVC*ESK.D	6.0	1.4	1.3	1.9
185	Q96BF6	BTBD14B BTB/POZ domain-containing protein 14B ENSG	BTBD14B	R.NTLANSC*GTGIR.S	6.0	1.2	4.1	13.8
186	P21333	FLNA Filamin-A	FLNA	K.AHVVPC*FDASK.V	6.0	1.4	1.2	1.4
187	O43681	CRABP2 Cellular retinoic acid-binding protein 2 EN	CRABP2	K.IDTHNIIVNQLVFPDPEKPC*K.M	6.1	1.0	1.0	1.1
188	P52272	HNRPM Isoform 1 of Heterogeneous nuclear ribonucle	HNRPM	R.GC*AVVEFK.M	6.1	1.0	1.8	1.6
189	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.SLHDALC*VVK.R	6.1	2.4	6.3	2.3
190	P50570	DNM2 98 kDa protein	DNM2	K.LQDAFSSIGQSC*HLDLPQIAVVGGQSAGK.S	6.1	1.4	1.9	1.7
191	P55263	ADK Isoform Long of Adenosine kinase	ADK	R.TGC*TFPEKPDFH.-	6.1	1.5	2.2	1.3
192	Q9C0C9	UBE2O Uncharacterized protein UBE2O	UBE2O	R.C*YNEMALIR.V	6.1	1.3	1.6	1.5
193	Q9GZZ9	UBE1DC1 Ubiquitin-activating enzyme E1 domain-cont	UBE1DC1	R.EGVC*AASLPTTMGVVAGILVQNVLK.F	6.1	1.3	7.7	6.5
194	P50990	CCT8 Uncharacterized protein CCT8	CCT8	K.IAVYSC*PFDGMITETK.G	6.1	1.1	1.0	1.3
195	Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	K.VVFC*PVK.E	6.1	0.9	0.9	2.1
196	P09429	HMG1L1 High-mobility group protein 1-like 1	HMG1L1	K.MSSYAFFVQTC*R.E	6.1	1.4	2.0	7.7
197	P07900	HSP90AA1 heat shock protein 90kDa alpha (cytosolic	HSP90AA1	R.VFIMDNC*EELIPEYLNFIR.G	6.2	1.2	1.2	1.3
198	P60709	ACTB Actin, cytoplasmic 2	ACTB	K.EKLC*YVALDFEQEMATAASSSSLEK.S	6.2	2.2	3.7	7.4
199	P54886	ALDH18A1 Isoform Long of Delta-1-pyrroline-5-carbo	ALDH18A1	K.LGSAVVTRGDEC*GLALGR.L	6.2	1.6	3.3	3.9
200	P84085	ARF5 ADP-ribosylation factor 5	ARF5	K.NIC*FTVWDVGGQDK.I	6.2	1.4	1.4	2.9
201	Q09666	AHNAK AHNAK nucleoprotein isoform 1	AHNAK	K.LEGDLTGPSVDVEVPDVELEC*PDAK.L	6.3	1.2	1.7	1.6
202	P49458	SRP9 hCG_1781062 Signal recognition particle 9 kDa	SRP9	K.VTDDLVC*LVYK.T	6.3	1.1	1.3	1.6
203	P13639	EEF2 Elongation factor 2	EEF2	R.YVEPIEDVPC*GNIVGLVGVDQFLVK.T	6.3	1.2	2.1	1.4
204	Q92598	HSPH1 Isoform Alpha of Heat shock protein 105 kDa	HSPH1	R.AGGIETIANEFSDRC*TPSVISFGSK.N	6.3	1.7	4.7	5.5

205	Q9UL46	_ Uncharacterized protein ENSP00000310225	_	K.C*GFLPGNEK.V	6.4	0.9	1.3	1.1
206	P57721	PCBP3 Poly(RC) binding protein 3	PCBP3	R.LVVPASQC*GSLIGK.G	6.4	1.1	1.6	2.2
207	Q15366	PCBP2 poly(rC)-binding protein 2 isoform a	PCBP2	R.AITIAGIPQSIIEC*VK.Q	6.4	1.0	1.1	1.6
208	P60174	TPI1 Isoform 1 of Triosephosphate isomerase	TPI1	R.IIYGGSVTGATC*K.E	6.4	0.9	1.1	1.2
209	P13489	RNH1 Ribonuclease inhibitor	RNH1	R.ELDLSNNC*LGDAGILQLVESVR.Q	6.5	1.2	1.3	1.5
210	O75348	FLJ25715 ATP6V1G1 Vacuolar ATP synthase subunit G	FLJ25715	R.GSC*STEVEKETQEK.M	6.5	1.0	1.9	1.8
211	Q9NTK5	OLA1 Isoform 1 of Putative GTP-binding protein 9 E	OLA1	K.STFFNVLTNSQASAENFPFC*TIDPNESR.V	6.5	1.1	1.3	1.2
212	P62937	_ Uncharacterized protein ENSP00000369516	_	R.IIPGFMC*QGGDFTR.H	6.6	0.8	0.8	1.2
213	Q8NBF2	NHLRC2 NHL repeat-containing protein 2	NHLRC2	K.AILFSQPLQITDTQQGC*IAPVELR.Y	6.6	1.3	3.8	2.3
214	Q16630	CPSF6 Isoform 2 of Cleavage and polyadenylation sp	CPSF6	R.ELHGQNPVVTPC*NK.Q	6.6	1.2	1.4	1.3
215	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.SIC*TTVLELLDK.Y	6.6	0.9	0.8	1.2
216	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	ECHS1	K.ALNALC*DGLIDELNQALK.T	6.6	2.2	5.6	1.6
217	P30153	PPP2R1A Serine/threonine-protein phosphatase 2A 65	PPP2R1A	R.LNIISNLDC*VNEVIGIR.Q	6.6	1.1	1.1	1.4
218	O15075	DCLK1 Isoform 2 of Serine/threonine-protein kinase	DCLK1	R.YQDDFLLDESEC*R.V	6.6	1.3	4.3	3.0
219	Q15185	PTGES3 19 kDa protein	PTGES3	K.HLNEIDLFHC*IDPNDSK.H	6.6	1.2	1.3	1.5
220	P51812	RPS6KA3 Ribosomal protein S6 kinase alpha-3	RPS6KA3	R.AENGLLMTPC*YTANFVAPEVLK.R	6.7	1.2	2.2	3.0
221	P18085	ARF4 similar to ADP-ribosylation factor 4	ARF4	K.NIC*FTVWDVGGQDR.I	6.7	1.4	2.1	3.9
222	O43684	BUB3 Mitotic checkpoint protein BUB3	BUB3	R.TPC*NAGTFSQPEK.V	6.7	1.4	2.3	1.7
223	Q93052	LPP Lipoma-preferred partner	LPP	K.TYITDPVSAPC*APPLQPK.G	6.7	1.5	2.8	1.5
224	P10768	ESD S-formylglutathione hydrolase	ESD	K.AETGKCPALYWLSGLTC*TEQNFISK.S	6.7	0.9	0.8	1.4
225	O14929	HAT1 Histone acetyltransferase type B catalytic su	HAT1	K.VDENFDC*VEADDVEGK.I	6.7	1.3	2.0	2.3
226	P00492	HPRT1 Uncharacterized protein HPRT1	HPRT1	K.SYC*NDQSTGDIK.V	6.7	1.0	1.3	1.3
227	P26641	EEF1G Elongation factor 1-gamma	EEF1G	K.AAAPAPEEEMDEC*EQALAAEPK.A	6.7	1.1	1.4	1.5
228	P12004	PCNA Proliferating cell nuclear antigen	PCNA	K.C*AGNEDIITLR.A	6.8	1.0	1.1	1.3
229	Q9UI30	HSPC152 TRM112-like protein	HSPC152	R.IC*PVEFNPNFVAR.M	6.8	1.1	1.8	1.7
230	P18669	PGAM1 hCG_2015138 Phosphoglycerate mutase 1	PGAM1	R.YADLTEDQLPSC*ESLK.D	6.8	1.0	1.8	1.3
231	P23921	RRM1 Ribonucleoside-diphosphate reductase large su	RRM1	K.IIDINYYPVPEAC*LSNK.R	6.8	1.3	2.3	3.1
232	Q15019	SEPT2 Septin-2	2-Sep	R.LTVVDTPGYGDAINC*R.D	6.8	1.7	2.4	1.6
233	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.YLAEVAC*GDDR.K	6.9	1.0	1.2	1.4
234	Q09666	AHNAK AHNAK nucleoprotein isoform 1	AHNAK	K.GPFVEAEVPDVDLEC*PDAK.L	6.9	1.1	1.8	1.4
235	P60763	RAC3 Ras-related C3 botulinum toxin substrate 3 pr	RAC3	R.AVLC*PPPVK.K	6.9	1.3	1.9	1.5
236	P22102	GART Isoform Long of Trifunctional purine biosynth	GART	K.QVLVAPGNAGTAC*SEK.I	7.0	1.4	2.4	1.2
237	P49327	FASN Fatty acid synthase	FASN	K.ADEASELAC*PTPK.E	7.0	1.4	2.0	1.6
238	P40926	MDH2 Malate dehydrogenase, mitochondrial precursor	MDH2	K.TIIPLISQC*TPK.V	7.0	1.8	2.9	1.8
239	P49915	GMPS GMP synthase	GMPS	K.TVGVQGDC*R.S	7.1	1.1	1.8	1.0
240	Q9NVG8	TBC1D13 TBC1 domain family, member 13	TBC1D13	R.LLQDYPITDVC*QILQK.A	7.1	1.1	1.3	1.5

241	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	R.AGAIAPC*EVTVPAQNTGLGPEK.T	7.1	1.8	3.1	2.5
242	Q15796	SMAD2 Isoform Long of Mothers against decapentaple	SMAD2	K.AITTQNC*NTK.C	7.1	1.7	2.0	3.7
243	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.LVVPATQC*GSLIGK.G	7.1	1.2	1.9	1.8
244	Q12849	GRSF1 G-rich RNA sequence binding factor 1 isoform	GRSF1	R.YIELFLNSC*PK.G	7.2	1.2	0.8	4.0
245	Q99439	CNN2 Calponin-2	CNN2	K.C*ASQVGMTAPGTR.R	7.3	2.2	0.7	2.2
246	P62829	RPL23 60S ribosomal protein L23	RPL23	R.ISLGLPVGAVINC*ADNTGAK.N	7.3	2.1	3.5	5.1
247	P60981	DSTN Destrin	DSTN	K.LGGSLIVAFEGC*PV.-	7.3	1.0	1.4	1.8
248	P52907	CAPZA1 F-actin-capping protein subunit alpha-1 ENS	CAPZA1	K.TIDGQQTIIAC*IESHQFQPK.N	7.4	1.0	0.8	1.6
249	P55212	CASP6 Isoform Alpha of Caspase-6 precursor	CASP6	R.GTC*ADRDNLTR.R	7.4	0.9	0.7	1.5
250	Q02790	FKBP4 FK506-binding protein 4	FKBP4	K.TQLAVC*QQR.I	7.4	1.1	1.1	1.1
251	P62826	RAN 26 kDa protein	RAN	R.VC*ENIPIVLCGNK.V	7.5	1.1	1.3	1.7
252	O15382	BCAT2 Branched chain aminotransferase 2, mitochond	BCAT2	R.EVFGSGTAC*QVCPVHR.I	7.5	1.2	1.2	1.7
253	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	R.QAVLGAGLPISTPC*TTINK.V	7.5	1.4	4.2	4.0
254	Q15631	TSN Translin	TSN	K.ETAAAC*VEK.-	7.5	1.2	3.0	2.5
255	P30281	CCND3 G1/S-specific cyclin-D3	CCND3	R.ASYFQC*VQR.E	7.6	1.4	3.1	2.0
256	P14618	PKM2 Uncharacterized protein PKM2	PKM2	R.NTGIIC*TIGPASR.S	7.6	0.9	3.0	1.1
257	P78347	GTF2I Isoform 1 of General transcription factor II	GTF2I	R.SILSPGGSC*GPIK.V	7.6	1.1	2.0	1.5
258	P36405	ARL3 ADP-ribosylation factor-like protein 3	ARL3	K.LSC*VPVLIFANK.Q	7.6	1.1	1.3	1.5
259	Q9UHX1	PUF60 Isoform 1 of Poly	PUF60	R.ALAIMC*R.V	7.6	0.9	0.9	1.5
260	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.YVLC*TAPR.A	7.7	1.6	1.9	2.4
261	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	K.TGQATVASGIPAGWMGLDC*GPESSK.K	7.7	0.9	1.1	1.1
262	P29590	PML Isoform PML-1 of Probable transcription factor	PML	R.LQDLSSC*ITQGK.D	7.7	3.5	5.9	1.9
263	Q15185	PTGES3 19 kDa protein	PTGES3	K.LTFSC*LGGSDNFK.H	7.9	0.8	0.8	0.9
264	Q9NUU7	DDX19B Isoform 1 of ATP-dependent RNA helicase DDX	DDX19B	K.VLVTTNVC*AR.G	8.0	1.3	2.5	5.2
265	P33316	DUT Isoform DUT-M of Deoxyuridine 5-triphosphate	DUT	R.IAQLIC*ER.I	8.1	1.3	1.9	1.8
266	P31948	STIP1 STIP1 protein	STIP1	K.ALDLDSSC*K.E	8.1	2.5	3.3	1.8
267	Q04917	YWHAH 14-3-3 protein eta	YWHAH	K.ELETVC*NDVLSLLDK.F	8.1	0.9	1.0	1.2
268	P49915	GMPS GMP synthase	GMPS	K.AC*TTEEDQEK.L	8.1	1.2	1.3	1.5
269	P49915	GMPS GMP synthase	GMPS	R.VICAEEPYIC*K.D	8.3	1.3	1.5	1.2
270	Q01518	CAP1 Adenylyl cyclase-associated protein 1	CAP1	R.ALLVTASQC*QQPAENK.L	8.7	1.0	1.0	1.1
271	Q00839	HNRNPU heterogeneous nuclear ribonucleoprotein U i	HNRNPU	K.AVVVC*PK.D	8.8	1.7	3.4	3.4
272	Q7RTV0	PHF5A PHD finger-like domain-containing protein 5A	PHF5A	R.ICDEC*NYGSYQGR.C	9.7	2.3	2.9	3.0
273	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit	PSMD2	R.C*ALGVFR.K	10.0	2.2	2.9	3.4
274	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.AITIAGVPQSVTEC*VK.Q	10.7	1.1	1.2	1.4
275	P04406	GAPDH 39 kDa protein	GAPDH	R.VPTANVSVVDLTC*R.L	11.2	0.4	1.7	0.5
276	P14868	DARS Aspartyl-tRNA synthetase, cytoplasmic	DARS	R.LEYC*EALAMLR.E	11.5	1.1	1.1	2.0
277	P45880	VDAC2 LOC729317 similar to voltage-dependent anion	VDAC2	R.PMC*IPPSYADLGK.A	12.7	2.2	4.1	3.7

278	O95833	CLIC3 Chloride intracellular channel protein 3 ENS	CLIC3	K.ASEDGESVGHC*PSC*QR.L	14.8	2.5	4.7	3.7

Table 3A-7. R-values from 1 mM MeGSH competitive transnitrosation experiment at 500 μM GSNO. A list of all identified peptides (* denotes labeled cysteine) is presented together with calculated Heavy:Light Ratios (R-values) in pre-treated with 1 mM MeGSH (light, n=3), or left untreated as a control (heavy, n=5), then transnitrosated by 500 μM GSNO and taken through the quantitative mass spectrometry workflow. Date were sorted by ΔR (R of control minus R of pre-treated sample) and numbered as "Peptide #".

Peptide #	Uniprot #	Description	Symbol	Sequence
1	O94906	PRPF6 Pre-mRNA-processing factor 6	PRPF6	R.AAQDLC*EEALR.H
2	P34896	SHMT1 Serine hydroxymethyltransferase, cytosolic	SHMT1	R.AVLEALGSC*LNNK.Y
3	P02795	MT2A Metallothionein-2	MT2A	K.C*AQGCICK.G
4	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	R.VGAFTMVC*K.D
5	Q13347	EIF3I Eukaryotic translation initiation factor 3 subunit	EIF3I	K.HVLTGSADNSC*R.L
6	P50995	ANXA11 Annexin A11	ANXA11	K.FNAVLC*SR.S
7	P31948	STIP1 Stress-induced-phosphoprotein 1	STIP1	K.ALDLDSSC*K.E
8	Q92616	GCN1L1 Translational activator GCN1	GCN1L1	K.C*LQNPSSDIR.L
9	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	R.QC*PIMDPAWEAPEGVPIDAIIFGGR.R
10	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.ALNALC*DGLIDELNQALK.T
11	Q04724	TLE1 Transducin-like enhancer protein 1	TLE1	K.SPVSQLDC*LNR.D
12	P07437	TUBB Tubulin beta chain	TUBB	K.LTTPTYGDLNHLVSATMSGVTTC*LR.F
13	P34932	HSPA4 Heat shock 70 kDa protein 4	HSPA4	R.AGGIETIANEYSDRC*TPACISFGPK.N
14	P50213	IDH3A Isocitrate dehydrogenase	IDH3A	R.IEAAC*FATIK.D
15	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.KLGNNC*VFAPADVTSEK.D
16	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.SLHDALC*VVK.R
17	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	K.C*PTSGR.L
18	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	R.GQPC*SQNYR.L
19	Q7L5Y1	ENOSF1 Mitochondrial enolase superfamily member 1	ENOSF1	K.ALQFLQIDSC*R.L
20	P83731	RPL24 60S ribosomal protein L24	RPL24	K.VELC*SFSGYK.I
21	P30519	HMOX2 Heme oxygenase 2	HMOX2	K.GALEGSSC*PFR.T
22	P33992	MCM5 DNA replication licensing factor MCM5	MCM5	R.C*SVLAAANSVFGR.W
23	Q68CP9	ARID2 AT-rich interactive domain-containing protein 2	ARID2	R.SC*SNAAFALK.Q
24	Q99798	ACO2 Aconitate hydratase, mitochondrial	ACO2	R.DLGGIVLANAC*GPCIGQWDR.K
25	Q96CD2	PPCDC Phosphopantothenoylcysteine decarboxylase	PPCDC	K.KLVC*GDEGLGAMAEVGTIVDK.V
26	O95747	OXSR1 Serine/threonine-protein kinase OSR1	OXSR1	K.C*QTSMDELLK.E
27	Q7Z406	MYH14 Myosin-14	MYH14	K.AEDMAELTC*LNEASVLHNLR.E
28	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	R.YVAAAFPSAC*GK.T
29	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	R.LC*PNSTGAEIR.S
30	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	K.LTFSC*LGGSDNFK.H
31	P10599	TXN Thioredoxin	TXN	K.C*MPTFQFFK.K
32	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	R.AVC*MLSNTTAIAEAWAR.L
33	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	R.NFILDQC*NVYNSGQR.R
34	P31948	STIP1 Stress-induced-phosphoprotein 1	STIP1	K.ALSVGNIDDALQC*YSEAIK.L
35	P07437	TUBB Tubulin beta chain	TUBB	K.TAVC*DIPPR.G
36	Q9H479	FN3K Fructosamine-3-kinase	FN3K	R.AFGGPGAGC*ISEGR.A
37	Q9Y3L5	RAP2C Ras-related protein Rap-2c	RAP2C	R.ALAQEWGC*PFMETSAK.S
38	Q9Y3E2	BOLA1 BolA-like protein 1	BOLA1	R.VC*LCQGSAGSGAIGPVEAAIR.T
39	Q27J81	INF2 Inverted formin-2	INF2	R.AVLLASDAQEC*TLEEVVER.L

Heavy : Light Ratio R										ΔR
500 μM GSNO (control)						1 mM MEGSH + 500 μM GSNO (sample)				Ctrl - Sample
1	2	3	4	5	average	1	2	3	average	
4.0	5.3	3.0	4.7	4.4	4.3	1.2	1.3	0.9	1.1	3.1
0.0	2.5	0.0	1.8	2.9	2.4	0.2	0.2	0.2	0.2	2.2
1.1	2.1	2.9	3.9	3.2	2.6	1.3	0.5	0.7	0.8	1.8
3.0	2.8	2.8	3.1	2.8	2.9	1.2	1.2	1.2	1.2	1.7
3.6	2.4	4.9	4.7	0.0	3.9	2.6	2.0	2.2	2.3	1.6
3.4	1.7	3.4	3.5	3.5	3.1	1.0	2.3	1.5	1.6	1.5
3.2	1.9	2.5	2.4	2.4	2.5	0.9	1.4	0.9	1.1	1.4
2.5	0.0	1.7	3.2	0.0	2.5	0.9	2.1	1.6	1.5	1.0
3.5	3.1	3.1	3.7	3.2	3.3	2.0	2.3	2.8	2.4	0.9
2.2	2.1	2.1	2.3	2.1	2.2	1.3	1.4	1.4	1.4	0.8
1.4	0.0	1.9	2.3	2.1	1.9	1.3	1.0	1.3	1.2	0.7
3.8	3.5	3.5	4.0	3.6	3.7	2.8	2.9	3.1	2.9	0.7
1.9	1.3	1.7	3.2	2.0	2.0	1.4	1.3	1.2	1.3	0.7
0.0	2.4	2.6	2.8	2.9	2.7	2.4	2.5	1.1	2.0	0.7
2.9	2.7	3.0	3.8	2.8	3.0	2.2	2.4	2.5	2.4	0.7
1.9	2.0	2.5	3.3	2.3	2.4	1.8	1.7	1.6	1.7	0.7
2.6	2.5	2.5	2.6	2.8	2.6	1.9	2.0	2.0	2.0	0.6
1.7	1.7	2.5	2.1	2.2	2.0	1.2	1.5	1.5	1.4	0.6
0.0	1.6	2.8	2.3	1.5	2.1	1.2	1.8	1.3	1.4	0.6
2.6	2.5	2.1	2.6	3.2	2.6	2.0	2.5	1.6	2.0	0.6
1.7	1.7	1.6	1.8	1.9	1.7	1.3	0.8	1.2	1.1	0.6
2.2	2.8	1.9	2.5	1.9	2.3	1.5	1.6	2.0	1.7	0.6
2.2	1.6	1.4	1.9	2.5	1.9	1.4	1.3	1.4	1.3	0.6
1.0	1.3	1.1	1.4	1.4	1.2	0.7	0.8	0.7	0.7	0.5
0.0	1.8	1.8	2.0	0.0	1.8	1.3	1.2	1.5	1.3	0.5
1.6	1.0	2.0	1.3	2.0	1.6	1.1	1.2	1.0	1.1	0.5
2.4	2.3	2.5	2.8	2.3	2.5	2.2	1.8	1.9	2.0	0.5
2.8	2.1	2.3	2.6	2.4	2.4	1.7	2.0	2.1	1.9	0.5
2.6	2.4	2.3	2.4	2.4	2.4	1.7	2.1	2.0	2.0	0.5
0.7	1.2	1.9	1.9	0.8	1.3	0.7	1.0	0.9	0.9	0.5
1.4	1.2	2.4	1.7	1.5	1.6	1.0	1.4	1.1	1.2	0.5
3.0	2.9	2.8	3.3	3.1	3.0	2.4	2.6	2.7	2.6	0.5
1.6	1.5	1.7	2.2	1.8	1.8	1.3	1.3	1.4	1.3	0.4
1.1	0.9	1.4	1.7	0.8	1.2	1.0	0.3	0.9	0.7	0.4
2.6	2.5	2.5	2.9	2.7	2.7	2.1	2.0	2.6	2.2	0.4
1.6	1.4	2.0	1.8	1.8	1.7	1.2	1.5	1.3	1.3	0.4
0.0	1.7	2.0	2.1	2.1	2.0	1.4	1.4	1.9	1.6	0.4
2.5	0.0	3.2	3.4	3.1	3.1	3.0	2.5	2.6	2.7	0.4
1.8	0.9	2.0	2.7	1.5	1.8	1.1	1.5	1.7	1.4	0.4

40	P62888	RPL30 60S ribosomal protein L30	RPL30	R.VC*TLAIIDPGDSDIIR.S
41	O43815	STRN Striatin	STRN	K.C*YIASAGADALAK.V
42	Q15019	SEPT2 Septin-2	2-Sep	R.LTVVDTPGYGDAINC*R.D
43	Q14318	FKBP8 Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8	K.C*LNNLAASQLK.L
44	P46013	MKI67 Antigen KI-67	MKI67	R.KADVEGELLAC*R.N
45	P23396	RPS3 40S ribosomal protein S3	RPS3	K.GC*EVVVSGK.L
46	P49721	PSMB2 Proteasome subunit beta type-2	PSMB2	R.NLADC*LR.S
47	P52943	CRIP2 Cysteine-rich protein 2	CRIP2	R.ASSVTTFTGEPNTC*PR.C
48	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	R.GQAGGGGPGTGPGLGEAGSLATC*ELPLAK.S
49	P25398	RPS12 40S ribosomal protein S12	RPS12	K.LGEWVGLC*K.I
50	P04183	TK1 Thymidine kinase, cytosolic	TK1	R.NTMEALPAC*LLR.D
51	P51946	CCNH Cyclin-H	CCNH	R.TC*LSQLLDIMK.S
52	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	K.C*AMTALSSK.L
53	P13489	RNH1 Ribonuclease inhibitor	RNH1	R.SNELGDVGVHC*VLQGLQTPSCK.I
54	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.GEETPVIVGSALC*ALEGR.D
55	Q9BUL9	RPP25 Ribonuclease P protein subunit p25	RPP25	R.SEEAPAGC*GAEGGGPGSGPFADLAPGAVHMR.V
56	P14678	SNRPB Small nuclear ribonucleoprotein-associated protein	SNRPB	R.C*ILQDGR.I
57	Q92879	CELF1 CUGBP Elav-like family member 1	CELF1	R.GC*AFVTFTTR.A
58	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	R.SVLDAAQIVGLNC*LR.L
59	Q9UL25	RAB21 Ras-related protein Rab-21	RAB21	K.VVLLGEGC*VGK.T
60	Q969Z0	TBRG4 Protein TBRG4	TBRG4	R.LATDLLSLMPSLTSGEVAHC*AK.S
61	P62280	RPS11 40S ribosomal protein S11	RPS11	K.C*PFTGNVSIR.G
62	Q5T4S7	UBR4 E3 ubiquitin-protein ligase UBR4	UBR4	K.AVQC*LNTSSK.E
63	Q9Y399	MRPS2 28S ribosomal protein S2, mitochondrial	MRPS2	R.DC*GEYAHTR.Y
64	Q9UBT2	UBA2 SUMO-activating enzyme subunit 2	UBA2	R.VLVVGAGGIGC*ELLK.N
65	Q9ULV4	CORO1C Coronin-1C	CORO1C	K.C*DLISIPK.K
66	Q15459	SF3A1 Splicing factor 3A subunit 1	SF3A1	R.EVLDQVC*YR.V
67	P13639	EEF2 Elongation factor 2	EEF2	K.IWC*FGPDGTGPNILTDITK.G
68	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	K.TRPDGNC*FYR.A
69	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.GIFPVLC*K.D
70	P02795	MT2A Metallothionein-2	MT2A	K.KSC*CSCCPVGCAK.C
71	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.AFAAGADIKEMQNLSFQDC*YSSK.F
72	P62873	GNB1 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB1	R.VSC*LGVTDDGMAVATGSWDSFLK.I
73	Q9C0C9	UBE2O Ubiquitin-conjugating enzyme E2 O	UBE2O	R.C*YNEMALIR.V
74	Q6P2I3	FAHD2B Fumarylacetoacetate hydrolase domain-containing pr	FAHD2B	K.TFDTFC*PLGPALVTK.D
75	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	R.TLSGMESYC*VR.A
76	Q86YS7	KIAA0528 Uncharacterized protein KIAA0528	KIAA0528	R.SAPPC*ANSTVGVVK.M
77	P07437	TUBB Tubulin beta chain	TUBB	K.NMMAAC*DPR.H
78	O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	R.ANSSVVSVNC*K.G
79	Q86XN7	PROSER1 Proline and serine-rich protein 1	PROSER1	K.DGEEC*TNEGK.G
80	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.YVLC*TAPR.A
81	P57678	GEMIN4 Gem-associated protein 4	GEMIN4	R.SDPDAC*PTMPLLAMLLR.G
82	P23528	CFL1 Cofilin-1	CFL1	K.AVLFC*LSEDK.K

2.1	1.9	1.8	2.2	2.0	2.0	1.5	1.6	1.7	1.6	0.4
1.5	1.5	0.0	0.0	2.3	1.8	1.7	1.4	1.1	1.4	0.4
1.8	1.6	1.6	1.9	1.8	1.7	1.4	1.4	1.4	1.4	0.4
1.8	1.8	2.2	2.3	1.9	2.0	1.6	1.6	1.7	1.6	0.4
0.0	1.3	1.3	2.2	1.0	1.4	1.3	1.2	0.8	1.1	0.4
2.3	3.1	2.6	2.5	2.7	2.6	2.2	2.4	2.2	2.3	0.4
1.8	1.3	1.2	1.2	1.3	1.4	1.1	1.0	1.0	1.0	0.3
1.1	0.9	1.1	1.2	1.0	1.0	0.8	0.6	0.7	0.7	0.3
1.1	1.0	0.9	1.2	1.1	1.1	0.7	0.8	0.7	0.7	0.3
2.5	2.5	2.5	3.2	2.4	2.6	2.1	2.0	2.6	2.2	0.3
3.0	2.4	3.1	3.7	3.1	3.1	1.9	3.2	3.0	2.7	0.3
1.5	0.0	1.2	1.3	1.3	1.3	0.8	1.0	1.0	1.0	0.3
1.8	2.4	1.5	1.7	1.4	1.8	1.4	1.6	1.3	1.4	0.3
1.0	0.7	1.0	0.9	0.9	0.9	0.6	0.6	0.5	0.6	0.3
2.3	2.1	2.2	2.5	2.4	2.3	1.1	2.9	1.8	1.9	0.3
1.4	1.5	1.5	1.5	1.5	1.5	1.1	1.2	1.2	1.2	0.3
1.3	0.0	1.2	1.6	1.5	1.4	1.1	1.1	1.1	1.1	0.3
1.8	1.5	1.5	1.5	1.7	1.6	1.2	1.3	1.3	1.3	0.3
2.0	1.5	3.0	3.0	3.0	2.5	2.1	2.2	2.3	2.2	0.3
1.4	1.4	1.4	1.6	1.5	1.4	1.1	1.1	1.2	1.1	0.3
1.7	1.8	1.7	2.0	1.6	1.8	1.3	1.4	1.6	1.4	0.3
2.3	2.2	1.9	2.4	2.8	2.3	1.9	2.0	2.2	2.0	0.3
2.0	1.2	1.3	0.9	1.3	1.4	1.5	0.9	0.8	1.1	0.3
1.4	1.7	2.9	2.7	2.4	2.2	1.5	2.1	2.2	1.9	0.3
1.6	1.5	1.6	1.7	1.5	1.6	1.2	1.3	1.4	1.3	0.3
1.3	1.4	1.5	1.6	1.4	1.4	1.1	1.3	0.9	1.1	0.3
0.0	1.2	0.9	1.6	1.5	1.3	1.0	1.0	0.9	1.0	0.3
2.3	1.1	1.1	1.0	1.1	1.3	1.1	1.2	0.8	1.0	0.3
1.3	1.2	0.0	0.0	1.0	1.2	0.8	1.0	0.9	0.9	0.3
0.8	1.0	1.2	1.0	1.0	1.0	0.9	0.5	0.7	0.7	0.3
1.4	1.6	1.8	2.7	1.6	1.8	1.6	1.1	1.9	1.5	0.3
2.0	1.9	1.8	2.0	1.9	1.9	1.5	1.9	1.6	1.6	0.3
3.0	1.6	1.7	0.0	1.2	1.9	1.9	1.6	1.4	1.6	0.3
1.2	1.3	1.2	1.5	1.5	1.3	1.1	0.9	1.2	1.1	0.3
2.1	0.0	2.0	2.5	2.1	2.2	1.9	1.6	2.4	1.9	0.3
1.3	1.4	1.4	1.6	1.3	1.4	1.7	1.5	0.3	1.2	0.3
1.1	0.0	1.1	1.6	1.4	1.3	0.9	1.0	1.3	1.0	0.3
2.9	2.6	2.6	3.0	2.8	2.8	2.4	2.5	2.7	2.5	0.3
1.7	1.9	1.4	1.8	1.9	1.7	1.4	1.6	1.5	1.5	0.2
1.4	1.2	1.2	0.0	0.0	1.3	0.9	1.2	1.1	1.0	0.2
1.6	1.5	1.6	1.6	1.6	1.6	1.2	1.4	1.5	1.4	0.2
1.8	0.0	1.4	1.8	0.0	1.7	1.6	1.3	1.4	1.4	0.2
0.8	1.0	1.1	0.8	0.9	0.9	0.8	0.7	0.6	0.7	0.2

83	P30281	CCND3 G1/S-specific cyclin-D3	CCND3	R.ASYFQC*VQR.E
84	P19838	NFKB1 Nuclear factor NF-kappa-B p105 subunit	NFKB1	R.YVC*EGPSHGGLPGASSEK.N
85	Q9H3P7	ACBD3 Golgi resident protein GCP60	ACBD3	K.QVLMGPYNPDTC*PEVGFFDVLGNDR.R
86	P33991	MCM4 DNA replication licensing factor MCM4	MCM4	K.AGIIC*QLNAR.T
87	P53384	NUBP1 Cytosolic Fe-S cluster assembly factor NUBP1	NUBP1	K.NC*DKGQSFFIDAPDSPATLAYR.S
88	Q14694	USP10 Ubiquitin carboxyl-terminal hydrolase 10	USP10	R.SSVELPPYSGTVLC*GTQAVDKLPDGQEYQR.I
89	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.YMAC*CLLYR.G
90	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.AEGSDVANAVLDGADC*IMLSGETAK.G
91	Q9Y277	VDAC3 Voltage-dependent anion-selective channel protein	VDAC3	K.VC*NYGLTFTQK.W
92	Q9NZL4	HSPBP1 Hsp70-binding protein 1	HSPBP1	R.LLDRDAC*DTVR.V
93	O43765	SGTA Small glutamine-rich tetratricopeptide repeat-cont	SGTA	R.AIC*IDPAYSK.A
94	Q8NBF2	NHLRC2 NHL repeat-containing protein 2	NHLRC2	K.AILFSQPLQITDTQQGC*IAPVELR.Y
95	Q15020	SART3 Squamous cell carcinoma antigen recognized by T-ce	SART3	K.C*AAVDVEPPSK.Q
96	P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	R.AALEALGSC*LNNK.Y
97	Q9Y3A3	MOB4 MOB-like protein phocein	MOB4	R.HTLDGAAC*LLNSNK.Y
98	P55263	ADK Adenosine kinase	ADK	R.TGC*TFPEKPDFH.-
99	Q96RQ3	MCCC1 Methylcrotonoyl-CoA carboxylase subunit alpha, mit	MCCC1	K.ESLC*QAALGLILK.E
100	Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	K.VVFC*PVK.E
101	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	R.IVDTPC*NEMNTDTFLEEINK.V
102	P63167	DYNLL1 Dynein light chain 1, cytoplasmic	DYNLL1	K.NADMSEEMQQDSVEC*ATQALEK.Y
103	P18669	PGAM1 Phosphoglycerate mutase 1	PGAM1	R.YADLTEDQLPSC*ESLK.D
104	P51553	IDH3G Isocitrate dehydrogenase	IDH3G	K.LGDGLFLQC*CR.E
105	Q02790	FKBP4 Peptidyl-prolyl cis-trans isomerase FKBP4	FKBP4	K.TQLAVC*QQR.I
106	Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	R.LSTLC*PSAVLQR.L
107	P49327	FASN Fatty acid synthase	FASN	K.ADEASELAC*PTPK.E
108	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	R.ISASC*QHPTAFEEAIPK.S
109	O43390	HNRNPR Heterogeneous nuclear ribonucleoprotein R	HNRNPR	K.SAFLC*GVMK.T
110	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	R.HIIEDPC*TLR.H
111	Q06330	RBPJ Recombining binding protein suppressor of hairless	RBPJ	R.IIQFQATPC*PK.E
112	P15924	DSP Desmoplakin	DSP	K.AC*GSEIMQK.K
113	Q8TAQ2	SMARCC2 SWI/SNF complex subunit SMARCC2	SMARCC2	R.NLAGDVC*AIMR.V
114	Q04760	GLO1 Lactoylglutathione lyase	GLO1	K.C*DFPIMK.F
115	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	K.SC*AHDWVYE.-
116	Q96CD2	PPCDC Phosphopantothenoylcysteine decarboxylase	PPCDC	K.ASC*PAAAPLMER.K
117	Q9H9P8	L2HGDH L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	R.GLMAIDC*PHTGIVDYR.Q
118	Q9NZB2	FAM120A Constitutive coactivator of PPAR-gamma-like protei	FAM120A	R.VAAASGHC*GAFSGSDSSR.T
119	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.GC*DVVVIPAGVPR.K
120	Q8N163	KIAA1967 DBIRD complex subunit KIAA1967	KIAA1967	R.VVTQNIC*QYR.S

1.5	1.5	1.3	1.5	1.5	1.4	1.3	1.1	1.3	1.2	0.2
1.5	1.5	1.5	1.6	1.5	1.5	1.1	1.2	1.5	1.3	0.2
0.0	1.0	1.2	1.2	1.0	1.1	0.7	1.0	0.9	0.9	0.2
2.1	1.2	0.0	0.0	1.7	1.6	1.6	1.4	1.3	1.4	0.2
2.0	2.1	1.6	2.5	1.7	2.0	2.0	1.1	2.2	1.8	0.2
1.1	1.2	1.2	1.4	1.1	1.2	1.0	1.2	0.6	1.0	0.2
2.5	2.3	2.3	2.6	2.4	2.4	2.1	2.1	2.3	2.2	0.2
0.0	0.9	1.2	1.1	1.0	1.1	0.8	0.9	0.9	0.8	0.2
0.0	1.3	1.9	1.6	1.0	1.4	1.3	1.2	1.3	1.2	0.2
1.2	1.2	1.4	1.3	1.3	1.3	1.1	1.0	1.1	1.1	0.2
1.5	1.1	1.1	1.2	1.1	1.2	1.1	1.2	0.6	1.0	0.2
1.3	1.1	1.3	1.3	1.4	1.3	0.9	1.2	1.0	1.0	0.2
1.1	0.8	1.3	1.2	1.6	1.2	0.6	1.3	1.0	1.0	0.2
0.0	1.3	1.3	1.6	1.1	1.3	1.1	1.2	1.0	1.1	0.2
1.4	1.4	1.4	1.5	1.4	1.4	1.2	1.1	1.2	1.2	0.2
1.4	1.4	1.4	1.8	1.5	1.5	1.3	1.4	1.2	1.3	0.2
1.4	2.0	1.4	1.6	1.6	1.6	1.4	1.4	1.3	1.4	0.2
1.0	0.8	0.8	1.0	0.8	0.9	0.6	0.7	0.7	0.7	0.2
1.1	1.0	0.9	1.1	1.1	1.0	0.8	0.9	0.8	0.8	0.2
0.9	1.0	0.9	0.9	1.0	1.0	0.6	0.9	0.7	0.7	0.2
1.0	0.9	1.1	0.9	0.8	1.0	0.8	0.9	0.5	0.7	0.2
2.2	2.2	2.0	2.4	2.3	2.2	1.2	2.2	2.6	2.0	0.2
0.8	1.1	1.0	1.4	1.2	1.1	0.9	1.1	0.8	0.9	0.2
0.7	1.8	2.0	1.3	1.2	1.4	1.4	0.8	1.4	1.2	0.2
1.3	1.3	1.3	1.4	1.4	1.3	0.9	1.3	1.1	1.1	0.2
1.3	1.3	1.3	1.4	1.4	1.3	1.0	1.2	1.1	1.1	0.2
2.1	1.1	1.3	1.3	1.2	1.4	1.1	1.2	1.2	1.2	0.2
1.6	1.2	1.3	1.6	1.4	1.4	1.4	1.1	1.2	1.2	0.2
1.1	2.0	1.0	0.0	1.7	1.4	1.5	0.9	1.3	1.2	0.2
1.5	1.3	1.2	1.2	1.2	1.3	1.2	1.2	0.9	1.1	0.2
1.0	0.9	1.0	1.1	1.0	1.0	0.9	0.8	0.8	0.8	0.2
1.0	0.9	1.2	1.3	0.9	1.1	0.8	0.9	0.9	0.9	0.2
1.4	1.4	1.0	1.0	1.2	1.2	1.1	1.1	0.8	1.0	0.2
1.4	1.5	1.7	1.8	1.6	1.6	1.1	1.5	1.6	1.4	0.2
0.0	3.8	4.0	4.8	0.0	4.2	4.3	3.6	4.2	4.0	0.2
2.3	1.7	2.0	2.5	2.0	2.1	1.6	2.0	2.2	1.9	0.2
3.3	2.5	3.0	3.6	2.2	2.9	2.4	3.6	2.2	2.7	0.2
1.8	2.4	1.9	2.0	2.5	2.1	1.9	2.1	1.8	1.9	0.2

121	Q7L2H7	EIF3M Eukaryotic translation initiation factor 3 subunit	EIF3M	K.VAASC*GAIQYIPTELDQVR.K
122	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.LFQEC*CPHSTDR.V
123	Q7L1Q6	BZW1 Basic leucine zipper and W2 domain-containing prot	BZW1	R.FDPTQFQDC*IIQGLTETGTDLEAVAK.F
124	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVDVEVPDVELEC*PDAK.L
125	P46782	RPS5 40S ribosomal protein S5	RPS5	K.TIAEC*LADELINAAK.G
126	O43865	AHCYL1 Putative adenosylhomocysteinase 2	AHCYL1	K.LC*VPAMNVNDSVTK.Q
127	P61981	YWHAG 14-3-3 protein gamma	YWHAG	K.NC*SETQYESK.V
128	P78347	GTF2I General transcription factor II-I	GTF2I	R.SILSPGGSC*GPIK.V
129	P15924	DSP Desmoplakin	DSP	R.DANSENC*NK.N
130	Q13542	EIF4EBP2 Eukaryotic translation initiation factor 4E-bindin	EIF4EBP2	R.TVAISDAAQLPHDYC*TTPGGTLFSTTPGGTR.I
131	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	R.EEFASTC*PDDEEIELAYEQVAK.A
132	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	R.SIQFVDWC*PTGFK.V
133	Q9BX63	BRIP1 Fanconi anemia group J protein	BRIP1	R.LANNSDC*ILAK.D
134	Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	R.NPVSQC*MR.G
135	Q9NQC3	RTN4 Reticulon-4	RTN4	K.YSNSALGHVNC*TIK.E
136	P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB2	K.AC*GDSTLTQITAGLDPVGR.I
137	Q05655	PRKCD Protein kinase C delta type	PRKCD	K.VLMSVQYFLEDVDC*K.Q
138	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	K.ASVGFGGSC*FQK.D
139	P36578	RPL4 60S ribosomal protein L4	RPL4	R.GPC*IIYNEDNGIIK.A
140	Q93052	LPP Lipoma-preferred partner	LPP	K.TYITDPVSAPC*APPLQPK.G
141	P11413	G6PD Glucose-6-phosphate 1-dehydrogenase	G6PD	R.TQVC*GILR.E
142	Q14847	LASP1 LIM and SH3 domain protein 1	LASP1	K.ACFHC*ETCK.M
143	O14964	HGS Hepatocyte growth factor-regulated tyrosine kinase	HGS	R.AC*GQIFCGK.C
144	P62241	RPS8 40S ribosomal protein S8	RPS8	K.NC*IVLIDSTPYR.Q
145	Q71U36	TUBA1A Tubulin alpha-1A chain	TUBA1A	R.TIQFVDWC*PTGFK.V
146	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	K.GLLDVTC*K.T
147	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	K.LGSAVVTRGDEC*GLALGR.L
148	P45984	MAPK9 Mitogen-activated protein kinase 9	MAPK9	R.TAC*TNFMMTPYVVTR.Y
149	P07858	CTSB Cathepsin B	CTSB	R.GQDHC*GIESEVVAGIPR.T
150	P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	K.LC*FSTAQHAS.-
151	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	K.FIC*EQDHQNFLR.L
152	P13639	EEF2 Elongation factor 2	EEF2	K.STLTDSLVC*K.A
153	O43684	BUB3 Mitotic checkpoint protein BUB3	BUB3	R.TPC*NAGTFSQPEK.V
154	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	R.SLLINAVEASC*IR.T
155	P46782	RPS5 40S ribosomal protein S5	RPS5	K.AQC*PIVER.L
156	P50990	CCT8 T-complex protein 1 subunit theta	CCT8	K.IAVYSC*PFDGMITETK.G
157	Q9Y3F4	STRAP Serine-threonine kinase receptor-associated protei	STRAP	K.IGFPETTEEELEEIASENSDC*IFPSAPDVK.A
158	P47756	CAPZB F-actin-capping protein subunit beta	CAPZB	K.DETVSDC*SPHIANIGR.L
159	P09429	HMGB1 High mobility group protein B1	HMGB1	K.MSSYAFFVQTC*R.E
160	O75153	KIAA0664 Clustered mitochondria protein homolog	KIAA0664	K.C*LTQQAVALQR.T
161	Q9UNH7	SNX6 Sorting nexin-6	SNX6	R.IGSSLYALGTQDSTDIC*K.F

1.4	1.1	1.2	1.3	1.2	1.2	0.9	1.1	1.2	1.1	0.2
1.2	1.1	1.3	1.3	1.2	1.2	1.1	1.0	1.0	1.0	0.2
1.4	1.1	1.2	1.2	1.2	1.2	1.0	1.1	1.1	1.0	0.2
0.0	1.1	1.1	1.4	1.2	1.2	0.9	1.3	1.0	1.1	0.2
1.7	1.6	1.6	1.8	1.7	1.7	1.4	1.5	1.6	1.5	0.2
1.2	1.0	1.4	1.2	1.4	1.3	1.2	0.9	1.2	1.1	0.2
0.9	0.9	1.0	0.9	0.9	0.9	0.6	1.0	0.8	0.8	0.2
1.1	1.0	1.1	1.2	1.2	1.1	0.9	1.1	0.9	1.0	0.2
1.2	1.6	1.8	2.1	1.4	1.6	1.4	1.3	1.7	1.5	0.2
1.5	1.4	1.9	2.1	1.7	1.7	1.2	1.8	1.7	1.5	0.2
0.9	1.0	1.3	1.1	1.1	1.1	0.9	1.1	0.7	0.9	0.2
2.5	2.4	2.4	2.8	2.5	2.5	2.3	2.3	2.5	2.4	0.2
1.1	1.1	1.3	1.3	1.2	1.2	1.0	1.2	1.0	1.0	0.2
1.5	1.3	1.3	1.5	1.4	1.4	1.1	1.3	1.3	1.2	0.2
1.1	1.5	1.0	1.3	1.5	1.3	1.2	1.1	1.1	1.1	0.2
2.8	2.2	2.5	2.8	2.6	2.6	2.7	2.1	2.5	2.4	0.2
0.0	1.2	1.5	0.0	1.5	1.4	1.3	1.2	1.3	1.2	0.2
1.2	1.0	1.9	1.0	1.1	1.2	1.0	1.2	1.0	1.1	0.2
0.0	3.1	2.2	0.0	2.5	2.6	2.4	2.3	2.7	2.5	0.2
1.4	1.4	1.4	1.7	1.5	1.5	1.2	1.4	1.3	1.3	0.2
1.4	1.3	1.5	1.7	1.4	1.5	1.3	1.4	1.3	1.3	0.2
0.6	0.5	0.7	0.6	0.7	0.6	0.4	0.6	0.4	0.5	0.2
1.0	0.7	0.9	1.2	0.9	0.9	0.6	0.8	0.9	0.8	0.2
2.6	3.2	3.2	3.7	3.5	3.2	2.8	2.5	3.9	3.1	0.2
2.4	2.4	2.3	2.7	2.5	2.4	2.2	2.3	2.4	2.3	0.2
1.1	1.1	1.1	1.1	1.1	1.1	0.9	1.0	0.9	1.0	0.2
1.7	1.5	1.5	1.7	1.6	1.6	1.3	1.5	1.5	1.4	0.2
1.6	1.4	1.6	1.6	1.7	1.6	1.5	1.4	1.4	1.4	0.2
4.1	3.0	3.1	2.5	2.5	3.0	2.7	2.8	3.2	2.9	0.2
1.3	1.2	1.1	1.1	1.1	1.2	1.1	1.2	0.8	1.0	0.1
1.0	1.0	1.1	1.3	1.2	1.1	0.8	1.1	1.1	1.0	0.1
1.3	1.1	1.2	1.3	1.5	1.3	1.1	1.1	1.2	1.1	0.1
1.2	1.5	1.3	1.6	1.2	1.4	1.0	1.6	1.1	1.2	0.1
2.7	2.2	2.6	2.9	2.6	2.6	2.4	2.5	2.5	2.4	0.1
1.6	1.6	1.3	1.7	1.6	1.6	1.4	1.4	1.5	1.4	0.1
1.1	1.0	1.0	1.2	1.1	1.1	0.9	1.0	0.9	0.9	0.1
1.0	1.1	1.3	1.4	1.2	1.2	0.9	1.1	1.1	1.0	0.1
1.0	1.0	1.2	1.0	0.9	1.0	0.9	1.0	0.9	0.9	0.1
1.4	1.7	1.4	1.4	1.4	1.4	1.0	1.6	1.3	1.3	0.1
1.3	1.2	1.2	1.3	1.3	1.3	0.9	1.3	1.1	1.1	0.1
1.1	1.0	1.1	1.2	1.2	1.1	1.0	0.9	1.1	1.0	0.1

162	Q4ZG55	GREB1 Protein GREB1	GREB1	R.LINSSC*LVR.T
163	Q9Y696	CLIC4 Chloride intracellular channel protein 4	CLIC4	K.AGSDGESIGNC*PFSQR.L
164	P42677	RPS27 40S ribosomal protein S27	RPS27	R.LTEGC*SFR.R
165	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	R.KENQWC*EEK.-
166	Q9UM54	MYO6 Unconventional myosin-VI	MYO6	R.C*GGIQYLQNAIESR.Q
167	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	K.GKEDKENRDQSAQC*TASK.S
168	P60709	ACTB Actin, cytoplasmic 1	ACTB	K.C*DVDIRKDLYANTVLSGGTTMYPGIADR.M
169	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	R.VDVAVNC*AGIAVASK.T
170	P30044	PRDX5 Peroxiredoxin-5, mitochondrial	PRDX5	K.ALNVEPDGTGLTC*SLAPNIISQL.-
171	Q99497	PARK7 Protein DJ-1	PARK7	K.VTVAGLAGKDPVQC*SR.D
172	Q6IA69	NADSYN1 Glutamine-dependent NAD(+) synthetase	NADSYN1	K.NSSQETC*TR.A
173	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.LVVPATQC*GSLIGK.G
174	Q9H0C8	ILKAP Integrin-linked kinase-associated serine/threonine	ILKAP	R.FILLAC*DGLFK.V
175	O43681	ASNA1 ATPase ASNA1	ASNA1	K.IDTHNIIVNQLVFPDPEKPC*K.M
176	P12004	PCNA Proliferating cell nuclear antigen	PCNA	K.C*AGNEDIITLR.A
177	Q15181	PPA1 Inorganic pyrophosphatase	PPA1	K.GISC*MNTTLSESPFK.C
178	Q9BY32	ITPA Inosine triphosphate pyrophosphatase	ITPA	R.GC*QDFGWDPCFQPDGYEQTYAEMPK.A
179	Q9Y224	C14orf166 UPF0568 protein C14orf166	C14orf166	K.LTALDYHNPAGFNC*K.D
180	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.IHMGSC*AENTAK.K
181	P28838	LAP3 Cytosol aminopeptidase	LAP3	R.SAGAC*TAAAFLK.E
182	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.TIIPLISQC*TPK.V
183	P46782	RPS5 40S ribosomal protein S5	RPS5	R.VNQAIWLLC*TGAR.E
184	Q7L5D6	GET4 Golgi to ER traffic protein 4 homolog	GET4	K.EQNYC*ESR.Y
185	Q9H3U1	UNC45A Protein unc-45 homolog A	UNC45A	R.AIQTVSCLLQGPC*DAGNR.A
186	P17858	PFKL 6-phosphofructokinase, liver type	PFKL	R.VFANAPDSAC*VIGLK.K
187	P30042	C21orf33 ES1 protein homolog, mitochondrial	C21orf33	K.NLSTFAVDGKDC*K.V
188	Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	K.LAAQSC*ALSLVR.Q
189	P10620	MGST1 Microsomal glutathione S-transferase 1	MGST1	K.VFANPEDC*VAFGK.G
190	Q86SX6	GLRX5 Glutaredoxin-related protein 5, mitochondrial	GLRX5	K.GTPEQPQC*GFSNAVVQILR.L
191	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	K.IGNC*PFSQR.L
192	P33240	CSTF2 Cleavage stimulation factor subunit 2	CSTF2	K.LC*VQNSPQEAR.N
193	Q9UNE7	STUB1 E3 ubiquitin-protein ligase CHIP	STUB1	R.AQQAC*IEAK.H
194	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.YLAEVAC*GDDR.K
195	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	R.VPTANVSVVDLTC*R.L
196	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	K.VDENFDC*VEADDVEGK.I
197	Q8TC07	TBC1D15 TBC1 domain family member 15	TBC1D15	R.TLLVNC*QNK.S
198	P10768	ESD S-formylglutathione hydrolase	ESD	K.AETGKCPALYWLSGLTC*TEQNFISK.S
199	Q12765	SCRN1 Secernin-1	SCRN1	K.TQSPC*FGDDDPAKKEPR.F
200	O95571	ETHE1 Protein ETHE1, mitochondrial	ETHE1	R.TDFQQGC*AK.T
201	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.NTGIIC*TIGPASR.S
202	P23528	CFL1 Cofilin-1	CFL1	K.HELQANC*YEEVK.D
203	P62241	RPS8 40S ribosomal protein S8	RPS8	K.LLAC*IASR.P

3.1	0.6	2.5	3.5	2.3	2.4	2.1	2.3	2.5	2.3	0.1
1.1	1.3	1.0	1.3	1.1	1.2	1.0	1.1	1.0	1.1	0.1
2.4	2.6	2.5	2.8	2.4	2.6	2.2	2.4	2.7	2.4	0.1
1.2	1.2	1.2	1.2	1.2	1.2	1.0	1.1	1.2	1.1	0.1
0.0	0.0	0.7	0.7	1.1	0.9	0.7	0.7	0.7	0.7	0.1
1.1	1.6	1.3	1.3	1.3	1.3	1.4	1.4	0.9	1.2	0.1
2.7	2.8	2.8	3.1	2.6	2.8	2.6	2.6	2.9	2.7	0.1
3.3	2.5	3.0	2.8	2.5	2.8	2.4	2.6	3.1	2.7	0.1
0.7	0.8	0.9	0.8	0.8	0.8	0.7	0.8	0.6	0.7	0.1
0.5	0.5	0.6	0.5	0.6	0.6	0.5	0.5	0.4	0.4	0.1
1.1	1.1	1.0	1.8	1.1	1.2	1.1	1.1	1.2	1.1	0.1
1.2	1.1	1.2	1.2	1.2	1.2	1.0	1.1	1.1	1.0	0.1
1.0	1.1	1.4	1.2	0.9	1.1	1.0	1.0	1.1	1.0	0.1
1.0	1.3	0.7	0.8	0.9	1.0	1.0	0.9	0.7	0.8	0.1
0.9	1.0	1.0	1.0	0.9	1.0	0.8	1.0	0.8	0.9	0.1
1.2	1.0	1.2	1.1	1.1	1.1	0.9	1.0	1.1	1.0	0.1
1.3	1.0	0.9	1.2	1.1	1.1	1.0	0.7	1.2	1.0	0.1
1.1	1.1	1.1	1.2	1.1	1.1	1.0	1.0	1.0	1.0	0.1
1.4	1.2	1.3	1.4	1.4	1.3	0.7	1.4	1.5	1.2	0.1
1.1	0.9	1.2	1.4	1.1	1.2	0.9	1.2	1.0	1.0	0.1
1.7	1.8	1.9	1.9	1.8	1.8	1.7	1.8	1.6	1.7	0.1
1.6	1.5	0.0	0.0	1.6	1.6	1.4	1.5	1.6	1.5	0.1
0.0	0.0	1.3	1.1	1.4	1.3	1.3	1.1	1.2	1.2	0.1
1.3	0.0	1.2	1.1	0.0	1.2	1.2	1.1	0.9	1.1	0.1
3.0	2.5	2.6	3.0	2.4	2.7	2.4	2.6	2.7	2.6	0.1
1.3	1.2	1.2	1.5	1.1	1.3	1.2	1.1	1.2	1.1	0.1
0.9	0.7	1.0	1.0	0.9	0.9	1.0	0.9	0.5	0.8	0.1
1.6	1.5	1.5	1.4	1.2	1.4	1.5	1.3	1.2	1.3	0.1
1.2	1.1	1.1	1.2	1.2	1.1	1.0	1.1	1.1	1.0	0.1
1.3	1.2	1.2	1.3	1.3	1.3	1.1	1.1	1.2	1.2	0.1
1.3	1.1	1.2	1.2	1.2	1.2	1.0	1.2	1.0	1.1	0.1
1.1	1.3	1.0	1.4	1.0	1.2	0.9	1.2	1.1	1.1	0.1
0.9	1.1	1.1	1.0	1.1	1.0	0.9	1.1	0.9	0.9	0.1
0.4	0.5	0.4	0.5	0.4	0.5	0.4	0.4	0.3	0.4	0.1
1.3	1.0	1.4	1.5	1.4	1.3	0.9	1.5	1.3	1.2	0.1
1.9	1.4	1.9	2.2	2.1	1.9	1.6	1.9	2.0	1.8	0.1
1.0	0.9	0.9	1.0	0.9	0.9	0.9	0.7	1.0	0.9	0.1
1.1	0.9	1.0	1.0	1.2	1.0	0.9	0.9	0.9	0.9	0.1
0.0	1.6	1.7	1.6	1.9	1.7	1.5	1.8	1.5	1.6	0.1
0.9	0.9	0.9	0.9	0.8	0.9	0.8	0.9	0.6	0.8	0.1
0.9	0.9	0.9	0.9	1.0	0.9	0.8	0.8	0.8	0.8	0.1
4.0	3.5	3.8	4.1	0.0	3.9	4.1	3.5	3.7	3.8	0.1

204	Q9UJW0	DCTN4 Dynactin subunit 4	DCTN4	R.LLQPDFQPVC*ASQLYPR.H
205	Q9HA64	FN3KRP Ketosamine-3-kinase	FN3KRP	R.ATGHSGGGC*ISQGR.S
206	Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	R.VGLGIC*YDMR.F
207	P30626	SRI Sorcin	SRI	R.CLTQSGIAGGYKPFNLETC*R.L
208	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.GSDFDC*ELR.L
209	P50914	RPL14 60S ribosomal protein L14	RPL14	R.ALVDGPC*TQVR.R
210	P20073	ANXA7 Annexin A7	ANXA7	R.LGTDESC*FNMILATR.S
211	P14649	MYL6B Myosin light chain 6B	MYL6B	K.ILYSQC*GDVMR.A
212	Q9UL46	PSME2 Proteasome activator complex subunit 2	PSME2	K.C*GFLPGNEK.V
213	Q92616	GCN1L1 Translational activator GCN1	GCN1L1	R.C*GLALALNK.L
214	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVGVEVPDVELEC*PDAK.L
215	P50213	IDH3A Isocitrate dehydrogenase	IDH3A	K.TFDLYANVRPC*VSIEGYK.T
216	Q9UI30	TRMT112 tRNA methyltransferase 112 homolog	TRMT112	R.IC*PVEFNPNFVAR.M
217	P53618	COPB1 Coatomer subunit beta	COPB1	K.ALSGYC*GFMAANLYAR.S
218	P46776	RPL27A 60S ribosomal protein L27a	RPL27A	R.NQSFC*PTVNLDK.L
219	Q9UQ35	SRRM2 Serine/arginine repetitive matrix protein 2	SRRM2	R.SVSPC*SNVESR.L
220	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	K.YAGLSTC*FR.Q
221	P00338	LDHA L-lactate dehydrogenase A chain	LDHA	R.VIGSGC*NLDSAR.F
222	P30041	PRDX6 Peroxiredoxin-6	PRDX6	R.DFTPVC*TTELGR.A
223	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	K.HLNEIDLFHC*IDPNDSK.H
224	P37235	HPCAL1 Hippocalcin-like protein 1	HPCAL1	R.LLQC*DPSSASQF.-
225	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	K.EGTDSSQGIPQLVSNISAC*QVIAEAVR.T
226	P29401	TKT Transketolase	TKT	K.QAFTDVATGSLGQGLGAAC*GMAYTGK.Y
227	P49207	RPL34 60S ribosomal protein L34	RPL34	R.AYGGSMC*AK.C
228	Q7Z406	MYH14 Myosin-14	MYH14	K.ADLLLEPC*SHYR.F
229	P62306	SNRPF Small nuclear ribonucleoprotein F	SNRPF	R.C*NNVLYIR.G
230	P49327	FASN Fatty acid synthase	FASN	K.AINC*ATSGVVGLVNCLR.R
231	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	K.C*LSVMEAK.V
232	O95336	PGLS 6-phosphogluconolactonase	PGLS	R.AAC*CLAGAR.A
233	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.AITIAGVPQSVTEC*VK.Q
234	Q9BWJ5	SF3B5 Splicing factor 3B subunit 5	SF3B5	K.MLQPC*GPPADKPEEN.-
235	Q9P258	RCC2 Protein RCC2	RCC2	K.AVQDLC*GWR.I
236	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	R.ISAFGYLEC*SAK.T
237	P62829	RPL23 60S ribosomal protein L23	RPL23	R.ISLGLPVGAVINC*ADNTGAK.N
238	P62820	RAB1A Ras-related protein Rab-1A	RAB1A	K.LLVGNKC*DLTTK.K
239	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	R.FC*PFAER.T
240	Q9P2T1	GMPR2 GMP reductase 2	GMPR2	K.VGIGPGSVC*TTR.K
241	O75874	IDH1 Isocitrate dehydrogenase	IDH1	K.SEGGFIWAC*K.N
242	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	K.ILSC*GEVIHVK.I
243	P62857	RPS28 40S ribosomal protein S28	RPS28	R.TGSQGQC*TQVR.V
244	Q5MNZ6	WDR45L WD repeat domain phosphoinositide-interacting prot	WDR45L	R.C*NYLALVGGGK.K
245	Q96AT9	RPE Ribulose-phosphate 3-epimerase	RPE	K.IGPSILNSDLANLGAEC*LR.M

1.3	1.4	1.0	1.0	1.3	1.2	1.2	0.9	1.2	1.1	0.1
1.2	1.4	1.2	0.0	1.4	1.3	1.1	1.2	1.2	1.2	0.1
1.4	1.1	1.0	1.2	1.3	1.2	1.0	1.2	1.1	1.1	0.1
1.1	0.0	1.0	1.0	1.1	1.0	0.9	1.1	0.8	0.9	0.1
1.1	1.3	1.3	1.2	1.3	1.2	1.1	1.2	1.1	1.1	0.1
2.5	2.1	2.1	2.7	2.3	2.3	2.2	2.2	2.3	2.2	0.1
1.5	1.3	1.2	1.4	1.4	1.3	1.2	1.4	1.2	1.3	0.1
0.9	1.0	1.1	1.0	1.0	1.0	0.9	1.0	0.9	0.9	0.1
0.9	0.8	0.9	1.0	0.9	0.9	0.8	0.9	0.7	0.8	0.1
3.2	2.1	2.3	3.1	2.5	2.6	2.2	3.1	2.4	2.5	0.1
1.1	1.1	1.2	1.5	1.1	1.2	1.2	1.2	0.9	1.1	0.1
2.7	0.0	1.5	3.0	1.5	2.2	1.8	2.3	2.2	2.1	0.1
0.9	1.2	1.2	1.2	1.2	1.1	1.1	1.2	0.8	1.0	0.1
2.1	1.5	1.9	2.3	2.3	2.0	1.7	2.3	1.9	2.0	0.1
2.3	1.8	1.8	2.0	1.7	1.9	1.8	1.7	2.1	1.9	0.1
1.1	1.5	1.1	1.2	1.1	1.2	1.1	1.0	1.2	1.1	0.1
1.2	1.1	1.1	1.2	1.2	1.1	1.0	1.1	1.1	1.1	0.1
1.1	1.1	1.2	1.1	1.1	1.1	0.9	1.1	1.1	1.0	0.1
1.0	0.5	0.5	0.5	0.5	0.6	0.4	0.6	0.6	0.5	0.1
1.2	1.1	1.1	1.2	1.2	1.2	1.1	1.1	1.1	1.1	0.1
0.0	1.2	1.3	1.3	1.3	1.2	1.1	1.2	1.2	1.2	0.1
0.0	1.4	1.4	1.5	1.5	1.4	1.4	1.5	1.3	1.4	0.1
3.2	2.5	2.5	2.6	2.4	2.6	2.5	2.6	2.6	2.6	0.1
2.5	2.3	2.5	2.9	2.3	2.5	2.6	2.2	2.5	2.5	0.1
1.7	1.8	1.6	1.9	1.8	1.7	1.9	1.4	1.8	1.7	0.1
1.2	1.1	1.1	1.2	1.2	1.2	1.1	1.1	1.1	1.1	0.1
1.3	1.4	1.3	1.5	1.1	1.3	1.2	1.3	1.3	1.2	0.1
1.2	1.0	0.9	1.0	1.1	1.0	1.0	1.0	0.9	1.0	0.1
1.2	1.2	1.1	1.3	1.3	1.2	1.2	1.1	1.1	1.1	0.1
1.0	1.2	1.1	0.9	1.1	1.1	1.1	1.1	0.8	1.0	0.1
1.0	0.7	1.0	1.3	0.0	1.0	0.9	0.9	1.1	0.9	0.1
1.3	1.1	1.2	1.3	1.3	1.2	1.0	1.2	1.4	1.2	0.1
1.9	1.2	1.8	1.8	1.5	1.6	1.4	1.7	1.6	1.6	0.1
2.2	1.9	2.0	2.3	2.2	2.1	2.0	2.1	2.1	2.0	0.1
1.0	0.0	1.0	1.2	0.0	1.1	1.1	1.0	0.9	1.0	0.1
1.1	1.0	1.1	1.1	1.1	1.0	0.9	1.1	1.0	1.0	0.1
1.6	0.0	1.0	1.0	1.3	1.2	1.2	1.2	1.2	1.2	0.1
0.9	0.9	0.8	0.9	1.0	0.9	1.0	0.9	0.8	0.9	0.1
0.9	1.0	0.8	1.2	1.1	1.0	1.0	1.0	0.8	0.9	0.1
1.0	1.1	1.1	1.1	1.1	1.1	1.1	1.0	1.0	1.0	0.1
1.1	1.2	1.0	1.1	1.2	1.1	1.1	1.0	1.2	1.1	0.1
0.8	1.0	1.4	0.8	0.9	1.0	0.8	1.3	0.7	0.9	0.0

246	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.INISEGNC*PER.I
247	Q9UBF6	RNF7 RING-box protein 2	RNF7	R.VQVMDAC*LR.C
248	Q66K14	TBC1D9B TBC1 domain family member 9B	TBC1D9B	R.AKNEC*YR.A
249	P15924	DSP Desmoplakin	DSP	R.GVITDQNSDGYC*QTGTMSR.H
250	O75223	GGCT Gamma-glutamylcyclotransferase	GGCT	R.NPSAAFFC*VAR.L
251	Q6P1X6	C8orf82 UPF0598 protein C8orf82	C8orf82	R.YEAAFPFLSPC*GR.E
252	Q52LJ0	FAM98B Protein FAM98B	FAM98B	R.EKTAC*AINK.V
253	Q2TAA2	IAH1 Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	R.VILITPTPLC*ETAWEEQCIIQGCK.L
254	Q96I99	SUCLG2 Succinyl-CoA ligase	SUCLG2	R.SC*NGPVLVGSPQGGVDIEEVAASNPELIFK.E
255	P26641	EEF1G Elongation factor 1-gamma	EEF1G	K.AAAPAPEEEMDEC*EQALAAEPK.A
256	Q8TB45	DEPTOR DEP domain-containing mTOR-interacting protein	DEPTOR	K.SPSSQETHDSPFC*LR.K
257	Q9BWD1	ACAT2 Acetyl-CoA acetyltransferase, cytosolic	ACAT2	R.ATVAPEDVSEVIFGHVLAAGC*GQNPVR.Q
258	Q96RS6	NUDCD1 NudC domain-containing protein 1	NUDCD1	R.DSAQC*AAIAER.L
259	Q13526	PIN1 Peptidyl-prolyl cis-trans isomerase NIMA-interacti	PIN1	K.IKSGEEDFESLASQFSDC*SSAK.A
260	P36969	GPX4 Phospholipid hydroperoxide glutathione peroxidase,	GPX4	R.YAEC*GLR.I
261	O15355	PPM1G Protein phosphatase 1G	PPM1G	K.C*SGDGVGAPR.L
262	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	K.EGC*TEVSLLR.V
263	P42025	ACTR1B Beta-centractin	ACTR1B	R.AC*YLSINPQKDEALETEK.V
264	Q9Y285	FARSA Phenylalanine--tRNA ligase alpha subunit	FARSA	K.VNLQMVYDSPLC*R.L
265	Q15149	PLEC Plectin	PLEC	K.AFC*GFEDPR.T
266	Q9NYL2	MLTK Mitogen-activated protein kinase kinase kinase MLT	MLTK	K.FDDLQFFENC*GGGSFGSVYR.A
267	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.HSMNPFC*EIAVEEAVR.L
268	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	R.C*MTNTPVVVR.E
269	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	R.VFIMDSC*DELIPEYLNFIR.G
270	P31947	SFN 14-3-3 protein sigma	SFN	K.GAVEKGEELSC*EER.N
271	P37802	TAGLN2 Transgelin-2	TAGLN2	K.NMAC*VQR.T
272	Q06323	PSME1 Proteasome activator complex subunit 1	PSME1	K.VDVFREDLC*TK.T
273	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	K.C*FIVGADNVGSK.Q
274	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	K.EADQKEQFSQGSPSNC*LETSLAEIFPLGK.N
275	Q9BW61	DDA1 DET1- and DDB1-associated protein 1	DDA1	R.FHADSVC*K.A
276	O43837	IDH3B Isocitrate dehydrogenase	IDH3B	K.LGDGLFLQC*CEEVAELYPK.I
277	P13639	EEF2 Elongation factor 2	EEF2	R.TFC*QLILDPIFK.V
278	Q9Y5P6	GMPPB Mannose-1-phosphate guanyltransferase beta	GMPPB	R.LC*SGPGIVGNVLVDPSAR.I
279	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.GPFVEAEVPDVDLEC*PDAK.L
280	Q9BYG5	PARD6B Partitioning defective 6 homolog beta	PARD6B	R.HGAGSGC*LGTMEVK.S
281	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	R.AQC*ETLSPDGLPEEQPQTTK.L
282	P00491	PNP Purine nucleoside phosphorylase	PNP	R.AC*VMMQGR.F
283	O75131	CPNE3 Copine-3	CPNE3	K.NC*LNPQFSK.T
284	P35270	SPR Sepiapterin reductase	SPR	R.TVVNISSLC*ALQPFK.G
285	Q9UHD8	SEPT9 Septin-9	9-Sep	R.SQEATEAAPSC*VGDMADTPR.D

1.1	1.1	1.1	1.2	1.1	1.1	1.0	1.1	1.1	1.1	0.0
1.1	1.4	1.1	1.1	1.1	1.2	1.3	1.0	1.0	1.1	0.0
1.4	1.6	1.4	1.7	1.8	1.6	1.3	1.7	1.6	1.5	0.0
0.0	2.0	1.5	2.5	1.6	1.9	1.7	1.7	2.1	1.8	0.0
0.8	0.0	1.0	0.9	0.9	0.9	0.9	1.0	0.5	0.8	0.0
1.3	1.1	1.2	1.3	1.2	1.2	1.1	1.3	1.1	1.2	0.0
0.0	0.0	1.1	1.1	1.2	1.2	1.1	1.0	1.2	1.1	0.0
1.2	1.1	1.1	1.3	1.3	1.2	1.2	1.0	1.2	1.2	0.0
1.6	1.4	1.4	1.7	1.6	1.5	1.6	1.5	1.4	1.5	0.0
1.1	1.1	1.2	1.1	1.1	1.1	1.0	1.1	1.1	1.1	0.0
1.0	1.2	1.2	1.0	1.0	1.1	0.8	1.3	1.0	1.0	0.0
0.0	0.7	0.7	0.8	0.6	0.7	0.5	0.7	0.7	0.6	0.0
1.2	1.4	1.1	1.0	1.1	1.2	1.0	1.2	1.1	1.1	0.0
1.1	1.1	1.1	1.3	1.2	1.2	1.2	1.1	1.1	1.1	0.0
1.1	1.0	1.1	1.2	1.2	1.1	0.9	1.0	1.3	1.1	0.0
1.3	1.5	1.5	1.5	1.5	1.4	1.3	1.5	1.5	1.4	0.0
1.3	1.2	1.2	1.3	1.3	1.3	1.1	1.4	1.2	1.2	0.0
2.1	2.0	1.9	2.4	1.9	2.1	1.8	2.1	2.2	2.0	0.0
1.1	1.5	1.6	2.0	1.6	1.5	1.5	1.5	1.5	1.5	0.0
1.1	1.1	1.0	1.2	1.1	1.1	1.0	1.1	1.1	1.1	0.0
1.2	1.0	1.1	1.5	1.4	1.2	1.1	1.2	1.2	1.2	0.0
1.1	1.0	1.3	1.3	1.2	1.2	1.1	1.2	1.1	1.1	0.0
2.7	2.4	2.5	2.7	2.3	2.5	2.2	2.5	2.7	2.5	0.0
1.1	1.3	1.2	1.2	1.3	1.2	1.1	1.3	1.2	1.2	0.0
1.0	1.0	1.1	1.1	1.0	1.0	1.0	1.0	1.0	1.0	0.0
1.3	1.0	0.9	1.0	1.1	1.1	1.0	1.1	1.0	1.0	0.0
1.2	1.2	1.3	1.5	1.3	1.3	1.2	1.4	1.2	1.3	0.0
2.0	1.8	1.9	2.1	2.0	1.9	1.8	1.9	2.1	1.9	0.0
1.3	1.4	1.2	1.0	1.2	1.2	1.4	1.0	1.3	1.2	0.0
1.1	1.2	1.1	1.0	1.1	1.1	0.9	1.3	1.0	1.1	0.0
0.0	2.6	2.3	2.2	2.0	2.3	2.0	2.4	2.4	2.2	0.0
1.0	1.1	1.0	1.1	1.0	1.0	1.1	1.0	1.0	1.0	0.0
1.0	1.0	1.0	1.0	1.1	1.0	1.0	1.0	1.1	1.0	0.0
1.0	1.1	1.1	1.1	1.0	1.1	1.0	1.1	1.0	1.0	0.0
0.0	0.0	1.2	1.4	1.1	1.2	1.1	1.1	1.4	1.2	0.0
0.0	0.0	1.1	1.1	1.0	1.1	1.1	1.1	1.0	1.1	0.0
0.7	1.1	1.0	0.7	0.8	0.9	0.8	1.1	0.8	0.9	0.0
1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.0
1.1	0.9	1.1	1.0	1.1	1.0	1.0	1.0	1.1	1.0	0.0
1.2	1.3	1.3	1.6	1.2	1.3	1.3	1.3	1.3	1.3	0.0

286	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.EVIAVSC*GPAQCQETIR.T
287	O14980	XPO1 Exportin-1	XPO1	K.LDINLLDNVVNC*LYHGEGAQQR.M
288	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	K.FLDGNELTLADC*NLLPK.L
289	P49458	SRP9 Signal recognition particle 9 kDa protein	SRP9	K.VTDDLVC*LVYK.T
290	O75934	BCAS2 Pre-mRNA-splicing factor SPF27	BCAS2	R.IENLELMSQHGC*NAWK.V
291	P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	K.KITIADC*GQLE.-
292	P61513	RPL37A 60S ribosomal protein L37a	RPL37A	K.YTCSFC*GK.T
293	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	K.IETELRDIC*NDVLSLLEK.F
294	P60981	DSTN Destrin	DSTN	K.LGGSLIVAFEGC*PV.-
295	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK.G
296	P60174	TPI1 Triosephosphate isomerase	TPI1	R.IIYGGSVTGATC*K.E
297	P51610	HCFC1 Host cell factor 1	HCFC1	K.LVIYGGMSGC*R.L
298	Q86Y56	HEATR2 HEAT repeat-containing protein 2	HEATR2	R.RPPEAC*EELR.L
299	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	R.YLLQYQEPIPC*EQLVTALCDIK.Q
300	P67936	TPM4 Tropomyosin alpha-4 chain	TPM4	K.EENVGLHQTLDQTLNELNC*I.-
301	Q99829	CPNE1 Copine-1	CPNE1	R.NC*SSPEFSK.T
302	P23396	RPS3 40S ribosomal protein S3	RPS3	R.GLC*AIAQAESLR.Y
303	P26368	U2AF2 Splicing factor U2AF 65 kDa subunit	U2AF2	K.SIEIPRPVDGVEVPGC*GK.I
304	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	K.C*CSGAIIVLTK.S
305	Q9Y5Q8	GTF3C5 General transcription factor 3C polypeptide 5	GTF3C5	R.VC*TNPVDR.K
306	P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	K.IIC*QGFTGK.Q
307	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.LVVPASQC*GSLIGK.G
308	O15355	PPM1G Protein phosphatase 1G	PPM1G	R.C*VVSEAGK.A
309	P62258	YWHAE 14-3-3 protein epsilon	YWHAE	K.LIC*CDILDVLDK.H
310	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.GLPFGC*SK.E
311	P30086	PEBP1 Phosphatidylethanolamine-binding protein 1	PEBP1	R.APVAGTC*YQAEWDDYVPK.L
312	Q9P1F3	ABRACL Costars family protein ABRACL	ABRACL	K.C*ANLFEALVGTLK.A
313	P60981	DSTN Destrin	DSTN	K.C*STPEEIKKR.K
314	P60174	TPI1 Triosephosphate isomerase	TPI1	K.VPADTEVVC*APPTAYIDFAR.Q
315	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	K.AAREEC*PVFTPPGGETLDQVK.M
316	P63220	RPS21 40S ribosomal protein S21	RPS21	K.C*SASNR.I
317	Q9Y2R9	MRPS7 28S ribosomal protein S7, mitochondrial	MRPS7	K.NC*EPMIGLVPILK.G
318	F5H284	PPIAL4D Peptidyl-prolyl cis-trans isomerase	PPIAL4D	R.IIPGFMC*QGGDFTR.H
319	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	R.ALANSLAC*QGK.Y
320	P0CW22	RPS17L 40S ribosomal protein S17-like	RPS17L	R.VC*EEIAIIPSK.K
321	Q14247	CTTN Src substrate cortactin	CTTN	K.C*ALGWDHQEK.L
322	P51659	HSD17B4 Peroxisomal multifunctional enzyme type 2	HSD17B4	K.IC*DFENASKPQSIQESTGSIIEVLSK.I
323	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	R.GNVC*GDSK.S
324	Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.GVPGAIVNVSSQC*SQR.A
325	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	R.AC*ALQVLSAILEGSK.Q
326	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.KGDEC*ELLGHSK.N
327	P22061	PCMT1 Protein-L-isoaspartate(D-aspartate) O-methyltransf	PCMT1	K.ALDVGSGSGILTAC*FAR.M
328	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.SQETEC*TYFSTPLLLGK.K

1.1	0.0	1.1	1.3	1.0	1.1	1.1	1.1	1.1	1.1	0.0
1.2	1.1	1.2	1.2	1.2	1.2	1.2	1.1	1.1	1.1	0.0
0.9	0.8	1.0	0.7	0.9	0.9	0.9	1.1	0.6	0.8	0.0
1.1	1.0	1.1	1.1	1.1	1.1	1.1	1.1	1.0	1.1	0.0
1.3	1.0	1.2	1.4	1.2	1.2	1.1	1.2	1.4	1.2	0.0
0.8	1.0	0.8	0.7	0.8	0.8	0.8	1.0	0.6	0.8	0.0
1.5	0.9	1.1	1.1	0.9	1.1	1.1	1.0	1.2	1.1	0.0
0.7	1.0	1.0	0.8	0.8	0.8	0.9	1.0	0.7	0.8	0.0
1.1	1.0	1.0	1.1	1.0	1.0	1.0	1.0	1.1	1.0	0.0
1.1	1.0	1.0	1.1	1.1	1.1	1.0	1.1	1.1	1.1	0.0
0.7	1.1	0.9	1.0	1.0	0.9	1.0	1.1	0.6	0.9	0.0
1.1	1.0	1.2	1.0	0.9	1.0	0.8	1.1	1.2	1.0	0.0
2.0	1.9	0.0	2.0	0.0	2.0	2.1	1.7	2.1	2.0	0.0
0.8	1.0	1.0	0.9	0.9	0.9	0.9	1.2	0.6	0.9	0.0
0.0	1.2	1.4	1.6	1.3	1.4	1.2	1.4	1.4	1.4	0.0
0.7	1.2	2.1	0.7	0.0	1.2	1.2	1.4	0.8	1.2	0.0
1.8	1.7	1.6	1.8	1.8	1.7	1.7	1.7	1.9	1.7	0.0
0.7	0.0	0.7	0.7	0.8	0.7	0.7	0.9	0.7	0.7	0.0
1.2	1.3	1.3	1.3	1.2	1.3	1.3	1.2	1.2	1.3	0.0
1.6	1.1	1.7	2.0	2.4	1.8	2.1	1.2	2.1	1.8	0.0
2.0	2.3	2.4	2.6	2.5	2.4	2.1	2.5	2.5	2.4	0.0
1.1	1.1	1.1	1.2	1.1	1.1	1.0	1.2	1.1	1.1	0.0
0.0	1.0	1.2	1.7	1.4	1.3	1.2	1.5	1.4	1.3	0.0
1.2	1.0	1.1	1.1	1.1	1.1	1.0	1.1	1.2	1.1	0.0
1.2	1.2	1.2	1.2	1.1	1.2	1.1	1.2	1.2	1.2	0.0
0.9	1.1	1.1	1.0	1.1	1.0	1.0	1.3	0.8	1.0	0.0
1.1	1.3	1.3	1.4	1.3	1.3	1.2	1.4	1.3	1.3	0.0
1.1	1.0	1.1	1.2	1.1	1.1	1.0	1.1	1.1	1.1	0.0
0.8	1.0	1.0	0.8	0.9	0.9	0.9	1.2	0.7	0.9	0.0
0.0	1.3	1.0	1.1	1.1	1.1	0.9	1.4	1.0	1.1	0.0
1.2	0.0	1.2	1.3	1.2	1.2	1.2	1.5	1.0	1.2	0.0
2.0	1.8	1.8	1.9	1.9	1.9	1.8	1.8	2.0	1.9	0.0
0.8	0.9	0.9	0.8	0.7	0.8	0.8	1.0	0.6	0.8	0.0
0.8	0.9	1.0	0.8	0.9	0.9	0.9	1.1	0.7	0.9	0.0
1.5	1.6	1.4	1.7	1.4	1.5	1.4	1.5	1.6	1.5	0.0
1.1	1.1	1.1	1.1	1.1	1.1	1.0	1.2	1.1	1.1	0.0
0.9	1.0	1.3	1.1	1.1	1.1	1.0	1.3	1.0	1.1	0.0
1.5	1.6	1.4	1.8	1.3	1.5	1.2	1.7	1.8	1.5	0.0
1.3	1.2	1.1	1.3	1.3	1.2	1.1	1.3	1.4	1.2	0.0
2.1	1.6	2.0	2.3	2.2	2.0	2.0	2.0	2.2	2.1	0.0
1.8	1.8	1.7	2.1	1.8	1.8	1.8	1.9	1.9	1.9	0.0
0.9	0.9	0.9	0.8	0.9	0.9	1.0	1.1	0.7	0.9	0.0
1.3	1.3	1.4	1.4	1.4	1.4	1.4	1.6	1.0	1.4	0.0

329	Q9NZZ3	CHMP5 Charged multivesicular body protein 5	CHMP5	K.APPPSLTDC*IGTVDSR.A
330	Q9UHD8	SEPT9 Septin-9	9-Sep	K.LTVIDTPGFGDHINNENC*WQPIMK.F
331	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.IC*PVETLVEEAIQCAEK.I
332	P25398	RPS12 40S ribosomal protein S12	RPS12	R.QAHLC*VLASNCDEPMYVK.L
333	Q9NX24	NHP2 H/ACA ribonucleoprotein complex subunit 2	NHP2	K.ADPDGPEAQAEAC*SGER.T
334	P31939	ATIC Bifunctional purine biosynthesis protein PURH	ATIC	R.VVAC*NLYPFVK.T
335	Q04917	YWHAH 14-3-3 protein eta	YWHAH	K.NC*NDFQYESK.V
336	O95295	SNAPIN SNARE-associated protein Snapin	SNAPIN	R.EQIDNLATELC*R.I
337	O15355	PPM1G Protein phosphatase 1G	PPM1G	R.GTEAGQVGEPGIPTGEAGPSC*SSASDK.L
338	P35250	RFC2 Replication factor C subunit 2	RFC2	K.VC*DEPHPLLVK.E
339	Q9NVS2	MRPS18A 28S ribosomal protein S18a, mitochondrial	MRPS18A	R.DNVC*YSR.T
340	Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	R.AITIAGIPQSIIEC*VK.Q
341	P07737	PFN1 Profilin-1	PFN1	K.C*YEMASHLR.R
342	P48047	ATP5O ATP synthase subunit O, mitochondrial	ATP5O	R.GEVPC*TVTSASPLEEATLSELK.T
343	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	K.TGQATVASGIPAGWMGLDC*GPESSKK.Y
344	P49327	FASN Fatty acid synthase	FASN	R.LGMLSPEGTC*K.A
345	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	R.ISSINSISALC*EATGADVEEVATAIGMDQR.I
346	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	K.KLVIVGDGAC*GK.T
347	Q96Q11	TRNT1 CCA tRNA nucleotidyltransferase 1, mitochondrial	TRNT1	K.YQGEHC*LLK.E
348	O15382	BCAT2 Branched-chain-amino-acid aminotransferase, mitoch	BCAT2	R.EVFGSGTAC*QVCPVHR.I
349	P22626	HNRNPA2B1 Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	K.LTDC*VVMRDPASK.R
350	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	R.QLC*DNAGFDATNILNK.L
351	O75874	IDH1 Isocitrate dehydrogenase	IDH1	K.DLAAC*IK.G
352	P62249	RPS16 40S ribosomal protein S16	RPS16	K.TATAVAHC*K.R
353	O00233	PSMD9 26S proteasome non-ATPase regulatory subunit 9	PSMD9	K.GIGMNEPLVDC*EGYPR.S
354	Q15370	TCEB2 Transcription elongation factor B polypeptide 2	TCEB2	R.ADDTFEALC*IEPFSSPPELPDVMKPQDSGSSANEQAVQ.-
355	Q9NP73	ALG13 UDP-N-acetylglucosamine transferase subunit ALG13	ALG13	K.ADLVISHAGAGSC*LETLEK.G
356	Q86YH6	PDSS2 Decaprenyl-diphosphate synthase subunit 2	PDSS2	R.C*LLSDELSNIAMQVR.K
357	P61158	ACTR3 Actin-related protein 3	ACTR3	R.YSYVC*PDLVK.E
358	P49327	FASN Fatty acid synthase	FASN	R.AAPLDSIHSLAAYYIDC*IR.Q
359	P53396	ACLY ATP-citrate synthase	ACLY	K.FIC*TTSAIQNR.F
360	P00390	GSR Glutathione reductase, mitochondrial	GSR	K.LGGTC*VNVGCVPK.K
361	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.NMITGTAPLDGC*ILVVAANDGPMPQTR.E
362	P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	K.QPAIMPGQSYGLEDGSC*SYKDFSESR.N
363	O00204	SULT2B1 Sulfotransferase family cytosolic 2B member 1	SULT2B1	R.APWC*ETIVGAFSLPDQYSPR.L
364	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	R.AVASQLDC*NFLK.V
365	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	K.LQGATC*NNNK.L
366	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.QGEYGLASIC*NGGGGASAMLIQK.L
367	P60174	TPI1 Triosephosphate isomerase	TPI1	K.IAVAAQNC*YK.V

1.0	1.1	1.1	1.1	1.0	1.1	1.1	1.1	1.1	1.1	0.0
1.6	1.7	1.6	1.7	1.5	1.6	1.6	1.5	1.8	1.7	0.0
0.8	0.9	0.9	0.9	0.8	0.8	0.8	0.9	0.8	0.9	0.0
0.6	0.6	0.6	0.7	0.7	0.6	0.7	0.6	0.7	0.7	0.0
0.9	1.0	1.0	1.3	0.0	1.1	1.2	1.1	1.0	1.1	0.0
0.8	0.8	1.0	0.7	0.0	0.8	0.8	1.0	0.8	0.9	0.0
0.9	1.1	0.9	0.9	1.0	0.9	0.8	1.4	0.8	1.0	0.0
0.0	1.4	1.0	1.2	1.1	1.2	1.2	1.3	1.1	1.2	0.0
1.2	1.1	1.2	1.3	1.2	1.2	1.1	1.1	1.4	1.2	0.0
2.2	2.4	2.3	2.9	2.4	2.4	2.2	2.4	2.8	2.5	0.0
1.6	1.1	0.0	1.4	1.2	1.3	1.3	1.3	1.4	1.3	0.0
1.0	1.0	1.0	0.9	1.0	1.0	1.1	1.1	0.7	1.0	0.0
0.9	0.9	0.8	0.8	0.9	0.9	1.0	1.0	0.7	0.9	0.0
1.5	1.5	1.3	1.5	1.5	1.4	1.7	1.4	1.3	1.5	0.0
0.9	1.0	1.0	0.7	1.0	0.9	1.0	1.1	0.7	0.9	0.0
2.7	2.8	2.6	3.3	2.4	2.8	2.7	2.7	3.0	2.8	0.0
0.9	1.1	1.0	0.9	1.1	1.0	1.0	1.2	1.0	1.0	0.0
1.9	1.5	1.4	1.8	1.6	1.6	1.7	1.7	1.7	1.7	0.0
1.3	1.0	1.1	1.1	0.9	1.1	1.1	1.1	1.1	1.1	0.0
1.1	1.2	1.1	1.1	1.4	1.2	1.1	1.2	1.4	1.2	0.0
0.9	0.8	1.1	0.9	0.8	0.9	1.1	1.0	0.8	1.0	0.0
2.0	1.6	1.6	1.7	1.2	1.6	1.4	1.6	2.0	1.7	0.0
0.0	1.0	1.1	0.9	1.2	1.0	1.0	1.2	1.1	1.1	0.0
2.0	1.9	2.3	2.3	1.9	2.1	1.8	2.5	2.1	2.1	0.0
1.3	1.2	1.2	1.3	1.1	1.2	1.0	1.3	1.5	1.3	-0.1
0.0	1.2	1.1	1.4	1.1	1.2	1.3	1.2	1.3	1.3	-0.1
1.3	1.3	1.3	1.5	1.3	1.3	1.3	1.3	1.6	1.4	-0.1
0.7	1.1	1.2	1.3	1.0	1.1	1.1	1.2	1.1	1.1	-0.1
0.9	1.0	1.0	0.9	1.1	1.0	1.0	1.1	1.0	1.0	-0.1
1.1	1.1	1.0	0.0	1.2	1.1	1.4	1.0	1.1	1.2	-0.1
1.3	1.0	1.0	1.2	1.7	1.2	1.5	1.3	1.1	1.3	-0.1
0.8	0.9	0.8	0.9	0.9	0.9	0.9	0.9	1.0	0.9	-0.1
2.7	2.7	2.5	3.0	3.2	2.8	2.7	3.0	2.9	2.9	-0.1
1.1	1.0	1.0	1.1	1.1	1.1	1.0	1.1	1.3	1.1	-0.1
1.3	1.0	1.1	0.8	0.9	1.0	1.3	1.0	0.9	1.1	-0.1
1.7	1.8	1.7	1.8	1.7	1.7	1.6	1.7	2.1	1.8	-0.1
1.8	1.9	1.5	2.2	0.7	1.6	1.7	1.9	1.5	1.7	-0.1
0.0	1.7	1.2	1.5	1.3	1.4	1.3	1.6	1.6	1.5	-0.1
0.8	0.9	0.9	0.7	0.9	0.8	0.9	1.2	0.6	0.9	-0.1

368	P62191	PSMC1 26S protease regulatory subunit 4	PSMC1	K.AIC*TEAGLMALR.E
369	P22234	PAICS Multifunctional protein ADE2	PAICS	K.ITSC*IFQLLQEAGIK.T
370	P37802	TAGLN2 Transgelin-2	TAGLN2	K.DGTVLC*ELINALYPEGQAPVK.K
371	P36507	MAP2K2 Dual specificity mitogen-activated protein kinase	MAP2K2	K.LC*DFGVSGQLIDSMANSFVGTR.S
372	P25398	RPS12 40S ribosomal protein S12	RPS12	K.LVEALC*AEHQINLIK.V
373	P62753	RPS6 40S ribosomal protein S6	RPS6	K.LNISFPATGC*QK.L
374	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.DLNYC*FSGMSDHR.Y
375	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	K.VGILDVDLC*GPSIPR.M
376	P61158	ACTR3 Actin-related protein 3	ACTR3	K.LGYAGNTEPQFIIPSC*IAIK.E
377	P10644	PRKAR1A cAMP-dependent protein kinase type I-alpha regulat	PRKAR1A	R.SLREC*ELYVQK.H
378	P15880	RPS2 40S ribosomal protein S2	RPS2	R.GC*TATLGNFAK.A
379	E9PPU0	EPPK1 Epiplakin	EPPK1	R.YLC*GLGAVGGVR.L
380	Q92947	GCDH Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	K.GYGC*AGVSSVAYGLLAR.E
381	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	R.IYGFYDEC*K.R
382	P14174	MIF Macrophage migration inhibitory factor	MIF	K.LLC*GLLAER.L
383	P53602	MVD Diphosphomevalonate decarboxylase	MVD	R.DGDPLPSSLSC*K.V
384	Q99873	PRMT1 Protein arginine N-methyltransferase 1	PRMT1	K.VIGIEC*SSISDYAVK.I
385	P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	R.LIGPNC*PGVINPGECK.I
386	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	R.FSPNSSNPIIVSC*GWDK.L
387	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	R.LQEALDAEMLEDEAGGGGAGPGGAC*K.A
388	P51812	RPS6KA3 Ribosomal protein S6 kinase alpha-3	RPS6KA3	R.AENGLLMTPC*YTANFVAPEVLK.R
389	O14561	NDUFAB1 Acyl carrier protein, mitochondrial	NDUFAB1	K.LMC*PQEIVDYIADKK.D
390	P60866	RPS20 40S ribosomal protein S20	RPS20	K.TPC*GEGSK.T
391	P62195	PSMC5 26S protease regulatory subunit 8	PSMC5	K.GVC*TEAGMYALR.E
392	P27635	RPL10 60S ribosomal protein L10	RPL10	K.MLSC*AGADR.L
393	Q9BTZ2	DHRS4 Dehydrogenase/reductase SDR family member 4	DHRS4	R.VNC*LAPGLIK.T
394	Q9Y2Q5	LAMTOR2 Ragulator complex protein LAMTOR2	LAMTOR2	K.FILMDC*MEGR.V
395	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	K.LNEC*VDHTPK.L
396	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.LGVENC*YFPMFVSQSALEK.E
397	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	R.GNHEC*ASINR.I
398	Q7Z2W4	ZC3HAV1 Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	K.NSNVDSSYLESLYQSC*PR.G
399	Q14247	CTTN Src substrate cortactin	CTTN	K.HC*SQVDSVR.G
400	P09467	FBP1 Fructose-1,6-bisphosphatase 1	FBP1	R.GTGELTQLLNSLC*TAVK.A
401	Q9BXV9	C14orf142 Uncharacterized protein C14orf142	C14orf142	R.VSC*EAPGDGDPFQGLLSGVAQMK.D
402	P21964	COMT Catechol O-methyltransferase	COMT	R.YLPDTLLLEEC*GLLR.K
403	Q8IY67	RAVER1 Ribonucleoprotein PTB-binding 1	RAVER1	R.ALSAVHSPTFCQLAC*GQDGQLK.G
404	P55786	NPEPPS Puromycin-sensitive aminopeptidase	NPEPPS	R.SKDGVC*VR.V
405	P62280	RPS11 40S ribosomal protein S11	RPS11	R.DVQIGDIVTVGEC*RPLSK.T
406	P50914	RPL14 60S ribosomal protein L14	RPL14	K.C*MQLTDFILK.F
407	Q86UU0	BCL9L B-cell CLL/lymphoma 9-like protein	BCL9L	K.TGNGGAQSQHQNVNQGPTC*NVGSK.G
408	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	R.AGAIAPC*EVTVPAQNTGLGPEK.T

1.5	1.4	1.6	1.6	1.4	1.5	1.3	1.6	1.8	1.6	-0.1
1.0	0.9	0.9	0.9	1.0	0.9	1.0	1.1	0.9	1.0	-0.1
0.9	1.0	1.0	0.9	0.9	0.9	1.0	1.1	0.8	1.0	-0.1
1.1	1.0	1.0	1.1	1.2	1.1	1.2	1.2	1.1	1.1	-0.1
0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.8	0.6	0.7	-0.1
2.0	1.8	1.9	2.2	2.0	2.0	1.9	2.1	2.2	2.1	-0.1
1.3	1.2	1.2	1.3	1.3	1.2	1.2	1.4	1.3	1.3	-0.1
2.1	1.7	2.0	2.7	1.9	2.1	2.0	2.0	2.5	2.2	-0.1
0.9	1.0	1.1	0.9	1.0	1.0	0.9	1.3	1.0	1.1	-0.1
2.2	3.1	2.4	2.5	2.8	2.6	2.7	2.4	2.9	2.7	-0.1
1.8	1.7	1.6	1.7	1.7	1.7	1.6	1.8	1.9	1.8	-0.1
1.4	1.6	1.3	1.5	1.6	1.5	1.6	1.4	1.8	1.6	-0.1
2.5	3.4	2.9	3.2	3.1	3.0	2.8	2.7	3.8	3.1	-0.1
2.9	1.8	0.0	0.0	2.4	2.4	2.2	2.6	2.6	2.5	-0.1
0.9	0.9	0.9	0.8	0.9	0.9	0.9	1.1	0.8	0.9	-0.1
1.1	1.1	1.1	1.2	1.1	1.1	1.0	1.3	1.2	1.2	-0.1
1.2	1.1	1.0	1.2	1.2	1.1	1.2	1.2	1.3	1.2	-0.1
1.7	1.6	1.6	1.7	1.8	1.7	1.5	2.1	1.7	1.7	-0.1
2.8	2.3	2.6	2.8	2.4	2.6	2.3	2.3	3.4	2.7	-0.1
0.8	0.9	1.0	1.0	1.0	0.9	0.9	1.1	1.1	1.0	-0.1
0.0	1.1	1.3	1.1	1.2	1.2	1.3	1.3	1.2	1.3	-0.1
0.9	0.0	1.3	0.9	1.2	1.1	1.3	1.1	1.0	1.1	-0.1
1.4	1.4	1.3	1.4	1.4	1.4	1.4	1.5	1.5	1.5	-0.1
1.6	1.6	1.5	1.9	1.6	1.6	1.6	1.7	1.8	1.7	-0.1
2.4	2.2	2.5	2.9	2.5	2.5	2.5	2.6	2.7	2.6	-0.1
2.1	1.7	1.8	1.9	1.7	1.9	1.8	2.0	2.0	1.9	-0.1
0.0	0.9	1.3	0.8	0.0	1.0	1.2	1.0	1.0	1.1	-0.1
1.0	1.3	1.0	1.0	1.0	1.1	1.4	1.1	0.9	1.1	-0.1
0.0	1.3	1.3	1.8	1.8	1.5	1.6	1.7	1.7	1.6	-0.1
2.2	2.0	2.2	2.4	2.2	2.2	2.2	2.2	2.5	2.3	-0.1
1.2	1.3	1.6	1.9	1.7	1.5	1.2	1.9	1.8	1.6	-0.1
1.1	0.9	1.1	1.1	1.0	1.0	0.8	1.6	1.0	1.1	-0.1
0.8	0.9	0.8	0.8	0.8	0.8	1.0	1.1	0.7	0.9	-0.1
0.0	1.2	1.1	1.1	0.8	1.0	0.8	1.7	1.0	1.2	-0.1
0.8	0.9	0.8	0.7	0.8	0.8	1.0	1.0	0.7	0.9	-0.1
1.0	0.0	0.9	1.1	0.9	1.0	0.7	1.0	1.6	1.1	-0.1
1.2	0.9	1.2	1.1	1.0	1.1	1.2	1.2	1.2	1.2	-0.1
2.9	2.5	2.5	3.1	2.7	2.7	2.8	2.7	3.1	2.8	-0.1
2.5	2.3	2.2	2.5	2.4	2.4	2.4	2.4	2.8	2.5	-0.1
1.0	1.6	0.0	0.0	1.6	1.4	1.1	1.7	1.8	1.5	-0.1
1.7	1.6	1.7	2.0	1.8	1.8	1.8	1.9	1.9	1.9	-0.1

409	P04632	CAPNS1 Calpain small subunit 1	CAPNS1	R.YSDESGNMDFDNFISC*LVR.L
410	P62633	CNBP Cellular nucleic acid-binding protein	CNBP	R.C*GESGHLAR.E
411	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	K.ATC*IGNNSAAAVSMLK.Q
412	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	R.YVDIAIPC*NNK.G
413	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.SIC*TTVLELLDK.Y
414	P50395	GDI2 Rab GDP dissociation inhibitor beta	GDI2	R.TDDYLDQPC*YETINR.I
415	P62633	CNBP Cellular nucleic acid-binding protein	CNBP	R.GFQFVSSSLPDIC*YR.C
416	Q01813	PFKP 6-phosphofructokinase type C	PFKP	R.NESC*SENYTTDFIYQLYSEEGK.G
417	P18085	ARF4 ADP-ribosylation factor 4	ARF4	K.NIC*FTVWDVGGQDR.I
418	P36578	RPL4 60S ribosomal protein L4	RPL4	R.SGQGAFGNMC*R.G
419	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	R.AVHQC*DR.G
420	O14976	GAK Cyclin-G-associated kinase	GAK	R.AIIQEVC*FMK.K
421	P82912	MRPS11 28S ribosomal protein S11, mitochondrial	MRPS11	K.ASHNNTQIQVVSASNEPLAFASC*GTEGFR.N
422	P10768	ESD S-formylglutathione hydrolase	ESD	K.C*FGGLQK.V
423	P49790	NUP153 Nuclear pore complex protein Nup153	NUP153	K.CVACETPKPGTC*VK.R
424	P51570	GALK1 Galactokinase	GALK1	R.RQC*EEVAR.A
425	Q9UHX1	PUF60 Poly(U)-binding-splicing factor PUF60	PUF60	R.ALAIMC*R.V
426	P35125	USP6 Ubiquitin carboxyl-terminal hydrolase 6	USP6	K.SGTSC*PSSK.N
427	P40925	MDH1 Malate dehydrogenase, cytoplasmic	MDH1	K.AIC*DHVR.D
428	Reverse_Q9H5V8	CDCP1 CUB domain-containing protein 1	CDCP1	R.SELCVFC*GPVFKR.S
429	Q9Y5M8	SRPRB Signal recognition particle receptor subunit beta	SRPRB	K.NTPSFLIAC*NK.Q
430	P37837	TALDO1 Transaldolase	TALDO1	K.ALAGC*DFLTISPK.L
431	P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	R.VFNVFC*LYGNVEK.V
432	Q9Y3D0	FAM96B Mitotic spindle-associated MMXD complex subunit MI	FAM96B	R.VAAALENTHLLEVVNQC*LSAR.S
433	P28331	NDUFS1 NADH-ubiquinone oxidoreductase 75 kDa subunit, mit	NDUFS1	K.VVAAC*AMPVMK.G
434	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	K.LEVDAIVNAANSSLLGGGGVDGC*IHR.A
435	Q9H0C8	ILKAP Integrin-linked kinase-associated serine/threonine	ILKAP	R.C*GVTSVPDIR.R
436	P62633	CNBP Cellular nucleic acid-binding protein	CNBP	R.DC*DHADEQK.C
437	P35270	SPR Sepiapterin reductase	SPR	R.AVC*LLTGASR.G
438	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.GANDFMC*DEMER.S
439	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.NMITGTSQADC*AVLIVAAGVGEFEAGISK.N
440	P55769	NHP2L1 NHP2-like protein 1	NHP2L1	K.KLLDLVQQSC*NYK.Q
441	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	R.ADHQPLTEASYVNLPTIALC*NTDSPLR.Y
442	Q07020	RPL18 60S ribosomal protein L18	RPL18	K.GC*GTVLLSGPR.K
443	P62826	RAN GTP-binding nuclear protein Ran	RAN	R.VC*ENIPIVLCGNK.V
444	P00492	HPRT1 Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	K.SYC*NDQSTGDIK.V
445	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	K.LNEDMAC*SVAGITSDANVLTNELR.L
446	P26599	PTBP1 Polypyrimidine tract-binding protein 1	PTBP1	K.LSLDGQNIYNAC*CTLR.I
447	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	K.LWNTLGVC*K.Y
448	E9PPU0	EPPK1 Epiplakin	EPPK1	R.LLDAQLATGGLVC*PAR.R

0.9	1.0	0.9	0.9	0.9	0.9	1.2	1.1	0.8	1.0	-0.1
1.1	1.2	1.4	1.4	1.4	1.3	1.4	1.4	1.4	1.4	-0.1
0.8	0.8	0.9	0.9	0.9	0.9	1.0	1.2	0.9	1.0	-0.1
1.4	1.2	1.4	1.5	1.3	1.3	1.4	1.5	1.6	1.5	-0.1
0.8	1.0	1.0	0.8	0.8	0.9	0.9	1.3	0.8	1.0	-0.1
0.9	1.0	1.0	0.8	1.0	0.9	0.9	1.4	0.8	1.1	-0.1
0.0	0.7	0.8	0.7	0.7	0.7	0.9	0.7	0.9	0.8	-0.1
2.7	2.3	2.3	2.9	2.8	2.6	2.6	2.6	2.9	2.7	-0.1
1.4	1.2	1.3	1.5	1.5	1.4	1.7	1.6	1.2	1.5	-0.1
1.9	2.1	2.2	2.6	2.5	2.3	2.2	2.3	2.8	2.4	-0.1
2.0	1.8	1.7	2.2	1.7	1.9	1.9	2.0	2.2	2.0	-0.1
0.0	1.5	1.4	1.5	1.3	1.4	1.4	1.4	1.9	1.6	-0.1
2.0	1.3	1.8	2.2	1.5	1.8	1.9	1.8	2.1	1.9	-0.1
0.0	0.9	1.0	0.8	0.9	0.9	1.0	1.3	0.7	1.0	-0.1
1.2	1.0	0.0	1.4	1.2	1.2	0.8	1.7	1.5	1.3	-0.1
1.7	0.0	1.4	1.6	1.3	1.5	1.8	1.4	1.8	1.7	-0.1
0.8	1.1	0.8	0.8	0.8	0.9	0.9	1.3	0.8	1.0	-0.1
1.5	1.5	1.9	1.8	1.6	1.7	1.7	1.7	2.0	1.8	-0.1
0.9	1.1	1.0	0.8	1.0	0.9	1.3	1.2	0.7	1.1	-0.1
0.0	2.3	2.2	3.3	0.0	2.6	2.2	3.6	2.4	2.7	-0.1
1.9	1.4	2.2	2.4	3.3	2.3	2.9	2.1	2.3	2.4	-0.1
0.0	1.0	0.0	0.9	1.2	1.0	1.2	1.4	0.8	1.2	-0.1
0.0	0.0	1.0	0.8	1.0	0.9	0.9	1.5	0.8	1.0	-0.1
0.7	0.8	0.6	0.6	0.7	0.7	0.9	0.8	0.8	0.8	-0.1
2.6	2.2	2.3	0.0	0.0	2.4	2.1	2.6	2.9	2.5	-0.2
1.1	1.0	1.0	1.0	1.2	1.1	1.2	1.2	1.2	1.2	-0.2
1.4	1.2	1.6	2.1	1.5	1.5	1.2	2.4	1.5	1.7	-0.2
0.0	0.7	0.8	0.9	0.0	0.8	0.8	1.0	1.0	0.9	-0.2
0.9	1.1	1.0	1.0	0.9	1.0	1.3	1.2	1.0	1.2	-0.2
2.8	2.0	2.0	2.8	2.8	2.5	3.1	2.5	2.2	2.6	-0.2
1.3	1.4	1.4	1.4	1.3	1.3	1.5	1.6	1.4	1.5	-0.2
1.3	1.3	1.2	1.3	1.3	1.3	1.4	1.4	1.5	1.4	-0.2
1.4	1.3	1.5	1.7	1.3	1.4	1.5	1.6	1.6	1.6	-0.2
1.9	1.7	1.8	2.0	2.0	1.9	2.1	2.0	2.0	2.0	-0.2
1.0	1.0	1.2	1.0	1.1	1.1	1.2	1.3	1.2	1.2	-0.2
1.0	1.1	0.9	1.0	1.0	1.0	1.5	1.0	1.1	1.2	-0.2
0.7	0.9	0.9	1.0	0.8	0.9	1.0	1.2	0.8	1.0	-0.2
1.0	0.7	1.2	1.0	1.1	1.0	1.2	0.9	1.4	1.2	-0.2
2.9	2.1	2.7	2.8	2.6	2.6	2.7	2.5	3.2	2.8	-0.2
2.5	2.1	2.4	2.2	2.3	2.3	2.2	2.8	2.4	2.5	-0.2

449	P63220	RPS21 40S ribosomal protein S21	RPS21	K.TYAIC*GAIR.R
450	P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	R.TIYAGNALC*TVK.C
451	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	R.QAVLGAGLPISTPC*TTINK.V
452	Q15054	POLD3 DNA polymerase delta subunit 3	POLD3	K.FSAIQC*AAAVPR.A
453	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	R.LDFVC*SFLQK.N
454	O43795	MYO1B Unconventional myosin-Ib	MYO1B	K.LVMSYVAAVC*GK.G
455	Q9Y6D5	ARFGEF2 Brefeldin A-inhibited guanine nucleotide-exchange	ARFGEF2	K.ANFIEADKYFLPFELAC*QSK.S
456	Q13418	ILK Integrin-linked protein kinase	ILK	K.FSFQC*PGR.M
457	O14545	TRAFD1 TRAF-type zinc finger domain-containing protein 1	TRAFD1	R.AVC*EADQSHGGPR.S
458	Q9H7X7	RABL5 Rab-like protein 5	RABL5	K.ILFVGPC*ESGK.T
459	P31949	S100A11 Protein S100-A11	S100A11	K.ISSPTETERC*IESLIAVFQK.Y
460	O75348	ATP6V1G1 V-type proton ATPase subunit G 1	ATP6V1G1	R.GSC*STEVEKETQEK.M
461	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	R.YNFFTGC*PK.A
462	P62266	RPS23 40S ribosomal protein S23	RPS23	K.ITAFVPNDGC*LNFIEENDEVLVAGFGR.K
463	Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.AVTNHSVYC*STK.G
464	O15075	DCLK1 Serine/threonine-protein kinase DCLK1	DCLK1	R.YQDDFLLDESEC*R.V
465	Q7L2J0	MEPCE 7SK snRNA methylphosphate capping enzyme	MEPCE	R.C*APSAGSPAAAVGR.E
466	Q9Y508	RNF114 RING finger protein 114	RNF114	K.SVVC*PICASMPWGDPNYR.S
467	Q96FJ2	DYNLL2 Dynein light chain 2, cytoplasmic	DYNLL2	K.NADMSEDMQQDAVDC*ATQAMEK.Y
468	P49327	FASN Fatty acid synthase	FASN	K.AFDTAGNGYC*R.S
469	O95757	HSPA4L Heat shock 70 kDa protein 4L	HSPA4L	R.GC*ALQCAILSPAFK.V
470	P51858	HDGF Hepatoma-derived growth factor	HDGF	K.C*GDLVFAK.M
471	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	K.C*EFQDAYVLLSEK.K
472	Q8TCU6	PREX1 Phosphatidylinositol 3,4,5-trisphosphate-dependent	PREX1	R.LC*VLNEILGTER.D
473	Q9BRA2	TXNDC17 Thioredoxin domain-containing protein 17	TXNDC17	K.DAGGKSWC*PDCVQAEPVVR.E
474	O95747	OXSR1 Serine/threonine-protein kinase OSR1	OXSR1	K.TFVGTPC*WMAPEVMEQVR.G
475	Q9BV86	NTMT1 N-terminal Xaa-Pro-Lys N-methyltransferase 1	NTMT1	R.IIC*SAGLSLLAEER.Q
476	P49327	FASN Fatty acid synthase	FASN	K.FC*FTPHTEEGCLSER.A
477	P07384	CAPN1 Calpain-1 catalytic subunit	CAPN1	R.LEIC*NLTPDALK.S
478	P28676	GCA Grancalcin	GCA	R.C*LTQSGINGTYSPFSLETCR.I
479	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.AYHEQLSVAEITNAC*FEPANQMVK.C
480	P36578	RPL4 60S ribosomal protein L4	RPL4	R.YAIC*SALAASALPALVMSK.G
481	B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	R.TAPGMGDQSGC*YR.C
482	P16455	MGMT Methylated-DNA--protein-cysteine methyltransferase	MGMT	R.VVC*SSGAVGNYSGGLAVK.E
483	P25398	RPS12 40S ribosomal protein S12	RPS12	K.VVGC*SCVVVK.D
484	Q15813	TBCE Tubulin-specific chaperone E	TBCE	R.NCAVSC*AGEK.G
485	Q12849	GRSF1 G-rich sequence factor 1	GRSF1	R.YIELFLNSC*PK.G
486	B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	K.IFVGNVSAAC*TSQELR.S
487	P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	K.YLEC*SALTQR.G
488	Q53H96	PYCRL Pyrroline-5-carboxylate reductase 3	PYCRL	R.SDVC*TPGGTTIYGLHALEQGGLR.A

1.2	1.7	1.2	1.4	1.5	1.4	1.6	1.6	1.5	1.6	-0.2
1.9	2.1	2.3	2.5	2.0	2.2	2.1	2.3	2.6	2.3	-0.2
1.3	1.4	1.4	1.4	1.4	1.4	1.4	1.8	1.5	1.6	-0.2
0.0	1.9	1.4	1.9	1.7	1.7	1.7	1.3	2.7	1.9	-0.2
1.2	1.1	1.0	1.1	1.1	1.1	0.9	1.0	1.8	1.3	-0.2
1.4	1.1	1.1	1.2	1.2	1.2	1.3	1.4	1.4	1.4	-0.2
0.0	0.0	1.7	1.6	1.6	1.6	1.3	2.3	1.8	1.8	-0.2
1.5	1.3	1.5	1.5	1.6	1.5	1.5	1.6	1.8	1.7	-0.2
1.2	1.2	1.3	1.5	1.6	1.3	1.4	1.5	1.6	1.5	-0.2
1.8	0.0	1.4	1.7	1.6	1.6	1.7	2.1	1.6	1.8	-0.2
0.6	1.0	0.9	0.9	0.8	0.8	1.3	1.1	0.7	1.0	-0.2
1.0	0.0	0.9	1.0	0.0	1.0	1.1	1.3	1.2	1.2	-0.2
2.2	2.0	2.1	2.6	2.1	2.2	2.3	2.3	2.6	2.4	-0.2
0.0	2.0	1.9	2.2	1.2	1.8	2.5	1.2	2.5	2.0	-0.2
1.3	1.5	1.3	1.2	1.1	1.3	1.4	1.6	1.5	1.5	-0.2
1.3	1.2	1.3	1.4	1.3	1.3	1.3	1.7	1.4	1.5	-0.2
1.2	0.0	1.1	1.1	1.0	1.1	1.4	1.3	1.4	1.3	-0.2
0.0	0.4	0.7	0.6	0.7	0.6	0.8	0.9	0.8	0.8	-0.2
0.8	0.8	1.2	0.8	0.9	0.9	1.1	1.3	1.0	1.1	-0.2
2.5	1.9	2.2	2.9	2.3	2.4	2.5	2.4	2.9	2.6	-0.2
1.6	1.7	1.5	1.5	1.7	1.6	2.1	1.4	2.1	1.8	-0.2
0.8	1.1	1.0	1.1	0.9	1.0	1.2	1.2	1.1	1.2	-0.2
1.1	1.2	1.1	1.2	1.2	1.2	1.5	1.6	1.1	1.4	-0.2
0.0	2.4	1.8	2.2	2.3	2.2	2.3	2.5	2.4	2.4	-0.2
1.2	1.1	1.1	1.2	1.2	1.1	1.3	1.4	1.5	1.4	-0.2
1.8	1.5	1.7	2.5	2.0	1.9	2.1	2.1	2.3	2.1	-0.2
1.3	1.2	1.1	1.2	1.1	1.2	1.4	1.5	1.4	1.4	-0.2
0.7	1.0	0.9	0.9	0.9	0.9	1.0	1.2	1.2	1.1	-0.3
1.9	1.7	1.9	2.4	1.5	1.9	1.9	2.3	2.1	2.1	-0.3
0.9	1.0	0.8	1.0	0.9	0.9	1.5	1.3	0.7	1.2	-0.3
3.3	3.0	3.1	3.5	3.3	3.2	3.2	3.5	3.9	3.5	-0.3
0.0	2.9	2.7	3.1	3.5	3.0	2.8	3.3	3.9	3.3	-0.3
0.0	0.8	0.8	1.2	0.0	0.9	1.0	1.4	1.1	1.2	-0.3
1.7	1.6	1.4	1.6	1.7	1.6	1.7	2.0	1.9	1.9	-0.3
0.0	0.6	0.7	0.7	0.7	0.7	0.8	1.3	0.8	1.0	-0.3
1.3	1.1	1.5	1.1	1.8	1.4	2.5	1.3	1.3	1.7	-0.3
1.1	0.0	0.9	1.0	0.0	1.0	0.8	1.2	1.9	1.3	-0.3
0.0	1.8	2.0	2.0	1.8	1.9	2.2	2.2	2.2	2.2	-0.3
0.8	1.3	1.0	0.9	0.9	1.0	1.6	1.4	0.9	1.3	-0.3
1.6	1.6	1.7	1.8	1.7	1.7	2.0	2.2	1.8	2.0	-0.3

489	P49327	FASN Fatty acid synthase	FASN	R.LLSAAC*R.L
490	O95671	ASMTL N-acetylserotonin O-methyltransferase-like protein	ASMTL	K.LTAC*QVATAFNLSR.F
491	P49327	FASN Fatty acid synthase	FASN	K.AC*LDTAVENMPSLK.M
492	P51153	RAB13 Ras-related protein Rab-13	RAB13	R.LLLGNKC*DMEAK.R
493	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	R.LC*ALRPDDSSSAR.T
494	P08559	PDHA1 Pyruvate dehydrogenase E1 component subunit alpha,	PDHA1	R.FAAAYC*R.S
495	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	R.SVC*TEAGMFAIR.A
496	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	K.GC*LLYGPPGTGK.T
497	P62910	RPL32 60S ribosomal protein L32	RPL32	K.SYC*AEIAHNVSSK.N
498	P62714	PPP2CB Serine/threonine-protein phosphatase 2A catalytic	PPP2CB	R.NVVTIFSAPNYC*YR.C
499	P60709	ACTB Actin, cytoplasmic 1	ACTB	K.EKLC*YVALDFEQEMATAASSSSLEK.S
500	P49327	FASN Fatty acid synthase	FASN	K.SFYGSTLFLC*R.R
501	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.FFSDC*K.I
502	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	K.QEPLGSDSEGVNC*LAYDEAIMAQQDR.I
503	P31749	AKT1 RAC-alpha serine/threonine-protein kinase	AKT1	K.TFC*GTPEYLAPEVLEDNDYGR.A
504	Q9Y676	MRPS18B 28S ribosomal protein S18b, mitochondrial	MRPS18B	K.VVGNPC*PICR.D
505	P27448	MARK3 MAP/microtubule affinity-regulating kinase 3	MARK3	K.LDTFC*GSPPYAAPELFQGK.K
506	P36578	RPL4 60S ribosomal protein L4	RPL4	R.FC*IWTESAFR.K
507	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	R.MLSAVSQQVQC*IQEALR.E
508	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.DLAGC*IHGLSNVK.L
509	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	R.LFC*VGFTK.K
510	P26440	IVD Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	R.GSNTC*ELIFEDCKIPAANILGHENK.G
511	E9PPU0	EPPK1 Epiplakin	EPPK1	R.YLQGTGC*IAGLLLPGSQER.L
512	Q9NRF9	POLE3 DNA polymerase epsilon subunit 3	POLE3	R.AASVFVLYATSC*ANNFAMK.G
513	P11498	PC Pyruvate carboxylase, mitochondrial	PC	R.FLYEC*PWR.R
514	P62701	RPS4X 40S ribosomal protein S4, X isoform	RPS4X	K.FDTGNLC*MVTGGANLGR.I
515	Q7L8W6	ATPBD4 ATP-binding domain-containing protein 4	ATPBD4	K.C*EGDEVEDLYELLK.L
516	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.VC*VETVESGAMTK.D
517	P49327	FASN Fatty acid synthase	FASN	R.WVC*SSLR.H
518	P24468	NR2F2 COUP transcription factor 2	NR2F2	R.FGSQC*MQPNNIMGIENICELAAR.M
519	P07437	TUBB Tubulin beta chain	TUBB	K.VSDTVVEPYNATLSVHQLVENTDETYC*IDNEALYDICFR.T
520	P49327	FASN Fatty acid synthase	FASN	R.DPETLVGYSMVGC*QR.A
521	Q96BF6	NACC2 Nucleus accumbens-associated protein 2	NACC2	R.NTLANSC*GTGIR.S
522	P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	R.LGGEVSC*LVAGTK.C
523	P62244	RPS15A 40S ribosomal protein S15a	RPS15A	K.C*GVISPR.F
524	P43897	TSFM Elongation factor Ts, mitochondrial	TSFM	R.FEC*GEGEEAAETE.-
525	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	K.IC*GDIHGQYYDLLR.L
526	O43290	SART1 U4/U6.U5 tri-snRNP-associated protein 1	SART1	K.SLPSAVYC*IEDK.M
527	Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	K.IVSLPEC*FNSPYGAK.Y
528	P40429	RPL13A 60S ribosomal protein L13a	RPL13A	R.C*EGINISGNFYR.N

2.6	0.0	2.5	2.6	2.3	2.5	2.6	2.7	3.1	2.8	-0.3
1.1	0.9	1.0	1.0	1.0	1.0	1.4	1.4	1.3	1.3	-0.3
0.8	0.9	0.8	1.2	0.8	0.9	1.2	1.3	1.1	1.2	-0.3
1.4	0.0	1.4	1.6	0.0	1.4	1.8	2.0	1.4	1.7	-0.3
2.0	1.5	1.8	2.0	1.9	1.8	2.1	2.1	2.3	2.2	-0.3
0.0	1.7	2.2	2.4	0.0	2.1	2.5	2.7	2.1	2.4	-0.3
0.0	1.5	2.0	2.3	2.1	2.0	2.4	2.2	2.2	2.3	-0.3
0.0	1.8	0.7	0.0	1.7	1.4	1.9	1.4	2.0	1.7	-0.3
1.6	1.7	1.7	1.7	1.8	1.7	1.9	1.9	2.4	2.0	-0.3
2.3	1.8	2.2	2.0	1.9	2.0	2.1	2.4	2.7	2.4	-0.4
2.2	2.1	2.2	2.4	2.1	2.2	2.5	2.4	2.7	2.6	-0.4
1.1	1.1	1.3	1.7	2.0	1.5	1.8	1.9	1.8	1.8	-0.4
1.4	1.2	1.5	1.3	1.3	1.3	1.6	1.8	1.8	1.7	-0.4
1.1	1.1	1.2	1.1	1.1	1.1	1.1	1.9	1.6	1.5	-0.4
3.6	2.9	2.9	3.2	2.9	3.1	2.8	2.8	4.9	3.5	-0.4
0.9	0.0	0.5	0.0	0.5	0.6	1.0	1.4	0.7	1.0	-0.4
1.5	1.6	1.6	3.1	1.7	1.9	2.1	2.1	2.6	2.3	-0.4
0.0	2.4	1.8	2.7	0.0	2.3	2.0	3.8	2.4	2.7	-0.4
2.1	2.0	1.8	2.3	1.6	2.0	2.1	2.6	2.4	2.4	-0.4
1.5	1.4	1.5	1.7	1.5	1.5	2.0	2.0	1.7	1.9	-0.4
1.6	1.6	1.7	1.7	1.1	1.5	1.9	2.0	2.0	2.0	-0.4
2.2	2.1	2.2	2.5	2.0	2.2	2.1	2.8	3.1	2.6	-0.4
2.1	2.4	0.0	0.0	1.7	2.1	2.7	2.6	2.3	2.5	-0.5
0.9	0.9	1.0	1.1	0.9	1.0	1.3	1.6	1.5	1.4	-0.5
1.5	1.5	1.4	1.4	1.6	1.5	2.1	1.4	2.2	1.9	-0.5
2.0	1.7	2.1	2.2	1.7	1.9	2.2	2.4	2.4	2.4	-0.5
0.0	0.0	1.4	2.0	1.7	1.7	1.5	2.3	2.7	2.2	-0.5
1.4	1.4	1.4	2.0	1.5	1.5	1.8	2.1	2.1	2.0	-0.5
1.5	1.2	1.5	1.4	1.5	1.4	1.9	1.8	2.1	1.9	-0.5
2.2	2.1	2.2	1.7	1.9	2.0	2.2	2.5	2.9	2.5	-0.5
2.7	2.7	2.4	2.4	2.7	2.6	3.4	2.6	3.2	3.1	-0.5
1.8	1.8	1.6	2.0	1.8	1.8	2.1	2.2	2.7	2.3	-0.5
1.3	1.6	0.7	0.0	1.4	1.2	1.5	1.8	2.0	1.8	-0.5
2.3	1.9	2.2	2.4	2.0	2.2	2.5	2.6	3.1	2.7	-0.5
1.4	1.7	1.7	1.9	1.5	1.6	2.4	1.8	2.2	2.2	-0.5
0.8	0.0	1.2	1.3	1.3	1.1	1.3	1.5	2.3	1.7	-0.5
2.8	0.0	3.1	3.4	2.4	2.9	3.4	3.6	3.5	3.5	-0.6
0.0	0.0	0.7	0.6	0.7	0.6	1.2	1.3	1.2	1.2	-0.6
1.5	0.0	1.4	1.3	1.5	1.4	1.8	2.4	1.9	2.0	-0.6
1.5	0.0	0.9	1.0	0.0	1.1	1.7	1.6	1.8	1.7	-0.6

529	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.SSGGFVWAC*K.N
530	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	R.DKMC*SMVK.K
531	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	K.AEMDAAIASC*K.R
532	P07741	APRT Adenine phosphoribosyltransferase	APRT	R.VVVVDDLLATGGTMNAAC*ELLGR.L
533	P49327	FASN Fatty acid synthase	FASN	R.DGLLENQTPEFFQDVC*KPK.Y
534	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	K.SGDAAIVEMVPGKPMC*VESFSQYPPLGR.F
535	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	K.ERVC*NLIDSGTK.E
536	P16278	GLB1 Beta-galactosidase	GLB1	K.TVGAALDILC*PSGPIK.S
537	Q96HY7	DHTKD1 Probable 2-oxoglutarate dehydrogenase E1 component	DHTKD1	R.VEELC*PFPLDSLQQEMSK.Y
538	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	K.TFTDC*FNCLPIAAIVDEK.I
539	Q02543	RPL18A 60S ribosomal protein L18a	RPL18A	R.DLTTAGAVTQC*YR.D
540	P26440	IVD Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	K.ACDEGHC*TAK.D
541	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.PMC*VESFSDYPPLGR.F
542	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.C*ATITPDEAR.V
543	Q6P2C8	MED27 Mediator of RNA polymerase II transcription subuni	MED27	K.LFQAPC*QR.C
544	P48556	PSMD8 26S proteasome non-ATPase regulatory subunit 8	PSMD8	K.C*GEELGR.L
545	Q9Y508	RNF114 RING finger protein 114	RNF114	R.DC*GGAAQLAGPAAEADPLGR.F
546	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	R.AGGIETIANEFSDRC*TPSVISFGSK.N
547	Q9GZZ9	UBA5 Ubiquitin-like modifier-activating enzyme 5	UBA5	R.EGVC*AASLPTTMGVVAGILVQNVLK.F
548	P07384	CAPN1 Calpain-1 catalytic subunit	CAPN1	R.C*LQSGTLFR.D
549	P78406	RAE1 mRNA export factor	RAE1	K.VFTASC*DK.T
550	P13674	P4HA1 Prolyl 4-hydroxylase subunit alpha-1	P4HA1	R.RPC*TLSELE.-
551	Q01813	PFKP 6-phosphofructokinase type C	PFKP	R.LPLMEC*VQMTQDVQK.A
552	Q96CM8	ACSF2 Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	R.MVSTPIGGLSYVQGC*TK.K
553	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	K.IISNASC*TTNCLAPLAK.V
554	P07339	CTSD Cathepsin D	CTSD	K.AIGAVPLIQGEYMIPC*EK.V

1.4	1.3	1.1	1.3	1.4	1.3	1.8	1.8	2.0	1.9	-0.6
1.4	1.3	1.3	1.4	1.3	1.3	1.8	1.9	2.1	1.9	-0.6
1.7	1.6	1.6	1.9	1.5	1.6	2.2	2.0	2.5	2.3	-0.6
1.0	1.1	1.1	1.1	1.1	1.1	1.8	2.0	1.4	1.7	-0.6
1.3	1.0	1.1	1.5	1.1	1.2	1.9	1.9	1.9	1.9	-0.7
1.6	1.6	1.8	1.9	1.6	1.7	2.3	2.7	2.2	2.4	-0.7
1.5	1.4	1.4	1.7	1.3	1.5	2.2	2.0	2.3	2.2	-0.7
2.4	2.3	2.3	2.6	2.1	2.3	3.3	3.1	2.8	3.0	-0.7
1.7	1.4	1.9	0.0	1.3	1.6	1.6	2.2	3.0	2.3	-0.7
0.0	1.7	2.6	2.4	2.4	2.3	3.3	2.5	3.3	3.0	-0.7
3.8	3.5	2.4	4.0	2.1	3.2	3.3	4.2	4.3	3.9	-0.7
3.6	2.5	2.9	2.9	3.3	3.1	4.0	3.3	4.2	3.8	-0.8
1.4	1.3	1.4	1.5	1.4	1.4	1.9	2.2	2.4	2.2	-0.8
1.7	1.5	1.9	1.8	1.6	1.7	2.4	2.2	2.9	2.5	-0.8
0.0	1.8	0.0	1.7	1.6	1.7	1.9	2.3	3.4	2.5	-0.8
2.3	1.4	1.0	0.0	0.0	1.5	2.0	2.8	2.5	2.4	-0.9
1.6	1.8	1.5	1.6	1.7	1.6	2.4	2.8	2.4	2.6	-0.9
1.6	1.6	1.6	0.9	1.6	1.5	2.2	2.4	2.6	2.4	-0.9
1.4	1.3	1.3	1.3	1.4	1.3	1.9	2.7	2.2	2.3	-0.9
2.3	2.2	1.9	2.4	2.5	2.3	2.8	3.4	3.6	3.3	-1.0
0.7	0.9	1.2	2.2	1.1	1.2	1.9	2.2	2.5	2.2	-1.0
5.0	4.0	4.4	5.9	4.2	4.7	5.2	5.4	6.9	5.8	-1.1
4.1	3.5	3.4	4.0	3.7	3.7	4.5	5.1	5.0	4.8	-1.1
1.9	1.8	1.6	1.8	1.7	1.8	2.4	3.4	3.1	2.9	-1.2
5.4	4.8	4.2	5.0	5.1	4.9	6.1	5.8	7.0	6.3	-1.4
3.4	3.2	4.0	4.7	3.7	3.8	7.8	7.3	8.9	8.0	-4.2

Table 3A-8. R-values from 1 mM ATP competitive transnitrosation experiment at 500 μM CoA-SNO. A list of all identified peptides (* denotes labeled cysteine) is presented together with calculated heavy:light ratios (R-values) in pre-treated with 1 mM ATP (light, n=2), or left untreated as a control (heavy, n=5), then transnitrosated by 500 μM CoA-SNO and taken through the quantitative mass spectrometry workflow. Date were sorted by ΔR (R of control minus R of pre-treated sample) and numbered as 'Peptide #".

Peptide #	Uniprot #	Description	Symbol	Sequence
1	Q01813	PFKP 6-phosphofructokinase type C	PFKP	R.LPLMEC*VQMTQDVQK.A
2	Q92947	GCDH Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	K.GYGC*AGVSSVAYGLLAR.E
3	P21333	FLNA Filamin-A	FLNA	K.AHVVPC*FDASK.V
4	Q68CP9	ARID2 AT-rich interactive domain-containing protein 2	ARID2	R.SC*SNAAFALK.Q
5	P31749	AKT1 RAC-alpha serine/threonine-protein kinase	AKT1	K.TFC*GTPEYLAPEVLEDNDYGR.A
6	Q8TCU6	PREX1 Phosphatidylinositol 3,4,5-trisphosphate-dependent	PREX1	R.LC*VLNEILGTER.D
7	P27708	CAD CAD protein	CAD	K.VHVDC*MTSQK.L
8	P10599	TXN Thioredoxin	TXN	K.LVVVDFSATWC*GPCK.M
9	P53384	NUBP1 Cytosolic Fe-S cluster assembly factor NUBP1	NUBP1	R.LC*ASGAGATPDTAIEEIKEK.M
10	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	K.KLMSSNSTDLPLNIEC*FMNDKDVSGK.M
11	P35914	HMGCL Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	R.GYVSCALGC*PYEGK.I
12	Q13418	ILK Integrin-linked protein kinase	ILK	K.FSFQC*PGR.M
13	Q9NP61	ARFGAP3 ADP-ribosylation factor GTPase-activating protein	ARFGAP3	K.LANTC*FNEIEK.Q
14	Q01813	PFKP 6-phosphofructokinase type C	PFKP	R.NESC*SENYTTDFIYQLYSEEGK.G
15	Q9Y3A3	MOB4 MOB-like protein phocein	MOB4	R.HTLDGAAC*LLNSNK.Y
16	Q9BSD7	NTPCR Cancer-related nucleoside-triphosphatase	NTPCR	R.NADC*SSGPGQR.V
17	P15924	DSP Desmoplakin	DSP	K.YQAEC*SQFK.A
18	P04183	TK1 Thymidine kinase, cytosolic	TK1	R.YSSSFC*THDR.N
19	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	K.HLC*QQLQAEQAAAEK.R
20	P55263	ADK Adenosine kinase	ADK	R.TGC*TFPEKPDFH.-
21	P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	K.ARDC*LIPMGITSENVAER.F
22	Q9UPN9	TRIM33 E3 ubiquitin-protein ligase TRIM33	TRIM33	R.C*DPVPAANGAIR.F
23	Q5MNZ6	WDR45L WD repeat domain phosphoinositide-interacting prot	WDR45L	R.C*NYLALVGGGK.K
24	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	R.MLSAVSQQVQC*IQEALR.E
25	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	R.YVAAAFPSAC*GK.T
26	O95833	CLIC3 Chloride intracellular channel protein 3	CLIC3	K.ASEDGESVGHC*PSCQR.L
27	P12532	CKMT1B Creatine kinase U-type, mitochondrial	CKMT1B	R.LGYILTC*PSNLGTGLR.A
28	P30519	HMOX2 Heme oxygenase 2	HMOX2	K.GALEGSSC*PFR.T
29	P61289	PSME3 Proteasome activator complex subunit 3	PSME3	R.LDEC*EEAFQGTK.V
30	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.VC*NFLASQVPFPSR.L
31	Q5VV41	ARHGEF16 Rho guanine nucleotide exchange factor 16	ARHGEF16	R.LPLLMDTLC*LK.T
32	P15924	DSP Desmoplakin	DSP	K.YC*YLQNEVFGLFQK.L
33	P13674	P4HA1 Prolyl 4-hydroxylase subunit alpha-1	P4HA1	R.RPC*TLSELE.-
34	P36578	RPL4 60S ribosomal protein L4	RPL4	R.YAIC*SALAASALPALVMSK.G
35	O00244	ATOX1 Copper transport protein ATOX1	ATOX1	K.VC*IESEHSMDTLLATLK.K
36	P49321	NASP Nuclear autoantigenic sperm protein	NASP	R.KPTDGASSSNC*VTDISHLVR.K
37	Q06203	PPAT Amidophosphoribosyltransferase	PPAT	K.C*ELENCQPFVVETLHGK.I

Heavy : Light Ratio R									ΔR
500 μM CoA-SNO (control)						1 mM ATP + 500 μM CoA-SNO (sample)			Ctrl - Sample
1	2	3	4	5	average	1	2	average	
8.7	10.6	9.4	10.7	9.2	9.7	4.8	5.1	4.9	4.8
11.4	10.6	9.4	10.7	9.2	10.3	5.6	5.4	5.5	4.7
9.5	0.0	4.7	4.1	4.7	5.8	1.3	1.3	1.3	4.4
5.0	5.3	4.9	0.0	4.5	4.9	1.1	1.8	1.5	3.5
8.8	11.6	14.6	11.7	8.0	10.9	6.6	8.7	7.7	3.3
9.0	8.3	4.9	8.1	9.8	8.0	4.6	5.8	5.2	2.8
5.7	4.4	7.0	2.1	0.0	4.8	2.2	2.2	2.2	2.6
6.0	7.7	3.3	5.2	4.4	5.3	2.3	3.8	3.0	2.3
2.4	3.9	0.0	0.0	3.4	3.2	1.0	1.0	1.0	2.3
6.7	4.0	4.1	4.1	3.8	4.5	3.3	1.5	2.4	2.1
2.5	4.4	6.3	0.0	0.0	4.4	2.9	2.1	2.5	1.9
4.5	3.6	2.8	0.0	2.6	3.4	1.6	1.7	1.6	1.8
0.0	0.0	4.1	3.2	1.2	2.9	1.4	0.8	1.1	1.8
7.2	7.8	6.5	6.4	5.9	6.8	5.2	4.9	5.1	1.7
6.5	7.6	6.4	7.7	6.0	6.9	5.2	5.4	5.3	1.6
9.0	7.9	8.3	0.0	8.2	8.3	6.9	6.7	6.8	1.6
7.4	9.9	6.7	4.6	5.1	6.7	5.4	5.3	5.4	1.4
0.0	7.9	6.4	5.4	5.2	6.2	4.3	5.6	5.0	1.3
0.0	4.1	3.7	2.8	3.9	3.6	3.0	1.9	2.4	1.2
0.0	2.1	2.6	2.3	1.8	2.2	1.0	1.1	1.1	1.2
4.7	5.0	4.4	4.5	3.6	4.4	2.7	3.9	3.3	1.2
3.9	0.0	3.2	0.0	1.0	2.7	1.8	1.5	1.6	1.1
4.5	5.0	4.6	6.3	4.7	5.0	3.3	4.6	3.9	1.1
4.6	2.5	3.3	0.0	2.2	3.2	1.2	2.9	2.1	1.1
5.6	6.3	5.3	4.2	5.6	5.4	3.5	5.3	4.4	1.0
6.3	5.3	1.8	5.4	4.6	4.7	2.8	4.6	3.7	1.0
0.0	4.3	3.2	3.8	3.5	3.7	2.5	2.9	2.7	1.0
2.6	3.1	2.4	0.0	2.4	2.6	1.7	1.7	1.7	0.9
7.4	0.0	6.0	0.0	3.6	5.7	3.9	5.6	4.8	0.9
0.0	5.9	6.6	6.8	0.0	6.4	5.0	6.1	5.5	0.9
3.2	4.8	4.2	0.0	6.5	4.7	4.2	3.3	3.7	0.9
6.0	5.5	5.3	5.5	5.8	5.6	4.9	4.5	4.7	0.9
9.9	8.2	7.5	7.2	8.3	8.2	7.9	6.8	7.3	0.9
7.5	6.4	5.5	5.7	5.8	6.2	5.3	5.4	5.3	0.9
3.9	0.0	0.0	3.6	3.0	3.5	3.6	1.6	2.6	0.9
0.0	4.8	0.0	3.5	3.7	4.0	3.3	3.0	3.2	0.8
4.7	3.9	5.1	3.5	4.7	4.4	3.7	3.4	3.6	0.8

38	Q9NZB2	FAM120A Constitutive coactivator of PPAR-gamma-like protei	FAM120A	R.VAAASGHC*GAFSGSDSSR.T
39	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	R.ISAFGYLEC*SAK.T
40	P13639	EEF2 Elongation factor 2	EEF2	K.DLEEDHAC*IPIK.K
41	Q9BRA2	TXNDC17 Thioredoxin domain-containing protein 17	TXNDC17	K.DAGGKSWC*PDCVQAEPVVR.E
42	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	R.C*MTNTPVVVR.E
43	P31153	MAT2A S-adenosylmethionine synthase isoform type-2	MAT2A	K.VAC*ETVAK.T
44	P62316	SNRPD2 Small nuclear ribonucleoprotein Sm D2	SNRPD2	K.NNTQVLINC*R.N
45	P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	R.VEQLFQVMNGILAQDSAC*SQR.A
46	P13639	EEF2 Elongation factor 2	EEF2	K.STLTDSLVC*K.A
47	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.NMITGTAPLDGC*ILVVAANDGPMPQTR.E
48	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	K.ELAPAVSVLQLFC*SSPK.A
49	P18085	ARF4 ADP-ribosylation factor 4	ARF4	K.NIC*FTVWDVGGQDR.I
50	Q96CM8	ACSF2 Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	R.MVSTPIGGLSYVQGC*TK.K
51	Q9NUU7	DDX19A ATP-dependent RNA helicase DDX19A	DDX19A	K.VLVTTNVC*AR.G
52	P83436	COG7 Conserved oligomeric Golgi complex subunit 7	COG7	K.YLSDSC*SPR.S
53	Q86Y56	HEATR2 HEAT repeat-containing protein 2	HEATR2	R.C*SLLDPFAAVR.R
54	Q00610	CLTC Clathrin heavy chain 1	CLTC	K.VIQC*FAETGQVQK.I
55	Q8NBF2	NHLRC2 NHL repeat-containing protein 2	NHLRC2	K.AILFSQPLQITDTQQGC*IAPVELR.Y
56	O14561	NDUFAB1 Acyl carrier protein, mitochondrial	NDUFAB1	K.LMC*PQEIVDYIADKK.D
57	Q8NFF5	FLAD1 FAD synthase	FLAD1	R.LHYGTDPC*TGQPFR.F
58	P45985	MAP2K4 Dual specificity mitogen-activated protein kinase	MAP2K4	K.LC*DFGISGQLVDSIAK.T
59	P07437	TUBB Tubulin beta chain	TUBB	K.TAVC*DIPPR.G
60	E9PPU0	EPPK1 Epiplakin	EPPK1	R.LLDAQLATGGLVC*PAR.R
61	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	R.QAVLGAGLPISTPC*TTINK.V
62	P53621	COPA Coatomer subunit alpha	COPA	R.TTYQALPC*LPSMYGYPNR.N
63	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	K.LEVDAIVNAANSSLLGGGGVDGC*IHR.A
64	Q9BTE3	MCMBP Mini-chromosome maintenance complex-binding protei	MCMBP	R.DASALLDPMEC*TDTAEEQR.V
65	Q96EY5	FAM125A Multivesicular body subunit 12A	FAM125A	R.GFSAISC*TVEGAPASFGK.S
66	P10599	TXN Thioredoxin	TXN	K.C*MPTFQFFK.K
67	P30042	C21orf33 ES1 protein homolog, mitochondrial	C21orf33	K.NLSTFAVDGKDC*K.V
68	P51812	RPS6KA3 Ribosomal protein S6 kinase alpha-3	RPS6KA3	R.AENGLLMTPC*YTANFVAPEVLK.R
69	P49903	SEPHS1 Selenide, water dikinase 1	SEPHS1	R.LGIGMDTC*VIPLR.H
70	O00148	DDX39A ATP-dependent RNA helicase DDX39A	DDX39A	R.AIVDC*GFEHPSEVQHECIPQAILGMDVLCQAK.S
71	P49327	FASN Fatty acid synthase	FASN	K.FC*FTPHTEEGCLSER.A
72	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	K.C*EYPAACNALETLLIHR.D
73	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.HSMNPFC*EIAVEEAVR.L
74	Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	R.AAEC*NIVVTQPR.R
75	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	R.YWLC*AATGPSIK.I
76	Q9UL15	BAG5 BAG family molecular chaperone regulator 5	BAG5	K.TELQGLIGQLDEVSLEKNPC*IR.E
77	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	R.AVHQC*DR.G

12.1	8.7	11.2	8.8	7.5	9.7	7.5	10.2	8.9	0.8
3.0	3.1	3.0	3.8	3.0	3.2	1.9	2.8	2.4	0.8
5.8	8.2	0.0	7.2	5.4	6.6	5.9	5.8	5.8	0.8
10.6	14.0	7.2	11.6	11.0	10.9	8.6	11.6	10.1	0.8
5.6	4.9	4.5	4.7	4.1	4.8	3.5	4.6	4.0	0.7
0.0	7.4	7.0	5.3	4.7	6.1	5.6	5.1	5.4	0.7
1.8	2.8	2.8	2.9	2.0	2.5	1.8	1.8	1.8	0.7
3.6	6.4	4.2	0.0	5.8	5.0	3.3	5.3	4.3	0.7
4.4	3.9	3.6	3.4	3.4	3.7	2.8	3.3	3.1	0.7
5.5	4.8	5.3	5.5	5.3	5.3	4.6	4.8	4.7	0.7
3.5	4.0	4.2	0.0	5.1	4.2	3.3	3.9	3.6	0.7
2.5	1.9	2.2	2.4	1.6	2.1	1.5	1.5	1.5	0.6
4.3	5.5	3.5	5.2	3.1	4.3	3.1	4.3	3.7	0.6
2.8	2.7	2.7	2.4	2.2	2.5	2.0	1.9	1.9	0.6
3.0	0.0	2.6	0.0	3.1	2.9	2.0	2.7	2.3	0.6
7.4	6.8	5.0	7.1	4.7	6.2	5.7	5.5	5.6	0.6
3.3	2.6	0.0	1.5	2.0	2.3	2.5	0.9	1.7	0.6
4.0	4.4	3.1	4.8	2.9	3.8	3.2	3.3	3.2	0.6
1.9	0.8	2.8	1.0	1.4	1.6	1.0	1.0	1.0	0.6
2.0	3.9	0.0	0.0	1.7	2.5	1.9	2.1	2.0	0.6
4.7	4.7	4.3	0.0	4.0	4.4	4.3	3.4	3.8	0.6
5.3	5.1	5.0	6.7	5.0	5.4	4.9	4.8	4.9	0.6
3.0	4.0	2.7	2.5	2.0	2.8	2.1	2.4	2.3	0.6
4.3	4.9	3.7	4.4	3.9	4.2	3.7	3.7	3.7	0.5
0.0	3.5	3.2	3.6	2.0	3.1	2.8	2.2	2.5	0.5
3.2	3.0	2.2	2.2	1.7	2.5	1.8	2.1	2.0	0.5
2.0	2.0	3.4	0.0	1.8	2.3	1.6	2.0	1.8	0.5
2.3	0.0	2.7	0.0	1.7	2.2	1.7	1.7	1.7	0.5
3.8	3.6	3.1	3.0	2.2	3.1	2.3	3.0	2.6	0.5
3.1	4.0	5.9	3.5	0.0	4.1	4.1	3.2	3.7	0.5
2.5	2.0	2.6	2.0	1.8	2.2	1.7	1.7	1.7	0.5
0.9	0.7	2.9	0.0	0.9	1.3	0.8	0.9	0.9	0.4
1.9	2.1	2.0	2.1	2.4	2.1	1.7	1.6	1.7	0.4
0.0	2.7	3.2	3.6	2.3	3.0	2.5	2.6	2.5	0.4
6.8	8.0	7.2	7.2	8.5	7.5	7.8	6.5	7.1	0.4
2.0	2.1	2.0	2.0	1.8	2.0	1.5	1.6	1.5	0.4
4.6	4.5	6.2	0.0	6.3	5.4	6.4	3.6	5.0	0.4
0.0	0.0	4.5	6.9	4.0	5.1	4.7	4.7	4.7	0.4
3.0	1.9	1.8	2.2	2.0	2.2	1.7	1.8	1.7	0.4
0.0	6.0	0.0	4.9	4.8	5.2	4.9	4.8	4.8	0.4

78	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	K.ERVC*NLIDSGTK.E
79	Q9Y3D0	FAM96B Mitotic spindle-associated MMXD complex subunit MI	FAM96B	R.VAAALENTHLLEVVNQC*LSAR.S
80	P22102	GART Trifunctional purine biosynthetic protein adenosin	GART	K.QVLVAPGNAGTAC*SEK.I
81	Q15019	SEPT2 Septin-2	2-Sep	R.LTVVDTPGYGDAINC*R.D
82	Q9HA64	FN3KRP Ketosamine-3-kinase	FN3KRP	R.ATGHSGGGC*ISQGR.S
83	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	K.VDENFDC*VEADDVEGK.I
84	Q86Y56	HEATR2 HEAT repeat-containing protein 2	HEATR2	R.RPPEAC*EELR.L
85	P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	R.QC*SSGLQAVASIAGGIR.N
86	P62306	SNRPF Small nuclear ribonucleoprotein F	SNRPF	R.C*NNVLYIR.G
87	Q27J81	INF2 Inverted formin-2	INF2	R.AVLLASDAQEC*TLEEVVER.L
88	Q6P2E9	EDC4 Enhancer of mRNA-decapping protein 4	EDC4	R.LC*TQLEGLQSTVTGHVER.A
89	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.QAIDDDC*NQTGQMTAGFLDWPQG TFASQVTLEGDKLK.V
90	P17858	PFKL 6-phosphofructokinase, liver type	PFKL	K.C*HDYYTTEFLYNLYSSEGK.G
91	Q92616	GCN1L1 Translational activator GCN1	GCN1L1	R.C*GLALALNK.L
92	P46734	MAP2K3 Dual specificity mitogen-activated protein kinase	MAP2K3	K.TMDAGC*KPYMAPER.I
93	Q5T9C2	FAM102A Protein FAM102A	FAM102A	K.VTIGMFLLSGDPC*FK.T
94	A6NDU8	C5orf51 UPF0600 protein C5orf51	C5orf51	R.C*PIQLNEGVSFQDLDTAK.L
95	Q9Y508	RNF114 RING finger protein 114	RNF114	R.DC*GGAAQLAGPAAEADPLGR.F
96	P09622	DLD Dihydrolipoyl dehydrogenase, mitochondrial	DLD	K.NETLGGTC*LNVGCIPSK.A
97	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitoch	MCCC2	K.AATGEEVSAEDLGGADLHC*R.K
98	Q00765	REEP5 Receptor expression-enhancing protein 5	REEP5	K.NC*MTDLLAK.L
99	P16455	MGMT Methylated-DNA--protein-cysteine methyltransferase	MGMT	R.VVC*SSGAVGNYSGGLAVK.E
100	P55769	NHP2L1 NHP2-like protein 1	NHP2L1	K.KLLDLVQQSC*NYK.Q
101	P13639	EEF2 Elongation factor 2	EEF2	R.ETVSEESNVLC*LSK.S
102	P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB2	K.AC*GDSTLTQITAGLDPVGR.I
103	P41240	CSK Tyrosine-protein kinase CSK	CSK	R.SVLGGDC*LLK.F
104	Q2TAY7	SMU1 WD40 repeat-containing protein SMU1	SMU1	K.SHVEC*AR.F
105	P45984	MAPK9 Mitogen-activated protein kinase 9	MAPK9	R.TAC*TNFMMTPYVVTR.Y
106	Q99829	CPNE1 Copine-1	CPNE1	R.NC*SSPEFSK.T
107	P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	R.LIGPNC*PGVINPGECK.I
108	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.SSGC*DVNLPGVNVK.L
109	Q12849	GRSF1 G-rich sequence factor 1	GRSF1	R.YIELFLNSC*PK.G
110	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.IC*PVETLVEEAIQCAEK.I
111	Q7L8W6	ATPBD4 ATP-binding domain-containing protein 4	ATPBD4	K.C*EGDEVEDLYELLK.L
112	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.GC*DVVVIPAGVPR.K
113	P51610	HCFC1 Host cell factor 1	HCFC1	R.AC*AAGTPAVIR.I
114	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit 2	PSMD2	R.NEC*DPALALLSDYVLHNSNTMR.L
115	Q5T0W9	FAM83B Protein FAM83B	FAM83B	R.LC*SSSDTLVSEGEENQKPK.K
116	O94760	DDAH1 N(G),N(G)-dimethylarginine dimethylaminohydrolase	DDAH1	K.SFC*SMAGPNLIAIGSSESAQK.A
117	Q8N335	GPD1L Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	R.IC*DEITGR.V

3.4	5.2	3.9	4.5	3.9	4.2	3.5	4.0	3.8	0.4
1.5	1.6	0.0	1.6	1.8	1.6	1.0	1.4	1.2	0.4
2.9	0.0	2.3	2.6	1.9	2.4	2.4	1.6	2.0	0.4
2.4	2.5	2.2	2.6	2.1	2.4	1.7	2.2	2.0	0.4
0.0	5.0	6.9	6.3	4.0	5.6	4.8	5.6	5.2	0.4
3.5	2.0	1.8	1.9	2.1	2.2	1.8	1.9	1.9	0.4
0.0	4.0	3.3	4.7	3.9	4.0	3.7	3.5	3.6	0.4
3.0	2.1	2.1	2.1	1.9	2.2	1.9	1.9	1.9	0.4
1.7	1.3	1.3	1.4	1.1	1.3	1.0	0.9	1.0	0.4
3.3	3.2	2.2	3.1	3.1	3.0	2.9	2.3	2.6	0.4
3.0	1.8	1.3	0.0	1.4	1.9	1.3	1.7	1.5	0.4
2.4	2.8	3.3	2.9	0.0	2.8	2.5	2.5	2.5	0.3
6.8	0.0	5.9	6.7	5.8	6.3	5.9	6.0	5.9	0.3
4.1	5.2	4.9	3.9	4.2	4.4	3.9	4.3	4.1	0.3
3.0	3.2	2.7	0.0	2.2	2.8	1.8	3.1	2.4	0.3
0.0	3.5	0.0	2.1	1.4	2.3	1.8	2.2	2.0	0.3
2.6	2.4	1.7	0.0	1.6	2.1	1.9	1.6	1.7	0.3
3.9	2.3	2.1	2.8	1.9	2.6	2.1	2.4	2.3	0.3
1.9	2.4	2.8	0.0	2.6	2.4	2.1	2.1	2.1	0.3
4.0	0.0	2.6	2.8	3.3	3.2	2.6	3.1	2.9	0.3
2.1	3.8	1.9	2.1	3.8	2.7	2.4	2.5	2.4	0.3
6.1	5.2	3.3	4.1	5.0	4.7	4.0	4.9	4.4	0.3
3.2	3.2	2.5	2.9	2.2	2.8	2.4	2.6	2.5	0.3
0.0	2.9	3.6	4.5	3.4	3.6	3.3	3.4	3.3	0.3
5.0	6.7	5.7	6.7	5.9	6.0	5.6	5.8	5.7	0.3
2.5	1.8	1.8	0.0	1.5	1.9	1.5	1.7	1.6	0.3
3.6	2.9	2.9	2.5	3.3	3.0	2.2	3.4	2.8	0.3
3.0	3.6	2.9	2.8	2.8	3.0	2.7	2.8	2.8	0.3
0.0	1.9	1.6	1.0	0.0	1.5	1.4	1.1	1.2	0.3
6.2	4.8	3.5	3.7	3.8	4.4	3.9	4.4	4.1	0.2
2.0	1.7	1.7	0.0	0.0	1.8	1.4	1.6	1.5	0.2
1.1	0.8	0.8	1.9	0.7	1.1	0.8	0.9	0.8	0.2
1.8	2.3	3.0	3.6	2.5	2.6	2.7	2.2	2.4	0.2
1.8	2.6	1.8	2.7	2.3	2.2	1.6	2.5	2.0	0.2
3.8	4.3	3.1	3.9	5.0	4.0	3.7	3.9	3.8	0.2
4.9	5.7	3.4	0.0	0.0	4.6	4.1	4.7	4.4	0.2
1.9	0.0	1.7	1.5	0.0	1.7	1.4	1.5	1.5	0.2
2.9	1.8	2.0	2.3	1.6	2.1	2.0	1.8	1.9	0.2
0.0	3.8	3.8	0.0	4.2	3.9	4.3	3.2	3.7	0.2
1.6	1.6	3.7	0.0	1.1	2.0	1.8	1.8	1.8	0.2

118	P46109	CRKL Crk-like protein	CRKL	K.RVPC*AYDK.T
119	P07339	CTSD Cathepsin D	CTSD	K.AIGAVPLIQGEYMIPC*EK.V
120	O95671	ASMTL N-acetylserotonin O-methyltransferase-like protein	ASMTL	K.LTAC*QVATAFNLSR.F
121	Q9UN37	VPS4A Vacuolar protein sorting-associated protein 4A	VPS4A	K.LLEPVVC*MSDMLR.S
122	Q96AT9	RPE Ribulose-phosphate 3-epimerase	RPE	K.IGPSILNSDLANLGAEC*LR.M
123	P60981	DSTN Destrin	DSTN	K.C*STPEEIK.K
124	Q9UHD8	SEPT9 Septin-9	9-Sep	R.SQEATEAAPSC*VGDMADTPR.D
125	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	K.EADQKEQFSQGSPSNC*LETSLAEIFP LGK.N
126	Q15796	SMAD2 Mothers against decapentaplegic homolog 2	SMAD2	K.AITTQNC*NTK.C
127	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.VMTIPYQPMPASSPVIC*AGGQDR.C
128	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	R.HIIEDPC*TLR.H
129	Q06210	GFPT1 Glucosamine--fructose-6-phosphate aminotransferase	GFPT1	K.C*QNALQQVVAR.Q
130	P23528	CFL1 Cofilin-1	CFL1	K.HELQANC*YEEVK.D
131	Q15813	TBCE Tubulin-specific chaperone E	TBCE	R.NCAVSC*AGEK.G
132	Q16630	CPSF6 Cleavage and polyadenylation specificity factor su	CPSF6	R.ELHGQNPVVTPC*NK.Q
133	Q8WTW3	COG1 Conserved oligomeric Golgi complex subunit 1	COG1	K.AQAISPC*VQNFCSALDSK.L
134	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	K.TSAPITC*ELLNK.Q
135	P62195	PSMC5 26S protease regulatory subunit 8	PSMC5	K.FVVDVDKNIDINDVTPNC*R.V
136	Q15208	STK38 Serine/threonine-protein kinase 38	STK38	K.LSDFGLC*TGLK.K
137	P49773	HINT1 Histidine triad nucleotide-binding protein 1	HINT1	K.C*AADLGLNK.G
138	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	K.EGTDSSQGIPQLVSNISAC*QVIAEAV R.T
139	P15924	DSP Desmoplakin	DSP	K.AC*GSEIMQK.K
140	Q00610	CLTC Clathrin heavy chain 1	CLTC	R.IHEGC*EEPATHNALAK.I
141	O75832	PSMD10 26S proteasome non-ATPase regulatory subunit 10	PSMD10	K.GAQVNAVNQNGC*TPLHYAASK.N
142	Q8WW01	TSEN15 tRNA-splicing endonuclease subunit Sen15	TSEN15	R.GDSEPTPGC*SGLGPGGVR.G
143	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	R.ISASC*QHPTAFEEAIPK.S
144	P51649	ALDH5A1 Succinate-semialdehyde dehydrogenase, mitochondria	ALDH5A1	R.WLPAAATFPVQDPASGAALGMVADC *GVR.E
145	P19367	HK1 Hexokinase-1	HK1	R.AILQQLGLNSTC*DDSILVK.T
146	P62873	GNB1 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB1	K.AC*ADATLSQITNNIDPVGR.I
147	A6NDG6	PGP Phosphoglycolate phosphatase	PGP	K.NNQESDC*VSK.K
148	P49327	FASN Fatty acid synthase	FASN	K.TGGAYGEDLGADYNLSQVC*DGK.V
149	O00233	PSMD9 26S proteasome non-ATPase regulatory subunit 9	PSMD9	K.GIGMNEPLVDC*EGYPR.S
150	O95782	AP2A1 AP-2 complex subunit alpha-1	AP2A1	K.TVFEALQAPAC*HENMVK.V
151	P18669	PGAM1 Phosphoglycerate mutase 1	PGAM1	R.YADLTEDQLPSC*ESLK.D
152	Q13158	FADD Protein FADD	FADD	R.SC*QMNLVADLVQEVQQAR.D
153	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	K.LWNTLGVC*K.Y
154	Q9GZQ3	COMMD5 COMM domain-containing protein 5	COMMD5	K.FVVSSLQGEDC*R.E
155	Q6P996	PDXDC1 Pyridoxal-dependent decarboxylase domain-containin	PDXDC1	R.HSC*DALNR.W

3.2	0.0	1.5	2.2	0.0	2.3	2.0	2.1	2.1	0.2
8.1	6.2	5.7	7.0	4.5	6.3	6.2	6.0	6.1	0.2
0.0	2.1	2.1	1.4	1.5	1.8	1.8	1.4	1.6	0.2
2.9	3.2	2.8	2.4	2.1	2.7	2.2	2.7	2.5	0.2
2.2	0.7	1.0	1.1	0.9	1.2	1.1	0.8	1.0	0.2
2.5	1.7	1.7	2.0	1.4	1.8	1.8	1.5	1.7	0.2
3.3	2.4	1.9	2.5	2.1	2.5	2.1	2.5	2.3	0.2
1.8	0.0	1.4	1.5	0.0	1.5	1.3	1.4	1.4	0.2
3.9	2.1	1.8	3.0	2.0	2.6	2.6	2.2	2.4	0.2
0.0	7.1	7.3	8.6	6.4	7.4	6.5	7.9	7.2	0.2
3.0	2.3	2.1	2.0	1.9	2.2	2.0	2.1	2.1	0.2
7.7	7.5	7.4	7.6	5.4	7.1	5.8	8.1	6.9	0.2
1.3	1.0	1.0	1.1	1.0	1.1	0.9	1.0	0.9	0.2
0.0	0.9	1.7	0.0	1.5	1.4	1.2	1.3	1.2	0.2
1.7	1.2	1.4	1.3	1.6	1.4	1.1	1.5	1.3	0.2
3.2	0.0	2.6	0.0	2.6	2.8	2.1	3.2	2.7	0.2
5.1	7.0	5.3	0.0	5.3	5.7	5.3	5.7	5.5	0.1
2.6	2.9	2.5	2.1	2.5	2.5	1.9	2.8	2.4	0.1
3.5	1.7	2.1	0.0	1.8	2.3	2.0	2.2	2.1	0.1
0.9	3.1	1.3	0.0	2.2	1.9	1.2	2.3	1.7	0.1
2.3	2.5	1.9	2.1	1.8	2.1	1.8	2.1	2.0	0.1
2.1	2.0	2.0	1.6	1.5	1.8	2.0	1.4	1.7	0.1
2.6	1.6	1.4	1.3	1.6	1.7	1.5	1.6	1.6	0.1
0.0	1.0	0.0	1.2	1.0	1.0	1.0	0.8	0.9	0.1
1.9	1.6	1.8	1.8	1.5	1.7	1.6	1.6	1.6	0.1
2.4	2.2	2.2	1.7	1.5	2.0	1.9	1.8	1.9	0.1
0.0	0.0	4.6	5.6	4.7	4.9	4.6	5.0	4.8	0.1
1.3	1.4	1.4	1.5	1.1	1.3	1.5	0.9	1.2	0.1
3.1	5.4	6.2	5.1	4.7	4.9	5.1	4.5	4.8	0.1
2.6	2.2	1.9	2.3	2.9	2.4	2.3	2.2	2.2	0.1
0.0	0.0	3.4	2.9	1.9	2.7	3.5	1.6	2.6	0.1
1.7	1.4	1.5	1.8	1.2	1.5	1.3	1.5	1.4	0.1
0.0	3.6	0.0	3.1	3.8	3.5	3.4	3.4	3.4	0.1
1.0	1.9	1.7	2.6	1.6	1.7	2.0	1.3	1.6	0.1
0.9	0.7	2.4	0.8	0.7	1.1	1.0	1.0	1.0	0.1
3.7	4.8	4.8	5.2	4.4	4.6	4.4	4.6	4.5	0.1
1.7	1.2	1.2	0.0	0.0	1.3	1.0	1.5	1.2	0.1
0.0	1.4	1.5	2.6	0.0	1.9	1.7	1.8	1.8	0.1

156	Q29RF7	PDS5A Sister chromatid cohesion protein PDS5 homolog A	PDS5A	R.ELLDLHKQPTSEANC*SAMFGK.L
157	Q13630	TSTA3 GDP-L-fucose synthase	TSTA3	R.KVVSCLSTC*IFPDK.T
158	Q5VYK3	ECM29 Proteasome-associated protein ECM29 homolog	ECM29	R.TIAALLPC*LLDK.G
159	P49588	AARS Alanine--tRNA ligase, cytoplasmic	AARS	K.C*LSVMEAK.V
160	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit 2	PSMD2	R.C*ALGVFR.K
161	Q52LJ0	FAM98B Protein FAM98B	FAM98B	R.EKTAC*AINK.V
162	Q9H3U1	UNC45A Protein unc-45 homolog A	UNC45A	R.AIQTVSCLLQGPC*DAGNR.A
163	Q9P2R7	SUCLA2 Succinyl-CoA ligase	SUCLA2	K.ILAC*DDLDEAAR.M
164	O15541	RNF113A RING finger protein 113A	RNF113A	K.AVDQVC*TFLFK.K
165	P35237	SERPINB6 Serpin B6	SERPINB6	K.SC*DFLSSFR.D
166	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	K.IAAYLQSDQFC*K.M
167	P07437	TUBB Tubulin beta chain	TUBB	K.LTTPTYGDLNHLVSATMSGVTTC*LR.F
168	Q99836	MYD88 Myeloid differentiation primary response protein M	MYD88	R.FITVCDYTNPC*TK.S
169	Q8NFG4	FLCN Folliculin	FLCN	K.VFEAEQFGC*PQR.A
170	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	K.TGQATVASGIPAGWMGLDC*GPESSK.K
171	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.AYHEQLSVAEITNAC*FEPANQMVK.C
172	P49327	FASN Fatty acid synthase	FASN	K.AINC*ATSGVVGLVNCLR.R
173	P53618	COPB1 Coatomer subunit beta	COPB1	K.ALSGYC*GFMAANLYAR.S
174	O14980	XPO1 Exportin-1	XPO1	K.DLLGLC*EQKR.G
175	O75934	BCAS2 Pre-mRNA-splicing factor SPF27	BCAS2	K.NDITAWQEC*VNNSMAQLEHQAVR.I
176	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.SSGGFVWAC*K.N
177	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	K.QEPLGSDSEGVNC*LAYDEAIMAQQDR.I
178	P53990	IST1 IST1 homolog	IST1	K.IVADQLC*AK.Y
179	Q9BXV9	C14orf142 Uncharacterized protein C14orf142	C14orf142	R.VSC*EAPGDGDPFQGLLSGVAQMK.D
180	P51610	HCFC1 Host cell factor 1	HCFC1	K.LVIYGGMSGC*R.L
181	Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	K.LAAQSC*ALSLVR.Q
182	P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.EVIAVSC*GPAQCQETIR.T
183	P30281	CCND3 G1/S-specific cyclin-D3	CCND3	R.ASYFQC*VQR.E
184	O00204	SULT2B1 Sulfotransferase family cytosolic 2B member 1	SULT2B1	R.APWC*ETIVGAFSLPDQYSPR.L
185	Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.GVPGAIVNVSSQC*SQR.A
186	O14964	HGS Hepatocyte growth factor-regulated tyrosine kinase	HGS	R.ACGQIFC*GK.C
187	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.ADIDVSGPKVDVEC*PDVNIEGPEGK.W
188	Q9NXG2	THUMPD1 THUMP domain-containing protein 1	THUMPD1	R.RC*DAGGPR.Q
189	Q13308	PTK7 Inactive tyrosine-protein kinase 7	PTK7	R.LPQPEGC*PSK.L
190	Q96TA1	FAM129B Niban-like protein 1	FAM129B	K.GPTKEELC*K.S
191	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.DLNYC*FSGMSDHR.Y
192	P49458	SRP9 Signal recognition particle 9 kDa protein	SRP9	K.VTDDLVC*LVYK.T
193	O60547	GMDS GDP-mannose 4,6 dehydratase	GMDS	K.YYRPTEVDFLQGDC*TK.A
194	P36969	GPX4 Phospholipid hydroperoxide glutathione peroxidase,	GPX4	R.ILAFPC*NQFGK.Q

2.9	2.3	0.0	2.6	1.9	2.4	2.5	2.2	2.3	0.1
0.0	4.4	0.0	4.3	3.8	4.2	3.9	4.2	4.1	0.1
0.0	0.0	2.0	2.9	2.4	2.4	2.5	2.2	2.3	0.1
1.6	1.3	1.5	1.4	1.2	1.4	1.2	1.4	1.3	0.1
1.3	1.3	1.6	0.0	1.4	1.4	1.0	1.6	1.3	0.1
2.8	1.7	1.5	0.0	1.4	1.9	1.8	1.8	1.8	0.1
1.4	1.0	0.0	1.1	0.9	1.1	1.7	0.4	1.1	0.1
2.0	0.0	1.8	2.3	0.0	2.0	2.9	1.0	2.0	0.1
8.5	3.8	2.3	0.0	2.2	4.2	3.4	4.9	4.1	0.1
2.2	0.0	1.3	1.3	0.9	1.4	1.1	1.6	1.4	0.1
1.0	1.3	0.8	0.9	0.7	0.9	0.8	0.9	0.9	0.1
5.3	5.7	5.2	5.3	4.8	5.3	5.1	5.3	5.2	0.1
3.8	3.1	3.3	0.0	3.0	3.3	2.9	3.6	3.2	0.1
2.3	2.4	3.0	3.5	2.0	2.6	2.6	2.5	2.6	0.1
0.8	1.0	1.1	1.9	1.0	1.2	1.1	1.1	1.1	0.1
6.6	5.7	5.6	5.7	5.2	5.8	5.6	5.8	5.7	0.1
2.3	1.3	1.4	1.5	1.3	1.6	1.7	1.4	1.5	0.0
3.1	3.7	3.6	2.9	3.3	3.3	3.2	3.3	3.2	0.0
3.2	4.1	2.2	3.1	1.9	2.9	2.5	3.2	2.9	0.0
3.9	3.6	3.4	3.4	2.8	3.4	3.2	3.5	3.4	0.0
1.8	1.5	1.1	1.2	1.0	1.3	1.2	1.3	1.3	0.0
2.1	1.6	1.7	1.6	1.4	1.7	1.6	1.7	1.6	0.0
2.2	1.8	1.6	0.0	1.3	1.7	1.7	1.7	1.7	0.0
1.5	1.3	0.3	1.5	1.3	1.2	0.9	1.4	1.1	0.0
1.4	1.5	1.3	1.4	1.1	1.3	1.3	1.4	1.3	0.0
1.3	1.2	1.4	1.0	1.1	1.2	1.0	1.3	1.2	0.0
2.2	2.2	2.4	3.4	1.8	2.4	2.4	2.4	2.4	0.0
3.8	3.3	3.7	2.8	2.5	3.2	3.1	3.3	3.2	0.0
1.3	1.3	1.5	1.3	1.4	1.4	1.3	1.4	1.3	0.0
2.5	3.2	2.8	2.9	2.6	2.8	2.6	2.9	2.8	0.0
2.3	1.1	1.2	0.9	1.1	1.3	1.0	1.5	1.3	0.0
1.4	1.4	1.4	1.2	1.1	1.3	1.3	1.3	1.3	0.0
0.0	1.6	0.0	1.4	1.7	1.5	1.4	1.6	1.5	0.0
4.9	5.7	5.6	0.0	5.0	5.3	6.1	4.5	5.3	0.0
1.8	1.6	0.0	1.3	1.2	1.5	1.4	1.5	1.4	0.0
2.1	2.2	2.1	2.4	2.0	2.2	2.1	2.2	2.1	0.0
1.5	1.3	1.2	1.3	1.2	1.3	1.3	1.3	1.3	0.0
2.3	2.0	1.7	2.0	1.7	1.9	2.1	1.7	1.9	0.0
0.0	1.8	2.7	1.1	3.7	2.3	1.5	3.1	2.3	0.0

195	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	R.AAVEEGIVLGGGC*ALLR.C
196	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	R.AVC*MLSNTTAIAEAWAR.L
197	P52895	AKR1C2 Aldo-keto reductase family 1 member C2	AKR1C2	R.EEPWVDPNSPVLLEDPVLC*ALAK.K
198	E9PPU0	EPPK1 Epiplakin	EPPK1	R.YLC*GLGAVGGVR.L
199	Q6P1X6	C8orf82 UPF0598 protein C8orf82	C8orf82	R.YEAAFPFLSPC*GR.E
200	Q15370	TCEB2 Transcription elongation factor B polypeptide 2	TCEB2	R.ADDTFEALC*IEPFSSPPELPDVMKPQ DSGSSANEQAVQ.-
201	P26599	PTBP1 Polypyrimidine tract-binding protein 1	PTBP1	K.LSLDGQNIYNAC*CTLR.I
202	Q8IUR0	TRAPPC5 Trafficking protein particle complex subunit 5	TRAPPC5	K.ENSTLNC*ASFTAGIVEAVLTHSGFPA K.V
203	O43390	HNRNPR Heterogeneous nuclear ribonucleoprotein R	HNRNPR	K.SAFLC*GVMK.T
204	P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	K.LC*FSTAQHAS.-
205	O95336	PGLS 6-phosphogluconolactonase	PGLS	R.AAC*CLAGAR.A
206	O60716	CTNND1 Catenin delta-1	CTNND1	K.TPAILEASAGAIQNLC*AGR.W
207	Q93009	USP7 Ubiquitin carboxyl-terminal hydrolase 7	USP7	K.GTC*VEGTIPK.L
208	P23528	CFL1 Cofilin-1	CFL1	K.AVLFC*LSEDK.K
209	O75439	PMPCB Mitochondrial-processing peptidase subunit beta	PMPCB	R.LC*TSVTESEVAR.A
210	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitoch	MCCC2	K.MVAAVAC*AQVPK.I
211	P22234	PAICS Multifunctional protein ADE2	PAICS	K.ITSC*IFQLLQEAGIK.T
212	P62910	RPL32 60S ribosomal protein L32	RPL32	K.SYC*AEIAHNVSSK.N
213	Q9UPM8	AP4E1 AP-4 complex subunit epsilon-1	AP4E1	R.SSC*STLPDYLLYQCQK.V
214	Q9NYL2	MLTK Mitogen-activated protein kinase kinase kinase MLT	MLTK	K.FDDLQFFENC*GGGSFGSVYR.A
215	P60981	DSTN Destrin	DSTN	K.LGGSLIVAFEGC*PV.-
216	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	R.AGAIAPC*EVTVPAQNTGLGPEK.T
217	Q12768	KIAA0196 WASH complex subunit strumpellin	KIAA0196	R.IVSC*GNAIIAELLR.L
218	Q96EY8	MMAB Cob(I)yrinic acid a,c-diamide adenosyltransferase,	MMAB	K.IQCTLQDVGSALATPC*SSAR.E
219	P31939	ATIC Bifunctional purine biosynthesis protein PURH	ATIC	R.VVAC*NLYPFVK.T
220	Q9UL40	ZNF346 Zinc finger protein 346	ZNF346	K.NQC*LFTNTQCK.V
221	P49327	FASN Fatty acid synthase	FASN	R.LSIPTYGLQC*TR.A
222	P21964	COMT Catechol O-methyltransferase	COMT	K.IVDAVIQEHQPSVLLELGAYC*GYSA VR.M
223	Q9Y296	TRAPPC4 Trafficking protein particle complex subunit 4	TRAPPC4	R.C*ELFDQNLK.L
224	Q9NZA1	CLIC5 Chloride intracellular channel protein 5	CLIC5	K.AGIDGESIGNC*PFSQR.L
225	P07437	TUBB Tubulin beta chain	TUBB	K.NMMAAC*DPR.H
226	Q9NXR7	BRE BRCA1-A complex subunit BRE	BRE	K.VGLDATNC*LR.I
227	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	R.LVSSPC*CIVTSTYGWTANMER.I
228	P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	R.LGGEVSC*LVAGTK.C
229	Q9NR33	POLE4 DNA polymerase epsilon subunit 4	POLE4	K.DAYC*CAQQGK.R
230	P49327	FASN Fatty acid synthase	FASN	K.ADEASELAC*PTPK.E
231	Q9BV86	NTMT1 N-terminal Xaa-Pro-Lys N-methyltransferase 1	NTMT1	R.IIC*SAGLSLLAEER.Q
232	P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitocho	LRPPRC	R.IHDVLC*K.L
233	Q01518	CAP1 Adenylyl cyclase-associated protein 1	CAP1	R.ALLVTASQC*QQPAENK.L

4.1	3.6	3.2	3.7	2.6	3.4	3.4	3.5	3.4	0.0
4.8	4.8	4.7	4.7	4.3	4.7	4.5	4.8	4.6	0.0
1.8	2.0	1.9	2.0	1.4	1.8	2.0	1.7	1.8	0.0
1.9	2.1	1.8	2.0	2.0	2.0	2.0	1.9	1.9	0.0
2.8	3.2	2.8	3.1	2.6	2.9	2.7	3.0	2.9	0.0
2.1	1.5	1.6	1.5	1.4	1.6	1.6	1.6	1.6	0.0
1.2	1.2	1.3	0.0	1.2	1.2	1.2	1.2	1.2	0.0
1.5	1.5	2.2	1.5	1.5	1.6	1.5	1.7	1.6	0.0
2.7	2.8	1.7	1.2	3.5	2.4	3.1	1.7	2.4	0.0
1.3	1.0	1.2	0.0	1.0	1.1	1.1	1.1	1.1	0.0
1.3	1.6	1.6	1.8	1.5	1.6	1.5	1.6	1.6	0.0
2.7	0.0	3.2	3.0	2.7	2.9	3.1	2.8	2.9	0.0
1.8	1.6	1.4	1.3	1.2	1.4	1.4	1.5	1.4	0.0
0.9	1.2	1.1	0.9	1.1	1.0	1.2	0.9	1.0	0.0
2.5	2.1	1.9	0.0	0.0	2.2	2.1	2.2	2.2	0.0
1.2	1.6	1.9	2.4	1.5	1.7	1.7	1.8	1.7	0.0
0.9	0.8	1.0	0.9	0.9	0.9	0.9	0.9	0.9	0.0
2.8	2.5	2.9	3.6	2.4	2.8	2.8	2.9	2.8	0.0
1.7	1.3	1.5	0.0	1.2	1.4	1.4	1.5	1.4	0.0
2.2	1.7	1.2	1.4	1.1	1.5	1.4	1.7	1.5	0.0
1.7	1.3	1.4	1.4	1.1	1.4	1.3	1.4	1.4	0.0
3.3	3.3	3.0	3.5	2.6	3.1	3.1	3.2	3.1	0.0
1.6	0.0	1.4	0.0	1.0	1.3	1.2	1.5	1.4	0.0
2.0	1.5	1.3	1.6	1.4	1.6	1.6	1.6	1.6	0.0
0.9	1.1	1.2	1.6	0.0	1.2	1.4	1.1	1.2	0.0
1.9	2.3	1.6	0.0	2.1	1.9	2.1	1.9	2.0	0.0
2.4	3.0	2.5	2.6	2.3	2.6	3.2	2.0	2.6	0.0
2.1	1.8	1.4	1.4	1.1	1.5	1.4	1.7	1.6	0.0
2.1	1.4	1.3	1.6	1.2	1.5	1.6	1.5	1.5	0.0
1.1	0.9	1.3	1.0	1.1	1.1	1.0	1.2	1.1	0.0
5.1	4.8	4.5	4.6	4.2	4.6	4.5	4.8	4.7	0.0
2.5	1.0	2.5	0.0	1.8	1.9	2.2	1.7	2.0	0.0
1.0	0.8	1.0	1.1	0.9	1.0	1.0	1.0	1.0	0.0
3.8	4.9	4.5	5.4	4.6	4.6	4.6	4.7	4.7	0.0
2.9	0.0	1.7	2.1	1.5	2.1	1.9	2.3	2.1	0.0
2.5	2.2	1.6	2.4	1.6	2.1	2.0	2.2	2.1	0.0
1.9	1.4	1.4	1.4	1.3	1.5	1.4	1.6	1.5	0.0
1.3	1.3	1.3	1.2	1.0	1.2	1.2	1.3	1.3	0.0
1.1	1.0	0.9	0.0	1.0	1.0	1.0	1.1	1.0	0.0

234	P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	K.AC*QIFVR.N
235	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	K.C*CSGAIIVLTK.S
236	O14818	PSMA7 Proteasome subunit alpha type-7	PSMA7	R.VEC*QSHR.L
237	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	R.IVDTPC*NEMNTDTFLEEINK.V
238	P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	K.GFGFVC*FSSPEEATK.A
239	Q86SX6	GLRX5 Glutaredoxin-related protein 5, mitochondrial	GLRX5	K.GTPEQPQC*GFSNAVVQILR.L
240	P04632	CAPNS1 Calpain small subunit 1	CAPNS1	R.YSDESGNMDFDNFISC*LVR.L
241	P52597	HNRNPF Heterogeneous nuclear ribonucleoprotein F	HNRNPF	R.DLSYC*LSGMYDHR.Y
242	P28838	LAP3 Cytosol aminopeptidase	LAP3	R.QVVDC*QLADVNNIGK.Y
243	Q96Q11	TRNT1 CCA tRNA nucleotidyltransferase 1, mitochondrial	TRNT1	K.YQGEHC*LLK.E
244	P55060	CSE1L Exportin-2	CSE1L	K.LSTAC*PGR.V
245	Q92879	CELF1 CUGBP Elav-like family member 1	CELF1	R.GC*AFVTFTTR.A
246	P04632	CAPNS1 Calpain small subunit 1	CAPNS1	K.TDGFGIDTC*R.S
247	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	K.FLDGNELTLADC*NLLPK.L
248	O60664	PLIN3 Perilipin-3	PLIN3	R.DIAQQLQATC*TSLGSSIQGLPTNVK.D
249	Q5TFE4	NT5DC1 5-nucleotidase domain-containing protein 1	NT5DC1	K.HFLSDTGMAC*R.S
250	O15355	PPM1G Protein phosphatase 1G	PPM1G	R.GTEAGQVGEPGIPTGEAGPSC*SSASDK.L
251	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.ALNALC*DGLIDELNQALK.T
252	Q5VTR2	RNF20 E3 ubiquitin-protein ligase BRE1A	RNF20	R.LTCPC*CNMR.K
253	Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	R.NPVSQC*MR.G
254	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	K.DVLNLVYLC*EALNLPEVAR.Y
255	Q9NQT5	EXOSC3 Exosome complex component RRP40	EXOSC3	K.LLAPDC*EIIQEVGK.L
256	P38606	ATP6V1A V-type proton ATPase catalytic subunit A	ATP6V1A	R.VLDALFPCVQGGTTAIPGAFGC*GK.T
257	Q14247	CTTN Src substrate cortactin	CTTN	K.HC*SQVDSVR.G
258	Q8IWX8	CHERP Calcium homeostasis endoplasmic reticulum protein	CHERP	K.LALEQQQLIC*K.Q
259	P52788	SMS Spermine synthase	SMS	R.LYC*PVEFSK.E
260	O15327	INPP4B Type II inositol 3,4-bisphosphate 4-phosphatase	INPP4B	K.SLNC*IIAMVDK.L
261	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.AITIAGVPQSVTEC*VK.Q
262	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.SQETEC*TYFSTPLLLGK.K
263	P21333	FLNA Filamin-A	FLNA	K.VGTEC*GNQK.V
264	P08107	HSPA1B Heat shock 70 kDa protein 1A/1B	HSPA1B	K.ELEQVC*NPIISGLYQGAGGPGPGGFGAQGPK.G
265	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK.G
266	Q9Y3C6	PPIL1 Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	R.VC*QGIGMVNR.V
267	Q7L1Q6	BZW1 Basic leucine zipper and W2 domain-containing prot	BZW1	K.ERFDPTQFQDC*IIQGLTETGTDLEAVAK.F
268	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.INISEGNC*PER.I
269	P53041	PPP5C Serine/threonine-protein phosphatase 5	PPP5C	R.TEC*AEPPRDEPPADGALKR.A
270	O75874	IDH1 Isocitrate dehydrogenase	IDH1	K.SEGGFIWAC*K.N
271	Q9Y696	CLIC4 Chloride intracellular channel protein 4	CLIC4	K.AGSDGESIGNC*PFSQR.L
272	Q96EY5	FAM125A Multivesicular body subunit 12A	FAM125A	K.SC*SPLAFSAFGDLTIK.S
273	Q14247	CTTN Src substrate cortactin	CTTN	K.C*ALGWDHQEK.L
274	Q9UL46	PSME2 Proteasome activator complex subunit 2	PSME2	K.C*GFLPGNEK.V

1.7	2.0	1.5	1.6	1.6	1.7	1.7	1.8	1.7	0.0
1.7	2.3	1.5	2.0	1.4	1.8	1.8	1.8	1.8	0.0
0.0	1.0	1.2	1.2	0.0	1.1	1.2	1.2	1.2	0.0
2.0	1.3	1.3	1.1	1.3	1.4	1.4	1.5	1.4	0.0
1.1	1.0	1.1	1.2	1.0	1.1	1.2	1.1	1.1	0.0
1.4	1.1	1.1	1.2	1.0	1.2	1.2	1.2	1.2	0.0
0.7	0.5	0.8	0.8	0.8	0.7	0.8	0.7	0.8	0.0
2.2	2.1	2.3	2.1	2.0	2.1	2.1	2.3	2.2	0.0
1.8	1.2	0.9	1.1	0.8	1.1	1.0	1.4	1.2	0.0
1.2	1.3	1.5	1.2	1.2	1.3	1.3	1.4	1.3	0.0
2.1	1.9	2.2	3.0	2.0	2.2	2.5	2.1	2.3	0.0
1.8	2.4	2.6	2.6	2.2	2.3	2.2	2.6	2.4	0.0
0.9	0.7	0.7	0.7	0.7	0.7	0.9	0.7	0.8	0.0
0.8	0.9	1.1	1.0	0.8	0.9	1.0	0.9	1.0	0.0
1.1	1.1	1.0	0.0	0.9	1.0	1.0	1.1	1.0	0.0
1.6	1.6	0.0	1.6	1.4	1.5	1.5	1.7	1.6	0.0
3.2	3.0	2.6	2.5	2.0	2.7	2.5	3.0	2.7	0.0
6.3	5.4	5.4	5.9	5.0	5.6	5.4	5.9	5.7	0.0
2.3	2.0	1.9	2.2	1.7	2.0	2.3	1.8	2.1	0.0
2.9	3.5	2.6	2.5	2.2	2.7	2.5	3.1	2.8	0.0
1.1	0.0	1.0	0.0	0.9	1.0	1.0	1.0	1.0	0.0
2.6	0.0	2.1	1.9	1.8	2.1	2.1	2.2	2.2	-0.1
2.2	2.9	2.4	2.4	2.0	2.4	2.4	2.5	2.4	-0.1
2.5	2.1	1.7	1.9	1.4	1.9	1.9	2.0	2.0	-0.1
2.5	2.3	1.9	0.0	1.6	2.1	2.1	2.1	2.1	-0.1
1.0	1.0	1.3	1.0	0.8	1.0	1.0	1.1	1.1	-0.1
2.1	0.0	1.9	1.7	0.0	1.9	1.7	2.2	1.9	-0.1
1.3	1.1	1.3	1.1	1.0	1.2	1.2	1.3	1.2	-0.1
1.8	1.8	2.0	1.8	1.8	1.8	2.1	1.6	1.9	-0.1
1.4	1.6	1.3	0.0	1.6	1.5	1.4	1.6	1.5	-0.1
0.0	1.0	0.9	0.8	0.9	0.9	1.1	0.8	1.0	-0.1
1.8	1.6	1.4	1.5	1.2	1.5	1.4	1.6	1.5	-0.1
0.8	0.4	0.0	1.4	0.0	0.8	1.4	0.4	0.9	-0.1
1.7	1.3	1.4	1.3	1.3	1.4	1.4	1.5	1.5	-0.1
2.0	1.7	1.5	1.9	1.4	1.7	1.7	1.9	1.8	-0.1
2.2	1.9	1.2	0.0	1.2	1.6	1.4	1.9	1.6	-0.1
0.8	0.8	0.8	0.8	0.8	0.8	0.9	0.9	0.9	-0.1
1.0	0.9	1.0	0.9	0.9	1.0	1.0	1.0	1.0	-0.1
1.9	1.9	1.7	1.3	1.4	1.6	1.7	1.7	1.7	-0.1
2.2	2.0	1.8	2.0	1.5	1.9	2.0	2.0	2.0	-0.1
1.6	1.3	1.1	1.3	1.1	1.3	1.2	1.5	1.3	-0.1

275	P49327	FASN Fatty acid synthase	FASN	R.AAPLDSIHSLAAYYIDC*IR.Q
276	O43865	AHCYL1 Putative adenosylhomocysteinase 2	AHCYL1	K.FDNLYC*CR.E
277	P49207	RPL34 60S ribosomal protein L34	RPL34	R.AYGGSMC*AK.C
278	P31947	SFN 14-3-3 protein sigma	SFN	K.GAVEKGEELSC*EER.N
279	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	K.AGSDGAKIGNC*PFSQR.L
280	P49327	FASN Fatty acid synthase	FASN	R.LGMLSPEGTC*K.A
281	F5H284	PPIAL4D Peptidyl-prolyl cis-trans isomerase	PPIAL4D	R.IIPGFMC*QGGDFTR.H
282	P53396	ACLY ATP-citrate synthase	ACLY	K.FIC*TTSAIQNR.F
283	Q9UNH7	SNX6 Sorting nexin-6	SNX6	R.IGSSLYALGTQDSTDIC*K.F
284	Q15631	TSN Translin	TSN	K.ETAAAC*VEK.-
285	P13489	RNH1 Ribonuclease inhibitor	RNH1	K.LSLQNCC*LTGAGCGVLSSTLR.T
286	P62753	RPS6 40S ribosomal protein S6	RPS6	K.LNISFPATGC*QK.L
287	O75828	CBR3 Carbonyl reductase	CBR3	R.ILVNAC*CPGPVK.T
288	Q13200	PSMD2 26S proteasome non-ATPase regulatory subunit 2	PSMD2	K.GTLTLC*PYHSDR.Q
289	P60604	UBE2G2 Ubiquitin-conjugating enzyme E2 G2	UBE2G2	R.VC*ISILHAPGDDPMGYESSAER.W
290	P49327	FASN Fatty acid synthase	FASN	R.DPETLVGYSMVGC*QR.A
291	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.DGLTDVYNKIHMGSC*AENTAK.K
292	P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	R.VFIMDSC*DELIPEYLNFIR.G
293	P22061	PCMT1 Protein-L-isoaspartate(D-aspartate) O-methyltransf	PCMT1	K.ALDVGSGSGILTAC*FAR.M
294	P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	K.ITIADC*GQLE.-
295	P33992	MCM5 DNA replication licensing factor MCM5	MCM5	K.C*SPIGVYTSGK.G
296	Q9BXJ9	NAA15 N-alpha-acetyltransferase 15, NatA auxiliary subun	NAA15	R.LFNTAVC*ESK.D
297	Q7Z2Z2	EFTUD1 Elongation factor Tu GTP-binding domain-containing	EFTUD1	R.ICDGCIIVVDAVEGVC*PQTQAVLR.Q
298	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	R.FC*PFAER.T
299	Q93052	LPP Lipoma-preferred partner	LPP	K.TYITDPVSAPC*APPLQPK.G
300	P55735	SEC13 Protein SEC13 homolog	SEC13	K.RFASGGC*DNLIK.L
301	Q9Y5Y2	NUBP2 Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	K.VGILDVDLC*GPSIPR.M
302	O00151	PDLIM1 PDZ and LIM domain protein 1	PDLIM1	K.C*GTGIVGVFVK.L
303	P49327	FASN Fatty acid synthase	FASN	K.AFDTAGNGYC*R.S
304	O43681	ASNA1 ATPase ASNA1	ASNA1	K.NQISPFISQMC*NMLGLGDMNADQLASK.L
305	Q9Y5X2	SNX8 Sorting nexin-8	SNX8	K.ESAQCVGDEFLNC*K.L
306	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.ERPTPSLNNNC*TTSEDSLVLYNR.V
307	P31689	DNAJA1 DnaJ homolog subfamily A member 1	DNAJA1	K.GAVEC*CPNCR.G
308	P60174	TPI1 Triosephosphate isomerase	TPI1	K.VPADTEVVC*APPTAYIDFAR.Q
309	O43707	ACTN4 Alpha-actinin-4	ACTN4	K.IC*DQWDALGSLTHSR.R
310	P21291	CSRP1 Cysteine and glycine-rich protein 1	CSRP1	K.SC*FLCMVCK.K
311	Q7Z406	MYH14 Myosin-14	MYH14	K.ADLLLEPC*SHYR.F
312	P50990	CCT8 T-complex protein 1 subunit theta	CCT8	K.IAVYSC*PFDGMITETK.G
313	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	R.VPTANVSVVDLTC*R.L
314	Q9BW61	DDA1 DET1- and DDB1-associated protein 1	DDA1	R.FHADSVC*K.A
315	P37235	HPCAL1 Hippocalcin-like protein 1	HPCAL1	R.LLQC*DPSSASQF.-
316	P14649	MYL6B Myosin light chain 6B	MYL6B	K.ILYSQC*GDVMR.A

1.1	1.1	1.4	1.5	1.2	1.3	1.3	1.4	1.3	-0.1
2.7	0.0	2.5	0.0	2.3	2.5	2.8	2.4	2.6	-0.1
4.1	3.4	3.2	4.1	3.2	3.6	3.8	3.5	3.7	-0.1
1.5	1.2	1.4	1.3	1.0	1.3	1.3	1.4	1.4	-0.1
1.0	0.9	1.0	1.0	1.0	1.0	1.1	1.0	1.1	-0.1
3.9	5.8	5.1	5.4	5.1	5.0	4.9	5.3	5.1	-0.1
0.7	0.7	0.9	0.9	0.8	0.8	0.9	0.9	0.9	-0.1
1.6	1.3	1.2	1.2	1.2	1.3	1.3	1.5	1.4	-0.1
1.1	0.7	0.9	1.1	0.9	0.9	1.1	1.0	1.0	-0.1
3.7	2.8	2.8	3.4	2.5	3.1	2.9	3.3	3.1	-0.1
0.0	0.5	0.5	0.5	0.5	0.5	0.6	0.6	0.6	-0.1
3.0	3.0	2.7	2.8	3.7	3.0	3.0	3.2	3.1	-0.1
0.0	0.3	0.3	0.7	0.3	0.4	0.6	0.5	0.5	-0.1
0.7	0.9	0.8	0.9	0.8	0.8	0.9	0.9	0.9	-0.1
1.5	1.0	1.1	0.0	0.9	1.1	1.0	1.4	1.2	-0.1
2.1	2.4	2.0	1.9	2.1	2.1	2.1	2.3	2.2	-0.1
3.3	3.4	2.7	3.2	3.0	3.1	3.2	3.2	3.2	-0.1
1.5	1.5	1.4	1.5	1.3	1.5	1.6	1.5	1.5	-0.1
1.0	1.0	1.1	1.0	0.9	1.0	1.1	1.0	1.1	-0.1
0.7	0.6	0.9	0.7	0.7	0.7	0.8	0.8	0.8	-0.1
1.6	1.2	1.2	0.0	1.2	1.3	1.4	1.4	1.4	-0.1
1.6	1.2	1.2	0.0	1.2	1.3	1.4	1.4	1.4	-0.1
2.6	3.5	2.7	1.4	1.8	2.4	2.3	2.6	2.5	-0.1
1.1	1.1	0.9	1.0	1.0	1.0	1.0	1.1	1.1	-0.1
3.6	3.4	2.5	2.7	1.8	2.8	2.9	2.9	2.9	-0.1
1.2	1.0	1.0	1.1	0.9	1.0	1.1	1.1	1.1	-0.1
7.1	8.0	6.3	5.9	6.1	6.7	7.0	6.5	6.7	-0.1
0.0	0.9	1.2	0.7	0.0	0.9	1.1	0.9	1.0	-0.1
3.6	4.1	3.2	3.1	2.9	3.4	3.5	3.4	3.5	-0.1
1.1	0.7	1.0	0.0	0.7	0.9	1.0	0.9	1.0	-0.1
1.5	1.2	0.7	0.0	1.3	1.2	1.3	1.3	1.3	-0.1
2.7	1.5	1.6	0.0	1.3	1.7	1.6	2.1	1.8	-0.1
4.1	0.0	4.2	0.0	2.1	3.4	4.3	2.7	3.5	-0.1
0.8	0.8	1.0	1.3	0.8	0.9	1.2	0.9	1.0	-0.1
0.9	0.0	0.8	0.0	0.8	0.8	1.0	0.8	0.9	-0.1
1.2	1.0	1.0	1.5	1.0	1.1	1.3	1.2	1.2	-0.1
2.7	2.4	3.1	0.0	2.2	2.6	2.9	2.5	2.7	-0.1
1.2	1.0	1.1	1.1	0.9	1.0	1.0	1.3	1.1	-0.1
0.7	2.0	2.1	2.2	1.4	1.7	2.1	1.5	1.8	-0.1
1.1	1.2	1.4	1.2	1.1	1.2	1.3	1.3	1.3	-0.1
2.3	1.9	1.7	1.9	1.6	1.9	1.9	2.0	2.0	-0.1
1.1	1.0	1.2	1.0	1.1	1.1	1.1	1.2	1.2	-0.1

317	Q8N987	NECAB1 N-terminal EF-hand calcium-binding protein 1	NECAB1	K.ETLNQLQSLQNSLEC*AMETTEEQTR.Q
318	O75131	CPNE3 Copine-3	CPNE3	K.NC*LNPQFSK.T
319	P37802	TAGLN2 Transgelin-2	TAGLN2	K.DGTVLC*ELINALYPEGQAPVK.K
320	P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	K.C*FIVGADNVGSK.Q
321	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	K.VVVVQAISALC*QK.Y
322	P14174	MIF Macrophage migration inhibitory factor	MIF	K.LLC*GLLAER.L
323	P78347	GTF2I General transcription factor II-I	GTF2I	R.SILSPGGSC*GPIK.V
324	Q14103	HNRNPD Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	K.FGEVVDC*TLKLDPITGR.S
325	Q52LJ0	FAM98B Protein FAM98B	FAM98B	K.SLC*NLEESITSAGR.D
326	Q9H1B7	IRF2BPL Interferon regulatory factor 2-binding protein-lik	IRF2BPL	K.EGVPGADMLPQPYLDASC*PMLPTALVSLSR.A
327	Q96HP0	DOCK6 Dedicator of cytokinesis protein 6	DOCK6	R.AGC*ALSAESSR.T
328	Q12765	SCRN1 Secernin-1	SCRN1	K.TQSPC*FGDDDPAKKEPR.F
329	P37802	TAGLN2 Transgelin-2	TAGLN2	K.NMAC*VQR.T
330	Q9NY27	PPP4R2 Serine/threonine-protein phosphatase 4 regulatory	PPP4R2	K.EVC*PVLDQFLCHVAK.T
331	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.PMC*VESFSDYPPLGR.F
332	P30041	PRDX6 Peroxiredoxin-6	PRDX6	R.DFTPVC*TTELGR.A
333	Q9UJU6	DBNL Drebrin-like protein	DBNL	R.AEEDVEPEC*IMEK.V
334	P21964	COMT Catechol O-methyltransferase	COMT	R.LITIEINPDC*AAITQR.M
335	Q96JB2	COG3 Conserved oligomeric Golgi complex subunit 3	COG3	R.ELLLGPSIAC*TVAELTSQNNR.D
336	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.KLGNNC*VFAPADVTSEK.D
337	Q96HE7	ERO1L ERO1-like protein alpha	ERO1L	K.HDDSSDNFC*EADDIQSPEAEYVDLLLNPER.Y
338	P46776	RPL27A 60S ribosomal protein L27a	RPL27A	R.NQSFC*PTVNLDK.L
339	P31350	RRM2 Ribonucleoside-diphosphate reductase subunit M2	RRM2	R.EFLFNAIETMPC*VK.K
340	Q9HAV7	GRPEL1 GrpE protein homolog 1, mitochondrial	GRPEL1	K.LYGIQAFC*K.D
341	P19367	HK1 Hexokinase-1	HK1	R.AAQLC*GAGMAAVVDK.I
342	P53618	COPB1 Coatomer subunit beta	COPB1	K.VLSEC*SPLMNDIFNK.E
343	Q7Z6Z7	HUWE1 E3 ubiquitin-protein ligase HUWE1	HUWE1	R.DQSAQC*TASK.S
344	P26599	PTBP1 Polypyrimidine tract-binding protein 1	PTBP1	K.RGSDELFSTC*VTNGPFIMSSNSASAANGNDSK.K
345	Q15691	MAPRE1 Microtubule-associated protein RP/EB family member	MAPRE1	R.NIELIC*QENEGENDPVLQR.I
346	Q15149	PLEC Plectin	PLEC	K.AFC*GFEDPR.T
347	Q9NTK5	OLA1 Obg-like ATPase 1	OLA1	K.STFFNVLTNSQASAENFPFC*TIDPNESR.V
348	P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.GLPFGC*SK.E
349	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	K.LCQDLPC*FSR.E
350	P10768	ESD S-formylglutathione hydrolase	ESD	K.AETGKCPALYWLSGLTC*TEQNFISK.S
351	Q9H0W8	SMG9 Protein SMG9	SMG9	R.REDFC*PR.K
352	Q2TAA2	IAH1 Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	R.VILITPTPLC*ETAWEEQCIIQGCK.L
353	P08107	HSPA1B Heat shock 70 kDa protein 1A/1B	HSPA1B	R.ARFEELC*SDLFR.S
354	P0CW22	RPS17L 40S ribosomal protein S17-like	RPS17L	R.VC*EEIAIIPSK.K
355	Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	K.IVSLPEC*FNSPYGAK.Y
356	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	K.LTFSC*LGGSDNFK.H

1.4	1.0	1.0	1.4	1.1	1.2	1.3	1.2	1.3	-0.1
1.6	1.4	1.4	1.4	1.1	1.4	1.5	1.5	1.5	-0.1
1.0	1.0	1.2	1.0	1.0	1.0	1.2	1.1	1.1	-0.1
3.6	3.0	2.8	3.0	2.6	3.0	2.8	3.4	3.1	-0.1
2.9	3.2	3.7	3.2	3.3	3.3	3.2	3.5	3.4	-0.1
0.8	0.7	0.9	0.7	0.8	0.8	0.9	0.9	0.9	-0.1
2.3	2.2	1.6	1.9	1.6	1.9	2.0	2.1	2.0	-0.1
0.8	0.9	1.0	0.0	0.8	0.9	1.0	1.0	1.0	-0.1
1.6	0.9	1.1	0.0	1.0	1.1	1.2	1.3	1.2	-0.1
0.0	2.4	2.2	2.6	1.5	2.2	2.2	2.3	2.2	-0.1
2.7	3.3	3.2	0.0	2.5	2.9	2.9	3.1	3.0	-0.1
1.2	1.2	1.0	1.0	1.1	1.1	1.2	1.2	1.2	-0.1
1.3	1.1	1.1	1.2	1.0	1.1	1.2	1.2	1.2	-0.1
1.6	1.7	2.1	2.0	1.7	1.8	2.1	1.7	1.9	-0.1
3.0	3.0	2.5	3.0	2.2	2.7	2.9	2.8	2.8	-0.1
0.4	0.9	0.9	1.1	0.7	0.8	1.0	0.8	0.9	-0.1
1.7	1.4	1.8	1.4	1.9	1.6	1.8	1.6	1.7	-0.1
1.3	1.2	1.2	0.0	0.9	1.1	1.2	1.3	1.2	-0.1
2.6	0.0	2.0	0.0	1.4	2.0	2.1	2.1	2.1	-0.1
5.1	7.7	7.5	7.7	7.6	7.1	6.9	7.5	7.2	-0.1
1.9	0.0	1.4	1.5	1.5	1.6	1.6	1.8	1.7	-0.1
2.8	2.6	3.1	3.0	2.4	2.8	2.6	3.1	2.9	-0.1
0.4	0.3	0.5	0.0	0.0	0.4	0.5	0.5	0.5	-0.1
1.6	1.6	1.2	1.4	1.3	1.4	1.6	1.4	1.5	-0.1
0.7	0.6	0.9	0.7	0.8	0.7	0.9	0.8	0.8	-0.1
2.5	2.5	2.4	0.0	2.5	2.5	2.6	2.5	2.6	-0.1
0.0	1.4	1.8	1.8	1.5	1.6	1.8	1.6	1.7	-0.1
1.8	2.3	2.3	0.0	1.6	2.0	2.3	1.9	2.1	-0.1
1.4	0.0	0.0	0.8	0.9	1.0	1.2	1.0	1.1	-0.1
1.4	1.3	1.2	0.0	1.1	1.3	1.4	1.4	1.4	-0.1
1.6	1.3	1.2	0.0	1.1	1.3	1.4	1.4	1.4	-0.1
1.4	1.5	1.5	1.4	1.4	1.4	1.5	1.6	1.6	-0.1
1.6	2.6	1.8	0.0	1.5	1.9	1.9	2.0	2.0	-0.1
0.9	0.8	0.8	0.8	0.9	0.8	1.0	0.9	0.9	-0.1
1.7	0.0	1.7	0.0	1.4	1.6	1.8	1.7	1.7	-0.1
1.8	1.7	1.6	1.9	1.4	1.7	1.6	2.0	1.8	-0.1
0.8	0.8	1.2	1.0	1.1	1.0	1.2	1.0	1.1	-0.1
2.4	2.5	2.1	2.7	2.0	2.3	2.5	2.4	2.5	-0.1
0.0	2.1	2.3	2.8	1.7	2.2	2.9	1.7	2.3	-0.1
0.7	0.8	0.9	0.7	0.8	0.8	0.9	0.9	0.9	-0.1

357	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	R.QFC*STQAALQAMER.E
358	E9PPU0	EPPK1 Epiplakin	EPPK1	R.YLEGTSC*IAGVLVPAK.D
359	P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	R.VFNVFC*LYGNVEK.V
360	Q9BSH4	TACO1 Translational activator of cytochrome c oxidase 1	TACO1	K.KLDSLGLCSVSC*ALEFIPNSK.V
361	Q96P48	ARAP1 Arf-GAP with Rho-GAP domain, ANK repeat and PH dom	ARAP1	R.AVFPEGPC*EEPLQLR.K
362	Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	K.HLNEIDLFHC*IDPNDSK.H
363	P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	K.LNEC*VDHTPK.L
364	Q14914	PTGR1 Prostaglandin reductase 1	PTGR1	R.IAIC*GAISTYNR.T
365	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.AFAAGADIKEMQNLSFQDC*YSSK.F
366	Q99873	PRMT1 Protein arginine N-methyltransferase 1	PRMT1	K.VIGIEC*SSISDYAVK.I
367	Q9P2R7	SUCLA2 Succinyl-CoA ligase	SUCLA2	R.IC*NQVLVCER.K
368	P60174	TPI1 Triosephosphate isomerase	TPI1	K.IAVAAQNC*YK.V
369	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.SVHYC*PATK.K
370	Q9P107	GMIP GEM-interacting protein	GMIP	R.LC*QAFENGR.A
371	Q9ULA0	DNPEP Aspartyl aminopeptidase	DNPEP	R.NDTPC*GTTIGPILASR.L
372	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	R.GQAGGGGPGTGPGLGEAGSLATC*ELPLAK.S
373	Q5VWZ2	LYPLAL1 Lysophospholipase-like protein 1	LYPLAL1	R.C*IVSPAGR.H
374	P49189	ALDH9A1 4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	K.GALMANFLTQGQVC*CNGTR.V
375	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	K.ILSC*GEVIHVK.I
376	Q9Y365	STARD10 PCTP-like protein	STARD10	R.MEC*CDVPAETLYDVLHDIEYR.K
377	Q9BXW7	CECR5 Cat eye syndrome critical region protein 5	CECR5	K.AQELSALLGC*EVDADQVILSHSPMK.L
378	P22626	HNRNPA2B1 Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	K.LTDC*VVMRDPASK.R
379	P47756	CAPZB F-actin-capping protein subunit beta	CAPZB	K.DETVSDC*SPHIANIGR.L
380	Q9UHX1	PUF60 Poly(U)-binding-splicing factor PUF60	PUF60	R.ALAIMC*R.V
381	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	K.TC*GFDFTGAVEDISK.I
382	Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	R.QC*PIMDPAWEAPEGVPIDAIIFGGR.R
383	Q04917	YWHAH 14-3-3 protein eta	YWHAH	K.NC*NDFQYESK.V
384	Q6KB66	KRT80 Keratin, type II cytoskeletal 80	KRT80	R.C*HIDLSGIVEEVK.A
385	P30041	PRDX6 Peroxiredoxin-6	PRDX6	K.DINAYNC*EEPTEK.L
386	Q9NZL4	HSPBP1 Hsp70-binding protein 1	HSPBP1	R.LLDRDAC*DTVR.V
387	Q04917	YWHAH 14-3-3 protein eta	YWHAH	K.ELETVC*NDVLSLLDK.F
388	P30153	PPP2R1A Serine/threonine-protein phosphatase 2A 65 kDa reg	PPP2R1A	R.ENVIMSQILPC*IK.E
389	Q9BWD1	ACAT2 Acetyl-CoA acetyltransferase, cytosolic	ACAT2	R.ATVAPEDVSEVIFGHVLAAGC*GQNPVR.Q
390	P53004	BLVRA Biliverdin reductase A	BLVRA	K.MTVC*LETEKK.S
391	P36969	GPX4 Phospholipid hydroperoxide glutathione peroxidase,	GPX4	R.YAEC*GLR.I
392	Q8N163	KIAA1967 DBIRD complex subunit KIAA1967	KIAA1967	R.VVTQNIC*QYR.S
393	Q9NZZ3	CHMP5 Charged multivesicular body protein 5	CHMP5	K.APPPSLTDC*IGTVDSR.A
394	Q96FW1	OTUB1 Ubiquitin thioesterase OTUB1	OTUB1	K.TRPDGNC*FYR.A
395	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.LSSC*DSFTSTINELNHCLSLR.T
396	Q9C0C9	UBE2O Ubiquitin-conjugating enzyme E2 O	UBE2O	R.C*YNEMALIR.V

3.5	3.2	2.7	3.7	2.6	3.1	3.5	3.1	3.3	-0.1
0.9	1.7	1.3	1.5	1.0	1.3	1.5	1.3	1.4	-0.1
1.1	1.0	1.1	0.0	1.0	1.1	1.0	1.4	1.2	-0.1
1.4	0.9	1.0	1.0	1.0	1.1	1.0	1.3	1.2	-0.1
1.9	1.8	1.2	1.3	1.5	1.5	1.6	1.7	1.7	-0.1
1.5	1.3	1.2	1.2	1.1	1.3	1.3	1.4	1.4	-0.1
1.0	0.8	1.0	0.8	0.9	0.9	1.0	1.1	1.0	-0.1
1.1	1.0	1.2	0.0	1.2	1.1	1.3	1.2	1.2	-0.1
8.8	8.2	8.1	10.0	8.3	8.6	7.9	9.6	8.8	-0.1
1.3	1.2	1.2	1.2	1.1	1.2	1.3	1.3	1.3	-0.1
2.2	1.8	2.1	1.9	1.9	2.0	2.4	1.8	2.1	-0.1
0.7	0.7	1.1	1.2	0.8	0.9	1.1	0.9	1.0	-0.1
0.0	2.6	2.6	2.6	2.8	2.6	2.7	2.8	2.8	-0.1
1.0	1.0	0.0	0.7	1.0	0.9	1.0	1.1	1.0	-0.1
1.4	2.2	2.3	2.6	1.5	2.0	2.4	1.9	2.1	-0.1
2.1	1.7	1.2	1.5	1.2	1.5	1.6	1.7	1.7	-0.1
2.1	1.6	1.8	1.9	1.8	1.8	1.9	2.1	2.0	-0.1
2.6	1.7	1.5	1.6	1.7	1.8	1.8	2.1	2.0	-0.1
0.9	0.7	0.9	0.8	0.8	0.8	1.0	0.9	1.0	-0.1
1.6	1.0	1.3	1.2	1.1	1.2	1.4	1.3	1.3	-0.1
0.8	1.8	2.2	0.0	2.7	1.9	2.3	1.8	2.0	-0.1
0.9	0.9	0.8	0.9	0.9	0.9	1.1	1.0	1.0	-0.1
1.5	1.4	1.4	1.4	1.2	1.4	1.5	1.6	1.5	-0.1
0.9	0.8	1.1	0.9	0.8	0.9	1.0	1.1	1.0	-0.1
2.0	0.0	3.0	4.5	2.7	3.1	3.4	3.0	3.2	-0.1
4.7	3.7	3.7	3.8	3.8	4.0	4.3	3.9	4.1	-0.1
1.2	0.9	1.0	1.0	0.9	1.0	1.1	1.2	1.1	-0.1
1.8	1.3	1.4	1.6	1.2	1.5	1.7	1.5	1.6	-0.1
1.2	1.2	1.5	1.6	1.3	1.3	1.8	1.2	1.5	-0.1
1.8	1.7	1.6	1.6	1.3	1.6	1.6	1.9	1.7	-0.1
1.1	0.8	1.1	1.1	0.9	1.0	1.2	1.0	1.1	-0.1
0.0	1.1	1.3	2.9	2.1	1.9	1.4	2.6	2.0	-0.1
1.3	1.8	1.8	1.9	1.5	1.7	1.6	2.0	1.8	-0.1
1.9	1.3	1.3	1.3	1.2	1.4	1.8	1.2	1.5	-0.1
1.5	1.2	1.2	1.3	1.1	1.2	1.3	1.5	1.4	-0.1
3.6	3.4	3.6	3.0	2.7	3.2	2.6	4.2	3.4	-0.1
1.7	1.5	1.5	1.4	1.3	1.5	1.6	1.7	1.7	-0.1
1.5	1.9	1.7	1.9	1.6	1.7	2.0	1.8	1.9	-0.1
1.5	1.2	1.5	1.5	1.1	1.3	1.6	1.4	1.5	-0.1
1.9	1.3	1.8	1.5	1.3	1.6	1.6	1.8	1.7	-0.1

397	P07384	CAPN1 Calpain-1 catalytic subunit	CAPN1	R.LEIC*NLTPDALK.S
398	P61158	ACTR3 Actin-related protein 3	ACTR3	R.LPAC*VVDCGTGYTK.L
399	P07737	PFN1 Profilin-1	PFN1	K.C*YEMASHLR.R
400	Q5T1V6	DDX59 Probable ATP-dependent RNA helicase DDX59	DDX59	K.NLPC*ANVR.Q
401	P40925	MDH1 Malate dehydrogenase, cytoplasmic	MDH1	K.AIC*DHVR.D
402	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	R.AC*ALQVLSAILEGSK.Q
403	Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	R.VGLGIC*YDMR.F
404	P33240	CSTF2 Cleavage stimulation factor subunit 2	CSTF2	K.LC*VQNSPQEAR.N
405	P60174	TPI1 Triosephosphate isomerase	TPI1	R.IIYGGSVTGATC*K.E
406	P67936	TPM4 Tropomyosin alpha-4 chain	TPM4	K.EENVGLHQTLDQTLNELNC*I.-
407	P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	K.ALYDTFSAFGNILSC*K.V
408	O14980	XPO1 Exportin-1	XPO1	K.LDINLLDNVVNC*LYHGEGAQQR.M
409	P57081	WDR4 tRNA (guanine-N(7)-)-methyltransferase subunit WDR	WDR4	K.SGDVYSFSVLEPHGC*GR.L
410	O43747	AP1G1 AP-1 complex subunit gamma-1	AP1G1	R.FTC*TVNR.I
411	P52943	CRIP2 Cysteine-rich protein 2	CRIP2	R.ASSVTTFTGEPNTC*PR.C
412	P29401	TKT Transketolase	TKT	R.MAAISESNINLC*GSHCGVSIGEDGPSQMALEDLAMFR.S
413	P30044	PRDX5 Peroxiredoxin-5, mitochondrial	PRDX5	K.ALNVEPDGTGLTC*SLAPNIISQL.-
414	Q9NXW9	ALKBH4 Probable alpha-ketoglutarate-dependent dioxygenase	ALKBH4	R.MGLYPGLEGFRPVEQCNLDYC*PER.G
415	P51946	CCNH Cyclin-H	CCNH	R.TC*LSQLLDIMK.S
416	P55212	CASP6 Caspase-6	CASP6	R.GTC*ADRDNLTR.R
417	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	K.ASVGFGGSC*FQK.D
418	P07900	HSP90AA1 Heat shock protein HSP 90-alpha	HSP90AA1	R.VFIMDNC*EELIPEYLNFIR.G
419	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.EGVVEC*SFVK.S
420	Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	R.SC*YLSSLDLLLEHR.L
421	P14868	DARS Aspartate--tRNA ligase, cytoplasmic	DARS	R.LEYC*EALAMLR.E
422	O95372	LYPLA2 Acyl-protein thioesterase 2	LYPLA2	K.TYPGVMHSSC*PQEMAAVK.E
423	Q969H4	CNKSR1 Connector enhancer of kinase suppressor of ras 1	CNKSR1	K.NLLQLC*PQSLEALAVR.S
424	P49915	GMPS GMP synthase	GMPS	K.AC*TTEEDQEK.L
425	Q9NVG8	TBC1D13 TBC1 domain family member 13	TBC1D13	R.LLQDYPITDVC*QILQK.A
426	P48739	PITPNB Phosphatidylinositol transfer protein beta isoform	PITPNB	R.VVLPC*SVQEYQVGQLYSVAEASK.N
427	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	K.ITGC*ASPGK.T
428	P25398	RPS12 40S ribosomal protein S12	RPS12	R.QAHLC*VLASNCDEPMYVK.L
429	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	R.YASIC*QQNGIVPIVEPEILPDGDHDLK.R
430	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	K.FIC*EQDHQNFLR.L
431	Q9UJW0	DCTN4 Dynactin subunit 4	DCTN4	R.LLQPDFQPVC*ASQLYPR.H
432	P08559	PDHA1 Pyruvate dehydrogenase E1 component subunit alpha,	PDHA1	R.FAAAYC*R.S
433	P11142	HSPA8 Heat shock cognate 71 kDa protein	HSPA8	K.VC*NPIITK.L
434	Q9Y2Q3	GSTK1 Glutathione S-transferase kappa 1	GSTK1	K.ETTEAAC*R.Y
435	Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.LVVPATQC*GSLIGK.G
436	P84085	ARF5 ADP-ribosylation factor 5	ARF5	K.NIC*FTVWDVGGQDK.I
437	P43034	PAFAH1B1 Platelet-activating factor acetylhydrolase IB subu	PAFAH1B1	R.MVRPNQDGTLIASC*SNDQTVR.V

2.6	2.4	1.9	2.1	1.5	2.1	2.4	2.1	2.3	-0.1
0.9	0.9	1.1	1.1	0.9	1.0	1.1	1.2	1.1	-0.2
0.8	0.9	1.1	1.0	0.8	0.9	1.1	1.0	1.1	-0.2
3.0	1.7	1.5	1.7	1.5	1.9	2.0	2.1	2.0	-0.2
0.7	0.7	1.1	1.0	0.9	0.9	1.0	1.0	1.0	-0.2
4.3	3.3	3.8	3.1	3.1	3.5	3.5	3.8	3.7	-0.2
1.2	1.0	1.0	1.0	1.0	1.0	1.1	1.3	1.2	-0.2
1.4	1.5	1.4	1.5	1.4	1.4	1.5	1.7	1.6	-0.2
0.9	1.0	1.3	1.4	1.0	1.1	1.4	1.1	1.3	-0.2
5.1	2.2	2.2	2.7	1.8	2.8	2.7	3.2	3.0	-0.2
0.9	0.8	1.1	0.8	0.9	0.9	1.0	1.1	1.0	-0.2
1.5	1.1	1.2	1.3	1.1	1.2	1.4	1.4	1.4	-0.2
1.1	1.2	0.0	1.0	0.9	1.1	1.1	1.3	1.2	-0.2
1.8	1.5	1.4	0.0	1.4	1.5	1.5	1.8	1.7	-0.2
0.7	0.0	1.2	0.0	1.6	1.2	1.3	1.4	1.3	-0.2
0.5	0.0	0.8	0.8	0.0	0.7	0.9	0.9	0.9	-0.2
1.1	0.9	0.9	0.9	0.9	1.0	1.0	1.2	1.1	-0.2
1.6	0.0	1.1	1.7	1.2	1.4	1.5	1.6	1.6	-0.2
2.4	2.3	2.1	2.4	1.7	2.2	2.1	2.6	2.3	-0.2
0.0	0.8	0.6	1.0	0.6	0.7	0.9	0.9	0.9	-0.2
1.6	1.0	1.3	1.5	0.9	1.3	1.5	1.4	1.4	-0.2
1.4	1.2	1.3	1.2	1.1	1.2	1.3	1.5	1.4	-0.2
1.2	0.9	1.5	1.3	1.4	1.3	1.6	1.2	1.4	-0.2
0.8	1.1	1.1	1.4	1.1	1.1	1.4	1.1	1.3	-0.2
1.5	1.1	1.2	1.1	0.9	1.1	1.3	1.3	1.3	-0.2
1.1	1.0	1.2	1.4	0.9	1.1	1.5	1.1	1.3	-0.2
0.0	1.3	1.2	1.3	1.1	1.2	1.4	1.3	1.4	-0.2
0.0	1.4	1.3	1.1	1.0	1.2	1.5	1.3	1.4	-0.2
1.7	1.2	1.2	1.3	1.1	1.3	1.5	1.5	1.5	-0.2
1.2	0.0	2.7	3.5	0.0	2.5	3.2	2.1	2.6	-0.2
3.0	3.1	2.2	2.3	2.5	2.6	2.1	3.5	2.8	-0.2
1.3	1.1	1.0	1.1	1.0	1.1	1.3	1.3	1.3	-0.2
0.9	1.4	1.6	2.0	1.2	1.4	1.8	1.4	1.6	-0.2
1.1	0.0	1.0	0.0	1.0	1.0	1.1	1.3	1.2	-0.2
1.6	1.4	1.2	1.6	1.2	1.4	1.7	1.4	1.5	-0.2
3.6	2.9	2.9	2.6	2.6	2.9	2.9	3.3	3.1	-0.2
0.8	0.9	1.1	1.5	1.0	1.1	1.3	1.2	1.2	-0.2
1.8	1.7	1.9	1.6	1.7	1.7	2.0	1.8	1.9	-0.2
2.3	2.0	1.9	1.9	1.6	1.9	2.0	2.2	2.1	-0.2
1.4	1.1	1.4	1.8	1.4	1.4	1.8	1.4	1.6	-0.2
5.1	4.8	4.6	5.6	5.3	5.1	5.1	5.4	5.3	-0.2

438	P31150	GDI1 Rab GDP dissociation inhibitor alpha	GDI1	K.NTNDANSC*QIIIPQNQVNR.K
439	Q7L2H7	EIF3M Eukaryotic translation initiation factor 3 subunit	EIF3M	K.VAASC*GAIQYIPTELDQVR.K
440	Q9Y266	NUDC Nuclear migration protein nudC	NUDC	R.WTQTLSELDLAVPFC*VNFR.L
441	Q9NQC3	RTN4 Reticulon-4	RTN4	K.YSNSALGHVNC*TIK.E
442	P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.LVVPASQC*GSLIGK.G
443	Q8TB45	DEPTOR DEP domain-containing mTOR-interacting protein	DEPTOR	K.SPSSQETHDSPFC*LR.K
444	P36507	MAP2K2 Dual specificity mitogen-activated protein kinase	MAP2K2	K.LC*DFGVSGQLIDSMANSFVGTR.S
445	Q9Y5P6	GMPPB Mannose-1-phosphate guanyltransferase beta	GMPPB	R.LC*SGPGIVGNVLVDPSAR.I
446	P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	R.FSPNSSNPIIVSC*GWDK.L
447	Q14694	USP10 Ubiquitin carboxyl-terminal hydrolase 10	USP10	R.TPSYSISSTLNPQAPEFILGC*TASK.I
448	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	R.YDDMAAC*MK.S
449	P61160	ACTR2 Actin-related protein 2	ACTR2	K.LC*YVGYNIEQEQK.L
450	P26641	EEF1G Elongation factor 1-gamma	EEF1G	K.AAAPAPEEEMDEC*EQALAAEPK.A
451	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.RSIQFVDWC*PTGFK.V
452	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.GPFVEAEVPDVDLEC*PDAK.L
453	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.SIC*TTVLELLDK.Y
454	Q9H6S3	EPS8L2 Epidermal growth factor receptor kinase substrate	EPS8L2	R.SGQAGYVPC*NILGEARPEDAGAPFEQAGQK.Y
455	Q9UI30	TRMT112 tRNA methyltransferase 112 homolog	TRMT112	R.IC*PVEFNPNFVAR.M
456	Q9UHD8	SEPT9 Septin-9	9-Sep	K.LTVIDTPGFGDHINNENC*WQPIMK.F
457	P38646	HSPA9 Stress-70 protein, mitochondrial	HSPA9	K.AKC*ELSSSVQTDINLPYLTMDSSGPK.H
458	Q9Y224	C14orf166 UPF0568 protein C14orf166	C14orf166	K.LTALDYHNPAGFNC*K.D
459	P31350	RRM2 Ribonucleoside-diphosphate reductase subunit M2	RRM2	K.LIGMNC*TLMK.Q
460	Q13526	PIN1 Peptidyl-prolyl cis-trans isomerase NIMA-interacti	PIN1	K.IKSGEEDFESLASQFSDC*SSAK.A
461	Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	R.AITIAGIPQSIIEC*VK.Q
462	O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	R.ANSSVVSVNC*K.G
463	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	R.AGGIETIANEFSDRC*TPSVISFGSK.N
464	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	R.TIC*AILENYQTEK.G
465	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	R.DHQPC*IIFMDEIDAIGGR.R
466	P49753	ACOT2 Acyl-coenzyme A thioesterase 2, mitochondrial	ACOT2	K.SEFYANEAC*KR.L
467	P63208	SKP1 S-phase kinase-associated protein 1	SKP1	R.KENQWC*EEK.-
468	P00492	HPRT1 Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	K.SYC*NDQSTGDIK.V
469	Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.AVTNHSVYC*STK.G
470	Q5RKV6	EXOSC6 Exosome complex component MTR3	EXOSC6	R.APPGGC*EER.E
471	Q9P1F3	ABRACL Costars family protein ABRACL	ABRACL	K.C*ANLFEALVGTLK.A
472	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitoch	MCCC2	K.NIAQIAVVMGSC*TAGGAYVPAMADENIIVR.K
473	P28838	LAP3 Cytosol aminopeptidase	LAP3	R.SAGAC*TAAAFLK.E
474	P26358	DNMT1 DNA (cytosine-5)-methyltransferase 1	DNMT1	K.NQLC*DLETK.L
475	B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	K.IFVGNVDGADTTPEELAALFAPYGTVMSC*AVMK.Q
476	E9PPU0	EPPK1 Epiplakin	EPPK1	R.TGGQALSTLEC*VKPYLEGSGCIAGVTVPSTR.E

1.0	0.9	1.3	0.0	1.0	1.0	1.4	1.0	1.2	-0.2
1.4	1.6	1.4	1.7	1.4	1.5	1.7	1.7	1.7	-0.2
0.0	1.5	1.3	0.0	1.3	1.4	1.5	1.6	1.5	-0.2
1.7	1.4	1.7	1.5	1.4	1.5	1.6	1.8	1.7	-0.2
1.9	1.6	1.6	1.5	1.4	1.6	1.7	1.8	1.8	-0.2
2.3	2.6	1.9	2.6	1.9	2.3	2.3	2.6	2.4	-0.2
1.4	1.0	1.2	1.3	1.1	1.2	1.4	1.4	1.4	-0.2
0.0	1.2	1.0	1.2	1.0	1.1	1.3	1.3	1.3	-0.2
3.5	5.1	4.5	4.9	3.9	4.4	4.3	4.9	4.6	-0.2
7.0	3.5	3.5	3.6	2.6	4.0	4.0	4.5	4.2	-0.2
0.7	0.7	1.1	1.0	1.0	0.9	1.2	1.0	1.1	-0.2
1.4	2.1	2.3	0.0	1.7	1.9	1.8	2.4	2.1	-0.2
1.7	1.4	1.3	1.5	1.1	1.4	1.6	1.7	1.6	-0.2
4.4	4.1	3.8	3.9	3.5	3.9	4.1	4.2	4.1	-0.2
1.9	2.0	1.8	1.7	1.6	1.8	1.9	2.0	2.0	-0.2
0.8	0.7	0.9	0.8	0.7	0.8	0.9	1.0	1.0	-0.2
1.1	1.2	1.2	1.0	1.1	1.1	1.4	1.2	1.3	-0.2
1.8	1.9	1.8	1.7	1.6	1.8	1.9	2.0	2.0	-0.2
2.9	2.7	2.6	3.1	2.4	2.8	2.9	3.0	3.0	-0.2
1.2	1.2	1.5	1.1	1.3	1.2	1.4	1.5	1.4	-0.2
1.4	1.4	1.3	1.5	1.2	1.4	1.5	1.6	1.6	-0.2
0.7	0.4	0.8	0.8	0.8	0.7	0.9	0.9	0.9	-0.2
3.7	2.9	2.4	3.7	2.3	3.0	3.2	3.2	3.2	-0.2
1.2	1.0	1.2	0.9	1.0	1.1	1.3	1.2	1.3	-0.2
2.4	2.3	2.0	2.7	1.8	2.2	2.2	2.7	2.4	-0.2
3.9	5.3	4.7	0.0	3.9	4.4	4.5	4.8	4.7	-0.2
1.2	0.9	1.2	0.0	1.0	1.1	1.3	1.2	1.3	-0.2
3.4	4.5	2.7	2.8	2.7	3.2	3.4	3.4	3.4	-0.2
1.4	1.0	1.0	1.0	1.1	1.1	1.2	1.4	1.3	-0.2
2.2	1.8	1.8	1.8	1.6	1.8	1.9	2.2	2.0	-0.2
1.6	1.1	1.2	1.4	1.2	1.3	1.4	1.6	1.5	-0.2
2.0	1.6	1.5	1.6	1.4	1.6	1.7	2.0	1.8	-0.2
1.5	0.0	0.0	1.3	1.0	1.3	1.4	1.6	1.5	-0.2
1.8	1.6	1.7	1.5	1.5	1.6	1.9	1.7	1.8	-0.2
2.0	0.0	2.0	1.8	1.5	1.8	2.0	2.1	2.0	-0.2
2.8	3.7	3.0	3.1	3.0	3.1	3.1	3.6	3.3	-0.2
1.6	0.0	1.6	1.8	0.8	1.4	1.6	1.7	1.7	-0.2
1.2	1.3	1.3	0.0	1.3	1.3	1.4	1.6	1.5	-0.2
2.5	0.0	1.8	2.2	2.5	2.3	2.2	2.7	2.5	-0.2

477	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	K.VQYPQSQAC*K.M
478	P00390	GSR Glutathione reductase, mitochondrial	GSR	K.LGGTC*VNVGCVPK.K
479	Q6GMV2	SMYD5 SET and MYND domain-containing protein 5	SMYD5	R.LFSQFC*NK.T
480	P53602	MVD Diphosphomevalonate decarboxylase	MVD	R.DGDPLPSSLSC*K.V
481	P30153	PPP2R1A Serine/threonine-protein phosphatase 2A 65 kDa reg	PPP2R1A	R.LNIISNLDC*VNEVIGIR.Q
482	Q9BV79	MECR Trans-2-enoyl-CoA reductase, mitochondrial	MECR	R.LALNC*VGGK.S
483	P55735	SEC13 Protein SEC13 homolog	SEC13	R.LATC*SSDR.S
484	O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	R.EEFASTC*PDDEEIELAYEQVAK.A
485	P29373	CRABP2 Cellular retinoic acid-binding protein 2	CRABP2	K.VGEEFEEQTVDGRPC*K.S
486	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	R.LDFVC*SFLQK.N
487	Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitoch	MCCC2	K.ITLIIGGSYGAGNYGMC*GR.A
488	P23396	RPS3 40S ribosomal protein S3	RPS3	R.GLC*AIAQAESLR.Y
489	P62993	GRB2 Growth factor receptor-bound protein 2	GRB2	K.VLNEEC*DQNWYK.A
490	P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	R.ALANSLAC*QGK.Y
491	P62258	YWHAE 14-3-3 protein epsilon	YWHAE	K.LIC*CDILDVLDK.H
492	P00338	LDHA L-lactate dehydrogenase A chain	LDHA	K.NRVIGSGC*NLDSAR.F
493	Q969Z0	TBRG4 Protein TBRG4	TBRG4	R.LATDLLSLMPSLTSGEVAHC*AK.S
494	Q92945	KHSRP Far upstream element-binding protein 2	KHSRP	K.VQQAC*EMVMDILR.E
495	Q9NVU0	POLR3E DNA-directed RNA polymerase III subunit RPC5	POLR3E	R.AAGTDSFNGHPPQGC*ASTPVAR.E
496	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.YDDMATC*MK.A
497	P46782	RPS5 40S ribosomal protein S5	RPS5	K.TIAEC*LADELINAAK.G
498	P61247	RPS3A 40S ribosomal protein S3a	RPS3A	R.LFC*VGFTK.K
499	P12004	PCNA Proliferating cell nuclear antigen	PCNA	K.C*AGNEDIITLR.A
500	Q9BSU1	C16orf70 UPF0183 protein C16orf70	C16orf70	R.LLAAGC*GPGLLADAK.M
501	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	K.EGC*TEVSLLR.V
502	P31947	SFN 14-3-3 protein sigma	SFN	K.VETELQGVC*DTVLGLLDSHLIK.E
503	P17676	CEBPB CCAAT/enhancer-binding protein beta	CEBPB	K.APPTAC*YAGAAPAPSQVK.S
504	P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.YMAC*CLLYR.G
505	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.LFQEC*CPHSTDR.V
506	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVGVEVPDVELEC*PDAK.L
507	O95571	ETHE1 Protein ETHE1, mitochondrial	ETHE1	R.TDFQQGC*AK.T
508	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	R.YLLQYQEPIPC*EQLVTALCDIK.Q
509	P10620	MGST1 Microsomal glutathione S-transferase 1	MGST1	K.VFANPEDC*VAFGK.G
510	Q9Y4P1	ATG4B Cysteine protease ATG4B	ATG4B	K.NFPAIGGTGPTSDTGWGC*MLR.C
511	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	K.ATC*IGNNSAAAVSMLK.Q
512	O15382	BCAT2 Branched-chain-amino-acid aminotransferase, mitoch	BCAT2	R.EVFGSGTAC*QVCPVHR.I
513	P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.YLAEVAC*GDDR.K
514	Q15459	SF3A1 Splicing factor 3A subunit 1	SF3A1	R.EVLDQVC*YR.V
515	A0AVT1	UBA6 Ubiquitin-like modifier-activating enzyme 6	UBA6	R.KPNVGC*QQDSEELLK.L
516	P49721	PSMB2 Proteasome subunit beta type-2	PSMB2	R.NLADC*LR.S
517	O75223	GGCT Gamma-glutamylcyclotransferase	GGCT	R.NPSAAFFC*VAR.L
518	P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.GSDFDC*ELR.L

3.9	3.6	2.8	3.1	3.1	3.3	3.4	3.6	3.5	-0.2
1.0	0.8	0.9	0.9	0.8	0.9	1.2	1.0	1.1	-0.2
1.6	1.3	1.1	1.4	1.2	1.3	1.4	1.7	1.5	-0.2
1.6	1.5	1.2	1.4	1.5	1.4	1.4	1.9	1.7	-0.2
1.5	1.1	1.1	1.3	0.6	1.1	1.4	1.3	1.3	-0.2
3.1	4.2	3.7	0.0	3.0	3.5	3.8	3.7	3.7	-0.2
0.8	1.1	1.7	0.0	0.9	1.1	1.5	1.2	1.3	-0.2
0.9	1.0	1.0	1.2	0.8	1.0	1.2	1.2	1.2	-0.2
1.0	0.8	1.3	1.0	0.9	1.0	1.4	1.1	1.2	-0.2
1.7	1.3	1.3	1.4	1.2	1.4	1.5	1.7	1.6	-0.2
1.4	1.0	0.0	1.3	0.9	1.2	1.6	1.2	1.4	-0.2
2.3	2.3	2.2	2.1	2.0	2.2	2.4	2.4	2.4	-0.2
1.4	1.3	1.1	1.3	1.2	1.3	1.4	1.6	1.5	-0.2
0.9	1.5	1.5	1.5	1.0	1.3	1.8	1.3	1.5	-0.2
1.0	0.9	1.1	0.9	0.9	1.0	1.1	1.3	1.2	-0.2
1.0	1.9	1.4	1.8	1.3	1.5	1.4	2.0	1.7	-0.2
1.9	2.6	3.0	2.5	2.6	2.5	2.9	2.7	2.8	-0.2
1.6	0.0	1.3	0.0	1.5	1.5	1.4	2.0	1.7	-0.2
0.0	1.8	1.4	2.0	1.4	1.7	1.9	1.9	1.9	-0.2
0.7	0.8	0.0	1.1	0.9	0.9	1.1	1.1	1.1	-0.2
3.3	2.8	2.5	2.5	2.3	2.7	2.8	3.0	2.9	-0.2
1.9	1.8	1.7	1.4	1.5	1.7	1.9	1.9	1.9	-0.2
1.2	1.0	1.1	1.2	0.9	1.1	1.3	1.3	1.3	-0.2
0.0	1.5	1.5	1.7	1.3	1.5	1.6	1.9	1.7	-0.2
1.8	1.5	1.4	1.6	1.5	1.6	1.7	1.9	1.8	-0.2
0.8	0.8	1.2	0.0	0.9	0.9	1.2	1.2	1.2	-0.2
0.0	2.4	1.9	2.5	1.6	2.1	2.4	2.3	2.3	-0.2
3.4	3.2	3.3	3.2	3.0	3.2	3.4	3.6	3.5	-0.2
1.7	1.4	1.5	1.6	1.4	1.5	1.7	1.8	1.8	-0.2
2.6	2.1	1.6	1.9	1.7	2.0	2.1	2.3	2.2	-0.2
2.6	1.8	1.5	1.4	1.5	1.8	1.9	2.1	2.0	-0.2
0.8	0.8	1.2	1.0	0.8	0.9	1.1	1.2	1.2	-0.2
1.2	1.1	1.0	0.0	1.0	1.1	1.2	1.4	1.3	-0.2
0.0	1.2	1.2	1.0	1.0	1.1	1.2	1.5	1.3	-0.2
0.7	1.0	1.3	1.2	0.8	1.0	1.3	1.2	1.3	-0.2
1.3	1.4	1.1	1.1	1.1	1.2	1.4	1.5	1.4	-0.2
1.6	1.2	1.2	1.0	1.1	1.2	1.3	1.6	1.4	-0.2
1.5	1.6	1.4	1.3	1.2	1.4	1.4	1.9	1.6	-0.2
1.4	1.2	1.3	1.3	1.2	1.3	1.5	1.6	1.5	-0.2
1.2	1.9	1.9	2.6	1.8	1.9	2.2	2.0	2.1	-0.2
0.8	0.8	1.4	0.7	1.1	0.9	1.3	1.1	1.2	-0.2
1.6	1.8	1.6	1.8	1.5	1.7	1.8	2.0	1.9	-0.2

519	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.GEETPVIVGSALC*ALEGR.D
520	Q96EI5	TCEAL4 Transcription elongation factor A protein-like 4	TCEAL4	R.KPEVTC*TLEDK.K
521	Q9Y315	DERA Putative deoxyribose-phosphate aldolase	DERA	K.GITTAAVC*VYPAR.V
522	P63220	RPS21 40S ribosomal protein S21	RPS21	K.TYAIC*GAIR.R
523	Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVDVEVPDVELEC*PDAK.L
524	P21333	FLNA Filamin-A	FLNA	K.THEAEIVEGENHTYC*IR.F
525	Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	R.KVEELQAC*VETAR.Q
526	P55060	CSE1L Exportin-2	CSE1L	K.NLFEDQNTLTSIC*EK.V
527	P25398	RPS12 40S ribosomal protein S12	RPS12	K.LVEALC*AEHQINLIK.V
528	P09467	FBP1 Fructose-1,6-bisphosphatase 1	FBP1	R.GTGELTQLLNSLC*TAVK.A
529	P50395	GDI2 Rab GDP dissociation inhibitor beta	GDI2	R.TDDYLDQPC*YETINR.I
530	P46782	RPS5 40S ribosomal protein S5	RPS5	R.VNQAIWLLC*TGAR.E
531	P22314	UBA1 Ubiquitin-like modifier-activating enzyme 1	UBA1	K.YFLVGAGAIGC*ELLK.N
532	P78347	GTF2I General transcription factor II-I	GTF2I	K.ITINPGC*VVVDGMPPGVSFK.A
533	Q9NS86	LANCL2 LanC-like protein 2	LANCL2	R.SVVC*QESDLPDELLYGR.A
534	Q9Y490	TLN1 Talin-1	TLN1	K.AGALQC*SPSDAYTK.K
535	P60174	TPI1 Triosephosphate isomerase	TPI1	K.DC*GATWVVLGHSER.R
536	Q8N6M0	OTUD6B OTU domain-containing protein 6B	OTUD6B	K.DC*ALTVVALR.S
537	P62304	SNRPE Small nuclear ribonucleoprotein E	SNRPE	R.IEGC*IIGFDEYMNLVLDDAEEIHSK.T
538	Q9HBM1	SPC25 Kinetochore protein Spc25	SPC25	K.STDTSC*QMAGLR.D
539	O95861	BPNT1 3(2),5-bisphosphate nucleotidase 1	BPNT1	K.TC*ATDLQTK.A
540	O43765	SGTA Small glutamine-rich tetratricopeptide repeat-cont	SGTA	R.AIC*IDPAYSK.A
541	P07900	HSP90AA1 Heat shock protein HSP 90-alpha	HSP90AA1	R.LVTSPC*CIVTSTYGWTANMER.I
542	P30086	PEBP1 Phosphatidylethanolamine-binding protein 1	PEBP1	R.APVAGTC*YQAEWDDYVPK.L
543	Q04760	GLO1 Lactoylglutathione lyase	GLO1	K.C*DFPIMK.F
544	P51858	HDGF Hepatoma-derived growth factor	HDGF	K.C*GDLVFAK.M
545	O75153	KIAA0664 Clustered mitochondria protein homolog	KIAA0664	K.C*LTQQAVALQR.T
546	Q12959	DLG1 Disks large homolog 1	DLG1	K.LLAVNNVC*LEEVTHEEAVTALK.N
547	P49327	FASN Fatty acid synthase	FASN	K.SFYGSTLFLC*R.R
548	O43865	AHCYL1 Putative adenosylhomocysteinase 2	AHCYL1	K.LC*VPAMNVNDSVTK.Q
549	O60701	UGDH UDP-glucose 6-dehydrogenase	UGDH	R.ISSINSISALC*EATGADVEEVATAIGMDQR.I
550	Q02790	FKBP4 Peptidyl-prolyl cis-trans isomerase FKBP4	FKBP4	K.TQLAVC*QQR.I
551	P00491	PNP Purine nucleoside phosphorylase	PNP	R.AC*VMMQGR.F
552	Q07020	RPL18 60S ribosomal protein L18	RPL18	K.GC*GTVLLSGPR.K
553	Q9Y3F4	STRAP Serine-threonine kinase receptor-associated protei	STRAP	K.IGFPETTEEELEEIASENSDC*IFPSAPDVK.A
554	P35270	SPR Sepiapterin reductase	SPR	R.AVC*LLTGASR.G
555	Q86YH6	PDSS2 Decaprenyl-diphosphate synthase subunit 2	PDSS2	R.C*LLSDELSNIAMQVR.K
556	Q15233	NONO Non-POU domain-containing octamer-binding protein	NONO	R.C*SEGSFLLTTFPRPVTVEPMDQLDDEEGLPEK.L
557	Q4ZG55	GREB1 Protein GREB1	GREB1	R.LINSSC*LVR.T
558	Q13404	UBE2V1 Ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	K.LPQPPEGQC*YSN.-
559	Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multif	AIMP2	K.FSIQTMC*PIEGEGNIAR.F

5.5	5.8	4.8	2.8	4.4	4.7	4.6	5.3	4.9	-0.2
1.2	1.1	1.1	1.0	1.3	1.1	1.4	1.4	1.4	-0.3
0.0	2.8	2.8	3.0	3.1	2.9	3.2	3.2	3.2	-0.3
3.6	3.1	2.8	2.4	2.3	2.8	3.1	3.0	3.1	-0.3
2.1	1.8	1.5	1.5	1.3	1.7	2.0	1.9	1.9	-0.3
2.8	0.0	2.8	2.5	1.7	2.5	2.4	3.0	2.7	-0.3
1.2	1.5	0.0	0.0	0.8	1.2	1.3	1.6	1.4	-0.3
2.0	2.9	4.4	3.5	3.1	3.2	3.6	3.3	3.4	-0.3
1.5	1.4	1.5	1.3	1.2	1.4	1.5	1.8	1.6	-0.3
0.7	0.6	0.8	0.7	0.8	0.7	1.1	0.9	1.0	-0.3
1.0	1.0	1.0	1.0	0.9	1.0	1.2	1.3	1.2	-0.3
2.4	2.5	2.6	2.3	1.8	2.3	2.6	2.6	2.6	-0.3
0.0	1.7	1.7	1.7	1.3	1.6	2.1	1.7	1.9	-0.3
1.4	1.0	1.0	1.1	1.3	1.2	1.2	1.7	1.5	-0.3
1.9	1.3	1.2	1.3	1.8	1.5	1.5	2.0	1.8	-0.3
1.0	1.3	1.4	0.0	1.0	1.2	1.7	1.2	1.4	-0.3
0.5	0.7	0.9	0.0	0.8	0.7	1.1	0.8	1.0	-0.3
2.0	1.3	1.2	0.0	1.3	1.4	1.8	1.6	1.7	-0.3
0.0	0.0	1.2	1.1	1.2	1.2	1.5	1.5	1.5	-0.3
1.3	1.2	2.0	0.0	1.2	1.4	1.6	1.8	1.7	-0.3
2.0	1.4	1.7	1.6	0.9	1.5	1.8	1.8	1.8	-0.3
2.1	1.3	1.4	1.2	1.4	1.5	1.4	2.0	1.7	-0.3
0.0	0.0	0.7	1.2	1.1	1.0	1.3	1.3	1.3	-0.3
1.3	1.4	1.5	1.3	1.1	1.3	1.7	1.5	1.6	-0.3
1.8	2.0	2.2	2.1	2.0	2.0	2.3	2.3	2.3	-0.3
1.6	1.6	2.0	1.5	1.9	1.7	2.1	1.9	2.0	-0.3
1.8	1.4	1.5	1.8	1.7	1.7	2.0	1.9	1.9	-0.3
1.2	0.8	1.0	0.8	0.0	0.9	1.3	1.2	1.2	-0.3
1.5	3.7	2.9	3.0	2.2	2.7	3.1	2.8	2.9	-0.3
1.4	1.2	1.2	1.2	1.4	1.3	1.5	1.6	1.5	-0.3
1.1	0.6	0.8	0.9	0.9	0.9	1.2	1.2	1.2	-0.3
1.1	1.0	1.1	1.2	1.0	1.1	1.3	1.5	1.4	-0.3
0.6	0.7	1.0	1.0	0.9	0.8	1.2	1.1	1.1	-0.3
3.0	3.3	2.7	2.8	3.0	2.9	3.1	3.4	3.2	-0.3
1.5	2.2	1.8	2.0	1.9	1.9	1.9	2.5	2.2	-0.3
3.1	2.8	2.8	2.1	2.4	2.6	2.9	3.0	2.9	-0.3
1.6	1.7	1.5	1.8	1.6	1.6	1.7	2.1	1.9	-0.3
2.7	2.7	1.9	0.0	2.1	2.4	2.6	2.7	2.6	-0.3
3.8	5.4	4.1	0.0	5.8	4.8	4.8	5.3	5.1	-0.3
0.6	0.5	1.0	0.6	1.1	0.7	1.2	0.9	1.0	-0.3
2.3	2.0	2.6	2.9	1.9	2.3	2.7	2.6	2.6	-0.3

560	Q96CD2	PPCDC Phosphopantothenoylcysteine decarboxylase	PPCDC	K.ASC*PAAAPLMER.K
561	P49915	GMPS GMP synthase	GMPS	R.VICAEEPYIC*K.D
562	Q06323	PSME1 Proteasome activator complex subunit 1	PSME1	K.VDVFREDLC*TK.T
563	P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	K.YAGLSTC*FR.Q
564	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	R.DLLVQQASQC*LSK.L
565	P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	K.YLEC*SALTQR.G
566	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	K.C*EFQDAYVLLSEK.K
567	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	K.C*AMTALSSK.L
568	P43897	TSFM Elongation factor Ts, mitochondrial	TSFM	R.FEC*GEGEEAAETE.-
569	P60763	RAC3 Ras-related C3 botulinum toxin substrate 3	RAC3	R.AVLC*PPPVK.K
570	P53582	METAP1 Methionine aminopeptidase 1	METAP1	R.VCETDGC*SSEAK.L
571	Q9UMS0	NFU1 NFU1 iron-sulfur cluster scaffold homolog, mitocho	NFU1	K.LQGSCTSC*PSSIITLK.N
572	Q15102	PAFAH1B3 Platelet-activating factor acetylhydrolase IB subu	PAFAH1B3	R.LGYTPVC*R.A
573	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.TLTSC*FLSCVVCVEGIVTK.C
574	P25205	MCM3 DNA replication licensing factor MCM3	MCM3	R.YVLC*TAPR.A
575	P48643	CCT5 T-complex protein 1 subunit epsilon	CCT5	R.VVYGGGAAEISCALAVSQEADKC*PTLEQYAMR.A
576	Q8TEW0	PARD3 Partitioning defective 3 homolog	PARD3	K.VTVC*FGR.T
577	P21964	COMT Catechol O-methyltransferase	COMT	R.YLPDTLLLEEC*GLLR.K
578	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	R.LQEALDAEMLEDEAGGGGAGPGGAC*K.A
579	P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	R.GDEC*GLALGR.L
580	Q9Y3D2	MSRB2 Methionine-R-sulfoxide reductase B2, mitochondrial	MSRB2	K.YC*SGTGWPSFSEAHGTSGSDESHTGILR.R
581	Q15369	TCEB1 Transcription elongation factor B polypeptide 1	TCEB1	K.VC*MYFTYK.V
582	Q6AI08	HEATR6 HEAT repeat-containing protein 6	HEATR6	R.LC*ALRPDDSSSAR.T
583	P52907	CAPZA1 F-actin-capping protein subunit alpha-1	CAPZA1	K.TIDGQQTIIAC*IESHQFQPK.N
584	P49841	GSK3B Glycogen synthase kinase-3 beta	GSK3B	R.TTSFAESC*KPVQQPSAFGSMK.V
585	P13639	EEF2 Elongation factor 2	EEF2	K.IWC*FGPDGTGPNILTDITK.G
586	P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	R.C*IPALDSLTPANEDQK.I
587	Q99497	PARK7 Protein DJ-1	PARK7	K.VTVAGLAGKDPVQC*SR.D
588	P46777	RPL5 60S ribosomal protein L5	RPL5	K.VGLTNYAAAYC*TGLLLAR.R
589	P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	R.SLLINAVEASC*IR.T
590	P61970	NUTF2 Nuclear transport factor 2	NUTF2	K.NINDAWVC*TNDMFR.L
591	Q7Z2W4	ZC3HAV1 Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	K.NSNVDSSYLESLYQSC*PR.G
592	Q9Y3B4	SF3B14 Pre-mRNA branch site protein p14	SF3B14	K.NACDHLSGFNVC*NR.Y
593	P02795	MT2A Metallothionein-2	MT2A	K.SC*CSCCPVGCAK.C
594	P37837	TALDO1 Transaldolase	TALDO1	K.ALAGC*DFLTISPK.L
595	Q71U36	TUBA1A Tubulin alpha-1A chain	TUBA1A	R.TIQFVDWC*PTGFK.V
596	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.TIIPLISQC*TPK.V
597	P52209	PGD 6-phosphogluconate dehydrogenase, decarboxylating	PGD	R.C*LSSLKDER.I
598	P49368	CCT3 T-complex protein 1 subunit gamma	CCT3	R.TLIQNC*GASTIR.L
599	P22102	GART Trifunctional purine biosynthetic protein adenosin	GART	R.FGDPEC*QVILPLLK.S
600	O15355	PPM1G Protein phosphatase 1G	PPM1G	K.C*SGDGVGAPR.L

3.0	2.2	2.1	2.2	1.6	2.2	2.3	2.8	2.5	-0.3
1.7	1.5	1.5	1.7	1.5	1.6	2.0	1.8	1.9	-0.3
2.0	1.8	1.8	0.0	1.7	1.8	2.0	2.2	2.1	-0.3
1.3	1.0	1.2	1.3	1.1	1.2	1.5	1.4	1.5	-0.3
3.7	3.3	3.7	2.9	2.7	3.3	3.6	3.5	3.6	-0.3
1.0	0.9	1.1	2.3	1.0	1.3	1.7	1.4	1.6	-0.3
2.3	2.2	2.3	2.3	1.8	2.2	2.4	2.6	2.5	-0.3
2.2	2.0	2.6	0.0	1.7	2.1	2.2	2.6	2.4	-0.3
0.7	1.5	2.1	0.0	2.3	1.6	2.3	1.6	1.9	-0.3
0.0	1.9	1.9	2.1	1.9	1.9	2.2	2.3	2.2	-0.3
0.0	5.8	2.6	2.9	1.9	3.3	3.2	4.0	3.6	-0.3
4.5	0.0	2.8	6.0	3.2	4.1	4.9	3.9	4.4	-0.3
0.7	1.2	1.2	0.0	1.1	1.0	1.4	1.3	1.3	-0.3
0.0	1.8	1.7	2.0	1.6	1.7	2.1	2.1	2.1	-0.3
2.0	2.0	2.1	2.1	1.6	2.0	2.1	2.4	2.3	-0.3
1.5	1.3	1.3	0.0	1.4	1.4	1.6	1.8	1.7	-0.3
0.0	1.9	2.3	2.1	1.9	2.0	2.2	2.5	2.3	-0.3
0.5	0.5	0.9	0.7	0.8	0.7	1.2	0.9	1.0	-0.3
1.4	1.3	1.5	1.4	1.5	1.4	1.8	1.7	1.7	-0.3
2.8	3.6	3.3	3.7	3.2	3.3	3.6	3.6	3.6	-0.3
1.8	3.8	1.7	1.5	1.5	2.1	2.6	2.2	2.4	-0.3
0.8	0.9	1.0	0.0	0.8	0.9	1.3	1.0	1.2	-0.3
3.4	3.4	2.7	3.2	2.3	3.0	3.4	3.2	3.3	-0.3
0.8	0.6	1.0	0.7	0.8	0.8	1.1	1.1	1.1	-0.3
4.8	0.0	2.7	3.9	3.4	3.7	3.7	4.3	4.0	-0.3
1.2	2.2	2.1	2.1	2.0	1.9	2.5	2.1	2.3	-0.3
3.2	3.3	2.7	3.1	2.4	2.9	3.1	3.4	3.3	-0.3
0.7	0.8	0.9	0.9	0.7	0.8	1.2	1.1	1.1	-0.3
1.0	1.4	2.2	1.7	1.7	1.6	1.5	2.4	1.9	-0.3
4.4	5.0	4.0	4.2	3.6	4.2	4.5	4.6	4.5	-0.3
0.9	1.0	1.2	1.2	1.0	1.1	1.4	1.4	1.4	-0.3
3.8	2.5	2.3	2.9	2.3	2.8	2.9	3.3	3.1	-0.3
3.0	0.0	2.4	2.1	0.0	2.5	2.4	3.2	2.8	-0.3
0.0	0.7	2.1	2.8	1.4	1.7	2.0	2.1	2.1	-0.3
2.0	0.0	3.0	2.4	0.0	2.4	2.8	2.7	2.8	-0.3
4.2	3.7	3.4	3.7	3.4	3.7	3.9	4.1	4.0	-0.3
2.7	3.0	3.2	3.1	2.6	2.9	3.4	3.1	3.2	-0.3
1.1	0.9	1.3	1.2	1.1	1.1	1.5	1.5	1.5	-0.3
0.0	2.2	1.9	0.0	1.8	2.0	2.4	2.3	2.3	-0.3
2.2	4.9	4.6	3.2	0.0	3.7	3.6	4.5	4.1	-0.3
2.1	2.1	2.2	2.2	2.0	2.1	2.4	2.5	2.5	-0.4

601	P13639	EEF2 Elongation factor 2	EEF2	R.VTDGALVVVDCVSGVC*VQTETVLR.Q
602	P62280	RPS11 40S ribosomal protein S11	RPS11	K.C*PFTGNVSIR.G
603	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	R.TLSGMESYC*VR.A
604	Q02543	RPL18A 60S ribosomal protein L18a	RPL18A	R.DLTTAGAVTQC*YR.D
605	Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multif	AIMP2	R.SC*ENLAPFNTALK.L
606	P13639	EEF2 Elongation factor 2	EEF2	R.YVEPIEDVPC*GNIVGLVGVDQFLVK.T
607	P21291	CSRP1 Cysteine and glycine-rich protein 1	CSRP1	R.C*SQAVYAAEK.V
608	P50213	IDH3A Isocitrate dehydrogenase	IDH3A	R.IEAAC*FATIK.D
609	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	K.C*LDEFPNLK.A
610	Q9BYT8	NLN Neurolysin, mitochondrial	NLN	R.IVHLQETC*DLGK.I
611	Q8NDH3	NPEPL1 Probable aminopeptidase NPEPL1	NPEPL1	R.DC*GGAAAVLGAFR.A
612	P35270	SPR Sepiapterin reductase	SPR	R.TVVNISSLC*ALQPFK.G
613	P63167	DYNLL1 Dynein light chain 1, cytoplasmic	DYNLL1	K.NADMSEEMQQDSVEC*ATQALEK.Y
614	P46782	RPS5 40S ribosomal protein S5	RPS5	K.AQC*PIVER.L
615	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	R.GC*ITIIGGGDTATCCAK.W
616	P31939	ATIC Bifunctional purine biosynthesis protein PURH	ATIC	K.VC*MVYDLYK.T
617	Q86VY4	TSPYL5 Testis-specific Y-encoded-like protein 5	TSPYL5	R.LPLDC*GLALR.A
618	Q15257	PPP2R4 Serine/threonine-protein phosphatase 2A activator	PPP2R4	R.IDYGTGHEAAFAAFLC*CLCK.I
619	Q9BT78	COPS4 COP9 signalosome complex subunit 4	COPS4	K.QIQSLC*FQVNNLLEK.I
620	Q9H9P8	L2HGDH L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	K.AC*FLGATVK.Y
621	P60866	RPS20 40S ribosomal protein S20	RPS20	R.KTPC*GEGSK.T
622	Q92797	SYMPK Symplekin	SYMPK	K.ATNLC*FAER.N
623	P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	K.IETELRDIC*NDVLSLLEK.F
624	P50213	IDH3A Isocitrate dehydrogenase	IDH3A	K.TFDLYANVRPC*VSIEGYK.T
625	P50991	CCT4 T-complex protein 1 subunit delta	CCT4	K.AQDIEAGDGTTSVVIIAGSLLDSC*TK.L
626	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	K.SC*AHDWVYE.-
627	Q9ULV4	CORO1C Coronin-1C	CORO1C	K.C*DLISIPK.K
628	Q99798	ACO2 Aconitate hydratase, mitochondrial	ACO2	R.DLGGIVLANAC*GPCIGQWDR.K
629	P50914	RPL14 60S ribosomal protein L14	RPL14	R.ALVDGPC*TQVR.R
630	P23921	RRM1 Ribonucleoside-diphosphate reductase large subunit	RRM1	K.IIDINYYPVPEAC*LSNK.R
631	Q7LG56	RRM2B Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	K.IEQEFLTEALPVGLIGMNC*ILMK.Q
632	Q9Y399	MRPS2 28S ribosomal protein S2, mitochondrial	MRPS2	R.DC*GEYAHTR.Y
633	Q9NQ88	TIGAR Fructose-2,6-bisphosphatase TIGAR	TIGAR	K.AAREEC*PVFTPPGGETLDQVK.M
634	P39687	ANP32A Acidic leucine-rich nuclear phosphoprotein 32 fami	ANP32A	K.SLDLFNC*EVTNLNDYR.E
635	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.VC*VETVESGAMTK.D
636	Q7L5D6	GET4 Golgi to ER traffic protein 4 homolog	GET4	K.EQNYC*ESR.Y
637	O43264	ZW10 Centromere/kinetochore protein zw10 homolog	ZW10	R.LAPILC*DGTATFVDLVPGFR.R
638	O43684	BUB3 Mitotic checkpoint protein BUB3	BUB3	R.TPC*NAGTFSQPEK.V
639	Q92598	HSPH1 Heat shock protein 105 kDa	HSPH1	R.SVLDAAQIVGLNC*LR.L
640	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.GIFPVLC*K.D

2.0	1.7	2.0	1.9	2.0	1.9	2.2	2.3	2.3	-0.4
3.2	3.5	3.2	3.2	2.9	3.2	3.6	3.5	3.5	-0.4
1.6	1.9	2.0	0.0	1.7	1.8	2.2	2.1	2.1	-0.4
4.3	3.7	4.0	5.7	1.8	3.9	4.6	4.0	4.3	-0.4
2.4	2.2	2.4	2.5	2.1	2.3	2.7	2.7	2.7	-0.4
1.3	2.2	2.2	2.6	1.6	2.0	2.7	2.0	2.3	-0.4
0.5	0.0	0.8	0.0	1.0	0.8	0.8	1.4	1.1	-0.4
4.2	4.4	4.2	5.6	3.2	4.3	4.0	5.3	4.7	-0.4
0.7	0.8	0.9	0.6	0.7	0.8	1.1	1.1	1.1	-0.4
1.2	0.0	2.1	0.0	1.5	1.6	2.1	1.9	2.0	-0.4
1.2	1.9	2.2	2.7	1.6	1.9	2.2	2.3	2.3	-0.4
4.1	5.0	3.3	6.0	5.0	4.7	3.6	6.5	5.1	-0.4
0.9	1.5	0.0	1.4	1.3	1.3	1.5	1.8	1.7	-0.4
2.0	2.3	1.7	2.0	2.0	2.0	2.3	2.4	2.3	-0.4
0.5	0.5	1.0	0.6	0.5	0.6	1.0	1.0	1.0	-0.4
0.7	0.9	1.8	2.3	0.9	1.3	1.8	1.6	1.7	-0.4
2.3	3.0	2.8	0.0	2.5	2.7	2.9	3.2	3.0	-0.4
0.7	1.2	1.9	1.9	1.0	1.4	2.2	1.2	1.7	-0.4
1.1	0.6	1.4	1.2	0.8	1.0	1.5	1.3	1.4	-0.4
3.7	3.7	3.8	0.0	3.4	3.6	4.2	3.8	4.0	-0.4
3.9	3.6	3.2	3.3	3.0	3.4	3.3	4.3	3.8	-0.4
2.1	1.5	1.9	1.9	2.1	1.9	2.3	2.3	2.3	-0.4
0.7	0.7	1.0	0.8	0.9	0.8	1.2	1.2	1.2	-0.4
3.9	4.3	2.8	0.0	3.7	3.7	4.2	4.0	4.1	-0.4
0.9	1.1	0.0	0.6	0.0	0.9	1.1	1.4	1.3	-0.4
1.2	1.6	1.9	2.0	1.7	1.7	2.3	1.9	2.1	-0.4
4.2	4.5	3.3	3.3	3.6	3.8	4.2	4.2	4.2	-0.4
2.3	2.0	1.7	2.5	1.8	2.1	2.3	2.6	2.5	-0.4
3.2	3.5	3.1	3.2	3.1	3.2	3.5	3.7	3.6	-0.4
2.5	2.4	2.2	2.5	2.0	2.3	2.5	2.9	2.7	-0.4
1.2	0.9	1.0	0.0	0.8	1.0	1.1	1.7	1.4	-0.4
1.1	0.0	2.6	3.3	0.0	2.3	2.4	3.1	2.7	-0.4
1.9	1.8	2.0	2.4	1.6	2.0	2.1	2.6	2.4	-0.4
0.5	0.7	0.0	0.0	0.6	0.6	1.2	0.8	1.0	-0.4
2.1	2.2	2.1	2.4	1.7	2.1	2.8	2.2	2.5	-0.4
2.4	1.9	1.9	1.6	1.5	1.8	2.1	2.4	2.2	-0.4
2.8	3.6	3.0	2.8	2.5	3.0	3.5	3.2	3.4	-0.4
1.4	2.5	2.9	2.9	2.0	2.3	3.1	2.4	2.7	-0.4
2.2	3.4	4.2	3.2	3.2	3.2	3.6	3.6	3.6	-0.4
1.2	2.6	3.3	3.6	2.5	2.6	3.6	2.6	3.1	-0.4

641	Q96FJ2	DYNLL2 Dynein light chain 2, cytoplasmic	DYNLL2	K.NADMSEDMQQDAVDC*ATQAMEK.Y
642	Q16854	DGUOK Deoxyguanosine kinase, mitochondrial	DGUOK	K.AC*TAQSLGNLLDMMYR.E
643	Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	K.SSVNC*PFSSQDMK.Y
644	P36578	RPL4 60S ribosomal protein L4	RPL4	R.SGQGAFGNMC*R.G
645	Q9NP73	ALG13 UDP-N-acetylglucosamine transferase subunit ALG13	ALG13	K.ADLVISHAGAGSC*LETLEK.G
646	P06733	ENO1 Alpha-enolase	ENO1	K.FGANAILGVSLAVC*K.A
647	B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	K.IFVGNVSAAC*TSQELR.S
648	Q9Y277	VDAC3 Voltage-dependent anion-selective channel protein	VDAC3	K.VC*NYGLTFTQK.W
649	P62857	RPS28 40S ribosomal protein S28	RPS28	R.TGSQGQC*TQVR.V
650	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.DLAGC*IHGLSNVK.L
651	P51659	HSD17B4 Peroxisomal multifunctional enzyme type 2	HSD17B4	K.IC*DFENASKPQSIQESTGSIIEVLSK.I
652	P28074	PSMB5 Proteasome subunit beta type-5	PSMB5	K.KVIEINPYLLGTMAGGAADC*SFWER.L
653	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.AEGSDVANAVLDGADC*IMLSGETAK.G
654	Q5VTL8	PRPF38B Pre-mRNA-splicing factor 38B	PRPF38B	K.TAGQTGMC*GGVR.G
655	P41250	GARS Glycine--tRNA ligase	GARS	R.SC*YDLSCHAR.A
656	O14745	SLC9A3R1 Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	R.IVEVNGVC*MEGK.Q
657	Q05655	PRKCD Protein kinase C delta type	PRKCD	K.VLMSVQYFLEDVDC*K.Q
658	Q8TEX9	IPO4 Importin-4	IPO4	R.APAALPALC*DLLASAADPQIR.Q
659	P41250	GARS Glycine--tRNA ligase	GARS	K.C*SVLPLSQNQEFMPFVK.E
660	P00966	ASS1 Argininosuccinate synthase	ASS1	R.FELSC*YSLAPQIK.V
661	Q9H3P7	ACBD3 Golgi resident protein GCP60	ACBD3	K.QVLMGPYNPDTC*PEVGFFDVLGNDR.R
662	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.NTGIIC*TIGPASR.S
663	Q9UBT2	UBA2 SUMO-activating enzyme subunit 2	UBA2	R.VLVVGAGGIGC*ELLK.N
664	Q969T9	WBP2 WW domain-binding protein 2	WBP2	K.DC*EIKQPVFGANYIK.G
665	P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.GYLGPEQLPDC*LK.G
666	E7EVH7	KLC1 Kinesin light chain 1	KLC1	R.YEVAVPLC*K.Q
667	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.SLHDALC*VVK.R
668	Q9NRF9	POLE3 DNA polymerase epsilon subunit 3	POLE3	R.AASVFVLYATSC*ANNFAMK.G
669	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	R.IQFVGAC*NPPTDPGR.K
670	P62829	RPL23 60S ribosomal protein L23	RPL23	R.ISLGLPVGAVINC*ADNTGAK.N
671	P55036	PSMD4 26S proteasome non-ATPase regulatory subunit 4	PSMD4	R.LQAQQDAVNIVC*HSK.T
672	P62424	RPL7A 60S ribosomal protein L7a	RPL7A	K.TC*TTVAFTQVNSEDKGALAK.L
673	Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	R.LSTLC*PSAVLQR.L
674	Q96I99	SUCLG2 Succinyl-CoA ligase	SUCLG2	R.SC*NGPVLVGSPQGGVDIEEVAASNPELIFK.E
675	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.IC*DDELILIK.N
676	P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.LGVENC*YFPMFVSQSALEK.E
677	O14545	TRAFD1 TRAF-type zinc finger domain-containing protein 1	TRAFD1	R.AVC*EADQSHGGPR.S
678	P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	K.LNEDMAC*SVAGITSDANVLTNELR.L
679	P15924	DSP Desmoplakin	DSP	K.NQC*TQVVQER.E

0.7	0.7	0.9	0.8	0.7	0.8	1.2	1.2	1.2	-0.4
1.3	1.1	1.4	0.0	1.6	1.3	1.7	1.8	1.7	-0.4
2.8	2.3	3.4	0.0	2.8	2.8	2.9	3.6	3.2	-0.4
5.0	5.1	4.9	4.2	4.0	4.6	5.0	5.1	5.1	-0.4
3.1	3.4	2.6	2.3	2.1	2.7	2.7	3.5	3.1	-0.4
0.0	0.5	0.0	1.0	0.8	0.8	1.3	1.1	1.2	-0.4
4.5	4.0	2.9	4.2	3.0	3.7	4.2	4.1	4.2	-0.4
1.9	1.9	1.7	1.2	1.6	1.7	2.3	1.9	2.1	-0.4
4.7	5.1	4.2	4.7	3.6	4.5	4.9	5.0	4.9	-0.4
2.7	2.9	1.8	2.7	2.3	2.5	2.8	3.0	2.9	-0.4
2.1	1.7	1.6	1.8	1.3	1.7	2.4	2.0	2.2	-0.4
1.1	1.8	2.1	2.2	1.7	1.8	2.2	2.3	2.2	-0.4
0.8	3.2	3.8	4.2	2.8	3.0	4.1	2.7	3.4	-0.4
0.0	4.4	0.0	3.9	3.9	4.1	5.1	3.9	4.5	-0.4
0.9	1.1	1.2	1.0	0.9	1.0	1.5	1.4	1.5	-0.4
1.4	1.2	1.4	1.1	0.0	1.3	1.4	2.1	1.7	-0.5
0.0	1.7	2.2	3.2	1.9	2.3	3.4	2.1	2.7	-0.5
0.0	1.9	2.2	1.8	1.6	1.9	2.0	2.7	2.3	-0.5
0.0	0.4	0.3	0.6	0.4	0.4	0.9	0.8	0.9	-0.5
1.5	2.2	1.9	2.0	1.8	1.9	2.3	2.3	2.3	-0.5
3.9	1.8	2.7	2.9	2.3	2.7	2.5	3.8	3.2	-0.5
0.9	2.8	3.2	3.4	2.4	2.5	3.2	2.8	3.0	-0.5
1.4	1.8	1.8	1.8	1.6	1.7	2.0	2.3	2.1	-0.5
2.0	2.0	2.1	1.8	1.8	1.9	2.5	2.4	2.4	-0.5
3.5	4.1	4.3	0.0	3.5	3.9	4.3	4.4	4.3	-0.5
1.5	1.6	1.9	0.0	1.6	1.6	2.2	2.1	2.1	-0.5
5.5	7.5	6.3	6.2	6.1	6.3	6.5	7.1	6.8	-0.5
2.9	1.4	1.3	1.4	1.0	1.6	2.0	2.1	2.1	-0.5
2.3	3.7	1.2	0.0	2.9	2.5	3.1	2.9	3.0	-0.5
3.9	3.6	3.3	3.3	3.3	3.5	4.0	4.0	4.0	-0.5
1.4	0.0	1.1	0.0	1.0	1.2	1.5	1.8	1.6	-0.5
2.2	2.0	1.9	0.0	1.8	1.9	2.1	2.7	2.4	-0.5
1.9	1.1	1.4	2.5	0.8	1.5	2.4	1.7	2.0	-0.5
2.8	2.8	2.9	2.7	2.7	2.8	3.4	3.1	3.3	-0.5
3.6	4.0	3.7	2.9	4.4	3.7	4.2	4.3	4.2	-0.5
2.6	2.8	2.4	2.3	2.2	2.4	3.0	2.9	3.0	-0.5
0.0	2.4	1.4	0.0	1.8	1.9	2.0	2.8	2.4	-0.5
0.8	1.1	1.2	1.1	1.1	1.1	1.5	1.7	1.6	-0.5
1.9	1.7	1.7	1.6	1.7	1.7	2.1	2.3	2.2	-0.5

680	O75940	SMNDC1 Survival of motor neuron-related-splicing factor 3	SMNDC1	K.VGVGTC*GIADKPMTQYQDTSK.Y
681	P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	R.TIYAGNALC*TVK.C
682	P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	K.IISNASC*TTNCLAPLAK.V
683	Q96RQ3	MCCC1 Methylcrotonoyl-CoA carboxylase subunit alpha, mit	MCCC1	K.ESLC*QAALGLILK.E
684	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	R.AVASQLDC*NFLK.V
685	P13639	EEF2 Elongation factor 2	EEF2	R.TFC*QLILDPIFK.V
686	Q5UIP0	RIF1 Telomere-associated protein RIF1	RIF1	K.SLIDNFALNPDILC*SAK.R
687	Q14152	EIF3A Eukaryotic translation initiation factor 3 subunit	EIF3A	K.NIC*QQVNIK.S
688	Q8N1F7	NUP93 Nuclear pore complex protein Nup93	NUP93	K.SSGQSAQLLSHEPGDPPC*LR.R
689	Q9H0C8	ILKAP Integrin-linked kinase-associated serine/threonine	ILKAP	R.FILLAC*DGLFK.V
690	P60953	CDC42 Cell division control protein 42 homolog	CDC42	K.YVEC*SALTQK.G
691	P11766	ADH5 Alcohol dehydrogenase class-3	ADH5	K.IDPLAPLDKVCLLGC*GISTGYGAAVNTAK.L
692	O94979	SEC31A Protein transport protein Sec31A	SEC31A	K.SC*ATFSSSHR.Y
693	Q9BX63	BRIP1 Fanconi anemia group J protein	BRIP1	K.QHC*LLESPTGSGK.S
694	Q14151	SAFB2 Scaffold attachment factor B2	SAFB2	K.ILDILGETC*K.S
695	P62249	RPS16 40S ribosomal protein S16	RPS16	K.TATAVAHC*K.R
696	P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.KGDEC*ELLGHSK.N
697	Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	K.AEMDAAIASC*K.R
698	P29401	TKT Transketolase	TKT	K.QAFTDVATGSLGQGLGAAC*GMAYTGK.Y
699	Q9Y2R9	MRPS7 28S ribosomal protein S7, mitochondrial	MRPS7	K.NC*EPMIGLVPILK.G
700	P61158	ACTR3 Actin-related protein 3	ACTR3	K.LGYAGNTEPQFIIPSC*IAIK.E
701	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	R.SVC*TEAGMFAIR.A
702	Q9Y285	FARSA Phenylalanine--tRNA ligase alpha subunit	FARSA	K.VNLQMVYDSPLC*R.L
703	Q6P2Q9	PRPF8 Pre-mRNA-processing-splicing factor 8	PRPF8	K.FIC*ISDLR.A
704	P49368	CCT3 T-complex protein 1 subunit gamma	CCT3	R.NLQDAMQVC*R.N
705	Q9BTZ2	DHRS4 Dehydrogenase/reductase SDR family member 4	DHRS4	R.VNC*LAPGLIK.T
706	P62714	PPP2CB Serine/threonine-protein phosphatase 2A catalytic	PPP2CB	R.NVVTIFSAPNYC*YR.C
707	P51553	IDH3G Isocitrate dehydrogenase	IDH3G	R.TSLDLYANVIHC*K.S
708	P33992	MCM5 DNA replication licensing factor MCM5	MCM5	R.C*SVLAAANSVFGR.W
709	P23921	RRM1 Ribonucleoside-diphosphate reductase large subunit	RRM1	R.NTAAMVC*SLENR.D
710	P15880	RPS2 40S ribosomal protein S2	RPS2	R.GC*TATLGNFAK.A
711	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	R.QLC*DNAGFDATNILNK.L
712	P27635	RPL10 60S ribosomal protein L10	RPL10	K.MLSC*AGADR.L
713	Q9P2X0	DPM3 Dolichol-phosphate mannosyltransferase subunit 3	DPM3	R.VATFHDC*EDAAR.E
714	Q9UQ35	SRRM2 Serine/arginine repetitive matrix protein 2	SRRM2	R.SVSPC*SNVESR.L
715	O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	R.GDFC*IQVGR.N
716	O43837	IDH3B Isocitrate dehydrogenase	IDH3B	K.LGDGLFLQC*CEEVAELYPK.I
717	P42025	ACTR1B Beta-centractin	ACTR1B	R.AC*YLSINPQKDEALETEK.V
718	P22695	UQCRC2 Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	R.NALANPLYC*PDYR.I
719	Q9UNE7	STUB1 E3 ubiquitin-protein ligase CHIP	STUB1	R.AQQAC*IEAK.H
720	Q16186	ADRM1 Proteasomal ubiquitin receptor ADRM1	ADRM1	R.VPQC*PSGR.V

1.9	1.6	1.7	1.4	1.4	1.6	1.7	2.4	2.1	-0.5
5.1	4.6	4.4	5.2	4.1	4.7	4.5	5.9	5.2	-0.5
6.3	5.3	6.7	7.3	6.4	6.4	6.5	7.3	6.9	-0.5
2.2	0.0	3.6	3.0	3.4	3.0	3.7	3.4	3.6	-0.5
2.9	3.2	2.8	2.7	2.6	2.8	3.3	3.5	3.4	-0.5
1.4	1.7	1.7	1.9	1.4	1.6	2.2	2.2	2.2	-0.5
3.0	3.4	2.9	0.0	3.0	3.1	4.6	2.7	3.6	-0.5
3.0	3.3	3.2	2.8	2.7	3.0	3.7	3.4	3.5	-0.5
1.3	1.4	0.0	1.3	1.1	1.3	1.9	1.7	1.8	-0.5
1.6	1.0	1.3	1.2	1.2	1.2	1.8	1.7	1.8	-0.5
0.0	0.9	1.7	0.9	0.7	1.0	1.7	1.4	1.6	-0.5
4.0	0.0	4.8	0.0	6.4	5.1	4.8	6.4	5.6	-0.5
0.0	4.7	3.5	0.0	4.0	4.0	4.9	4.3	4.6	-0.5
2.6	5.4	0.0	0.0	3.6	3.9	5.6	3.2	4.4	-0.5
2.5	1.5	2.6	1.6	1.7	2.0	2.9	2.1	2.5	-0.6
4.0	4.1	3.5	3.9	3.3	3.8	4.3	4.3	4.3	-0.6
3.7	5.0	3.9	4.3	3.8	4.1	4.9	4.5	4.7	-0.6
3.5	4.0	4.4	3.7	4.0	3.9	4.1	4.8	4.5	-0.6
1.8	2.7	3.0	0.0	2.7	2.5	3.3	3.0	3.1	-0.6
2.6	2.6	2.7	2.5	2.5	2.6	3.3	3.0	3.2	-0.6
1.0	2.3	2.7	3.1	2.3	2.3	3.0	2.7	2.8	-0.6
5.2	4.6	4.3	4.5	3.7	4.5	5.2	4.9	5.0	-0.6
2.9	3.0	2.5	2.4	2.0	2.5	3.6	2.7	3.1	-0.6
0.8	0.0	2.6	0.0	2.1	1.8	2.4	2.5	2.4	-0.6
1.9	1.8	2.1	0.0	2.1	2.0	2.6	2.6	2.6	-0.6
0.0	3.3	3.2	2.9	3.0	3.1	3.6	3.8	3.7	-0.6
1.6	2.3	2.8	2.5	1.8	2.2	3.2	2.5	2.8	-0.6
4.9	0.0	4.2	0.0	4.9	4.7	5.3	5.2	5.3	-0.6
4.9	6.8	4.9	5.1	5.6	5.4	6.0	6.1	6.0	-0.6
2.2	0.0	2.1	2.9	1.5	2.2	2.2	3.4	2.8	-0.6
3.1	2.8	2.4	2.8	2.3	2.7	3.0	3.6	3.3	-0.6
2.6	1.9	2.5	2.2	1.5	2.1	2.6	2.9	2.8	-0.6
5.6	4.8	4.4	4.2	4.1	4.6	4.7	5.7	5.2	-0.6
2.0	2.1	0.0	0.0	2.2	2.1	3.4	2.1	2.7	-0.6
0.0	5.1	4.2	4.8	3.8	4.5	5.0	5.2	5.1	-0.6
1.0	3.1	3.2	3.2	2.5	2.6	3.3	3.2	3.2	-0.6
0.0	3.2	0.0	3.1	2.9	3.1	3.5	3.9	3.7	-0.6
4.1	5.2	3.5	4.3	2.7	3.9	4.5	4.7	4.6	-0.6
2.5	2.8	2.6	2.8	2.1	2.6	3.4	3.0	3.2	-0.6
2.3	2.1	2.1	1.5	1.8	1.9	2.2	2.9	2.6	-0.6
0.0	4.2	7.0	5.4	4.0	5.2	5.8	5.9	5.8	-0.6

721	P40227	CCT6A T-complex protein 1 subunit zeta	CCT6A	K.NAIDDGC*VVPGAGAVEVAMAEALIK.H
722	Q5VT52	RPRD2 Regulation of nuclear pre-mRNA domain-containing p	RPRD2	R.LNLFYLANDVIQNC*K.R
723	P57678	GEMIN4 Gem-associated protein 4	GEMIN4	R.SDPDAC*PTMPLLAMLLR.G
724	P07741	APRT Adenine phosphoribosyltransferase	APRT	R.VVVVDDLLATGGTMNAAC*ELLGR.L
725	P23396	RPS3 40S ribosomal protein S3	RPS3	R.AC*YGVLR.F
726	P31949	S100A11 Protein S100-A11	S100A11	K.ISSPTETERC*IESLIAVFQK.Y
727	Q9H7X7	RABL5 Rab-like protein 5	RABL5	K.ILFVGPC*ESGK.T
728	P60981	DSTN Destrin	DSTN	K.AVIFC*LSADKK.C
729	Q13185	CBX3 Chromobox protein homolog 3	CBX3	R.LTWHSC*PEDEAQ.-
730	P00558	PGK1 Phosphoglycerate kinase 1	PGK1	K.AC*ANPAAGSVILLENLR.F
731	P13639	EEF2 Elongation factor 2	EEF2	K.EGALC*EENMR.G
732	Q7Z406	MYH14 Myosin-14	MYH14	R.C*NGVLEGIR.I
733	P62280	RPS11 40S ribosomal protein S11	RPS11	R.DVQIGDIVTVGEC*RPLSK.T
734	Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	K.DC*EVVMMIGLPGAGK.T
735	P40939	HADHA Trifunctional enzyme subunit alpha, mitochondrial	HADHA	R.C*LAPMMSEVIR.I
736	Q96RS6	NUDCD1 NudC domain-containing protein 1	NUDCD1	R.DSAQC*AAIAER.L
737	P48047	ATP5O ATP synthase subunit O, mitochondrial	ATP5O	R.GEVPC*TVTSASPLEEATLSELK.T
738	P23921	RRM1 Ribonucleoside-diphosphate reductase large subunit	RRM1	R.NTAAMVCSLENRDEC*LMCGS.-
739	Q15181	PPA1 Inorganic pyrophosphatase	PPA1	K.GISC*MNTTLSESPFK.C
740	P08243	ASNS Asparagine synthetase	ASNS	R.IGC*LLSGGLDSSLVAATLLK.Q
741	P13639	EEF2 Elongation factor 2	EEF2	K.YRC*ELLYEGPPDDEAAMGIK.S
742	P13639	EEF2 Elongation factor 2	EEF2	R.C*LYASVLTAQPR.L
743	O43795	MYO1B Unconventional myosin-Ib	MYO1B	K.LVMSYVAAVC*GK.G
744	Q8TAQ2	SMARCC2 SWI/SNF complex subunit SMARCC2	SMARCC2	R.NLAGDVC*AIMR.V
745	Q9P258	RCC2 Protein RCC2	RCC2	K.AVQDLC*GWR.I
746	Q96FV9	THOC1 THO complex subunit 1	THOC1	K.SQNTVFC*GR.I
747	O75663	TIPRL TIP41-like protein	TIPRL	K.VAC*AEEWQESR.T
748	P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	R.VGAFTMVC*K.D
749	Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	R.GQPC*SQNYR.L
750	Q7Z406	MYH14 Myosin-14	MYH14	K.AEDMAELTC*LNEASVLHNLR.E
751	P55263	ADK Adenosine kinase	ADK	R.SLIANLAAANC*YK.K
752	P62266	RPS23 40S ribosomal protein S23	RPS23	K.ITAFVPNDGC*LNFIEENDEVLVAGFGR.K
753	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	R.YVDIAIPC*NNK.G
754	Q07960	ARHGAP1 Rho GTPase-activating protein 1	ARHGAP1	K.IIVFSAC*R.M
755	Q92879	CELF1 CUGBP Elav-like family member 1	CELF1	K.AMHQAQTMEGC*SSPMVVK.F
756	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	K.TFTDC*FNCLPIAAIVDEK.I
757	P49915	GMPS GMP synthase	GMPS	K.TVGVQGDC*R.S
758	P21266	GSTM3 Glutathione S-transferase Mu 3	GSTM3	K.RYTC*GEAPDYDR.S
759	P60981	DSTN Destrin	DSTN	K.HEC*QANGPEDLNR.A
760	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	R.GNHEC*ASINR.I
761	P34896	SHMT1 Serine hydroxymethyltransferase, cytosolic	SHMT1	K.NTC*PGDR.S

1.2	2.9	2.0	2.4	1.9	2.1	2.6	2.8	2.7	-0.6
1.9	2.7	2.3	0.0	2.1	2.2	3.0	2.7	2.9	-0.6
2.4	2.2	2.3	2.1	1.7	2.1	3.0	2.6	2.8	-0.6
1.1	1.2	1.4	1.3	1.1	1.2	2.1	1.6	1.9	-0.6
2.4	1.8	2.2	2.1	2.3	2.2	2.5	3.1	2.8	-0.6
0.9	0.6	1.3	0.8	1.3	1.0	2.2	1.0	1.6	-0.6
4.0	0.0	3.6	0.0	2.3	3.3	4.0	3.9	4.0	-0.6
0.9	1.3	1.1	1.1	0.8	1.1	1.6	1.8	1.7	-0.6
4.1	4.1	2.9	4.2	3.2	3.7	4.2	4.5	4.3	-0.6
1.0	1.5	0.0	2.8	1.3	1.6	2.1	2.5	2.3	-0.7
1.0	3.2	3.5	3.4	3.9	3.0	3.7	3.6	3.7	-0.7
4.0	0.0	4.8	3.5	3.8	4.0	4.3	5.1	4.7	-0.7
4.9	4.8	4.4	5.1	4.2	4.7	5.4	5.3	5.3	-0.7
2.8	1.8	1.9	1.8	1.7	2.0	2.3	3.0	2.7	-0.7
3.3	4.3	4.4	3.8	4.4	4.0	4.1	5.4	4.7	-0.7
3.2	2.1	1.9	1.9	1.5	2.1	2.5	3.0	2.8	-0.7
2.5	1.9	2.1	2.2	2.0	2.1	2.6	3.0	2.8	-0.7
2.2	1.5	2.1	2.9	1.8	2.1	2.2	3.4	2.8	-0.7
2.5	1.9	1.5	1.5	1.3	1.7	2.6	2.2	2.4	-0.7
1.7	3.6	3.4	0.0	2.3	2.8	3.3	3.6	3.4	-0.7
1.6	1.8	0.0	1.8	2.3	1.9	3.2	1.9	2.6	-0.7
0.9	3.0	2.9	3.1	3.2	2.6	3.3	3.4	3.3	-0.7
1.5	1.1	1.2	1.1	1.1	1.2	1.6	2.2	1.9	-0.7
2.0	3.9	2.6	3.2	3.0	2.9	4.1	3.2	3.7	-0.7
2.2	2.1	1.8	3.3	1.6	2.2	3.1	2.7	2.9	-0.7
1.8	0.0	0.4	0.0	1.0	1.1	1.5	2.1	1.8	-0.7
2.0	0.0	0.0	1.6	1.4	1.6	1.6	3.1	2.3	-0.7
3.2	2.9	1.7	3.0	3.5	2.8	4.2	2.9	3.6	-0.7
1.9	2.2	1.9	2.3	1.5	1.9	3.0	2.3	2.7	-0.7
4.7	5.4	4.8	0.0	5.1	5.0	4.8	6.7	5.7	-0.7
1.8	1.9	2.5	3.9	2.0	2.4	3.6	2.7	3.2	-0.7
4.5	0.0	3.1	0.0	3.4	3.7	3.1	5.7	4.4	-0.7
1.8	3.0	2.7	0.0	2.7	2.6	3.3	3.3	3.3	-0.7
1.7	0.0	2.8	0.0	1.3	1.9	2.8	2.4	2.6	-0.7
1.2	1.3	1.3	1.3	1.1	1.2	1.7	2.3	2.0	-0.7
2.7	0.0	2.1	2.7	2.0	2.4	3.3	3.0	3.1	-0.7
2.2	1.8	1.6	0.0	1.5	1.8	2.5	2.5	2.5	-0.8
1.5	1.6	1.5	1.7	1.1	1.5	1.9	2.6	2.2	-0.8
1.9	2.3	2.4	2.6	1.9	2.2	2.8	3.2	3.0	-0.8
3.2	2.6	2.6	2.5	2.3	2.6	3.3	3.5	3.4	-0.8
0.8	2.1	1.8	2.3	1.5	1.7	2.8	2.1	2.5	-0.8

762	P35658	NUP214 Nuclear pore complex protein Nup214	NUP214	K.AC*FQVGTSEEMK.M
763	E2QRD5	C15orf38-AP3S2 Protein C15orf38-AP3S2	C15orf38-AP3S2	K.C*NFTGDGK.T
764	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	R.ITNQVIYLNPPIEEC*R.Y
765	Q8TC07	TBC1D15 TBC1 domain family member 15	TBC1D15	R.TLLVNC*QNK.S
766	P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	K.IIC*QGFTGK.Q
767	Q13636	RAB31 Ras-related protein Rab-31	RAB31	K.VC*LLGDTGVGK.S
768	Q9BYG5	PARD6B Partitioning defective 6 homolog beta	PARD6B	R.HGAGSGC*LGTMEVK.S
769	P54136	RARS Arginine--tRNA ligase, cytoplasmic	RARS	K.NC*GCLGASPNLEQLQEENLK.L
770	O95747	OXSR1 Serine/threonine-protein kinase OSR1	OXSR1	K.TFVGTPC*WMAPEVMEQVR.G
771	P49327	FASN Fatty acid synthase	FASN	K.AC*LDTAVENMPSLK.M
772	Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	K.AVVVC*PK.D
773	P62701	RPS4X 40S ribosomal protein S4, X isoform	RPS4X	K.FDTGNLC*MVTGGANLGR.I
774	P62826	RAN GTP-binding nuclear protein Ran	RAN	R.VC*ENIPIVLCGNK.V
775	P31153	MAT2A S-adenosylmethionine synthase isoform type-2	MAT2A	K.TC*NVLVALEQQSPDIAQGVHLDR.N
776	P17858	PFKL 6-phosphofructokinase, liver type	PFKL	R.VFANAPDSAC*VIGLK.K
777	Q92599	SEPT8 Septin-8	8-Sep	R.QYPWGVVQVENENHC*DFVK.L
778	P60900	PSMA6 Proteasome subunit alpha type-6	PSMA6	K.C*DPAGYYCGFK.A
779	P49327	FASN Fatty acid synthase	FASN	R.DGLLENQTPEFFQDVC*KPK.Y
780	P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.QGEYGLASIC*NGGGGASAMLIQK.L
781	P60709	ACTB Actin, cytoplasmic 1	ACTB	K.EKLC*YVALDFEQEMATAASSSSLEK.S
782	P34896	SHMT1 Serine hydroxymethyltransferase, cytosolic	SHMT1	R.AVLEALGSC*LNNK.Y
783	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	R.ALC*QITDSTMLQAIER.Y
784	P50914	RPL14 60S ribosomal protein L14	RPL14	K.C*MQLTDFILK.F
785	O14929	HAT1 Histone acetyltransferase type B catalytic subunit	HAT1	K.C*NTNTAIELK.L
786	Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	K.GNGIVEC*LGPK.-
787	Q04637	EIF4G1 Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	R.LQGINC*GPDFTPSFANLGR.T
788	P61158	ACTR3 Actin-related protein 3	ACTR3	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSC*IK.H
789	P46734	MAP2K3 Dual specificity mitogen-activated protein kinase	MAP2K3	R.FSPEFVDFTAQC*LR.K
790	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	K.GC*LLYGPPGTGK.T
791	P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	K.IC*GDIHGQYYDLLR.L
792	P49720	PSMB3 Proteasome subunit beta type-3	PSMB3	K.NC*VAIAADR.R
793	P21281	ATP6V1B2 V-type proton ATPase subunit B, brain isoform	ATP6V1B2	R.GPVVLAEDFLDIMGQPINPQC*R.I
794	Q9GZZ9	UBA5 Ubiquitin-like modifier-activating enzyme 5	UBA5	R.EGVC*AASLPTTMGVVAGILVQNVLK.F
795	P62241	RPS8 40S ribosomal protein S8	RPS8	K.NC*IVLIDSTPYR.Q
796	Q96QR8	PURB Transcriptional activator protein Pur-beta	PURB	R.GGGGGPC*GFQPASR.G
797	P51553	IDH3G Isocitrate dehydrogenase	IDH3G	K.LGDGLFLQC*CR.E
798	P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	K.C*DENILWLDYK.N
799	P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.C*ATITPDEAR.V
800	O75150	RNF40 E3 ubiquitin-protein ligase BRE1B	RNF40	R.LTCPC*CNTR.K
801	P62191	PSMC1 26S protease regulatory subunit 4	PSMC1	K.AIC*TEAGLMALR.E
802	P09429	HMGB1 High mobility group protein B1	HMGB1	K.MSSYAFFVQTC*R.E

1.6	1.6	2.5	0.0	1.4	1.8	2.0	3.1	2.5	-0.8
3.0	3.2	2.8	0.0	2.1	2.8	3.1	4.0	3.5	-0.8
1.5	1.5	1.6	0.0	1.6	1.5	2.2	2.5	2.3	-0.8
3.4	4.6	3.2	0.9	2.8	3.0	3.8	3.8	3.8	-0.8
4.8	5.3	5.8	4.5	5.1	5.1	5.8	6.0	5.9	-0.8
1.9	2.7	2.2	2.3	2.1	2.2	3.2	2.9	3.1	-0.8
3.0	1.9	1.9	2.3	1.4	2.1	3.2	2.7	2.9	-0.8
5.9	6.6	4.9	6.0	4.7	5.6	6.1	6.8	6.5	-0.8
2.7	4.6	4.0	3.8	3.8	3.8	4.3	4.9	4.6	-0.8
1.2	1.7	1.2	1.4	1.7	1.4	2.5	2.0	2.3	-0.8
3.4	3.8	3.5	3.2	3.1	3.4	3.7	4.7	4.2	-0.8
2.1	2.3	2.2	1.8	2.1	2.1	2.9	2.9	2.9	-0.8
1.1	1.3	1.4	1.6	1.2	1.3	2.3	2.0	2.2	-0.8
6.0	5.5	4.8	5.0	3.6	5.0	5.2	6.5	5.8	-0.8
5.6	5.9	5.6	5.5	5.2	5.5	6.2	6.6	6.4	-0.8
2.2	1.5	1.5	1.3	0.0	1.6	2.2	2.7	2.5	-0.9
1.1	1.9	2.2	2.3	2.0	1.9	2.4	3.2	2.8	-0.9
3.9	6.0	5.3	0.0	4.3	4.9	5.6	5.9	5.7	-0.9
2.9	2.8	2.4	2.5	2.5	2.6	4.1	2.9	3.5	-0.9
3.0	3.6	3.7	3.7	3.7	3.5	4.3	4.5	4.4	-0.9
0.5	1.1	0.9	1.0	0.7	0.8	1.7	1.7	1.7	-0.9
4.4	4.7	4.5	0.0	3.5	4.3	4.7	5.7	5.2	-0.9
3.3	3.7	3.2	3.4	3.2	3.4	3.6	5.0	4.3	-0.9
2.3	3.0	1.8	0.0	2.3	2.3	3.5	3.0	3.3	-0.9
0.7	0.8	0.6	0.8	0.5	0.7	2.2	1.0	1.6	-0.9
0.0	2.6	1.8	2.3	1.9	2.2	2.6	3.5	3.1	-0.9
0.0	1.9	2.4	2.4	1.9	2.2	3.3	2.9	3.1	-0.9
6.3	6.8	5.0	6.4	5.0	5.9	6.6	7.1	6.8	-0.9
2.1	3.0	0.9	3.0	3.0	2.4	3.0	3.8	3.4	-1.0
3.9	2.7	2.1	2.2	2.4	2.7	3.2	4.1	3.6	-1.0
1.1	1.3	2.1	2.5	1.7	1.7	2.5	2.9	2.7	-1.0
2.2	2.0	1.6	0.0	1.6	1.9	3.2	2.5	2.8	-1.0
0.0	0.0	7.9	8.2	7.7	7.9	7.4	10.5	8.9	-1.0
4.2	4.5	4.5	4.7	4.0	4.4	4.9	5.9	5.4	-1.0
0.0	3.0	2.4	2.9	2.9	2.8	4.0	3.6	3.8	-1.0
3.1	4.3	3.0	3.2	3.1	3.3	4.8	3.9	4.3	-1.0
1.3	0.0	2.4	2.5	0.0	2.1	3.1	3.0	3.1	-1.0
2.7	2.3	2.6	2.8	2.5	2.6	4.2	3.0	3.6	-1.0
2.7	2.3	1.5	0.0	2.5	2.3	2.7	3.9	3.3	-1.0
2.3	2.5	2.5	2.5	2.1	2.4	3.7	3.2	3.4	-1.0
0.0	0.0	3.4	4.1	3.3	3.6	4.2	5.0	4.6	-1.0

803	Q6IA69	NADSYN1 Glutamine-dependent NAD(+) synthetase	NADSYN1	K.NSSQETC*TR.A
804	Q06587	RING1 E3 ubiquitin-protein ligase RING1	RING1	R.FC*SDCIVTALR.S
805	P83731	RPL24 60S ribosomal protein L24	RPL24	K.VELC*SFSGYK.I
806	P62820	RAB1A Ras-related protein Rab-1A	RAB1A	K.LLVGNKC*DLTTK.K
807	Q9UL25	RAB21 Ras-related protein Rab-21	RAB21	K.VVLLGEGC*VGK.T
808	Q9Y678	COPG1 Coatomer subunit gamma-1	COPG1	K.HPSAVTAC*NLDLENLVTDSNR.S
809	P33992	MCM5 DNA replication licensing factor MCM5	MCM5	K.AIAC*LLFGGSR.K
810	A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	R.ADHQPLTEASYVNLPTIALC*NTDSPLR.Y
811	P35250	RFC2 Replication factor C subunit 2	RFC2	R.FALAC*NASDK.I
812	Q6P2I3	FAHD2B Fumarylacetoacetate hydrolase domain-containing pr	FAHD2B	K.TFDTFC*PLGPALVTK.D
813	Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	K.LQGATC*NNNK.L
814	Q07864	POLE DNA polymerase epsilon catalytic subunit A	POLE	R.IHC*GLQDSQK.A
815	Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	R.YNFFTGC*PK.A
816	P35568	IRS1 Insulin receptor substrate 1	IRS1	K.LC*GAAGGLENGLNYIDLDLVK.D
817	P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	R.AALEALGSC*LNNK.Y
818	P55809	OXCT1 Succinyl-CoA:3-ketoacid coenzyme A transferase 1,	OXCT1	K.C*TLPLTGK.Q
819	P22102	GART Trifunctional purine biosynthetic protein adenosin	GART	R.SAGVQC*FGPTAEAAQLESSK.R
820	P61158	ACTR3 Actin-related protein 3	ACTR3	R.YSYVC*PDLVK.E
821	P53618	COPB1 Coatomer subunit beta	COPB1	K.VLSECSPLMNDIFNKEC*R.Q
822	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	R.RGNVC*GDSK.S
823	P23919	DTYMK Thymidylate kinase	DTYMK	K.LVEALC*AAGHR.A
824	P50570	DNM2 Dynamin-2	DNM2	K.TEHAEFLHC*K.S
825	P62888	RPL30 60S ribosomal protein L30	RPL30	R.VC*TLAIIDPGDSDIIR.S
826	P51610	HCFC1 Host cell factor 1	HCFC1	R.VAGINAC*GR.G
827	P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.GANDFMC*DEMER.S
828	P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.NMITGTSQADC*AVLIVAAGVGEFEAGISK.N
829	Q9Y5M8	SRPRB Signal recognition particle receptor subunit beta	SRPRB	K.NTPSFLIAC*NK.Q
830	Q04726	TLE3 Transducin-like enhancer protein 3	TLE3	K.SPISQLDC*LNR.D
831	P27448	MARK3 MAP/microtubule affinity-regulating kinase 3	MARK3	K.LDTFC*GSPPYAAPELFQGK.K
832	P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	K.KLVIVGDGAC*GK.T
833	Q05639	EEF1A2 Elongation factor 1-alpha 2	EEF1A2	K.SGDAAIVEMVPGKPMC*VESFSQYPPLGR.F
834	P42677	RPS27 40S ribosomal protein S27	RPS27	R.LTEGC*SFR.R
835	P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	R.NVC*TEAGMFAIR.A
836	Q9H773	DCTPP1 dCTP pyrophosphatase 1	DCTPP1	K.YTELPHGAISEDQAVGPADIPC*DSTGQTST.-
837	Q53H96	PYCRL Pyrroline-5-carboxylate reductase 3	PYCRL	R.SDVC*TPGGTTIYGLHALEQGGLR.A
838	P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	R.LC*PNSTGAEIR.S
839	Q9UEW8	STK39 STE20/SPS1-related proline-alanine-rich protein ki	STK39	K.C*QTSMDELLK.E
840	O95757	HSPA4L Heat shock 70 kDa protein 4L	HSPA4L	R.GC*ALQCAILSPAFK.V
841	Q13572	ITPK1 Inositol-tetrakisphosphate 1-kinase	ITPK1	K.NGLTFPFIC*K.T
842	P60709	ACTB Actin, cytoplasmic 1	ACTB	K.C*DVDIRK.D
843	P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.IC*PVETLVEEAIQC*AEK.I

0.0	1.2	1.3	2.4	1.2	1.5	2.3	2.8	2.6	-1.0
3.5	2.9	2.9	4.0	3.7	3.4	3.2	5.6	4.4	-1.1
5.2	4.2	4.4	2.5	3.8	4.0	5.9	4.3	5.1	-1.1
1.3	2.5	3.0	1.4	0.0	2.1	3.3	3.0	3.1	-1.1
2.9	2.6	2.3	2.4	2.3	2.5	3.3	4.0	3.7	-1.2
4.1	3.3	0.0	5.4	4.3	4.3	5.0	6.0	5.5	-1.2
0.0	3.0	3.6	4.2	3.8	3.7	5.1	4.6	4.8	-1.2
1.8	3.1	2.9	2.9	3.2	2.8	3.9	4.1	4.0	-1.2
5.1	3.8	0.0	0.0	4.7	4.5	5.4	6.2	5.8	-1.3
2.7	2.8	3.3	0.0	3.3	3.0	4.7	3.9	4.3	-1.3
1.9	3.6	3.0	3.4	2.2	2.8	3.4	4.8	4.1	-1.3
3.5	2.8	0.0	0.0	1.4	2.6	3.1	4.6	3.9	-1.3
2.3	3.3	2.9	0.0	2.6	2.7	3.6	4.6	4.1	-1.3
5.1	0.0	4.2	0.0	5.1	4.8	6.1	6.1	6.1	-1.3
1.3	4.3	3.7	2.2	3.2	3.0	4.9	3.7	4.3	-1.3
2.6	4.1	3.7	0.0	3.1	3.4	5.7	3.8	4.7	-1.4
5.3	0.0	0.0	4.6	5.4	5.1	5.9	7.1	6.5	-1.4
1.0	2.4	1.8	2.0	1.8	1.8	2.9	3.5	3.2	-1.4
1.4	0.0	0.7	2.5	0.0	1.5	3.0	2.9	2.9	-1.4
0.0	3.5	4.2	3.5	4.7	4.0	5.5	5.5	5.5	-1.5
1.8	3.2	0.0	3.2	2.9	2.8	4.0	4.7	4.3	-1.5
4.1	0.0	2.2	2.8	0.0	3.0	3.4	5.7	4.6	-1.6
9.9	8.2	8.4	8.7	8.2	8.7	10.6	9.9	10.2	-1.6
7.1	9.9	8.3	0.0	7.2	8.1	7.8	11.6	9.7	-1.6
4.1	0.0	5.1	4.3	3.9	4.4	6.3	5.6	6.0	-1.6
1.4	1.8	2.1	2.1	2.0	1.9	3.2	3.8	3.5	-1.6
3.7	3.5	3.5	2.0	3.1	3.2	4.0	5.6	4.8	-1.6
3.2	0.0	3.7	0.0	2.5	3.1	4.2	5.3	4.8	-1.7
3.3	0.0	3.2	0.0	3.1	3.2	4.4	5.4	4.9	-1.7
2.5	2.8	2.7	3.4	2.5	2.8	4.5	4.5	4.5	-1.8
2.2	3.8	4.2	4.7	3.2	3.6	5.0	5.8	5.4	-1.8
5.4	5.8	5.0	5.0	4.8	5.2	6.6	7.4	7.0	-1.8
0.0	3.2	3.2	2.6	0.0	3.0	4.4	5.6	5.0	-2.0
2.3	1.7	2.3	1.7	1.7	1.9	3.2	4.7	3.9	-2.0
11.5	9.0	0.0	8.8	7.8	9.3	11.3	11.2	11.3	-2.0
4.7	4.1	4.9	4.6	4.6	4.6	5.9	7.4	6.6	-2.0
0.0	1.0	2.1	1.0	1.0	1.3	3.1	3.5	3.3	-2.1
4.4	4.2	4.4	4.1	4.4	4.3	6.6	6.4	6.5	-2.2
1.8	2.2	0.0	0.0	3.3	2.4	4.0	5.6	4.8	-2.4
3.8	3.9	5.0	4.9	4.2	4.4	6.8	7.0	6.9	-2.5
2.6	2.7	2.9	3.2	2.5	2.8	5.5	5.5	5.5	-2.7

844	Q9Y265	RUVBL1 RuvB-like 1	RUVBL1	K.VPFC*PMVGSEVYSTEIK.K
845	Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.FGRVDVAVNC*AGIAVASK.T
846	Q1KMD3	HNRNPUL2 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL2	R.NFILDQC*NVYNSGQR.R
847	P04183	TK1 Thymidine kinase, cytosolic	TK1	R.NTMEALPAC*LLR.D
848	P53384	NUBP1 Cytosolic Fe-S cluster assembly factor NUBP1	NUBP1	R.GASC*QGCPNQR.L

2.0	5.8	3.6	3.0	4.1	3.7	6.0	7.0	6.5	-2.8
4.7	5.5	5.7	6.8	7.1	5.9	8.9	9.2	9.0	-3.1
3.3	3.8	2.8	3.4	2.8	3.2	6.6	6.1	6.4	-3.1
7.0	8.5	8.5	7.0	8.2	7.9	12.8	10.3	11.6	-3.7
6.9	7.2	7.1	7.4	8.9	7.5	11.8	11.6	11.7	-4.2

Table 4A-1. A list of glutathionylated proteins identified in mass analysis that have a high spectral count and a high enrichment in positive over negative samples.

Gene	Protein	Neg[(1)]	Pos[(1)]	Loc[(2)]	Function[(3)]	Process[(4)]	G[(5)]	S[(6)]
ACE	Angiotensin-converting enzyme	0	79.8	EC	Peptidase	Cell proliferation	+	-
TBA1A	Tubulin alpha-1A chain	0	59.5	C	GTPase	Cell division	+	-
CTPS1	CTP synthase 1	0	43.5	C	ligase	B cell proliferation	-	+
RRM1	Ribonucleoside-diphosphate reductase large subunit	0	35	C	ATP binding	Cell proliferation	-	+
GMPS	GMP synthase	0	30.5	C	Ligase	Metabolic	-	+
PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	0	29	C	Phosphatase regulatory	Apoptosis	-	-
NPEPPS	Puromycin-sensitive aminopeptidase	0	28.8	C, N	Peptidase	Stress response	-	-
DHX15	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase	0	28.3	N	Helicase	mRNA processing	+	-
GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	0	24.8	C	GTPase	Cell cycle	-	+
PARP1	Poly [ADP-ribose] polymerase 1	0	23.5	N	Glycosyltransferase	DNA repair	+	-
NAA15	N-alpha-acetyltransferase 15, NatA auxiliary subunit	0	23	C	Acetyltransferase	Angiogenesis	+	+
VARS	Valine-tRNA synthetase	0	20	C	Ligase	Protein biosynthesis	-	+
CAND1	Cullin-associated NEDD8-dissociated protein 1	0	19.5	C, N	Ubiquitin conjugation	Proteolysis	-	+
CSTB	Cystatin-B	0	19	C, N	Peptidase inhibitor	proteolysis	-	-
USP7	Ubiquitin carboxyl-terminal hydrolase 7	0	18	C, N	Peptidase	DNA repair	-	-
DIS3	Exosome complex exonuclease RRP44	0	18	C,N	Endonuclease	rRNA processing	-	-
TUBA3D	Tubulin alpha-3C/D chain	0	18	C	GTPase	Protein folding	-	
TPP2	Tripeptidyl-peptidase 2	0	17.5	C, N	Peptidase	Proteolysis	+	+
RBBP7	Histone-binding protein RBBP7	0	16.8	N	RNA binding	DNA replication	+	-
HSPA4L	Heat shock 70 kDa protein 4L	0	16.8	C, N	Chaperone	Stress response	-	+
MAP4	Microtubule-associated protein 4	0	16.3	C	Microtubule binding	Cell division	+	+
HSPH1	Heat shock protein 105 kDa	0	15.8	C	ATP binding	Stress response	-	+
TIPRL	TIP41-like protein	0	14.8	C	PP2A inhibitor	Cell cycle	+	-
HUWE1	E3 ubiquitin-protein ligase	0	14.8	C, N	Ligase	DNA repair	-	+
PPP2R2A	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	0	14.5	C	Phosphatase	Cell cycle	-	+
MCMBP	Mini-chromosome maintenance complex-binding protein	0	14.3	N	Chromatin binding	Cell cycle	+	-
UBA6	Ubiquitin-like modifier-activating enzyme 6	0	14.3	C	ATP binding	Protein ubiquitination	+	+
USP5	Ubiquitin carboxyl-terminal hydrolase 5	0	14.3	L	Hydrolase	Protein catabolism	-	-
SNRNP200	U5 small nuclear ribonucleoprotein 200 kDa helicase	0	14.3	N	Helicase	mRNA processing	-	-
GSTM3	Glutathione S-transferase Mu 3	0	14	C	Glutathione binding	Detoxification	+	-
DNM1L	Dynamin-1-like protein	0	14	C	Hydrolase	Apoptosis	+	-
KHSRP	Far upstream element-binding protein 2	0	14	N	DNA binding	mRNA processing	-	-

AIMP2	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	0	14	C, N	Development-al protein	Apoptosis	+	+
PABPC4	Polyadenylate-binding protein 4	0	14	C	mRNA binding	mRNA processing	-	+
NCAPD2	Condensin complex subunit 1	0	14	N	Chromatin binding	Cell cycle	-	+
MARS	Methionine--tRNA ligase, cytoplasmic	0	13.8	C	tRNA ligase	Gene expression	-	-
UNC45A	Protein unc-45 homolog A	0	13.8	C	Chaperone	Cell differentiation	-	-
STIP1	Stress-induced-phosphoprotein 1	0	13.5	C, N	RNA binding	Stress response	+	+
CORO1C	Coronin-1C	0	12.8	C	Actin binding	cytokinesis	-	+
MSH6	DNA mismatch repair protein Msh6	0	12.5	N	DNA binding	DNA repair	+	-
IARS	Isoleucine--tRNA ligase, cytoplasmic	0	12.5	C	tRNA editing	Gene expression	-	-
PABPC1	Polyadenylate-binding protein 1	0	12	C, N	RNA binding	mRNA processing	-	+
EIF4G1	Eukaryotic translation initiation factor 4 gamma 1	0	12	C	Translation factor	Translation	-	+
SPAG9	C-Jun-amino-terminal kinase-interacting protein 4	0	11.5	C	Kinase binding	Cell differentiation	-	-
KHDRBS1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	0	11.5	N	DNA binding	Cell cycle	-	-
PSMD2	26S proteasome non-ATPase regulatory subunit 2	0	11.3	C	MAPKK activator	Cell proliferation	+	-
ABCE1	ATP-binding cassette sub-family E member 1	0	11	C	ATPase activity	RNA catabolism	-	+
GFPT1	Glucosamine--fructose-6-phosphate aminotransferase 1	0	11	C	Carbohydrate binding	metabolism	-	+
SND1	Staphylococcal nuclease domain-containing protein 1	0	11	C, N	Nuclease	Transcription	+	-
RNPEP	Aminopeptidase B	0	10.8	EC	peptidase	Proteolysis	-	-
SMC4	Structural maintenance of chromosomes protein 4	0	10.8	N	ATP binding	Cell cycle	-	-
IPO11	Importin-11	0	10.5	C	Protein transporter	Protein transport	-	-
USP9X	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	0	10.5	C	Hydrolase	Cell cycle	-	-
CRKL	Crk-like protein	0	10.3	C	MAPKK activator	Cell proliferation	+	+
TBCD	Tubulin-specific chaperone D	0	10.3	C	chaperone	Protein folding	+	-
PSMD1	26S proteasome non-ATPase regulatory subunit 1	0	10.3	C	MAPKK activator	Cell proliferation	+	-
GTF2I	General transcription factor II-I	0	10.3	C, N	DNA binding	Transcription	+	+
LARP1	La-related protein 1	0	10.3	C	mRNA binding	Cell proliferation	+	+
TTLL12	Tubulin--tyrosine ligase-like protein 12	0	10	C	ATP binding	Tubulin PTM	-	-
EPRS	Bifunctional glutamate/proline--tRNA ligase	1	68.5	C	Ligase	Translation	-	+
PFAS	Phosphoribosylformylglycinamidine synthase	0.7	34.5	C	Ligase	Purine biosynthesis	-	+
NASP	Nuclear autoantigenic sperm protein	0.7	33	C, N	Protein binding	cell proliferation	+	+
UBE2L3	Ubiquitin-conjugating enzyme E2 L3	0.7	32.8	C, N	Transferase	Transcription	-	-
GARS	Glycine--tRNA ligase	0.7	32	C	Ligase	Translation	-	+
PRMT1	Protein arginine N-methyltransferase 1	0.7	25	N	Methyl transferase	Gene expression	-	+
FSCN1	Fascin	0.7	25	C	Actin binding	Cell migration	+	-
HNRNPK	Heterogeneous nuclear ribonucleoprotein K	1	36.8	C, N	Pre-mRNA binding	Apoptosis	-	+

XPO1	Exportin-1	1	36.5	C, N	Protein transporter	Gene expression	+	+
PPA1	Inorganic pyrophosphatase	1	31	C	Phosphatase	Gene		
expression	-	+						
PAICS	Multifunctional protein ADE2	0.7	20.3	C	Decarboxy-lase	Purine biosynthesis	-	+
PREP	Prolyl endopeptidase	0.7	20.3	C	Peptidase	Proteolysis	-	+
CSE1L	Exportin-2	0.7	18	C, N	Protein transport	Apoptosis	-	+
EEF2	Elongation factor 2	8.3	201.3	C, N	GTPase	Translation	-	+
PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	2.3	54.3	C	Methyl transferase	Protein repair	-	-
NPM1	Nucleophosmin	1	23	N	Chaperone	Cell proliferation	-	-
PLS3	Plastin-3	1.3	27.5	C	Calcium binding	Cell differentiation	-	+
IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	0.7	13.8	C, N	Oxidoredu-ctase	Purine biosynthesis	-	-
CLTC	Clathrin heavy chain 1	1.7	33.5	C	Protein or RNA binding	Protein transport	-	+
PRKDC	DNA-dependent protein kinase catalytic subunit	2.3	46.8	N	kinase	DNA repair	+	+
YWHAQ	14-3-3 protein theta	0.7	13.3	C	Protein binding	Apoptosis	-	+
ACLY	ATP-citrate synthase	2	39.5	M	Transferase	Lipid metabolism	+	+
EEF1G	Elongation factor 1-gamma	3	58.3	C	Transferase	Gene expression	-	+
RCC2	Protein RCC2	1.3	25.3	N	GTPase activator	Cell cycle	+	+
GART	Trifunctional purine biosynthetic protein adenosine-3	5	78.8	C	Ligase	Purine biosynthesis	-	+
CPNE1	Copine-1	0.7	10.5	N	Repressor	Differentiation	-	+
CCT2	T-complex protein 1 subunit beta	4.3	66.5	C	Chaperone	Protein folding	-	+
FASN	Fatty acid synthase	11	165.3	C	Hydrolase, Transferase	Fatty acid biosynthesis	-	+
AHCY	Adenosylhomocysteinase	1.3	20	C	Hydrolase	One-carbon metabolism	-	-
DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	1.3	19.5	C	ATPase	Transport	-	+
PTBP1	Polypyrimidine tract-binding protein 1	1.7	24	N	Pre-mRNA binding	mRNA processing	-	+
TARS	Threonine--tRNA ligase, cytoplasmic	1	13.3	C	Ligase	Translation	-	-
HSP90AB1	Heat shock protein HSP 90-beta	10.7	137.3	C	Chaperone	Stress response	-	+
DDX3X	ATP-dependent RNA helicase DDX3X	1	12.8	N	Helicase/ ATPase	Transcription	+	+
TCP1	T-complex protein 1 subunit alpha	2.7	33.8	C	Chaperone	Protein folding		+
IPO5	Importin-5	1.7	21	C, N	GTPase inhibitor	Protein transport	+	+
GSPT2	Eukaryotic peptide chain release factor GTP-binding subunit ERF3B	1	12.5	C	GTPase	Cell cycle	-	-
CFL1	Cofilin-1	4.7	56.8	N	Actin binding	Cytokinesis	-	+
CCT6A	T-complex protein 1 subunit zeta	1	11	C	Chaperone	Protein folding	-	+
PRDX2	Peroxiredoxin-2	2.3	24.3	C, M	Peroxidase	Oxidative stress response	-	-
PHGDH	D-3-phosphoglycerate dehydrogenase	1.3	13.8	C	Oxidoredu-ctase	Amino-acid biosynthesis	-	+
GCN1L1	Translational activator GCN1	2.3	21.5	C	RNA binding	Translation	-	+
PRDX1	Peroxiredoxin-1	2.7	24.5	C, M	Peroxidase	Oxidative stress response	-	-
UBA1	Ubiquitin-like modifier-activating enzyme 1	6.7	57.3	C,M	Ligase	proteolysis	+	+

PKM	Pyruvate kinase isozymes M1/M2	6.3	53.5	C, N	Kinase	Glycolysis	-	+
RPL18A	60S ribosomal protein L18a	2	16.3	C	RNA binding	Translation	-	-
DDX1	ATP-dependent RNA helicase	1.3	10.8	N	Helicase	Transcription	+	-
HNRNPF	Heterogeneous nuclear ribonucleoprotein F	1.7	11.5	N	RNA binding	mRNA processing	-	+
HSP90AA1	Heat shock protein HSP 90-alpha	20.7	140.5	C	Chaperone	Stress response	-	+
PRDX6	Peroxiredoxin-6	6	38	C	peroxidase	Oxidative stress response	+	+
QARS	Glutamine--tRNA ligase	1.7	10.5	C, M	Ligase	Translation	-	+
HNRNPL	Heterogeneous nuclear ribonucleoprotein L	5	25.5	C, N	RNA binding	mRNA processing	-	+
EEF1A2	Elongation factor 1-alpha 2	12.3	60.5	N	GTPase	Translation	-	-
XRCC6	X-ray repair cross-complementing protein 6	2.7	13	N	Helicase	DNA repair	-	-
XRCC5	X-ray repair cross-complementing protein 5	6.3	29.5	N	Helicase	DNA repair	-	+
EIF5AL1	Eukaryotic translation initiation factor 5A-1-like	5.7	25.8	C, N	mRNA binding	mRNA transport	-	-
EEF1A1	Elongation factor 1-alpha 1	18.3	79.8	C, N	GTPase	Translation	-	+
CAD	CAD protein	2.7	11.5	C, N	Hydrolase, ligase	Pyrimidine biosynthesis	-	-
YWHAE	14-3-3 protein epsilon	4	14.8	C	HDAC binding	Apoptosis	-	+
HSPA8	Heat shock cognate 71 kDa protein	3	11	C	ATPase, Chaperone	Transcription	-	+
ALDOA	Fructose-bisphosphate aldolase A	3	10	C	Lyase	Glycolysis	+	+
RPL10	60S ribosomal protein L10	4.7	14	C	RNA binding	Translation	-	+
CCT5	T-complex protein 1 subunit epsilon	6	16	C	ATP binding	Protein folding	-	+
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	30.7	77.3	C	Oxidoreductase/transferase	Glycolysis	-	+
MCM3	DNA replication licensing factor MCM3	4	10	N	Helicase	DNA replication	+	+
NME1	Nucleoside diphosphate kinase A	7.3	18.3	C, N	Kinase	Cell differentiation	-	-
PGAM1	Phosphoglycerate mutase 1	8	17.5	C	Isomerase	Glycolysis	+	-
PPIA	Peptidyl-prolyl cis-trans isomerase A	7.7	15.5	C, EC	Isomerase	Protein folding	+	-

(1) Neg and Pos: spectral count of the negative and positive samples, respectively.

(2) Loc: Localization (C: cytosol, N: nucleus, EC: extracellular, L: lysosome, M- mitochondrion).

(3) Function: molecular function determined by DAVID GO analysis.

(4) Process: biological processes determined by DAVID GO analysis.

(5) G: glutathionylation proteomic result by exogenous H_2O_2.

(6) S: sulfenylation proteomic result by exogenous H_2O_2.