
iTRAQ Data Analysis Report

NHLBI Zile/Grant, Aged Rat

November 19, 2007

1 Introduction

This document summarizes an analysis of relative protein expression using iTRAQ. The reporter ion peak area measurements supplied by the ABI software are used to estimate treatment-dependent peptide and protein relative expression. Estimation is accomplished using a Bayesian approach with the model given below. The document includes a protein relative expression summary and a per-protein detailed analysis. The document is internally hyperlinked and linked externally to NCBI.

2 Experiment and Model Description

2.1 Experiment Design

The report summarizes data from one or more iTRAQ experiments addressing a common comparison. The experiment design, used in this analysis, is given in the table below.

	Experiment	Treatment	Channel	Sample
1	A	C	114	H1
2	A	D	115	H2
3	A	D	116	H3
4	A	D	117	H4
5	B	C	114	H1
6	B	D	115	H6
7	B	D	116	H7
8	B	D	117	H8

2.2 Input Files

Data for this analysis was extracted from the following tandem mass spectra (MSMS) summary files.

Experiment	MSMS Summary File
A	../DataSets/Zile/JEG_I_33_Standard_peptide_full_MSMS.txt
B	../DataSets/Zile/JEG_I_43_peptide_full_MSMSsummary.txt

2.3 Statistical Model

The following statistical model was used to estimate the treatment-dependent effects.

$$\text{LogIntensity} \sim \text{Spectrum} + \text{Protein} + \text{Peptide} + \text{Treatment} + \text{Protein:Treatment} + \text{Peptide:Treatment}$$

3 Data Summary

The data supplied in the MSMS summary is filtered to remove unidentified proteins, contaminants, and peptides containing selected modifications. The following table summarizes the data provided and used in the analysis.

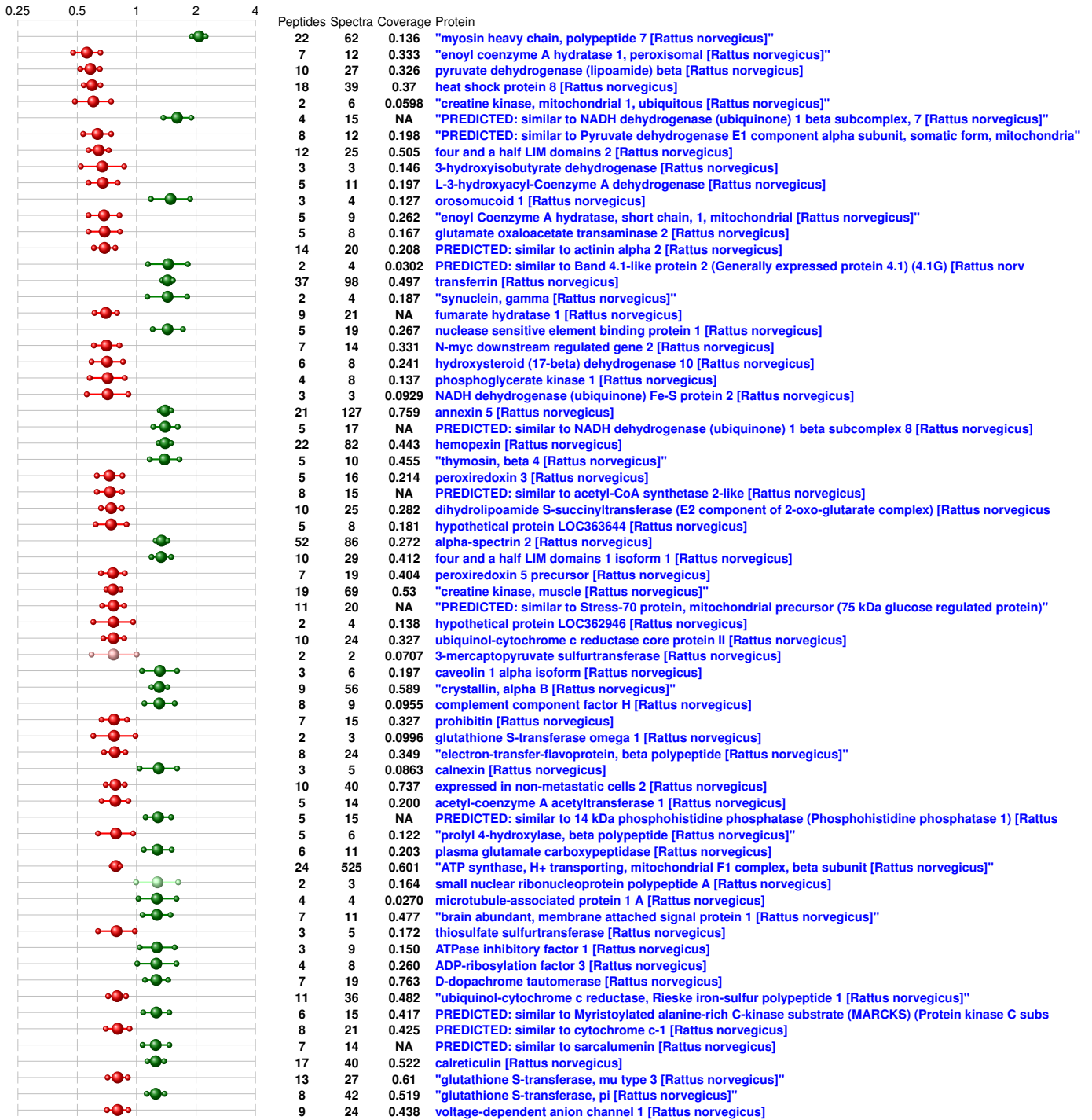
	A	B	Combined
Supplied Spectra	35597	35699	71296
Unidentified Spectra	26560	31757	58317
Disallowed Modifications	475	193	668
Spectra from Contaminants	0	0	0
Missing Data	0	5	5
Remaining Spectra			12306
Unique Proteins			1040
Unique Peptides			4085
Model R^2			0.965

4 Protein Summary

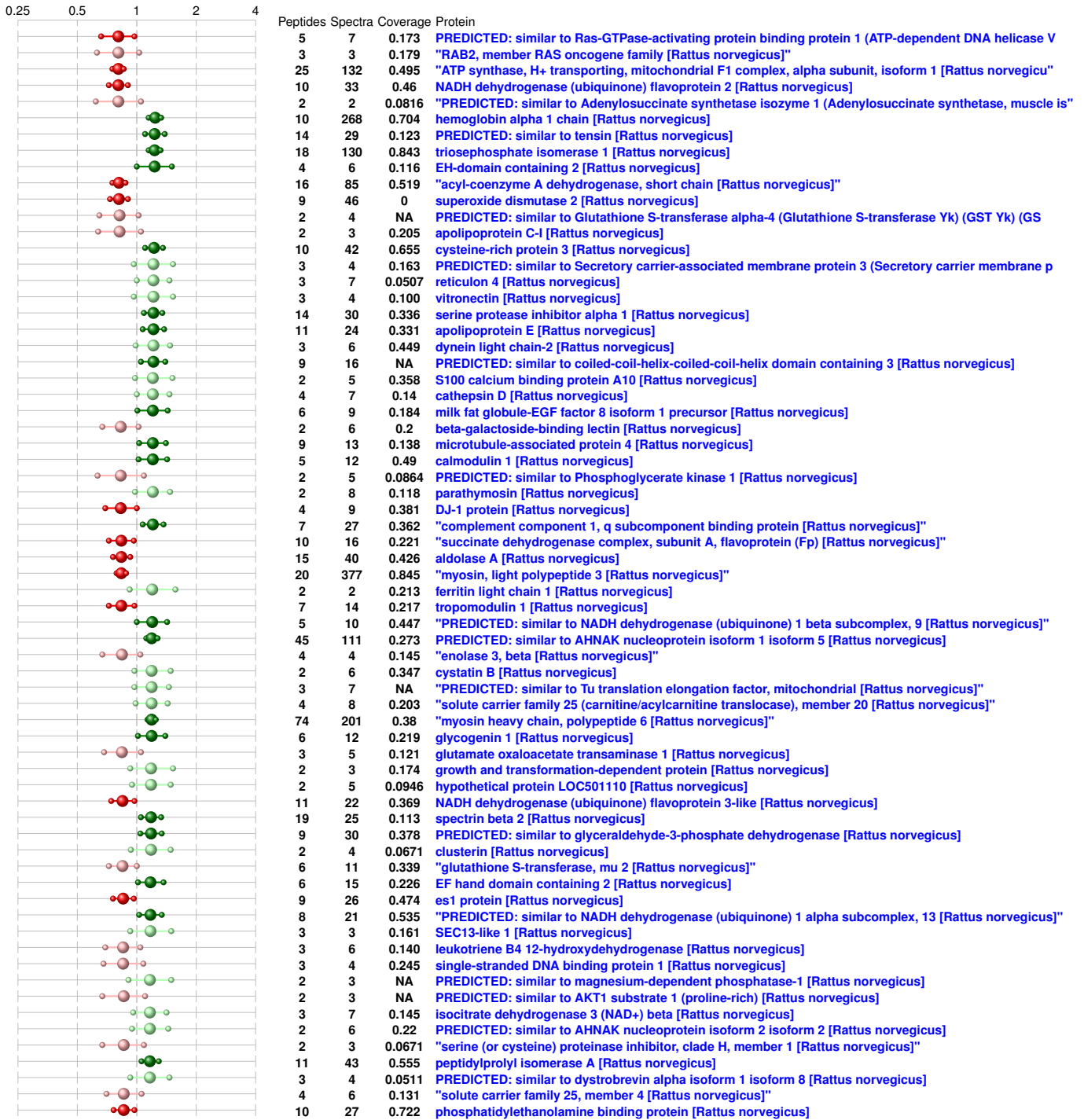
Each protein identified in one or more of the MSMS summaries is listed below in decreasing order of expression change magnitude. The median and estimated credible interval for each protein is given to the left in the table. Proteins identified by a single peptide are listed in a separate table.

4.1 Identified Proteins

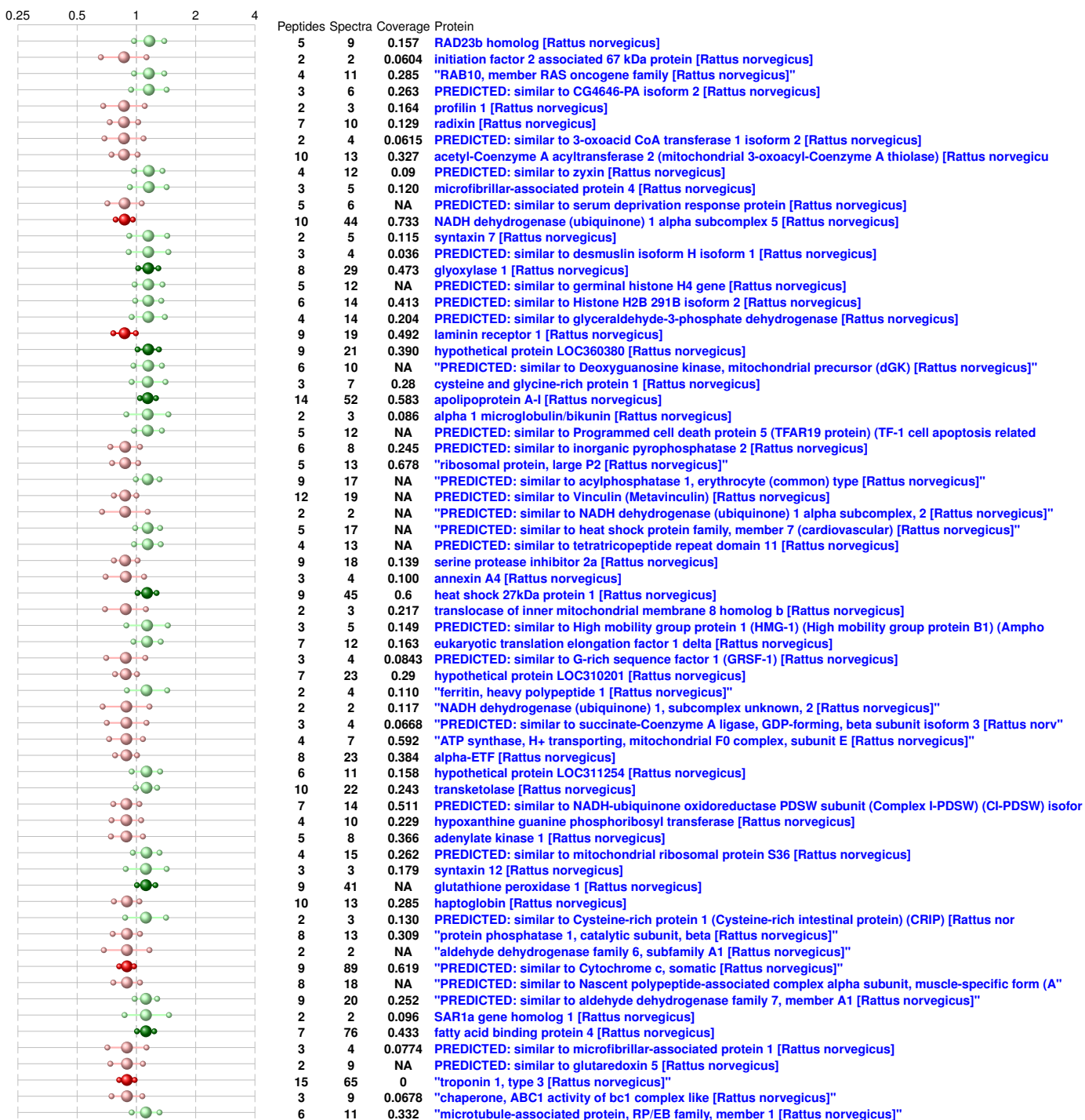
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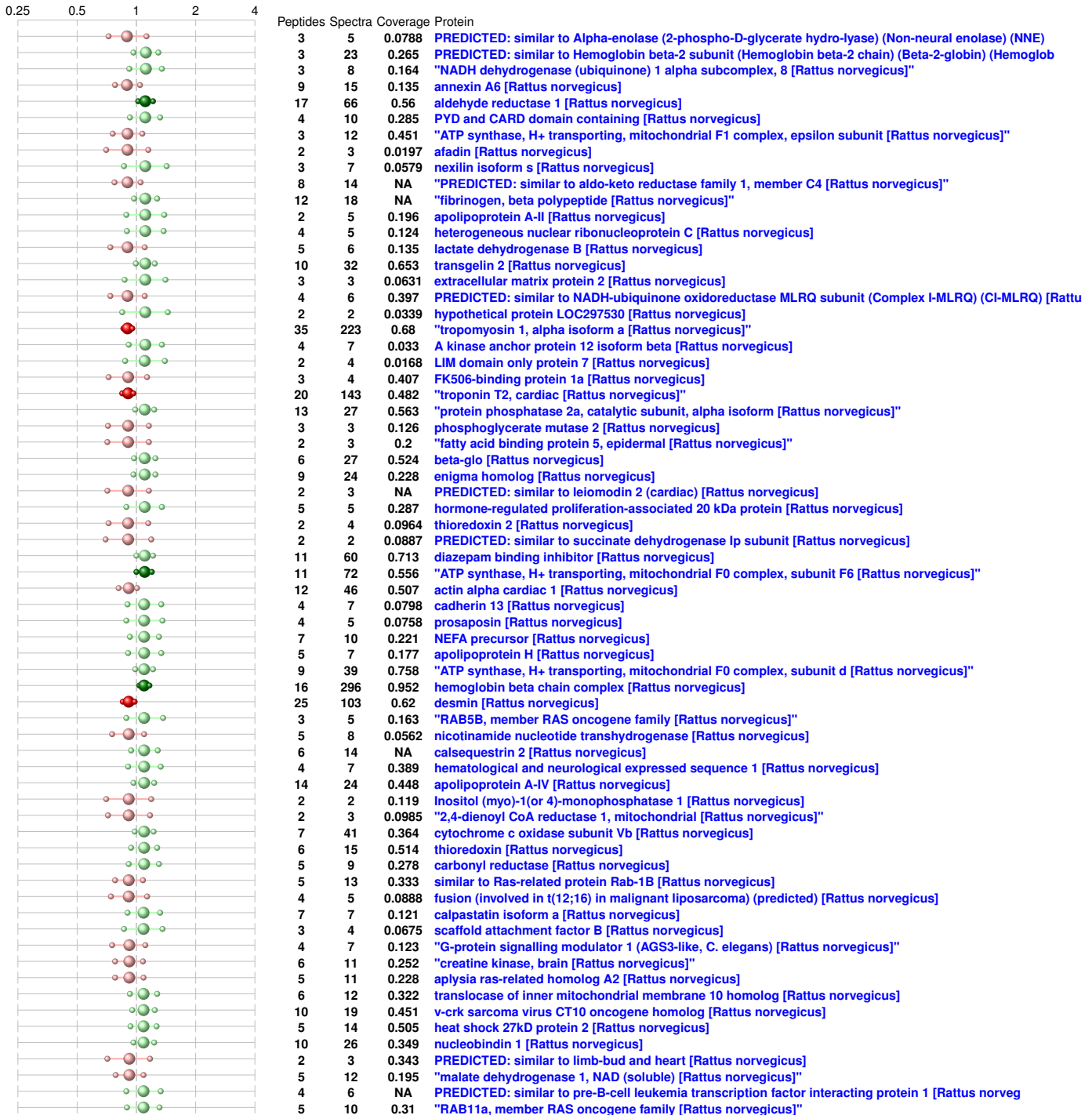
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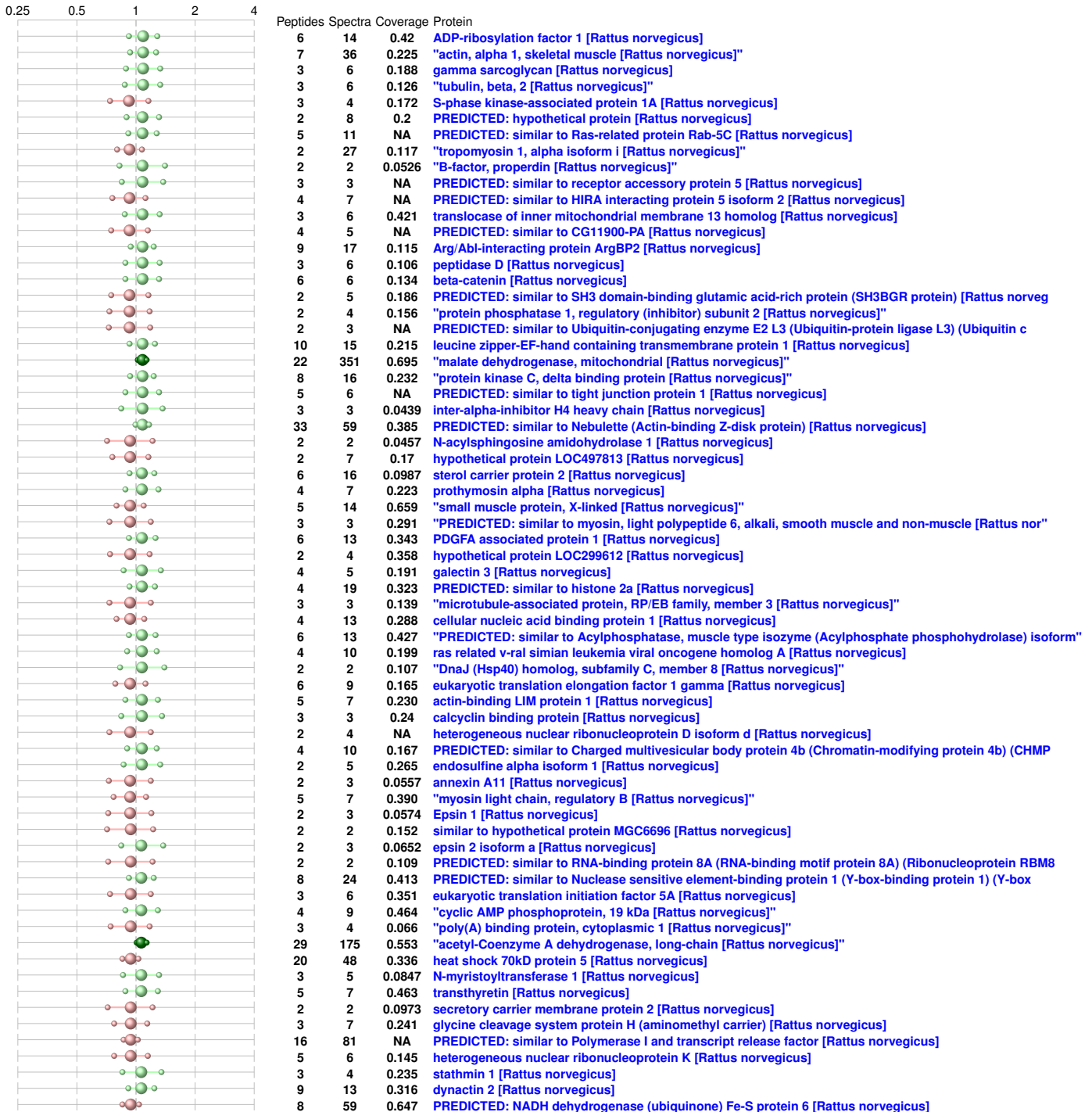
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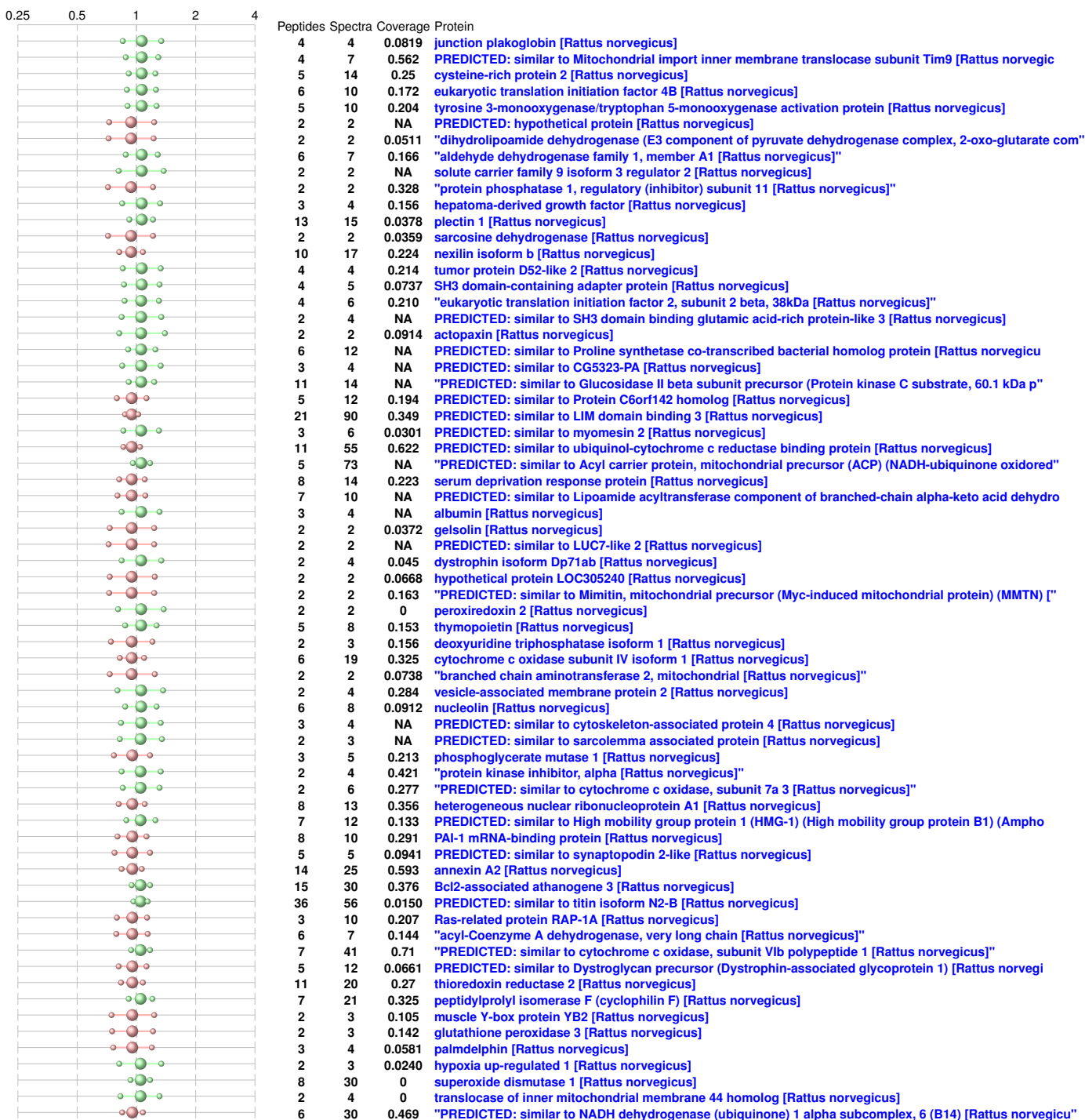
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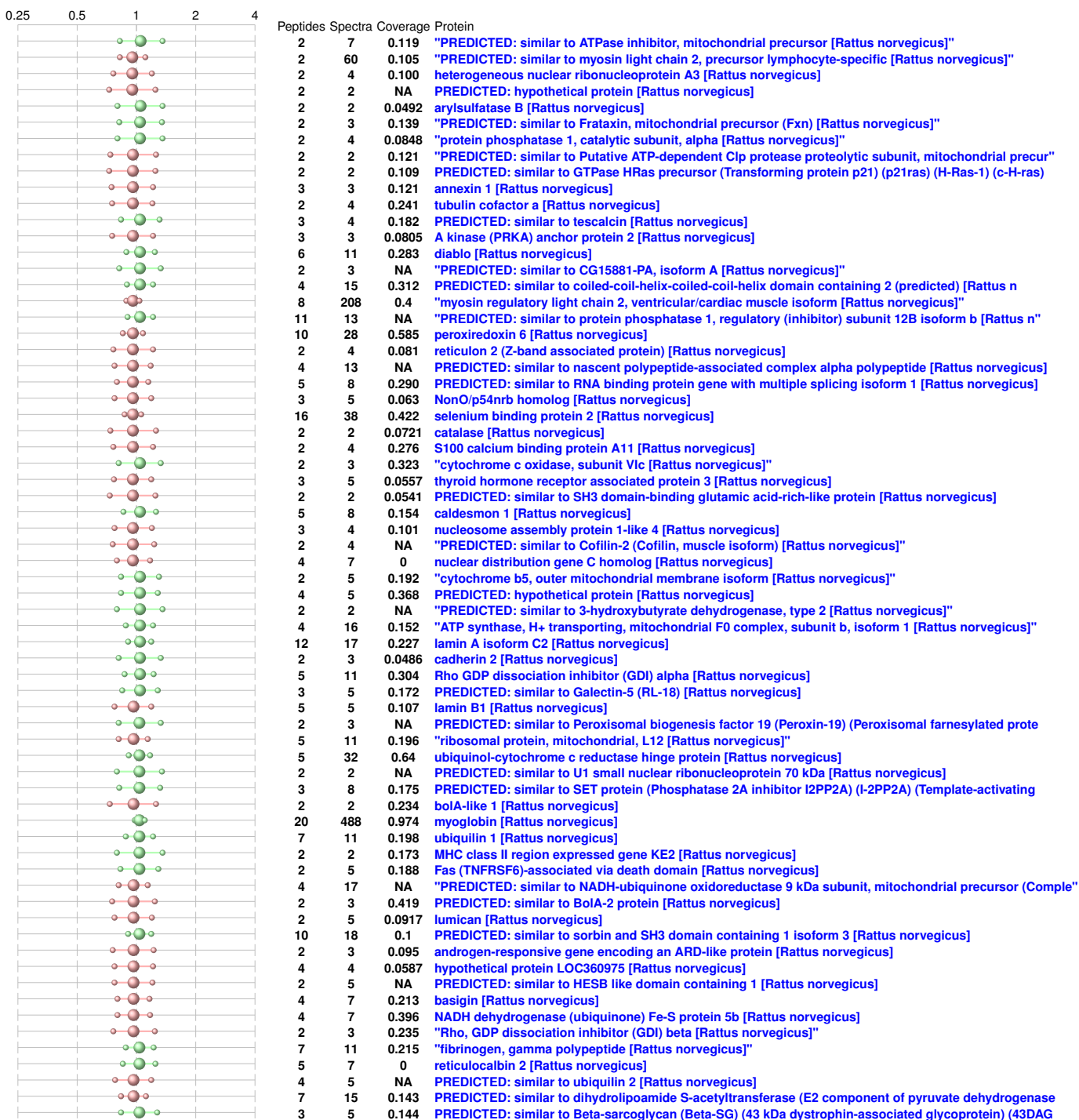
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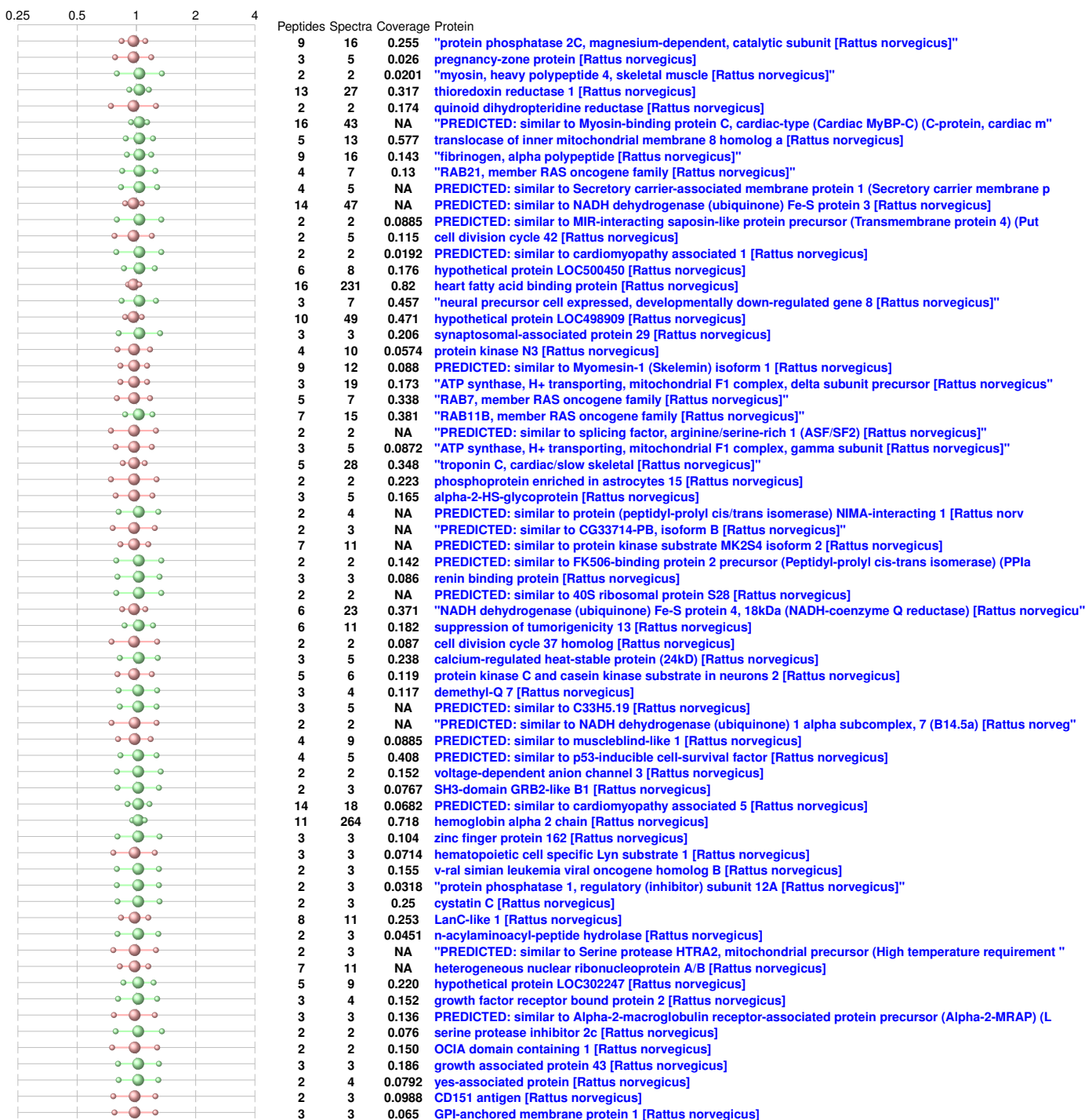
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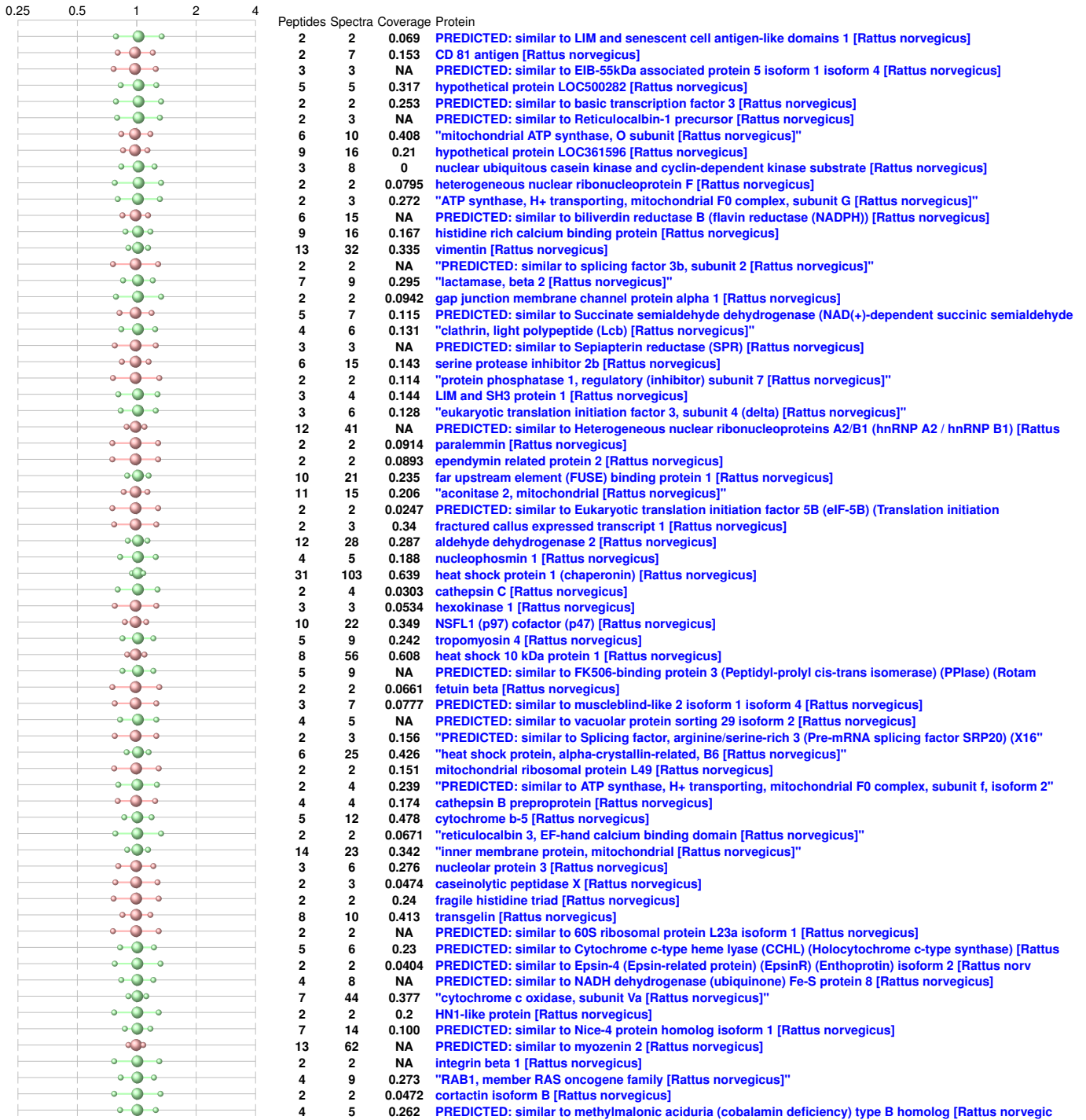
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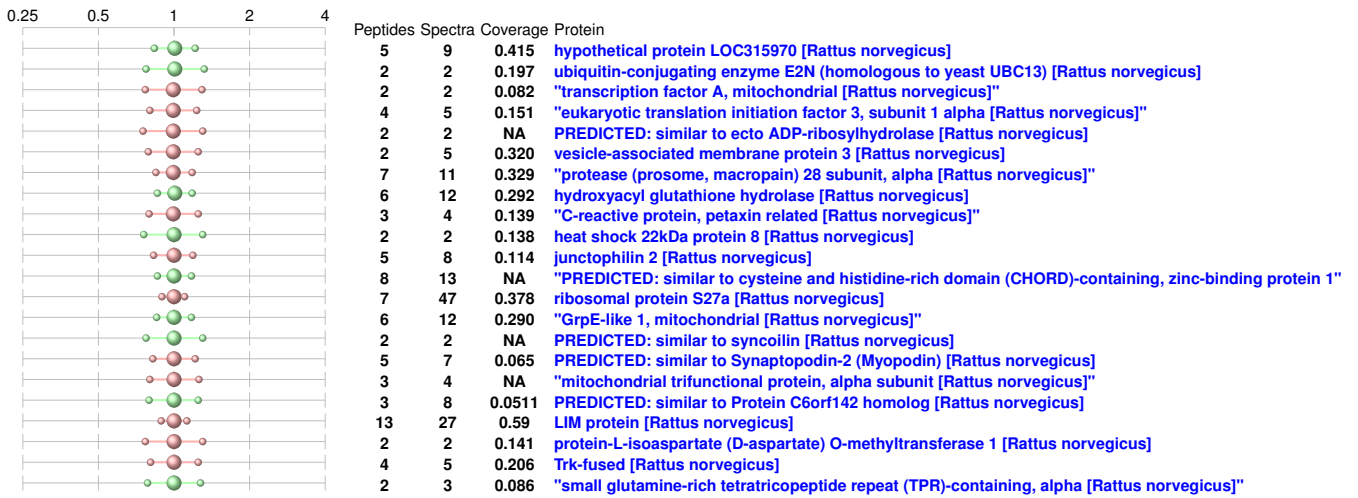


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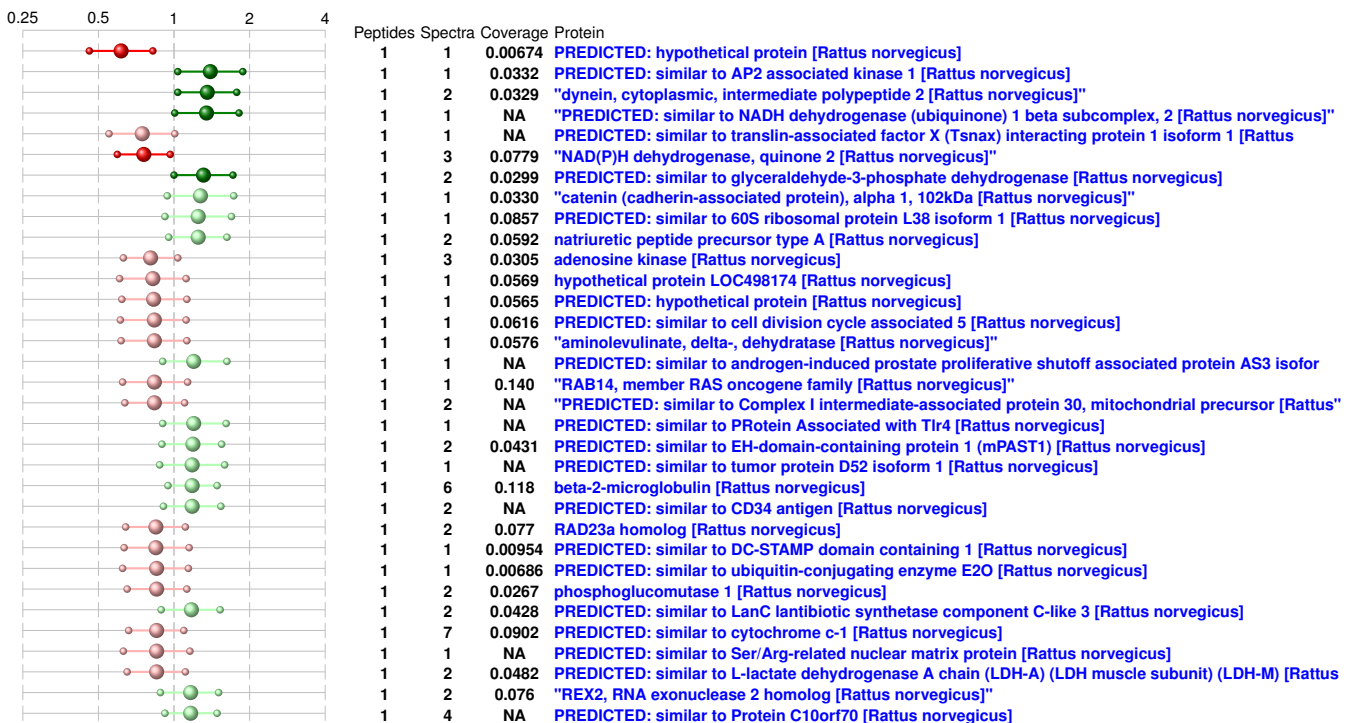


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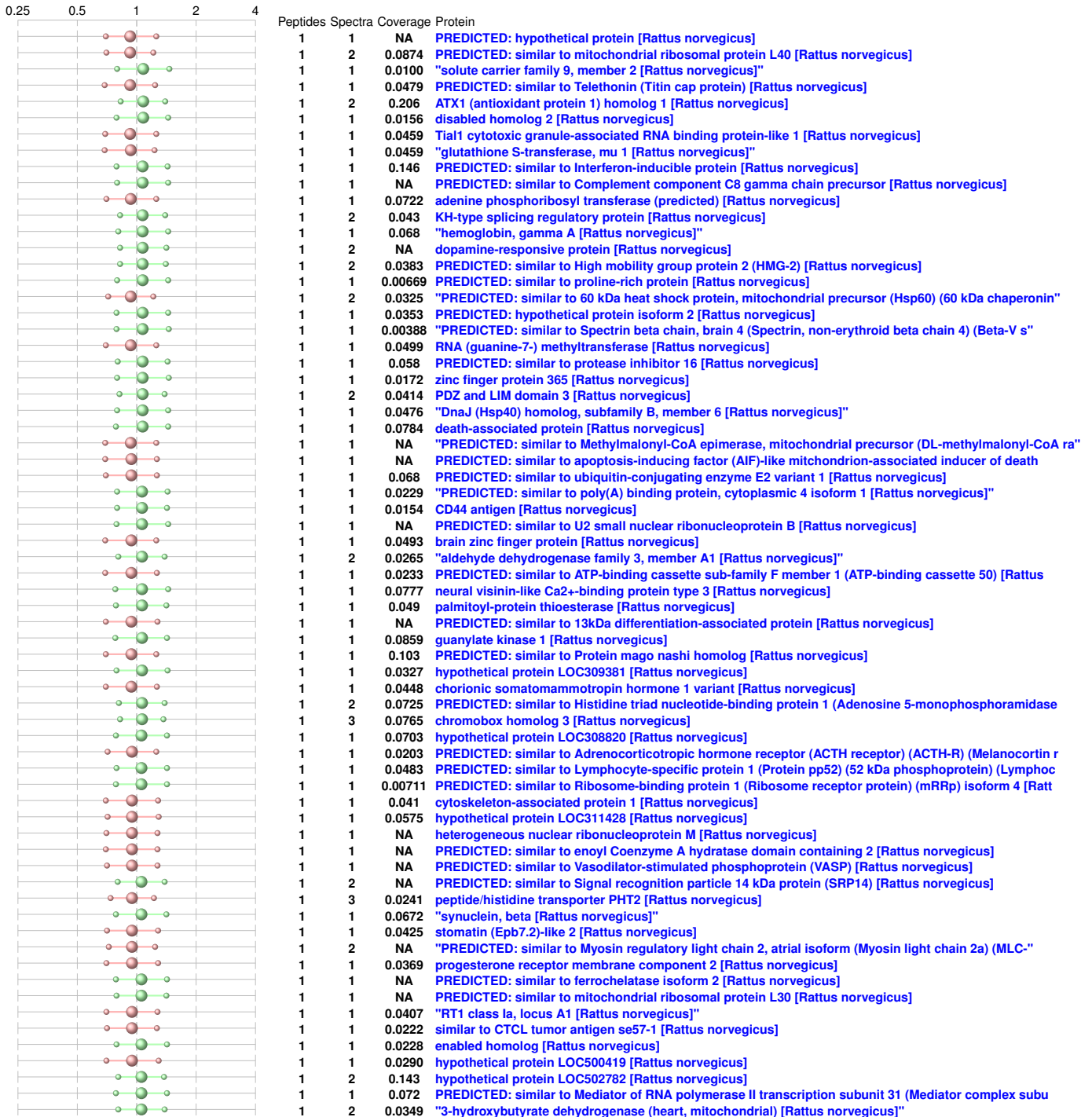
4.2 Proteins Identified by a Single Peptide



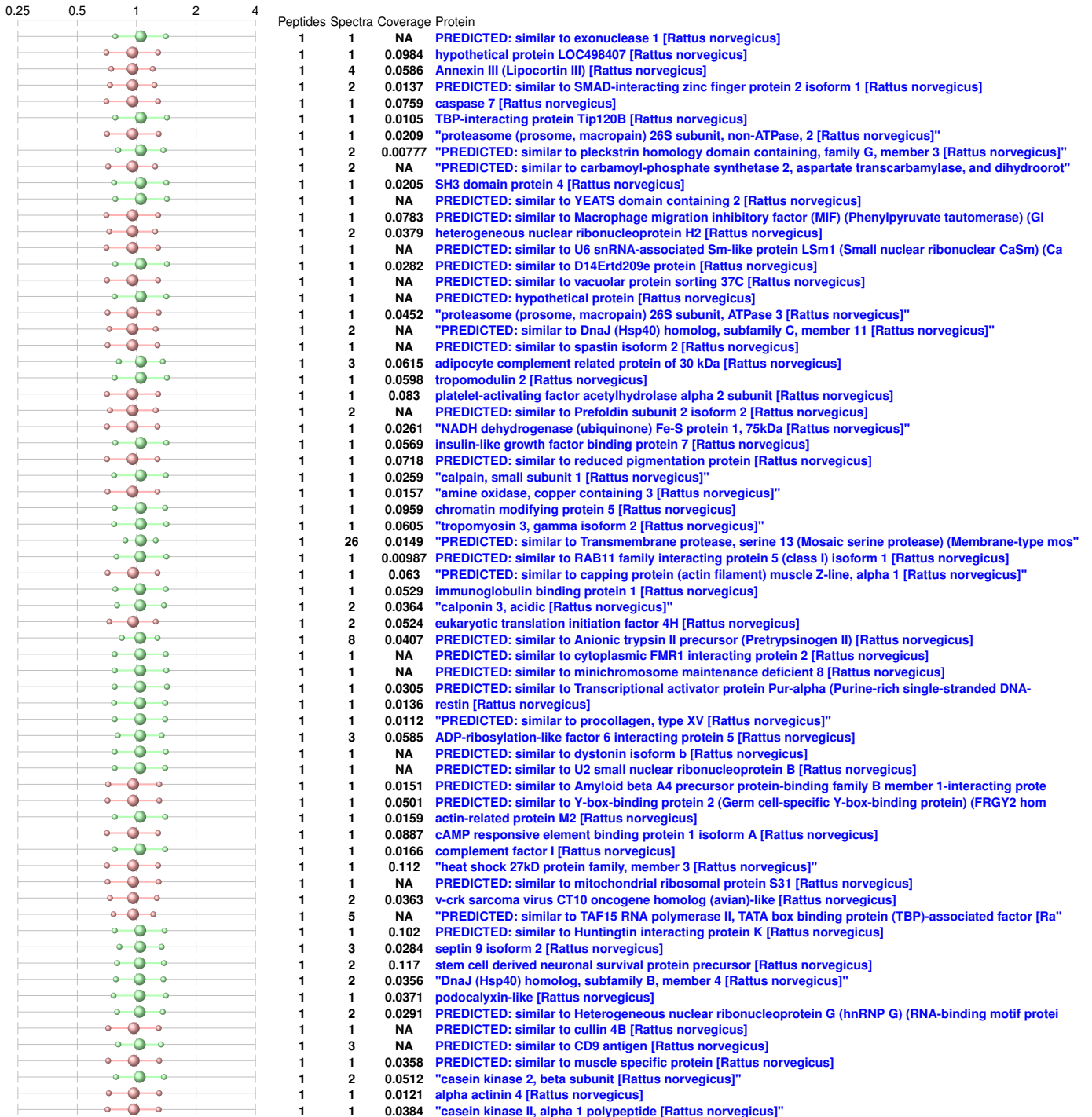
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0.25	0.5	1	2	4	Peptides	Spectra	Coverage	Protein
					1	1	0.0187	hypothetical protein LOC498332 [Rattus norvegicus]
					1	1	0.051	hypothetical protein LOC619440 [Rattus norvegicus]
					1	1	0.100	"COP9 (constitutive photomorphogenic) homolog, subunit 8 [Rattus norvegicus]"
					1	2	0.0498	glutathione S-transferase A5 [Rattus norvegicus]
					1	1	0.0467	PREDICTED: similar to developmental pluripotency-associated 3 [Rattus norvegicus]
					1	1	NA	PREDICTED: similar to transforming growth factor beta 1 induced transcript 4 isoform 1 isoform 1 [Rattus norvegicus]
					1	1	0.0189	"mitochondrial trifunctional protein, beta subunit [Rattus norvegicus]"
					1	1	0	xanthine dehydrogenase [Rattus norvegicus]
					1	1	0.0714	PREDICTED: similar to RuvB-like 2 (p47 protein) [Rattus norvegicus]
					1	3	0.00748	cell division cycle 5-like [Rattus norvegicus]
					1	2	0.122	"protein phosphatase 1, regulatory (inhibitor) subunit 14C [Rattus norvegicus]"
					1	2	NA	PREDICTED: similar to sorting nexin associated golgi protein 1 [Rattus norvegicus]
					1	1	0.00318	unc-13 homolog C [Rattus norvegicus]
					1	1	0.0653	PREDICTED: similar to Nucleoside diphosphate linked moiety X motif 13 (Nudix motif 13) [Rattus norvegicus]
					1	3	0.0447	PREDICTED: similar to Acyl-CoA thioesterase 4 (Peroxisomal acyl coenzyme A thioester hydrolase Ib) [Rattus norvegicus]
					1	2	NA	PREDICTED: similar to target of myb1-like 2 isoform 2 [Rattus norvegicus]
					1	1	0.0147	PREDICTED: hypothetical protein [Rattus norvegicus]
					1	1	0.158	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 isoform 1 [Rattus norvegicus]
					1	2	0.0315	"protein kinase, cAMP dependent regulatory, type I, alpha [Rattus norvegicus]"
					1	3	0.013	E74-like factor 1 [Rattus norvegicus]
					1	4	0.0465	similar to TSC22 domain family protein 4 (TSC22-related-inducible leucine zipper protein 2) [Rattus norvegicus]
					1	3	0	ribosomal protein S15 [Rattus norvegicus]
					1	1	0.0285	PREDICTED: similar to ring finger protein 186 [Rattus norvegicus]
					1	1	0	synaptopodin [Rattus norvegicus]
					1	1	NA	PREDICTED: similar to supervillin isoform 1 [Rattus norvegicus]
					1	1	0.0342	PREDICTED: similar to glycerol-3-phosphate dehydrogenase 1-like [Rattus norvegicus]
					1	1	0.00753	PREDICTED: similar to D10Ert802e protein [Rattus norvegicus]
					1	1	0.0263	microtubule-associated protein 6 [Rattus norvegicus]
					1	1	0.026	"serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4 "
					1	1	0.0137	PREDICTED: similar to Sphingomyelin phosphodiesterase 3 (Neutral sphingomyelinase 2) (Neutral sphingomyelinase 2) [Rattus norvegicus]
					1	1	0.0543	hypothetical protein LOC288683 [Rattus norvegicus]
					1	1	0.0558	methionine sulfoxide reductase A [Rattus norvegicus]
					1	1	0.0774	PREDICTED: interferon-stimulated protein (predicted) [Rattus norvegicus]
					1	3	NA	"PREDICTED: similar to LSM3 homolog, U6 small nuclear RNA associated [Rattus norvegicus]"
					1	2	0.160	PREDICTED: similar to Protein C6orf115 [Rattus norvegicus]
					1	1	0.103	adipsin [Rattus norvegicus]
					1	1	0.00551	PREDICTED: similar to talin 2 isoform 2 [Rattus norvegicus]
					1	1	NA	PREDICTED: similar to Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like protein) (ABP-280-like p) [Rattus norvegicus]
					1	1	0.00221	PREDICTED: similar to AHNAK nucleoprotein isoform 1 [Rattus norvegicus]
					1	1	0.154	PREDICTED: similar to basic transcription factor 3 [Rattus norvegicus]
					1	1	0.0160	PREDICTED: similar to Y50C1A.1 [Rattus norvegicus]
					1	4	0.0784	PREDICTED: similar to eukaryotic translation initiation factor 5A2 [Rattus norvegicus]
					1	1	0.00333	PREDICTED: similar to hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC) [Rattus norvegicus]
					1	1	NA	glutaminase [Rattus norvegicus]
					1	2	0.108	nuclear protein E3-3 isoform a [Rattus norvegicus]
					1	1	0.0244	"tumor necrosis factor (ligand) superfamily, member 10 [Rattus norvegicus]"
					1	1	0.0787	S100 calcium binding protein A6 (calcyclin) [Rattus norvegicus]
					1	7	0.212	phospholamban [Rattus norvegicus]
					1	2	0.0577	emerin [Rattus norvegicus]
					1	1	0.0664	PREDICTED: similar to Dual specificity protein phosphatase 3 (T-DSP11) [Rattus norvegicus]
					1	1	0.0394	PREDICTED: similar to peptide deformylase-like protein [Rattus norvegicus]
					1	1	0.0691	secernin 3 [Rattus norvegicus]
					1	1	NA	PREDICTED: similar to N-acetylneuraminic acid synthase (sialic acid synthase) [Rattus norvegicus]
					1	4	0.145	PREDICTED: similar to carnitine deficiency-associated gene expressed in ventricle 3 isoform CDV3B [Rattus norvegicus]
					1	1	NA	PREDICTED: similar to acyl-Coenzyme A oxidase-like [Rattus norvegicus]
					1	1	0.0445	"solute carrier family 16 (monocarboxylic acid transporters), member 1 [Rattus norvegicus]"
					1	1	0.00355	PREDICTED: similar to centromere protein F (350/400kD) [Rattus norvegicus]
					1	2	0.0156	PREDICTED: similar to Collagen alpha-1(VI) chain precursor [Rattus norvegicus]
					1	2	0.0345	"PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 [Rattus norvegicus]"
					1	1	0.0421	pyridoxine 5-phosphate oxidase [Rattus norvegicus]
					1	3	NA	PREDICTED: similar to pentatricopeptide repeat domain 2 [Rattus norvegicus]
					1	1	0.00657	vanilloid receptor-like protein 1 [Rattus norvegicus]
					1	3	0.0104	PREDICTED: similar to CG10632-PA [Rattus norvegicus]
					1	1	NA	PREDICTED: hypothetical protein [Rattus norvegicus]
					1	1	NA	"ATPase, Na+/K+ transporting, beta 1 polypeptide [Rattus norvegicus]"
					1	1	0.00862	neural stem cell-derived dendrite regulator [Rattus norvegicus]
					1	4	0.259	dapit protein [Rattus norvegicus]

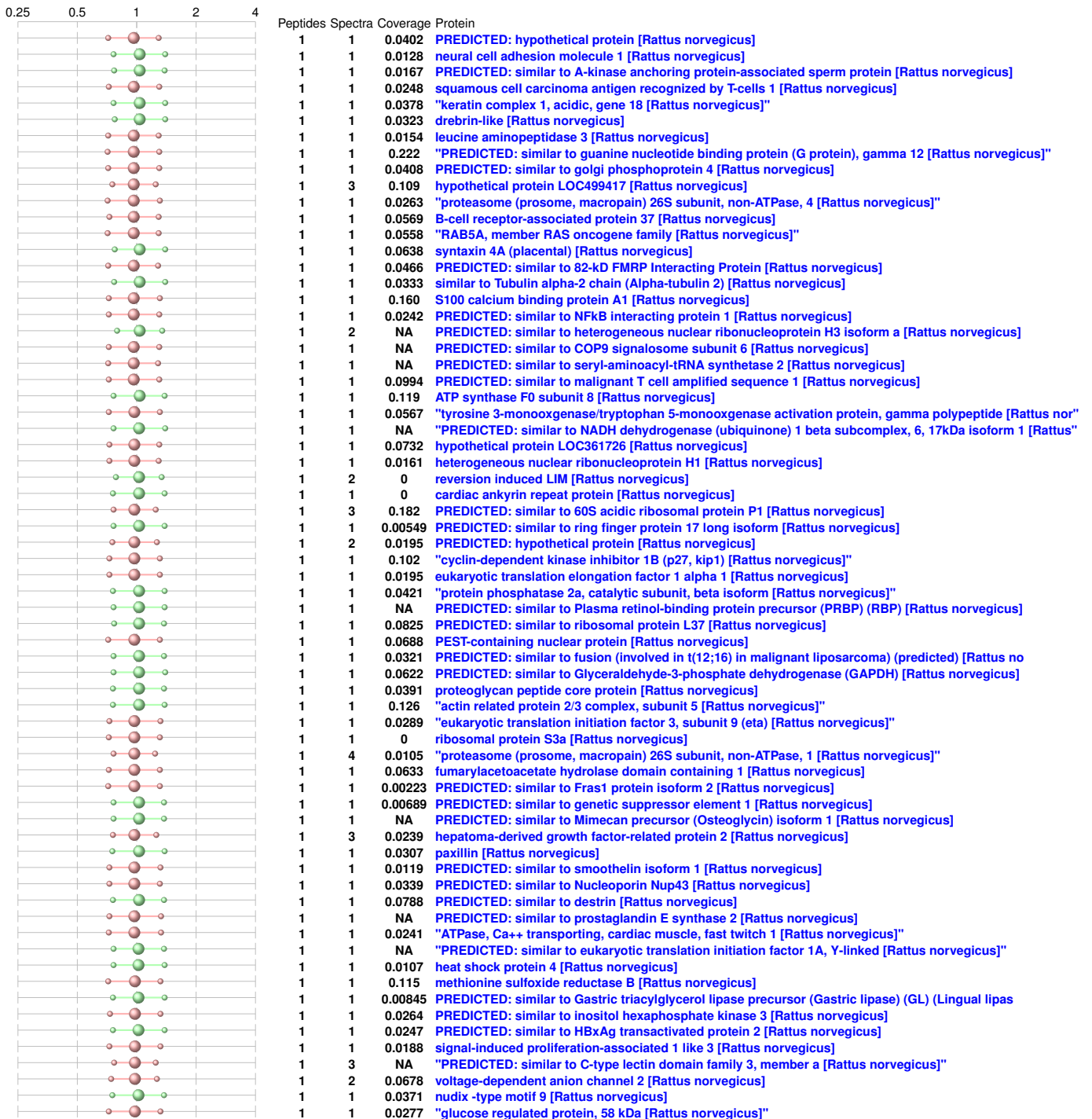
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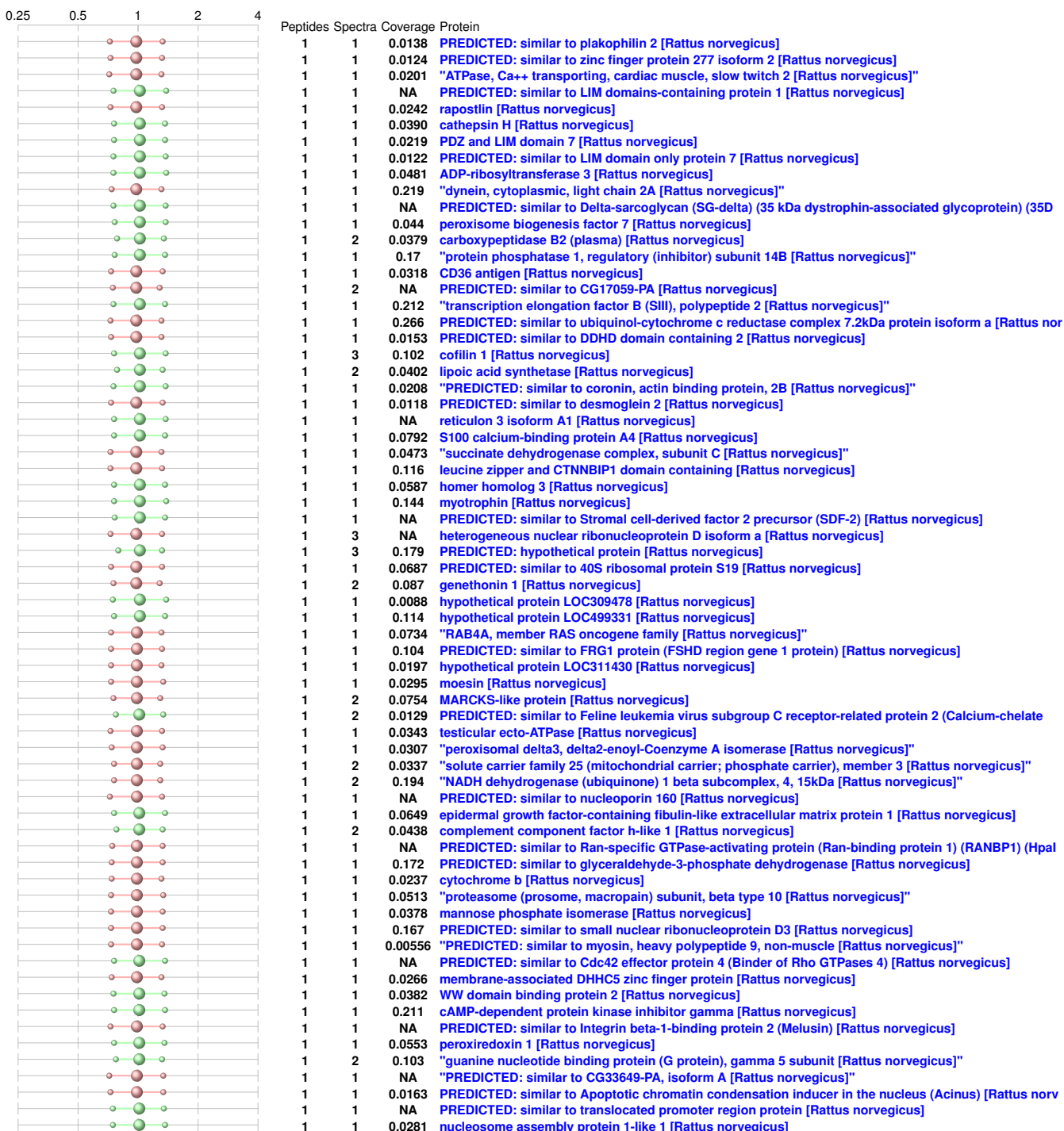
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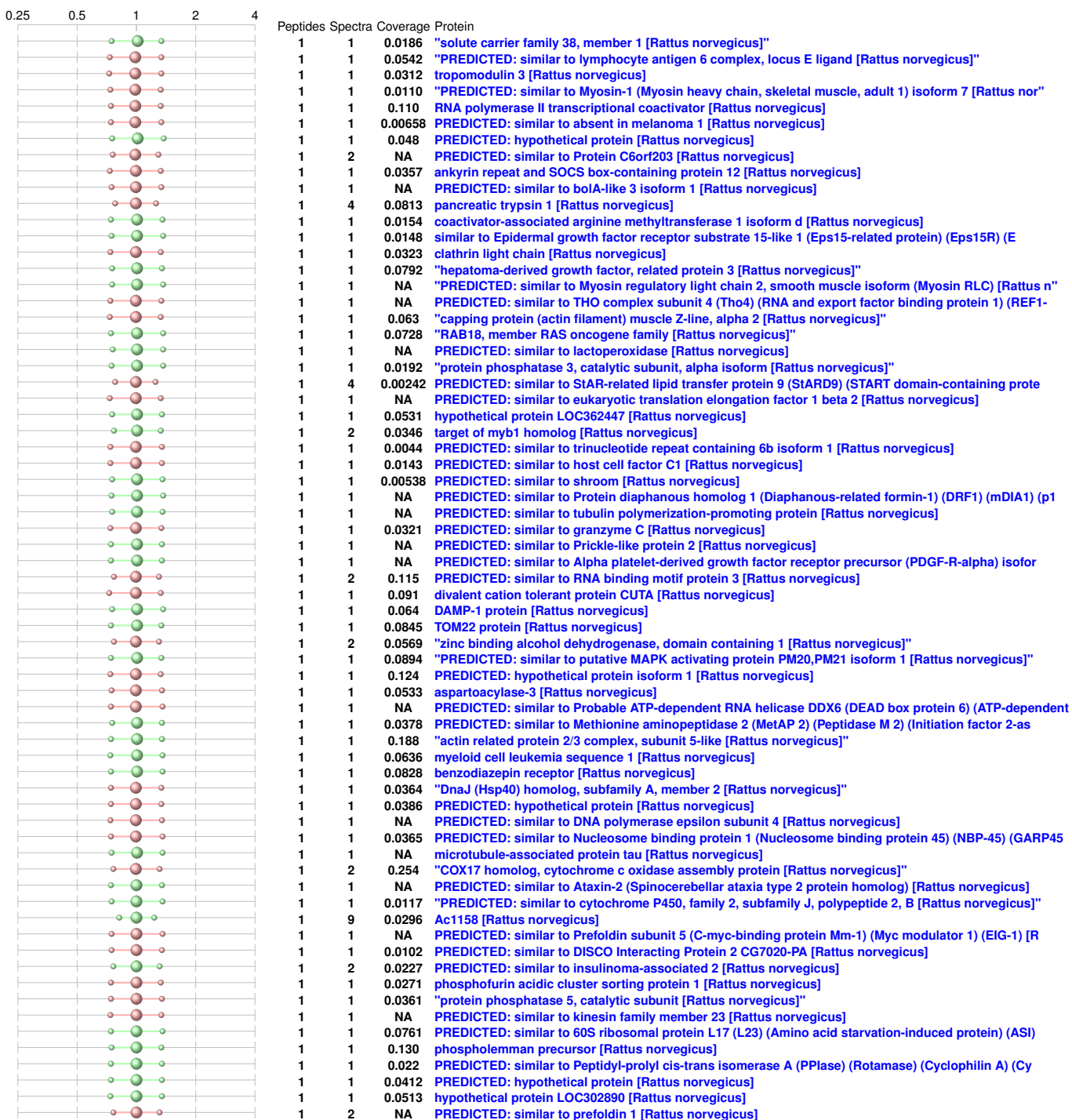
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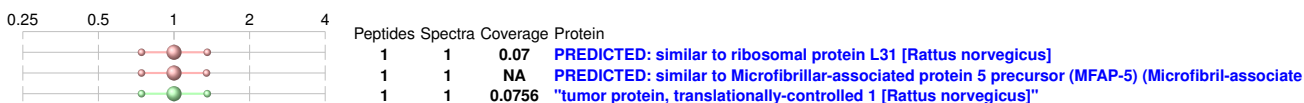


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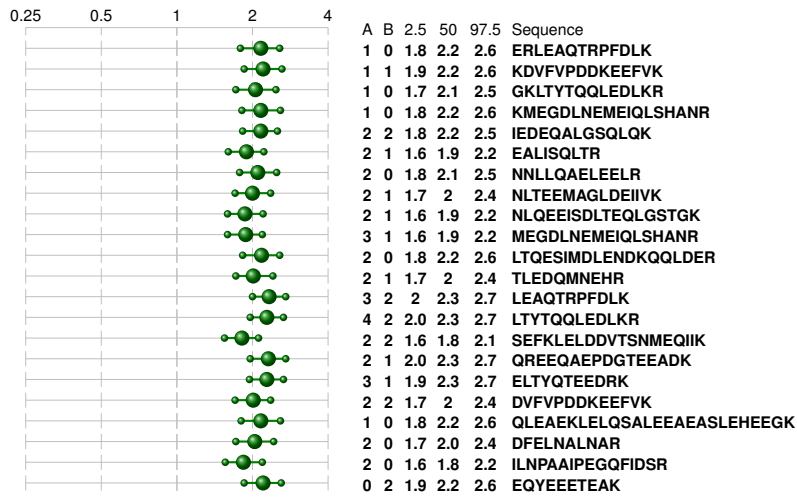
5 Protein Details

A detailed summary of each protein is given below. These sections include peptide relative expression estimates in addition to protein-level estimates.

5.1 "myosin heavy chain, polypeptide 7 [Rattus norvegicus]"

Protein Accession	gij8393807	
Mean Expression Ratio	2.07	
Median Expression Ratio	2.06	
Credible Interval	(1.91, 2.24)	
Associated Peptides	22	
Associated Spectra	62	
Coverage	0.136	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.23	1.40
Avg..iTRAQ.Ratio....116.114.	1.44	1.15
Avg..iTRAQ.Ratio....117.114.	2.17	1.95

1	MADREMAAFG	AGAPFLRKSE	KERLEAQTRP	FDLKKDVFVP	DDKEEFVKAK	IVSREGGKVT	AETENGKTVT	VKEDQVMQQN
81	PPKFDKIEDM	AMTLFLHEPA	VLNLIKERYA	SWMIYTYSGL	FCVTVNPYKW	LPVYNAQVVA	AYRGKKRSEA	PPHIFSISDN
161	AYQYMLTDRE	NQSILITGES	GAGKTVNTRK	VIQYFAVIAA	IGDRSKKDDT	PGKGTLEDQI	IQANPALEAF	GNAKTVRNDN
241	SSRFQKFI	HFGATGKLAS	ADIETYLLEK	SRVIFQLKAE	RDYHIFYQIL	SNKKPELLDM	LLITNNPYDY	AFFSQGETTV
321	ASIDDSEEHM	ATDSAFDVLG	FTPEEKNSIY	KLGTAIMHFG	NMKFKQKQRE	EQAEPDGTTE	ADKSAYLMGL	NSADLLKGLC
401	HPRVKVGNEY	VTGQNVQVQV	AYAIGALAKS	VYEKMFNMWV	TRINATLETK	QPRQYFIGVL	DIAGFEIFDF	NSFEQLCINF
481	TNEKLQQFFN	HHMFVLEQEE	YKKEGIEWTF	IDFGMDLQAC	IDLIEKPMGI	MSILEEECMF	PKATDMTFKA	KLYDNHHLGKS
561	NNFQKPRNIK	GKQEAHFSLI	HYAGTVDYNI	LGWLQKNKDP	LNETHVVGLYQ	KSSLEKLLSNL	FANYAGADAP	VDKGKGKAKK
641	GSSFQTVSAL	HRENLNKLMT	NLRSTHPHFV	RCHIPNETKS	PGVMDNPLVM	HQLRCNGVLE	GIRICRKFPP	NRILYGDFRQ
721	RYRILNPAAI	PEGQFIDSRK	GAEKLLGSLD	IDHNQYKFGH	TKVFFKAGLL	GLLEEMRDER	LSRIITRIQA	QSRGVLSRME
801	FKKLLERRDS	LLIIQWNIRA	FMGVKNWPM	KLYFKIKPLL	KSAETEKEMA	NMKEEFGRVK	DALEKSEARR	KELEEKMVSL
881	LQEKNDLQLQ	VQAEQDNLAD	AEERCDQLIK	NKIQLKAVK	EMTERLEDEE	EMNAELTAKK	RKLEDECSSEL	KRDIIDLELT
961	LAKVEKEKHA	TENKVKNLTE	EMAGLDEIIV	KLTKKALQ	EAHQQALDDL	QAEEDKVNTL	TKAKVKLEQQ	VDDLEGLSDQ
1041	DKKVRMDLER	AKRKLKGLD	LTQESIMDLE	NDKQQLDERL	KKKDFELNAL	NARIEDEQAL	GSQQLQKLLKE	LQARIEELEEE
1121	ELEAERTARA	KVEKLRSDLS	RELEEISERL	EEAGGATSVQ	IEMNKKREAE	FQKMRDLEE	ATLQHEATAA	ALRKKHDSV
1201	AELGEQIDNL	QRVKQKLEKE	KSEFKLELDD	VTSNMEQIIK	AKANLEKMC	TLEDQMNEHR	SKAEETQRSV	NDLTRQRAKL
1281	QTENGELSRQ	LDEKEALISQ	LTRGKLTYTQ	QLEDLKRQLE	EVEKAKNALA	HALQSARHDC	DLLREQYEEE	TEAKAELQRV
1361	LSKANSEVAQ	WRTKYETDAI	QRTEELEBAK	KKLAQRLQDA	EEAVEAVNAK	CSSLEKTKHR	LQNEIEDLMV	DVERSNAAAA
1441	ALDKKQRNFD	KILVEWKQKY	EESQSELESS	QKEARSLSTE	LFKLNAYEE	SLEHLETFKR	ENKNLQEEIS	DLTEQLGSTG
1521	KSIEHELEKIR	KQLEAEKLEL	QSALEAEAS	LEHEEGKILR	AQLEFNQIKA	EIERKLAEKD	EEMEQAQRNH	LRVVDLSQTS
1601	LDAETRSRNE	ALRVKKMEG	DLNEMEIQLS	HANRMAAEAQ	KQVKSLSQSL	KDTQIQLDLDA	VRANDDLKEN	IAIVERNNL
1681	LQAELEELRA	VVEQTTERS	LAEQELIETS	ERVQLLSQSN	TSLINQKKKM	DADLSQLQTE	VEEAVQECRN	AEEKAKKAIT
1761	DAAMMAEELK	KEQDTSAHLE	RMKNMNETI	KDLQHRHDEA	EQIALKGGKK	QLQKLEARVR	ELENELEAEQ	KRNESVKG
1841	RKSERRIKEL	TYQTEEDRKN	LLRLQDLVDK	LQLKVKAYKR	QAEEAEQAN	TNLSKFRKVV	HELDEAEERA	DIAESQVKNL
1921	RAKSRDIGAK	GLNEE						

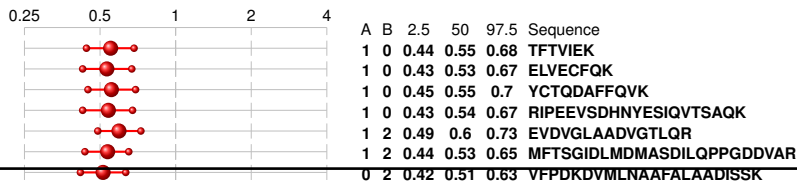


5.2 "enoyl coenzyme A hydratase 1, peroxisomal [Rattus norvegicus]"

Protein Accession	gij12018256	
Mean Expression Ratio	0.557	
Median Expression Ratio	0.558	
Credible Interval	(0.477, 0.653)	
Associated Peptides	7	
Associated Spectra	12	
Coverage	0.333	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.565	0.409
Avg..iTRAQ.Ratio....116.114.	0.478	0.419
Avg..iTRAQ.Ratio....117.114.	0.371	0.629

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1      MATAMTVSSK LLGLLMQQIR GTRQLYFNVS LRLSLSSSAQE ASKRIPPEEVS DHNYESIQVT SAQKHVHLHVQ LNRPEKRNAM
81     NRAFWRELVE CFQKISKDSD CRAVVVSGAG KMFTSGIDLMDMASDILQPPP GDDVARIAWY LRDLLISRYQK TFTVIEKCPK
161    PVITAIHGGC IGGGVDLISA CDIRYCTQDA FFQVKEVDVG LAADVGTLQR LPKVIIGNRSL VNELTFTARK MMADEALDSG
241    LVSRVFPDKD VMLNAAFALA ADISSKSPVA VQGSKINLIY SRDHSVDESL DYMATWNMSM LQTQDIKSV QAAMEKKDSK
321    SITFSKL
    
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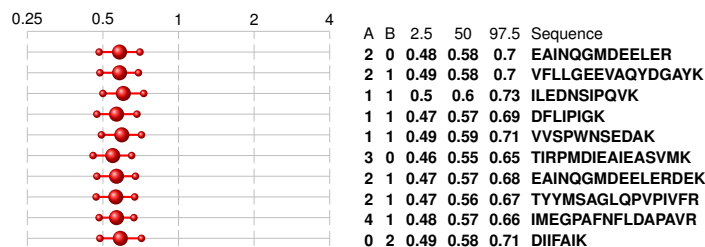


5.3 pyruvate dehydrogenase (lipoamide) beta [Rattus norvegicus]

Protein Accession	gij56090293	
Mean Expression Ratio	0.582	
Median Expression Ratio	0.582	
Credible Interval	(0.517, 0.652)	
Associated Peptides	10	
Associated Spectra	27	
Coverage	0.326	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.593	0.43
Avg..iTRAQ.Ratio....116.114.	0.477	0.42
Avg..iTRAQ.Ratio....117.114.	0.56	0.77

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1   MAAVAGLVRG PLRQASGLLK RRFHRSAPAA VQLTVREAIN QGMDEELERD EKVFLLGEEV AQYDGAYKVS RGLWKKYGDK
81  RIIDTPISEM GFAGIAVGAA MAGLRPICEF MTFNFMSQAI DQVINSAAKT YYMSAGLQPV PIVFRGPNGA SAGVAAQHSQ
161 CFAAWYGHCP GLKVVSPWNS EDAKGLIKSA IRDDNPVVML ENELMYGVAF ELPTEAQSKD FLIPIGKAKI ERQGTHTVTV
241 AHSRPVGHCL EAAAVLSKEG IECEVINLRT IRPMDIEAIE ASVMKTNHLV TVEGGWPFQFV VGAEICARIM EGPAPNFLDA
321 PAVRVTGADV PMPYAKILED NSIPQVKDII FAIKKTLNI
  
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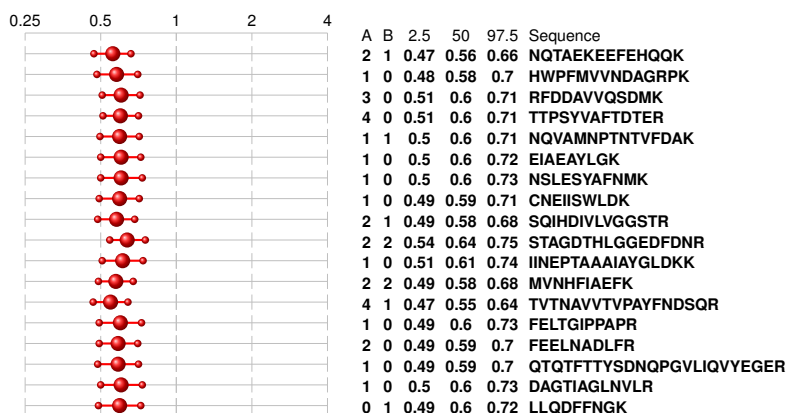
5.4 heat shock protein 8 [Rattus norvegicus]

Protein Accession	gij13242237	
Mean Expression Ratio	0.596	
Median Expression Ratio	0.596	
Credible Interval	(0.54, 0.657)	
Associated Peptides	18	
Associated Spectra	39	
Coverage	0.37	

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.649	0.427
Avg..iTRAQ.Ratio....116.114.	0.506	0.548
Avg..iTRAQ.Ratio....117.114.	0.585	0.72

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1   MSKGPVAVGID LGTTYSCVGV FQHGKVEIIA NDQGNRTTPS YVAFTDTERL IGDAAKNQVA MNPNTVFD A KRLIGRRFDD
81  AVVQSDMKHW PFMVVDAGR PKVQVEYKGE TKSFYPEEVS SMVLTMKMEI AEAYLGKTVT NAVVTVPAYF NDSQRQATKD
161 AGTIAGLNLV RIINEPTAAA IAYGLDKKVG AERNVLIFDL GGCTFDVSI L TIEDGIFEVK STAGDTHLGG EDFDNRMVNH
241 FIAEFKRKHK KDISENKRAV RRLRTACERA KRTLSSSTQA SIEIDSLYEG IDFYTSITRA RFEELNADLF RGTLDPVEKA
321 LRDAKLDKSO IHDIVLVGGS TRIPKIQKLL QDFFNQKELN KSINPDEAVA YGAAVQAAIL SGDKSENVQD LLLLDVTPLS
401 LGIETAGGVM TVLIKRNTTI PTKQTQFTT YSDNQPGVLI QVYEGERAMT KDNLLGKFE LTGIPPAPRG VPQIEVTFDI
481 DANGILNVSA VDKSTGKENK ITITNDKGR L SKEDIERMVQ EAEKYKAED E KQRDKVSSKN SLESYAFNMK ATVEDEKLQG
561 KINDEDKQKI LDKCNEIISW LDKNQTAEKE EFEHQQKLE KVCNPIITKL YQSAGGMPGG MPGGFPGGGA PPSGGASSGP
641 TIEEVD
    
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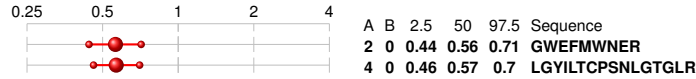


5.5 "creatine kinase, mitochondrial 1, ubiquitous [Rattus norvegicus]"

Protein Accession	gij60678254
Mean Expression Ratio	0.602
Median Expression Ratio	0.602
Credible Interval	(0.486, 0.742)
Associated Peptides	2
Associated Spectra	6
Coverage	0.0598
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.557
Avg..iTRAQ.Ratio....116.114.	0.422
Avg..iTRAQ.Ratio....117.114.	0.423


```

1      MAGPFSRLLS  ARPGLKLLAL  AGAGSLAAGI  LLRPESVRAA  TGERRRLYPP  SAEYPLDRKH  NNCMASHLTP  AVYARLCKDT
81     TPTGWTLQDC  IQTGVNPGH  PFIKTVGMVA  GDEETYEVFA  ELFDVPVIER  HNGYDFRTMK  HTDLDLASKI  RSGYFDERYV
161    LSSRVRTGRS  IRGLSLPPAC  TRAERREVER  VVVDALSGLK  GDLAGRYRL   SEMTEAEQQQ  LIDDDHFLDK  PVSPLLTAAG
241    MARDWPDARG  IWHNNEKSL  IWNNEEDHTR  VISMEKGGNM  KRVERFCRG   LKEVEKLIQE  RGWEFMWNER  LGYILTCPSN
321    LTGLRAGVH  VKLPLLSKDS  RFPKILENLR  LQKRGTTGGVD  TAATGSVFDI  SNLDRLGKSE  VELVQLVIDG  VNYLIDCERR
401    LEKGQDIRIP  PPLVHGKH
    
```

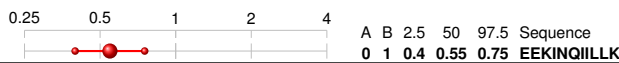


5.6 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gij109460243
Mean Expression Ratio	0.617
Median Expression Ratio	0.616
Credible Interval	(0.46, 0.825)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00674
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.106
Avg..iTRAQ.Ratio....116.114.	0.142
Avg..iTRAQ.Ratio....117.114.	0.132

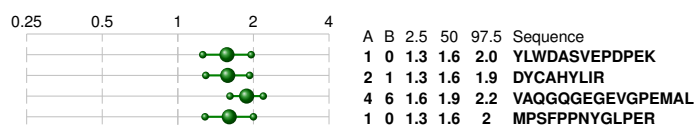
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1      MAQMCFKDWD  GFAVAVLWVQ  GFPSQNVHVF  NDNTICYPSG  NYVIFINLET  KKKTVLQGIN  GIVGVMATNV  PGEVVAFSDR
81     RLKPIIYIYS  FPSLTKIKL  KGDILLDYNL  LCFSYCGTYL  ASYSSLPEFE  LALWNWEANV  ILCKKSNPGM  DVSQMTFNP
161    NWRQMCLSSP  SAVSVWTIER  SNQEHFRIR  LVKLPQEDGT  LSNETDMLFP  TSLPKDLIYG  PVLPLSAIAG  LVGEEAETFR
241    PKDDIYPLLH  PTMHCWTPSS  DLYVGCBEHG  LLMINTECLK  VTVLQKLEEF  PVLDTGAQLIN  PLTLVYQKDG  ILASGIDGVI
321    YSFIKDKTKY  EVKPFLEFDG  PVAHLAFSPS  YKMLLIQTDK  GSVYIYTFGT  EPVLDKLLA   CDGKVVQAI   ITPGNKYFLT
401    LTSSGEVSI  SIEDGTCTGR  IFLRTHATTL  ACSPSSSSAA  MGTVDGSVVF  LNILDVESPO  LIHQAFLSKS  PVKILYDQR
481    GIFLLVGTTE  GKIFVIDARP  SKSFQIFGYT  ESSKMDLQIS  TVSHVESDVV  EVLVLSPLSE  TGRSRLEYFT  LPIMLPQVVP
561    ENFADERGRL  KDNFTHRYLY  EVEHALSSAV  LGSFESKIYG  FCSQVPIYCS  YTMPVKEHTG  ICILKPPQKV  QSKQYAGATI
641    YLSSHGLWLI  TIAKCGVLCI  RDMFSLDTFV  RCRSHSHHGQ  GIQNMKMSMD  GQHILVNGKD  DNTLVYLNK  RLGSNIANEI
721    FEHCHQLMLS  LAKTVETECD  YLASPDYQCV  PPEEETTEFQ  KKLKSLYSSQE  ELAIDLNKIP  WIQRKMEEAV  KKEVRIFTPR
801    RKEIKRGIKE  LAQIIAAMME  ENEKLDTIK  LDEQEFCLEDA  EELERLHDEC  EEEVSKIRKD  VEMHNLAKSY  LTELKKEECW
881    NSMAVKGRAL  KCFHIPYVVD  NFPMKERTEE  ELLELSKVIQ  QKKTIEIECLK  LRKEIVEAQS  AATMVKKHHE  EEEEEEEDE
961    EKVVKSTSLP  NYLLGSLSTD  FGADTSLLTN  QLELHSREK  INQIILLKDI  IYNIKKTFFNS  EFDAAAYKQKE  IEIARVQEK
1041   VRIAEIISDL  ELEEKVWQPV  FEDSEKPERA  LVVEDDEISL  QKYFAPWHKT  KAELLTAFDA  ERLQARLSD  ARHRGLMDMM
1121   GGVLEVKKED  ILRMVIPQPP  FMSKPDALWS  EEERKQFKEY  EKKVKELNEE  RDKYRKSLEA  ELKKLQNAIQ  ENTQNFDEHL
1201   KRLFERRVKA  EMVINQEELK  INNIVFSLLL  DEELSSREQF  LNNYLQKKQD  EKVLDRSFKK  EFSDISGHQV  DVLYKLFKRR
1281   PRVPKQKTQT  EVNTLVVYGE  RPSGSKLNKE  TFAQLMKSM  ELDNVSNMPE  GLDPSVWEHF  CATRRRAVEN  EYKVKQKAC
1361   LLEMTTFLRK  RMEDDDVVH  ETIRVFHEL  RLQDEKVKFO  VNLTVQILK  QGQVELENFO  LTLEYSDAIL  INKNIIEELN
1441   SVIRTQGGQK  VASMMESKEV  HKGIYQIEWE  HKKMEMEMED  LNQKAWDIQM  LFFSRDRQKY  LNEPNYEGVI  AIQIGIMEQT
1521   ISVIDKNHKK  NVENCKLLK  KLGKCSNQKD  VANYNLSCNL  REELVAVSER  QDICNEIGSK  LTCEKIARER  YDNLMKQQKL
1601   TNISKQQAEO  ISILQAEVER  LRMKTFPALV  PM
    
```



5.7 "PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 [Rattus norvegicus]"

Protein Accession	gij109508678	
Mean Expression Ratio	1.60	
Median Expression Ratio	1.61	
Credible Interval	(1.36, 1.89)	
Associated Peptides	4	
Associated Spectra	15	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.11	2.51
Avg..iTRAQ.Ratio....116.114.	1.59	2.81
Avg..iTRAQ.Ratio....117.114.	1.29	3.53

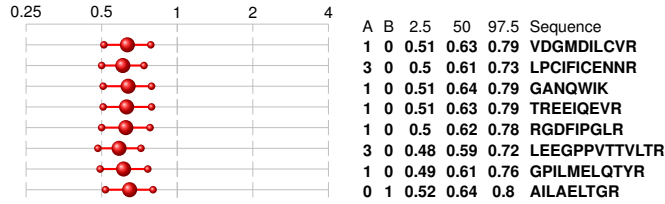


5.8 "PREDICTED: similar to Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondria"

Protein Accession	gij109503594	
Mean Expression Ratio	0.631	
Median Expression Ratio	0.632	
Credible Interval	(0.537, 0.741)	
Associated Peptides	8	
Associated Spectra	12	
Coverage	0.198	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.593	0.758
Avg..iTRAQ.Ratio....116.114.	0.505	0.569
Avg..iTRAQ.Ratio....117.114.	0.556	1.05

```

1      MRKMLAAVSR VLAGAAQKPI LNGNLALQAS RVLVASRNFA NDATFEIKKC DLHRLEEGPP VTTVLTR EDG LKYYRMMQTV
81     RRMELKAFQL YKQKIIRGFC HLCDDGQEACC VGLEAGINPT DHLITAYRAH GFTFTRGLPV RAILAELTGR RGGCAKGGG
161    SMHMYAKNFY GGNGIVGAQV PLGAGIALAC KYNGKDEVCL TLYGDGAANQ GQIFEAYDMA ALWKLPCIFI CENNRYGMGT
241    SVERAAASTD YYKRGDFIPG LRV DGM DILC VREATKFAAA YCRSGKGPIL MELQTYRYHG HSMSPGVSY RTREEIQEVR
321    SKSDPIMLLK DRMVNSNLAS VEELKEIDVE VRKEIEDAAQ FATADPEPPL EELGYHIYSS DPPFEVRGAN QWIKFKSVI
    
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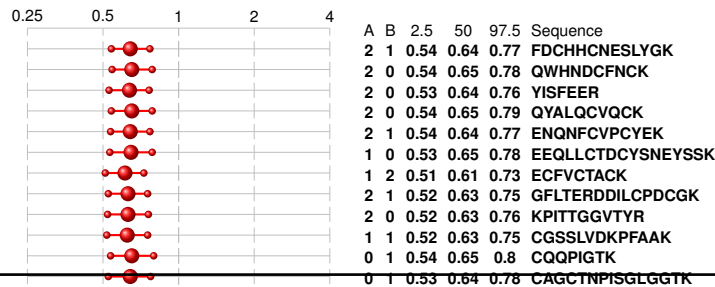


5.9 four and a half LIM domains 2 [Rattus norvegicus]

Protein Accession	gij13928940	
Mean Expression Ratio	0.644	
Median Expression Ratio	0.644	
Credible Interval	(0.569, 0.724)	
Associated Peptides	12	
Associated Spectra	25	
Coverage	0.505	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.731	0.573
Avg..iTRAQ.Ratio....116.114.	0.6	0.615
Avg..iTRAQ.Ratio....117.114.	0.61	0.36

```

1      MTERFDCHHC NESLYGKKYI LKEENPHCVA CFEELYANTC EECGTPIGCD CKDLSYKDRH WHEGCFHCSR CGSSLVDKPF
81     AAKEEQLLCT DCYSNEYSSK CQECKKTIMP GTRKMEYKGS SWHETCFTCQ RCQQPIGTKS FIPKENQNF VPCYEKQYAL
161    QCVQCKKPI TGGVTYRDQP WHRECFVCTA CKRQLSGQRF TARDEFPYCL TCFCDLYAKK CAGCTNPISG LGGTKYISFE
241    ERQWHNDCFN CKKCSLSLVG RGFILTERDDI LCPDCGKDI
    
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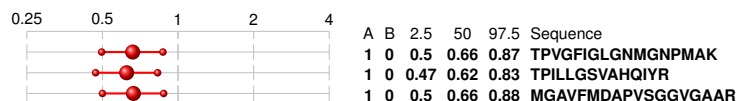


5.10 3-hydroxyisobutrate dehydrogenase [Rattus norvegicus]

Protein Accession	gij83977457
Mean Expression Ratio	0.67
Median Expression Ratio	0.67
Credible Interval	(0.521, 0.863)
Associated Peptides	3
Associated Spectra	3
Coverage	0.146
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.608
Avg..iTRAQ.Ratio....116.114.	0.392
Avg..iTRAQ.Ratio....117.114.	0.42

```

1   MAASLGFRGA ASGLRYWGR RRPVGSAAV CSRSMAKTP VGFIFLGNMG NPMKLNLIKH GYPLILYDVF PDVCKEFKEA
81  GEQVASSPAD VAEKADRIIT MLPSSMNSIE VYSGANGILK KVKKGSLLID SSTIDPSVSK ELAKEVEKMG AVFMDAPVSG
161 GVGARSGNL TFMVGGVENE FAAAQELLGC MGSNVLYCGA VSGGQSAKIC NNMLLAISMI GTAEAMNLGI RSGLDPKLLA
241 KILNMSSGRC WSSDTYNPVP GVMDGVPSSN NYQGGFGTTL MAKDLGLAQD SATSTRTPIL LGSVAHQIYR MMCSKGYSKK
321 DFSSVFQYLR EETTF
  
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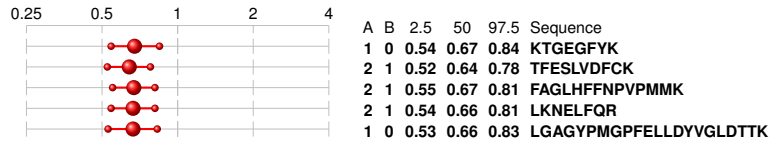


5.11 L-3-hydroxyacyl-Coenzyme A dehydrogenase [Rattus norvegicus]

Protein Accession	gij17105336	
Mean Expression Ratio	0.675	
Median Expression Ratio	0.675	
Credible Interval	(0.572, 0.799)	
Associated Peptides	5	
Associated Spectra	11	
Coverage	0.197	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.662	0.567
Avg..iTRAQ.Ratio....116.114.	0.667	0.458
Avg..iTRAQ.Ratio....117.114.	0.628	0.42

```

1      MAFVTRQFVR SMSSSSSSASA AAKKILIKHV TVIGGGLMGA GIAQVAAATG HTVVLVDQTE DILAKSKKGI EESLKRMAKK
81     KFTENPKAAD EFVEKTLSSL STSTDAASVV HSTDLVVEAI VENLKLKNEF FQRLDKFAAE HTIFASNTSS LQITNIANAT
161    TRQDRFAGLH FFNPVPMMLL VEVIKTPMST QKTFESLVDF CKTLGKHPVS CKDTPGFIVN RLLVPYLIEA IRLHERGDAS
241    KEDIDTAMKL GAGYPMGPFE LDYVGLDFT KFILDGWHEM DPENPLFQPS PSMNNLVAQK KLGGKTGEGF YKYK
    
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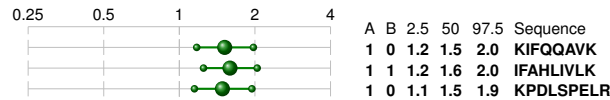


5.12 orosomuroid 1 [Rattus norvegicus]

Protein Accession	gij16757980	
Mean Expression Ratio	1.48	
Median Expression Ratio	1.48	
Credible Interval	(1.18, 1.86)	
Associated Peptides	3	
Associated Spectra	4	
Coverage	0.127	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.49	3.05
Avg..iTRAQ.Ratio....116.114.	1.71	2.21
Avg..iTRAQ.Ratio....117.114.	2.31	3.76

```

1      MALHMLVLVL SLLPLLEAQN PEPANITLGI PITNETLKWL SDKWFMGAA FRDPVFKQAV QTIQTEYFYL TPNLINDTIE
81     LREFQTDDQ CVYNFTHLGV QRENGTLSKC AGAVKIFAHL IVLKKGHTFM LAFNLTDENR GLSFYAKKPD LSPELRKKIFQ
161    QAVKDVGMDE SEIVFVDWTK DKCSEQQKQQ LELEKETKKE TKKDP
    
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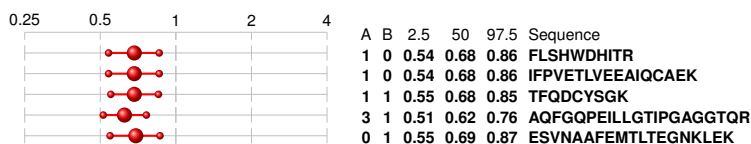


5.13 "enoyl Coenzyme A hydratase, short chain, 1, mitochondrial [Rattus norvegicus]"

Protein Accession	gij17530977	
Mean Expression Ratio	0.684	
Median Expression Ratio	0.683	
Credible Interval	(0.571, 0.82)	
Associated Peptides	5	
Associated Spectra	9	
Coverage	0.262	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.618	0.579
Avg..iTRAQ.Ratio....116.114.	0.625	0.711
Avg..iTRAQ.Ratio....117.114.	0.524	0.47

```

1   MAALRALLPK ACNSLLSPVR CPEFRRFASG ANFYIITEK KGNSSVGLI QLNRPKALNA LCNGLIEELN QALETFEEDP
81  AVGAIIVLTGG EKAFPAAGADI KEMQNRTFQD CYSGKFLSHW DHITRIIKKPV IAAVNGYALG GGCELAMMCD IYAGEKAQF
161 GQPEILLGTI PGAGGTQRLT RAVGKSLAME MVLTGDRISA QDAKQAGLVS KIFPVETLVE EEAIQCAEKIA NNSKIIVAMA
241 KESVNAAFEM TLTEGNKLEK KLFYSTFATD DRREGMSAFV EKRRANFKDH
  
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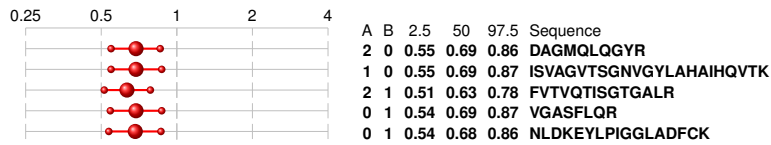
5.14 glutamate oxaloacetate transaminase 2 [Rattus norvegicus]

Protein Accession	gij6980972	
Mean Expression Ratio	0.687	
Median Expression Ratio	0.688	
Credible Interval	(0.572, 0.823)	
Associated Peptides	5	
Associated Spectra	8	
Coverage	0.167	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.738	0.542
Avg..iTRAQ.Ratio....116.114.	0.59	0.332
Avg..iTRAQ.Ratio....117.114.	0.586	0.631

NHLBI Zile/Grant, Aged Rat

```

1      MALLHSGRVL SGMAAAFHPG LAAAASARAS SWWTHVEMGP PDPI LGVTEA FKRDTNSKKM NLGVGAYRDD NGKPYVLPSPV
81     RKAEAQIAGK NLDKEYLPIG GLADFCASASA ELALGENSEV LKSGRFVTVQ TISGTGALRV GASFLQRFFK FSRDVFLPKP
161    SWGNHTPIFR DAGMQLQGYR YYDPKTCGFD FSGALEDISK IPEQSVLLH ACAHNPTGVD PRPEQWKEMA AVVKKKNLFA
241    FFDMAYQGFA SGDGDKDAWA VRHFIEQGIN VCLCQSYAKN MGLYGERVGA FTVVCKDAEE AKRVESQLKI LIRPLYSNPP
321    LNGARIAATI LTSPDLRKQW LQEVKGMADR IISMRTQLVS NLKKEGSSHN WQHITDQIGM FCFTGLKPEQ VERLTKEFSPV
401    YMTKDGRI SV AGVTSGNVGY LAHAHQVTK
  
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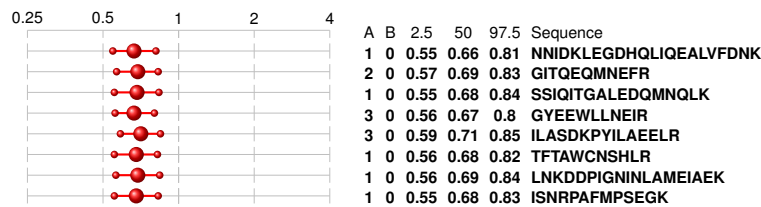


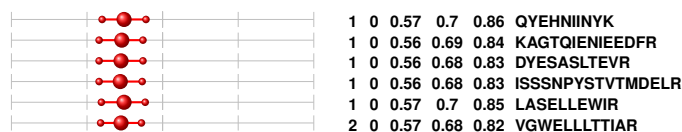
5.15 PREDICTED: similar to actinin alpha 2 [Rattus norvegicus]

Protein Accession	gij109506033
Mean Expression Ratio	0.689
Median Expression Ratio	0.689
Credible Interval	(0.608, 0.782)
Associated Peptides	14
Associated Spectra	20
Coverage	0.208
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.767
Avg..iTRAQ.Ratio....116.114.	0.581
Avg..iTRAQ.Ratio....117.114.	0.709

```

1      MNQIEPGVQY NYVYDEDEYM IQEEEWDRDL LLDPAWEKQQ RKTF TAWCNS HLRKAGTQIE NIEEDFRNGL KMLLLEVIS
81     GERLPKPD RG KMRFHKIANV NKALDYIASK GVKLVSIGAE EIVDGNVKMT LGMIWTIILR FAIQDISVEE TSAKEGLLLW
161    CQRKTAPYRN VNIQNFHTSW KDGLGLCALI HRRRPDLIDY SKLNKDDPIG NINLAMEIAE KHLDIPKMLD AEDIVNTPKP
241    DERAIMTYVS CFYHAFAGAE QVLLPCARSE PRCSSVCACL PKNDLYSVAE TAANRICKVL AVNQENERLM EEEYERLASEL
321    LEWIRRTIPW LENRTPEKTM QAMQKKLEDF RDYRRKHKPP KVQEKQLEI NFNTLQTKLR ISNRP AFMPS EGK MVSDIAG
401    AWQRLEQAEK GYEEWLLNEI RRLERLEHLA EKFRQKASTH ETWAYGKEQI LLQKDYESAS LTFVRALLRK HEAFESDLAA
481    HQDRVEQIAA IAQELNELDY HDAVNVDNRC QKICDQWDRL GTLTQKRREA LERTEKLET IDQLHLEFAK RAAPFNNWME
561    GAMEDLQDMF IVHSIEEIQS LITAHEQFKA TLPEADGERQ SILAIQNEVE KVIQSYSIRI SSSNPYSTVT MDELNRNKWD
641    VKQLVPVRDQ SLQEELARQH ANERLRRQFA AQANAIGPWI QNKMEIARS SIQITGALED QMNQLKQYEH NIINYKNID
721    KLEGDHQLIQ EALVFDNKHT NYTMEHIRVG WELLLTTIAR TINEVETQIL TRDAKGITQE QMNEFRASFN HFDRRKNGLM
801    DHEDFRACLI SMGYDLGEAE FARIMTLVDP NGQGTVTFQS FIDFMTRETA DTDTAEQVIA SFRILASDKP YILAEELRRE
881    LPPDQAQYCI KRMPYSGPG SVPGALDYTA FSSALYGESD L
  
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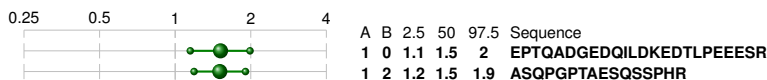


5.16 PREDICTED: similar to Band 4.1-like protein 2 (Generally expressed protein 4.1) (4.1G) [Rattus norv

Protein Accession	gij109460528	
Mean Expression Ratio	1.44	
Median Expression Ratio	1.45	
Credible Interval	(1.14, 1.82)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.0302	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	2.49	1.59
Avg..iTRAQ.Ratio....116.114.	1.9	1.61
Avg..iTRAQ.Ratio....117.114.	2.83	1.73

```

1   MTTEVASASE VKKGSDPSGA DAHKEKAKEV VENEQTAASE LDEGKASQPG PTAESQSSPH RRKRKGPSE NRGISRFIPP
81  WLKKQKSYSL VVAKDGGDKK EPTQADGEDQ ILDKEDTLPE EESRAKGDAA EMAQRKHLEV KVEVREEKSA LKSSAEIQPA
161 EQVRKDKKEE VIQDIQEEEL EGGAAKRETK EVQTSELKAE VASQKAAKKT KTVLAKVTLL DGTEFSCDLE KRKRGQALFD
241 RVCEHLNLEL KDYFGLIFQE HPEQKNWLDP AKEIKRQLRS LPWLFTFNVK FYPPDPSQLT EDITRYFLCL QLRQDISSGR
321 LPCSFVTHAL LGSYTLQAEH GDYDPEEYDS IDLGDFQFAP THNKELEEKV AELHKTHRGL SPAQADSQFL ENAKRLSMYG
401 VDLHHAADSE GVDIKLGVCA NGLLIYKDR L RINRFAPFKI LKISYKRSNF YIKVRFGELE QFESTIGFKL PNHRAAKRLW
481 KVCVEHHTFY RLVSPQQPK TKFLTLGSKF RYSGRTQAQT REASTLIDRP APQFERASSK RVSRSLDGAP IGVVDQSLMK
561 DFPGPPGEGS VPGPGVVSYT TVQDGRRDGK SPTKVTPLLA EGKVRPLALC CCGGCSDERP LPLVLVEDSV SCHCVVYAYN
641 LRCFKWSCYF ALLFLTFLFL FFRVKYLFQY KLYFPEVDLL SDISEEDPFG EADETTLDSF ELLSVGGASE QGDPEVATLD
721 SVLDPVEAPP QFEGPSMHEK TLEPAVPKDA ELGSFAFTFH KCFASGLPSL LDEDGYLAFP SLPKLWVSFL PADVRHHVPI
801 TSPSFIPSLV LSFGLLLSAS QSVAFSLTFS LPLALALCYL EGKATSLHGS YDCDLNDKPE EEEAGRWKDA ELCREQDLDK
881 AQEAILKHQA SVSELKRNFM ESTPEPRPSE WEKRRVTPLS CQILASLEEE ITSILFSGQG FSHSVKASFP SATTWTAEGT
961 VVNANAPREP LSSAPFSRLP ETPRALVSEG PCTGTRDAVK SSHETLNVVE EKKRAEVGKG ESVITEEMNG KELSPGSGPG
1041 ETRKVEPMAH KDSTLSLSES SSSSESEED VGEYQPHHRV TEGTIREEQE YEELEEEEPG QGAKVVEREA AMPEAIPDRQ
1121 AGASVLPVET EAQENVVAQK LPGEKGAHRG TAEQDMSEEA EEDQHRVNGE VPHLDIDGLP EIVCPSEPPV VKTEMVITSD
1201 ASQRTEISTK EVPIVQTEK TITYESPQID GGAGGDSGVL LTAQTITSES ASTTTTTTHIT KTVKGGISET RIEKRIVITG
1281 DAALDHDQAL AQAIAREAREQ HPDMSVTRVV VHKETELAAE GED
    
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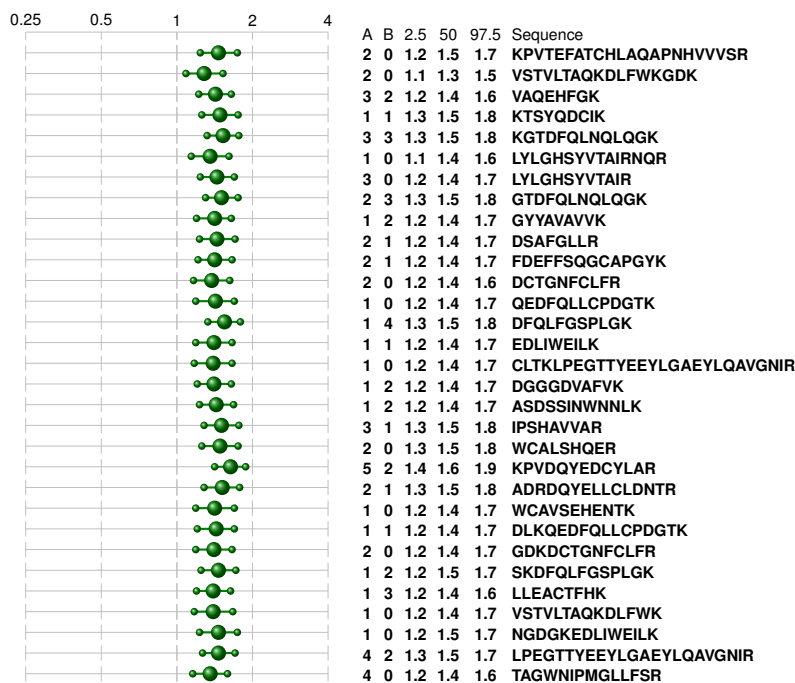


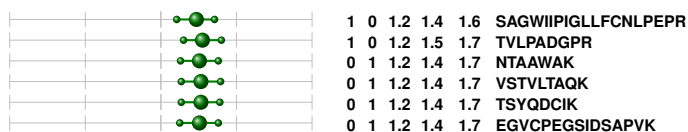
5.17 transferrin [Rattus norvegicus]

Protein Accession	gi 61556986	
Mean Expression Ratio	1.44	
Median Expression Ratio	1.44	
Credible Interval	(1.34, 1.53)	
Associated Peptides	37	
Associated Spectra	98	
Coverage	0.497	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.39	1.37
Avg..iTRAQ.Ratio....116.114.	1.29	0.921
Avg..iTRAQ.Ratio....117.114.	1.79	2.19

```

1   MRFAVGALLA CAALGLCLAV PDKTVKCAV SEHENTKCIS FRDHMKTVLP ADGPRRLACVK KTSYQDCIKA ISGGEADAIT
81  LDGGWVYDAG LTPNNLKPVA AEFYGSLEHP QTHYLAVAVV KKGTFDFQLNQ LQGKKSCHTG LGRSAGWIIP IGLLFCNLPE
161 PRKPLEKAVA SFFSGSCVPC ADPVAFQQLC QLCPGCGCSP TQPFPGYVGA FKCLRGGGD VAFVKHTTIF EVLPQKADR
241 QYELLCLDNT RKPVDQYEDC YLARIPSHAV VARNGDGKED LIWEILKVAQ EHFQKGSKD FQLFGSPLGK DLLFKDSAFG
321 LLRVPPRMDY RLYLGHSYVT AIRNQRREGVC PEGSIDSAPV KWALSHQER AKCDEWSVSS NGQIECESAE STEDCIDKIV
401 NGEADAMSLD GGHAYIAGQC GLVPVMAENY DISSCTNPQS DVFPKGYAV AVVKASDSSI NWNLLKGGKS CHTGVDRTAG
481 WNIPMGLLFS RINHCKFDEF FSQGCAPGYK KNSTLCLDCI GPAKCAPNNR EGYNGYTGA FQCLVEKGDVA FVKHQTVLEN
561 TNGKNTAAWA KDLKQEDFQL LCPDGTKKPV TEFATCHLAQ APNHVVVSRK EKAARVSTVL TAQKDLFWKG DKDCTGNFCL
641 FRSTKDLLF RDDTKCLTKL PEGTTYEYEL GAEYLQAVGN IRKCTSRLLE EACTFHKS
    
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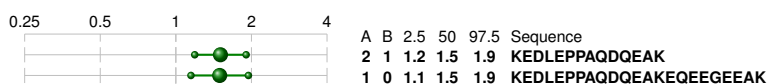




5.18 "synuclein, gamma [Rattus norvegicus]"

Protein Accession	gij13928954	
Mean Expression Ratio	1.44	
Median Expression Ratio	1.43	
Credible Interval	(1.13, 1.80)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.187	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.82	2.15
Avg..iTRAQ.Ratio....116.114.	1.44	1.72
Avg..iTRAQ.Ratio....117.114.	2.59	3.03

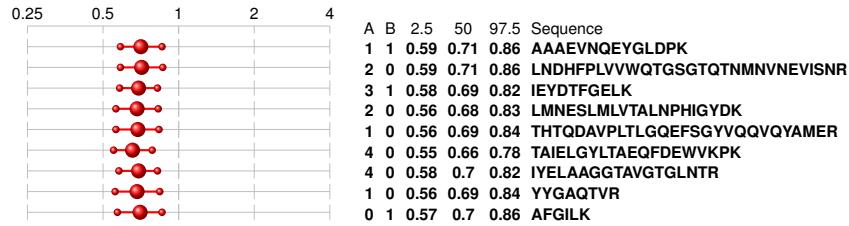
1 MDVFKKGFSI AREGVVGAVE KTTQGVTEAA EKTKEGVMYV GAKTKGERGT SVTSVAEKTQ EQANAVSEAV VSSVNTVATE
 81 TVEEAENIVV TTGVVRKEDL EPPAQDQEAQ EQEEGEEAKS GGD



5.19 fumarate hydratase 1 [Rattus norvegicus]

Protein Accession	gij8393358	
Mean Expression Ratio	0.698	
Median Expression Ratio	0.698	
Credible Interval	(0.613, 0.794)	
Associated Peptides	9	
Associated Spectra	21	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.691	0.623

Avg..iTRAQ.Ratio....116.114.	0.735	0.577
Avg..iTRAQ.Ratio....117.114.	0.616	0.636

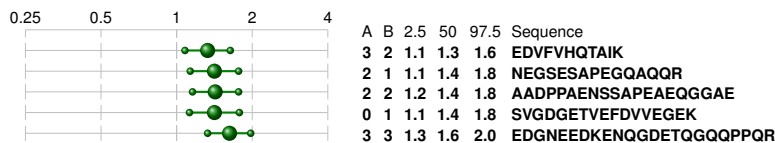


5.20 nuclease sensitive element binding protein 1 [Rattus norvegicus]

Protein Accession	gi 92373398
Mean Expression Ratio	1.43
Median Expression Ratio	1.43
Credible Interval	(1.20, 1.71)
Associated Peptides	5
Associated Spectra	19
Coverage	0.267
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.38
Avg..iTRAQ.Ratio....116.114.	1.37
Avg..iTRAQ.Ratio....117.114.	1.71

```

1      MSSEAETQQP PAAPAAALSA ADTKPGSTGS GAGSGGPGGL TSAAPAGGDK KVIATKVLGT VKWFNVRNGY GFINRNDTKE
81     DVFVHQTAIK KNNPRKYLRS VGDGETVEFD VVEGEGKGAEA ANVTGPGGVP VQGSKYAADR NHYRRYPRRR GPPRNYQQNY
161    QNSESGEKNE GSESAPEGQA QQRPPYRRRR FPPYMRPPY ARRPPQYSNPP VQGEVMEGAD NQGAGEQGRP VRQNMYRGYR
241    PRFRRGPPRQ RQPREDGNEE DKENQGDETQ GQQPPQRRYR RNFNYRRRRP ENPKPQDGKE TKAADPPAEN SSAPAEAEQGG
321    AE
    
```

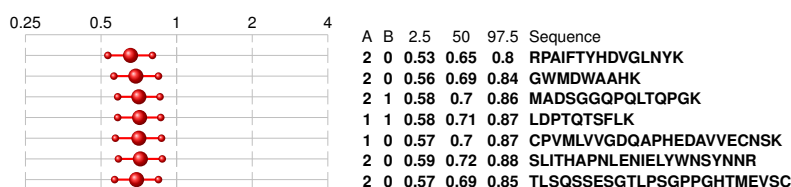


5.21 N-myc downstream regulated gene 2 [Rattus norvegicus]

Protein Accession	gij19424278	
Mean Expression Ratio	0.704	
Median Expression Ratio	0.704	
Credible Interval	(0.607, 0.816)	
Associated Peptides	7	
Associated Spectra	14	
Coverage	0.331	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.757	0.718
Avg..iTRAQ.Ratio....116.114.	0.627	0.506
Avg..iTRAQ.Ratio....117.114.	0.596	1.01

```

1   MAELQEVQIT EEKPLLPGQT PEAAKTHSVE TPYGSVTFV YGTPKPKRPA IFTYHDVGLN YKSCFQPLFQ FGD MQEIIQN
81  FVRVHVDAPG MEEGAPVFPL GYQYPSQDQL ADMIPCILQY LNFSTIIGVG VGAGAYILSR YALNHPDVE GLVLINIDPN
161 AKGMDWAH KLTGLTSSIP EMILGHLFSQ EELSGNSELI QKYRSLITHA PNLENIELYW NSYNNRDLN FERGGEMTLK
241 CPVMLVVG DQ APHEDAVVEC NSKLDPTQTS FLKMADSGGQ PQLTQPGKLT EAFKYFVQGM GYMASSCMTR LSRSR TASLT
321 SAASIDGSR SRSRTLSQSSE SGTLPSPGPPG HTMEVSC
  
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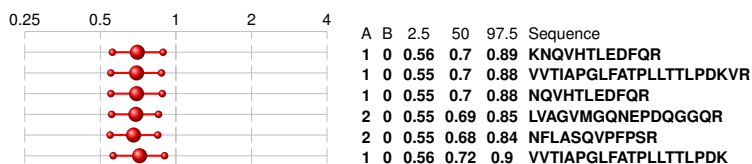


5.22 hydroxysteroid (17-beta) dehydrogenase 10 [Rattus norvegicus]

Protein Accession	gij13994225	
Mean Expression Ratio	0.708	
Median Expression Ratio	0.708	
Credible Interval	(0.592, 0.851)	
Associated Peptides	6	
Associated Spectra	8	
Coverage	0.241	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.668	
Avg..iTRAQ.Ratio....116.114.	0.624	
Avg..iTRAQ.Ratio....117.114.	0.642	

```

1      MAAACRSVKG LVAVITGGAS GLGLSTAKRL VGQGATAVLL DVPNSEGETE AKKLGNCIF APANVTSEKE VQAALTLAKE
81     KFRGRIDAVN CAGIAVAIKT YHEKKNQVHT LEDFQRVINV NLIGTFNVIR LVAGVMGQNE PDQGGQRGVI INTASVAAFE
161    GQVGQAAYSA SKGGIVGMTL PIARDLAPIG IRVVTIAPGL FATPLLTLP DKVRNFLASQ VPFFPSRLGDP AEYAHLVQMV
241    IENFFLNGEV IRLDGAIQMP P
    
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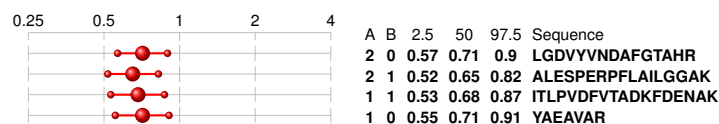


5.23 phosphoglycerate kinase 1 [Rattus norvegicus]

Protein Accession	gij40254752
Mean Expression Ratio	0.712
Median Expression Ratio	0.713
Credible Interval	(0.579, 0.869)
Associated Peptides	4
Associated Spectra	8
Coverage	0.137
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.709
Avg..iTRAQ.Ratio....116.114.	0.591
Avg..iTRAQ.Ratio....117.114.	0.546

```

1      MSLSNKLTLD KLDVKGKRVV MRVDFNVPMK NNQITNNQRI KAAVPSIKFC LDNGAKSVVL MSHLGRPDGV PMPDKYSLEP
81     VADELKSLG KDVFLKDCV GSEVENACAN PAAGTVILLE NLRFHVEEEG KGKDASGNKV KAEPAKIDAF RASLSKLDGV
161    YVNDAFGTAH RAHSSMVGVN LPQKAGGFLL KKELNYPKA LESPERPFLA ILGGAKVADK IQLINMLDK VNEMIIGGGM
241    AFTFLKVLNN MEIGTSLYDE EGAKIVKDLM AKAENGVKI TLPVDFVTAD KFDENAKTGQ ATVASGIPAG WMGLDCGTES
321    SKKYAEAVAR AKQIVWNGPV GVFWEAFAR GTKSLMDEVV KATSRGCITI IGGGDATATCC AKWNTEKVS HVSTGGGASL
401    ELLEGKVLPG VDALS NV
    
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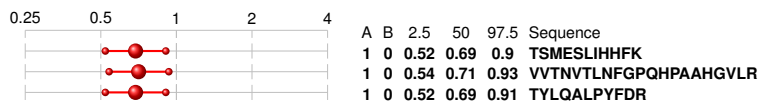


5.24 NADH dehydrogenase (ubiquinone) Fe-S protein 2 [Rattus norvegicus]

Protein Accession	gij58865384
Mean Expression Ratio	0.712
Median Expression Ratio	0.714
Credible Interval	(0.557, 0.909)
Associated Peptides	3
Associated Spectra	3
Coverage	0.0929
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.685
Avg..iTRAQ.Ratio....116.114.	0.563
Avg..iTRAQ.Ratio....117.114.	0.418

```

1      MAALRAVCSL  RGVAQVLR  GSGIRLPSQP  SRGARRWQPD  IEWAEQFSGA  VMYPKETAH  WKPPPNDVD  VLKEKVVTVN
81     TLNFGPQHPA  AHGVLRLVLE  LSGEMVRKCD  PHIGLLHRGT  EKLIYKTYL  QALPYFDRLD  YVSMCNEQA  YSLAVEKLLN
161    IQPPFRAQWI  RVLFGIEITRI  LNHIMAVTTH  ALDIGAMTFF  FWMFEEREKM  FEFYERVSGA  RMHAAYIRPG  GVHQDLPPLG
241    MDDIYEFSKN  FSLRIDEVEE  MLTNNRIWRN  RTVDIGVSA  EDALNYGFSG  VMLRSGSIQW  DLRKTQPYDV  YDQVEFDVPI
321    GSRGDCYDRY  LCRVEEMRQS  LRIIEQCLNK  MPPGEIKVDD  AKVSPKRAE  MKTSMESLIH  HFKLYTEGYQ  VPPGATYTAI
401    EAPKGEFGVY  LVSDGSSRPY  RCKIKAPGFA  HLAGLDKMSK  GHMLADVVAI  IGTQDIVFGE  IDR
    
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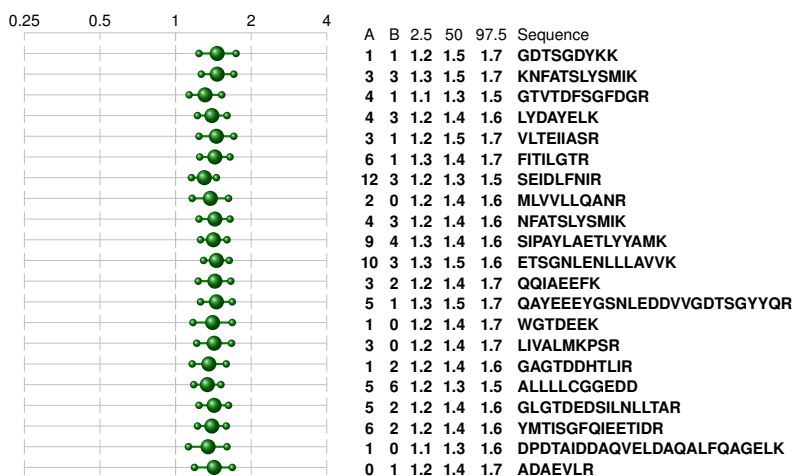
5.25 annexin 5 [Rattus norvegicus]

Protein Accession	gij6978505	
Mean Expression Ratio	1.4	
Median Expression Ratio	1.4	
Credible Interval	(1.31, 1.50)	
Associated Peptides	21	
Associated Spectra	127	
Coverage	0.759	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.21	1.63
Avg..iTRAQ.Ratio....116.114.	1.29	1.75
Avg..iTRAQ.Ratio....117.114.	1.48	1.51

NHLBI Zile/Grant, Aged Rat

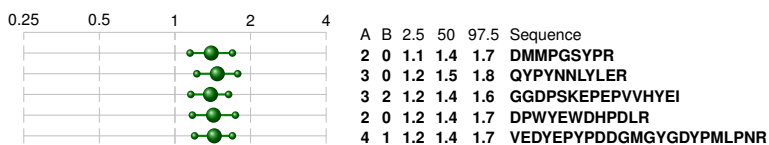
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1      MALRGTVTFD SGFDGRADAE VLRKAMKGLG TDEDSILNLL TARSNAQRQQ IAEEFKTLFG RDLVNDMKSE LTGKFEKLIV
81     ALMKPSRLYD AYELKHALKG AGTDERVLTE IIASRTPEEL RAIKQAYEEE YGSNLEDDVV GDTSGYYQRM LVVLLQANRD
161    PDTAIDDAQV ELDAQALFQA GELKKGTDDEE KFITILGTRS VSHLRRVFDK YMTISGFQIE ETIDRETSGN LENLLLAVVK
241    SIRSIPAYLA ETLTYAMKGA GTDDHTLIRV IVSRSEIDLF NIRKEFRKNF ATSLYSMIKG DTSGDYKKAL LLLCGGEDD
  
```



5.26 PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 [Rattus norvegicus]

Protein Accession	gij109463999	
Mean Expression Ratio	1.40	
Median Expression Ratio	1.4	
Credible Interval	(1.21, 1.62)	
Associated Peptides	5	
Associated Spectra	17	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.32	1.60
Avg..iTRAQ.Ratio....116.114.	1.87	1.36
Avg..iTRAQ.Ratio....117.114.	1.81	0.7

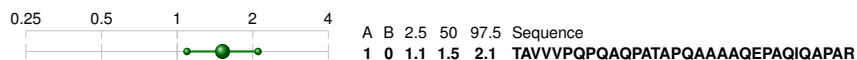


5.27 PREDICTED: similar to AP2 associated kinase 1 [Rattus norvegicus]

Protein Accession	gij109473794
Mean Expression Ratio	1.39
Median Expression Ratio	1.39
Credible Interval	(1.04, 1.88)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0332
Experiment	A
Avg..iTRAQ.Ratio....115.114.	4.3
Avg..iTRAQ.Ratio....116.114.	7.1
Avg..iTRAQ.Ratio....117.114.	3.40

```

1      MKKFFDSRRE QGSSGLGSGS SGGGGSSSGL GSGYIGRVFG IGRQQVTVDE VLAEGGFALV FLVRTSNGVK CALKRMFVNN
81     EHDLQVCKRE IQIMRDLSGH KNIVGYIDSS INNVS SGD VW EVLILMDFCR GGQVVNLMNQ RLQTGFENE VLQIFCDTCE
161    AVARLHQCKT PIIHRDLKVE NILLHDRGHY VLCDFGSATN KFQNPQAEV NAVEDIKKY TLSYRAPEM VNLYSGKIIT
241    TKADIWALGC LLYKLCYFTL PFGESQVAIC DGSFTIPDNS RYSQDMHCLI RYMLEPDPDK RPDYQVSYF SFKLLKKECP
321    VPNVQNSPIP TKLPEPVKAS EAAVKKTQPK ARLTDPIPTT ETSIAPRQRP KAGQTQPNPG ILFIQPALTP RKRATVQPLP
401    QATGFSNQPS LLASVSQPKA QATPSQPLQS SQPKQPQAPP TPQQTAPAPQT QGLPTQAQAT PQHQQLLLK QQQQQQQQQQ
481    QQQPQPPTAP PQPSGTFYQQ QPQQQQAQT QPFQAVHPAA QQSVTAQFPV VSQGGSQQL MQNFYQQQQQ QQQQQQQQ LMA
561    QQAALQQKTA VVVPQQAQP ATAPQAAAAQ EPAQIQAPAR QQPKVQTTFP PTIQGQKVG S LTPPSSPKTQ RAGHRRILSD
641    VTHSAVFGVP ASKSTQLLHA AAAEASLSKS KSATTTSPGS PRTSQQNVSN ASEGSTWNP F DDDNFSKLT A EELLNKDFAK
721    LGEKLPPEKL GSAESLIPG FQATQGD AFA TSSFSAGTAE KRKGGQAVDS GIPLLSVSDP FIPLQVPDAP EKLI E GLKSP
801    DTSLLLPDLL PMTDFPGSTS DAVIEKADAA VESLIPGLEP PVAQRLPSHT ESVTSNRTDS LTGEDSLDC SLLSNPTADL
881    LDEFAPIALS ASTHKAEDS NLISGFGVAE GSEKVAEDEF DPIPVLITKN TQGGHSRNS S GSSESLPNL ARSLLLV DQL
961    IDL
  
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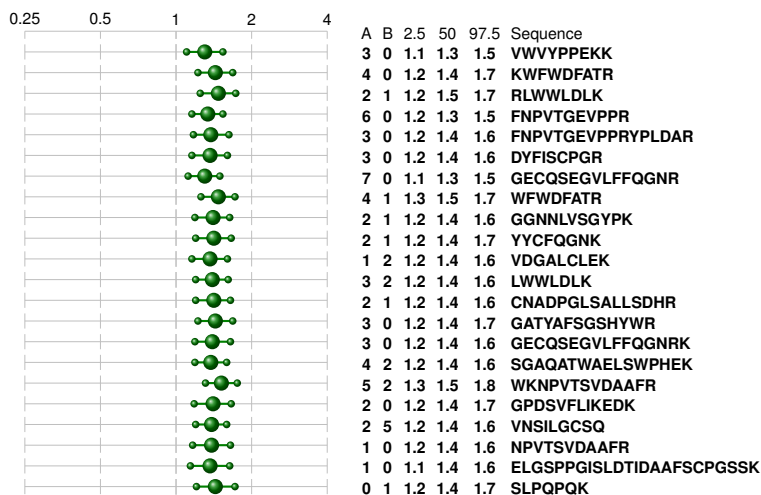
5.28 hemopexin [Rattus norvegicus]

Protein Accession	gij16758014
Mean Expression Ratio	1.39
Median Expression Ratio	1.39
Credible Interval	(1.29, 1.5)
Associated Peptides	22
Associated Spectra	82
Coverage	0.443

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.37	1.52
Avg..iTRAQ.Ratio....116.114.	1.23	1.36
Avg..iTRAQ.Ratio....117.114.	1.6	1.78

```

1   MARTVVALNI  LVLLGLCWSL  AVANPLPAAH  ETVAKGENGT  KPDSDVIEHC  SDAWSFDATT  MDHNGTMLFF  KGEFVWRGHS
81  GIRELISERW  KNPVTSVDA  FRGPDVFLI  KEDKVWVYPP  EKKENGYPKL  FQEESPGIPY  PPDAAVECHR  GECQSEGVLF
161 FQGNRKWFWD  FATRTQKERS  WPAVGNCTAA  LRWLERYYCF  QGNKFLRFNP  VTGEVPPRYP  LDARDYFISC  PGRGHGKLRN
241 GTAHGNSTHP  MHSRCNADPG  LSALLSDHRG  ATYAFSGSHY  WRDSSRDGW  HSWPIAHHP  QGPSAVDAAF  SWDEKVYLIQ
321 GTQVYVFLTK  GGNNLVSGYP  KRLEKELGSP  PGISLDTIDA  AFSCPGSSKL  YVTSGRRLW  LDLKSGAQAT  WAELSWPHEK
401 VDGALCLEKS  LGPYSCSSNG  PNLFFIHGPN  LYCYSSIDKL  NAAKSLPQPQ  KVNLSILGCSQ
    
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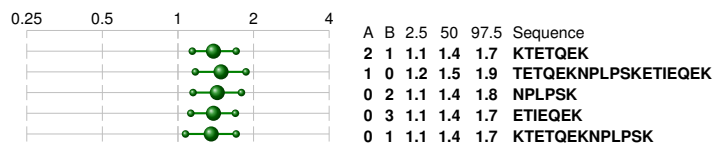


5.29 "thymosin, beta 4 [Rattus norvegicus]"

Protein Accession	gij13592119	
Mean Expression Ratio	1.38	
Median Expression Ratio	1.39	
Credible Interval	(1.16, 1.64)	
Associated Peptides	5	
Associated Spectra	10	
Coverage	0.455	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.53	1.27
Avg..iTRAQ.Ratio....116.114.	1.27	1.16

Avg..iTRAQ.Ratio....117.114. 3.1 1.47

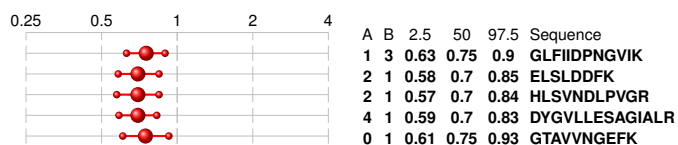
1 MSDKPDMAEI EKFDKSKLKK TETQEKNPLP SKETIEQEKQ AGES



5.30 peroxiredoxin 3 [Rattus norvegicus]

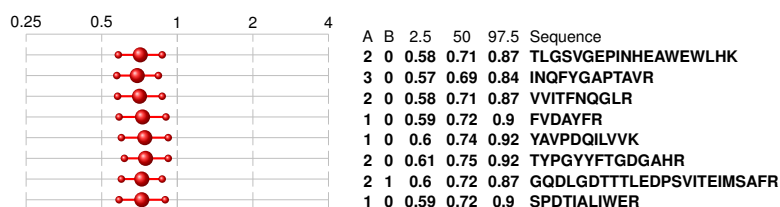
Protein Accession	gij11968132	
Mean Expression Ratio	0.729	
Median Expression Ratio	0.729	
Credible Interval	(0.629, 0.847)	
Associated Peptides	5	
Associated Spectra	16	
Coverage	0.214	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.692	0.567
Avg..iTRAQ.Ratio....116.114.	0.578	0.63
Avg..iTRAQ.Ratio....117.114.	0.58	0.99

1 MAAAAGRLLW SSVARPASTI FRISISASTVL RPVASRRCTL TDMLWSACPQ AKFAFSTSSS FHTPAVTQHA PHFKGTAVVN
 81 GEFKELSLDD FKGKYLVLFF YPLDFTFVCP TEIVAFSDKA NEFHDVNCEV VAVSVDSHFS HLAWINTPRK NGGLGHMNIT
 161 LLSDLTKQIS RDYGVLLESA GIALRGLFII DPNGVIKHLS VNDLPVGRSV EEPLRLVKAF QFVETHGEVC PPNWTPESPT
 241 IKPSPTASKE YFEKVHQ



5.31 PREDICTED: similar to acetyl-CoA synthetase 2-like [Rattus norvegicus]

Protein Accession	gi 109468951	
Mean Expression Ratio	0.729	
Median Expression Ratio	0.73	
Credible Interval	(0.629, 0.841)	
Associated Peptides	8	
Associated Spectra	15	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.823	0.646
Avg..iTRAQ.Ratio....116.114.	0.77	0.453
Avg..iTRAQ.Ratio....117.114.	0.543	1.20



5.32 "dynein, cytoplasmic, intermediate polypeptide 2 [Rattus norvegicus]"

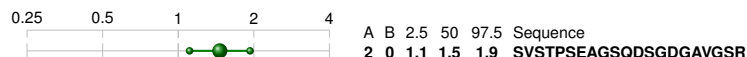
Protein Accession	gi 16758748
Mean Expression Ratio	1.35
Median Expression Ratio	1.35
Credible Interval	(1.03, 1.78)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0329
Experiment	A
Avg..iTRAQ.Ratio....115.114.	2.33
Avg..iTRAQ.Ratio....116.114.	1.92
Avg..iTRAQ.Ratio....117.114.	3.92

NHLBI Zile/Grant, Aged Rat

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1   MSDKSELKAE LERKKQRLAQ IREEKRRKEE ERKKKETDQK KEAAVSQVEE SDLEKKRREA EALLQSMGLT TDSPIVFSEH
81  WVPPPMSPSS KSVSTPSEAG SQDSGDGAVG SRTLHWDTDP SALQLHSDSD LGRGPIKLG M AKITQVDFPP REIVTYTKET
161 QTPVTAQPK EDEEEDDVAA PKPPVEPEEE KILKDEEND SKAPPHELTE EEKQQILHSE EFLSFFDHST RIVERALSEQ
241 INIFFDYSGR DLEDKEGEIQ AGAKLSLNRO FFERWSKHR VVSCLDWSSQ YPELLVASYN NNEEAPHEPD GVALVWNMKY
321 KKTTPPEYVFR CQSAVMSATF AKFHPNLVVG GTYSGQIVLW DNRSNKRTPV QRTPLSAAAH THPVYCVNVV GTQNAHNLIS
401 ISTDGKICSW SLDMLSHPDQ SMELVHKQSK AVAVTSMSPF VGDVNNFVVG SEEGSVYTAC RHGSKAGISE MFEGHQGPIT
481 GIHCHAAVGA VDFSHLFVTS SFDWTVKLWS TKNNKPLYSF EDNSDYVYDV IGSPTHPALF ACVDGMGRLD LWNLNNDTEV
561 PTASISVEGN PALNRVRWTH SGREIAVGDS EGQIVIVYDV EQIAVPRNDE WARFGRTLAE INASRADAE EAAATRIPA

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5.33 "PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 [Rattus norvegicus]"

Protein Accession	gij109473378
Mean Expression Ratio	1.35
Median Expression Ratio	1.35
Credible Interval	(1.01, 1.82)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	3.69
Avg..iTRAQ.Ratio....116.114.	2.57
Avg..iTRAQ.Ratio....117.114.	3.45



5.34 dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Rattus norvegicus]

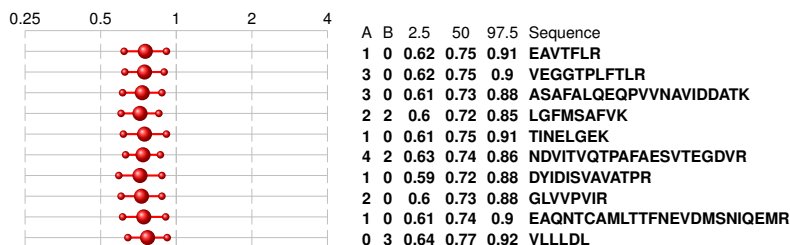
Protein Accession	gij55742725
Mean Expression Ratio	0.743
Median Expression Ratio	0.744
Credible Interval	(0.658, 0.84)

Associated Peptides	10	
Associated Spectra	25	
Coverage	0.282	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.714	0.692
Avg..iTRAQ.Ratio....116.114.	0.788	0.623
Avg..iTRAQ.Ratio....117.114.	0.713	0.69

```

1      MLSRSRCVSR AFSRSLSAFQ KGNCPLGRRS LPGVSLCQGP GYPDSRKMVI NNSSVFSVRF FQTTAVCKND VITVQTPAFA
81     ESVTEGDVRVW EKAVGDVAE DEVVCEIETD KTSVQVPSPA NGIIEALLVP DGGKVEGGTP LFTLRKTGAA PAKAKPAEAP
161    ATAYKAAPEA PAAPPPVPAP VPTQMPPVPS PSQPPSSKPV SAIKPTAAPP LAEAGAAGKL RSEHREKMNR MRQRIAQRK
241    EAQNTCAMLT TFNEVDMSNI QEMRARHKDA FLKKNHLKLG FMSAFVKASA FALQEQPVVN AVIDDATKEV VYRDYIDISV
321    AVATPRGLV PVIRNVETMN YADIERTINE LGEKARKNEL AIEDMDGGTF TISNGGVFGS LFGTPIINPP QSAILGMHGI
401    FDRPVAVGK VEVREPMYVA LTYDHLRIDG REAVTFLRKI KAAVEDPRVL LDDL

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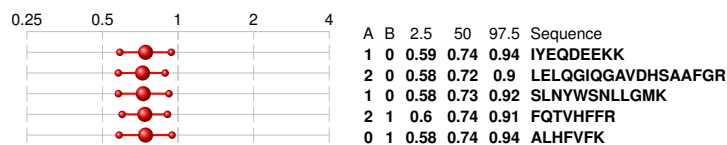
5.35 hypothetical protein LOC363644 [Rattus norvegicus]

Protein Accession	gi 62079189	
Mean Expression Ratio	0.744	
Median Expression Ratio	0.744	
Credible Interval	(0.619, 0.89)	
Associated Peptides	5	
Associated Spectra	8	
Coverage	0.181	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.697	0.579
Avg..iTRAQ.Ratio....116.114.	0.561	0.722
Avg..iTRAQ.Ratio....117.114.	0.636	1.17

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1      MVTRRALHFV FKVGNRFQTV HFFRDVLGMQ VLRHEEFEEG CKAACNGPYD GKWSKTMVGF GPEDDHFVAE LTYNYGIGDY
81     KLGNDFMGLT LASSQAVSNA RRLEWPLSKV AEGVFETEAP GGYKFYLQDR SPSQSDPVLK VTLAVSDLQK SLNYWSNLLG
161    MKIYEQDEEK KWALLGYADD QCKLELQGIO GAVDHSAAFG RIAFSQPKE LPDLEDLMKR ESQSILTPLV SLDTPGKATV
241    QVVILADPDG HEICFVGDEA FRELSKMDPK GSKLLDDAMA ADKSDSEWFAT RNKPKASG

```



5.36 PREDICTED: similar to translin-associated factor X (Tsnax) interacting protein 1 isoform 1 [Rattus

Protein Accession	gij109508694
Mean Expression Ratio	0.747
Median Expression Ratio	0.747
Credible Interval	(0.551, 1.01)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.433
Avg..iTRAQ.Ratio....116.114.	0.52
Avg..iTRAQ.Ratio....117.114.	0.155

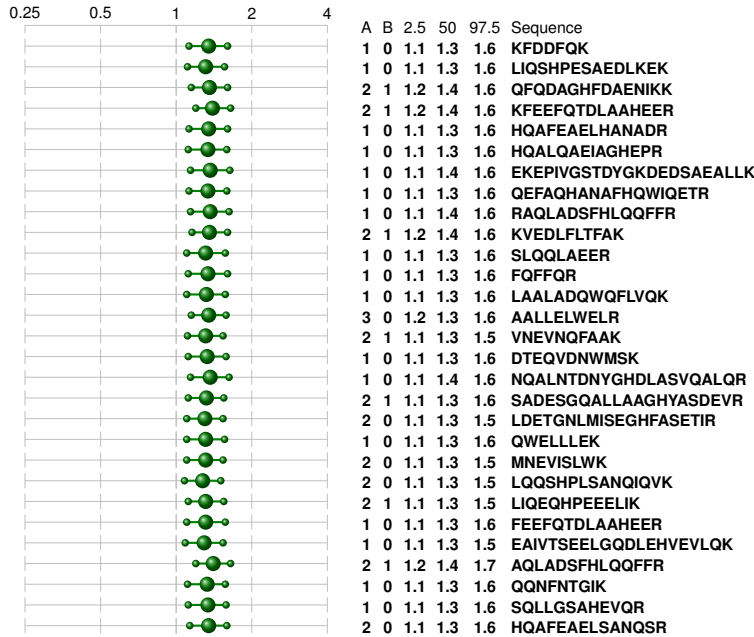


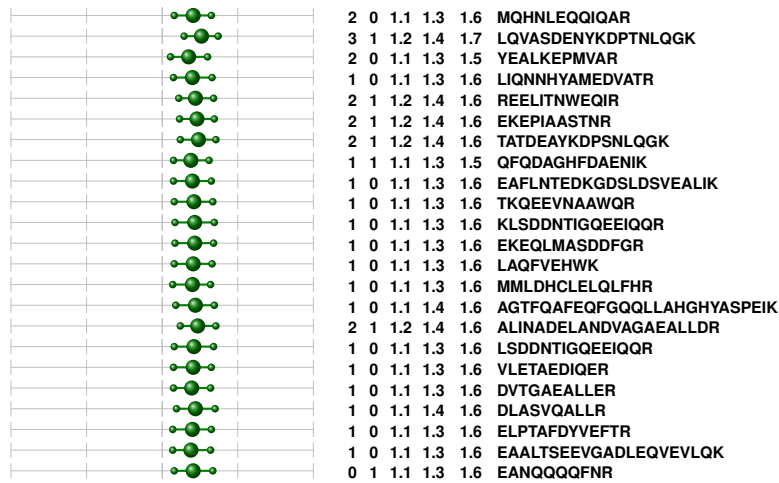
5.37 alpha-spectrin 2 [Rattus norvegicus]

Protein Accession	gij31543764	
Mean Expression Ratio	1.33	
Median Expression Ratio	1.34	
Credible Interval	(1.24, 1.43)	
Associated Peptides	52	
Associated Spectra	86	
Coverage	0.272	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.30	1.24

Avg..iTRAQ.Ratio....116.114. 1.24 1.18
 Avg..iTRAQ.Ratio....117.114. 1.69 1.72

1	MDPSGVKVL	TAEDIQERRQ	QVLDRYHRFK	ELSTLRRQKL	EDSYRFQFFQ	RDAAEELEKWI	QEKLQVASDE	NYKDPTNLQG
81	KLQKHQAFEA	EVQANSQAIV	KLDEGTGNLMI	SEGHFASETI	RTRLMLHRQ	WELLLLEKMRE	KGIKLLQAQK	LVQYLRECED
161	VMDWINDKEA	IVTSEELGQD	LEHVEVLQKK	FEFQTDLAA	HEERVNEVNO	FAAKLIQEQH	PEEELIKTKQ	EEVNAAWQRL
241	KGLALQRQGK	LFGAAEVQRF	NRDVDEITGW	IKEKEQLMAS	DDFGRDLASV	QALLRKHEGL	ERDLAALEDK	VKALCAEADR
321	LQQSHPLSAN	QIQVKREELI	TNWEQIRTLA	AERHARLDD	YRLQRFLADF	RDLTSSWVTEM	KALINADELA	NDVAGAEALL
401	DRHQEHKGEI	DAHEDSFKSA	DESGQALLAA	GHYASDEVRE	KLSILSEERA	ALLELWELRR	QQVEQCMDLQ	LFYRDTEQVD
481	NWMSKQEAFL	LNEDLGDSLD	SVEALLKKEH	DFEKLSAQE	EKITALDEFA	TKLIQNNHYA	MEDVATRDRDA	LLSRRNALHE
561	RAMHRRQA	DSFHLQQFFR	DSDELKSWVN	EKMKTATDEA	YKDPNQLQGG	VQKHQAFEA	LSANQSRIDA	LEKAGQKLLD
641	VNHYAKEEVA	ARMNEVISLW	KKLEATELQ	GVKLEARNQ	QQFNRRNVEDI	ELWLVEVEGH	LASDDYDGKDL	TNVQNLQKKH
721	ALLEADVAAH	QDRIDGITIQ	ARQFQDAGHF	DAENIKKKQE	ALVARYEALK	EPMVARKKQKL	ADSLRRLQQLF	RDVEDEETWI
801	REKEPIAAS	NRGKDLIGVQ	NLLKKHQALQ	AEIAGHEPRI	KAVTQKGNAM	VEEGHFAAED	VKAKLSELNQ	KWEALKAAS
881	QRRQDLEDL	QAQQYFADAN	EAESWMREKE	PIVGSTDYGK	DEDSAEALLK	KHEALMSDLS	AYGSSIQALR	EQAQSCROQV
961	APMDDDETGE	LVLALYDYQE	KSPREVTMCK	GDILTLLNST	NKDWWKVEVN	DRQGFVPAAY	VKKLDPAQSA	SRENLEEQG
1041	SIADLRQGD	NQTRITKEAG	SVSLRMKQVE	ELYQSLLELG	EKKRGMLEKS	CKKFMLFREA	NELQQWINEK	EAAITSEEVG
1121	ADLEQVEVLQ	KKFDFFQKDL	KANESRLKDI	NKVAEDLESE	GLMAEEVQAV	QQQVEVGMMP	RDEADSKTAS	PWKSARLMVH
1201	TVATFNISKE	LNERWRSLLQ	LAEBERSQLLG	SAHEVQRFHR	DADETKEWIE	EKNQALNTDN	YGHDLASVQA	LQRKHEGFER
1281	DLAALGDKVN	SLGETAQRLL	QSHPEAEDL	KEKCTELNQA	WTSLGKRADQ	RKAKLGDSDH	LQRFSLDFRD	LMSWINGIRG
1361	LVSSELEAKD	VTGAEALLER	HQEHRTIDA	RAGTFQAFEQ	FGQQLLAHGH	YASPEIKEKL	DILDQERTDL	EKANVQRMM
1441	LDHCLELQLF	HRDCQEAENW	MAAREAFLENT	EDKGDLSLVS	EALIKKHEDF	DKAINVQEEK	IAALQAFADQ	LIALDHYAKG
1521	DIANRRNEVL	DRWRLKAQM	IEKRSKLGES	QTLQQFSRDV	DEIEAWISEK	LQTASDESYSK	DPTNIQSKHQ	KHQAFAELH
1601	ANADRIIRGVI	DMGNSLIERG	ACAGSEDAVK	ARLAALADQW	QFLVQKSAEK	SQKLKEANKQ	QNFNTGIKDF	DFWLSEVAL
1681	LASEDYGKDL	ASVNNLLKKH	QLEADISAH	EDRLKDLNSQ	ADSLMTSSAF	DTSQVKEKRD	TINGRFQKIK	SMATSRRAKL
1761	SESHRLHGF	RDMDDEESWI	KEKLLVSSSE	DYGRDLTVGQ	NLRKKHRRLE	AELAAHEPAI	QGVLDTGKKL	SDDNTIGQEE
1841	IQQLAQFVE	HWKELQLAA	ARGQRLAESL	EYQQFVANVE	EEEAWINEKM	TLVASEDYGD	TLAAIQGLLK	KHEAFETDFT
1921	VHKDRVNDVC	TNGQDLIKKN	NHHEENISSK	MKGLNGKVS	LEKAAAQRKA	NVDENSALFQ	FNWKADVVES	WIGEKENSLK
2001	TDDYGRDLSS	VQTLTKQET	FDAGLQAFQ	EGANITALK	DQLLAAKHQ	SKAIEARHAS	LMKRWQQLLA	NSATRKKLL
2081	EAQSHFRKVE	DLFLTFAKKA	SAFNWVFENA	EEDLTDVPR	NLEEEKALR	EAHADFRSSL	SSAQADFNQL	AELDRQIKSF
2161	RVASNPYTF	TMEALEETWR	NLQKIKERE	LEIQKEQRRQ	EENDNVRFQF	AQHANAFAHQW	IQETRTYLLD	GSCMVEESGT
2241	LESQLEATKR	KHQEIRAMRS	QLKKIEDLGA	AMEEALILDN	KYTEHSTVGL	AQQWDQLDQL	GMRMQHNLEQ	QIQARNTGTV
2321	TEEALKEFSM	MFKHFDKDKS	GRLNHQEFKS	CLRSLGYDLP	MVEEGEPDE	FEAILDTPDP	NRDGHVSLQE	YMAFMISRET
2401	ENVKSSSEIE	SAFRALSSEG	KPYVTKEELY	QNLTREQADY	CVSHMKPYVD	KGKRELPTAF	DYVEFTRSLF	VN



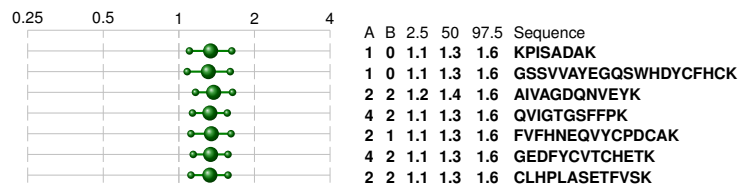


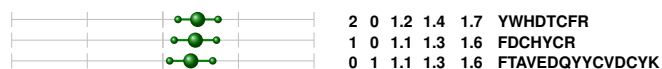
5.38 four and a half LIM domains 1 isoform 1 [Rattus norvegicus]

Protein Accession	gij76781465	
Mean Expression Ratio	1.33	
Median Expression Ratio	1.33	
Credible Interval	(1.19, 1.50)	
Associated Peptides	10	
Associated Spectra	29	
Coverage	0.412	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.26	1.38
Avg..iTRAQ.Ratio....116.114.	1.39	1.55
Avg..iTRAQ.Ratio....117.114.	1.56	1.02

```

1   MASQRHSGPS SYKVGTMSEK FDCHYCRDPL QGKKYVQKDG RHCLLCKFDK FCANTCVECR KPISADAKEV HYKNRYWHD
81  CFRCAKCLHP LASETFVSKD GKILCNKCAT REDSPRCKGC FKAIVAGDQN VEYKGTIWHK DCFTCSNCKQ VIGTGSFFPK
161 GEDFYCVTCH ETKFAKHCVK CNKAITSGGI TYQDQPWHA ECFVVTCSKK LAGQRF TAVE DQYYCVD CYK NFAVAKK CAG
241 KNPITGFGKG SSVVAYEGQS WHDYCFHCKK CSVNLANKRF VFHNEQVYCP DCAKKL
    
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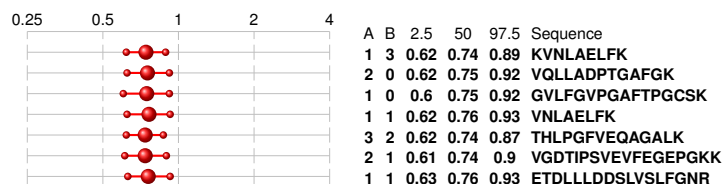




5.39 peroxiredoxin 5 precursor [Rattus norvegicus]

Protein Accession	gi 16758404	
Mean Expression Ratio	0.756	
Median Expression Ratio	0.756	
Credible Interval	(0.659, 0.869)	
Associated Peptides	7	
Associated Spectra	19	
Coverage	0.404	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.738	0.654
Avg..iTRAQ.Ratio....116.114.	0.808	0.76
Avg..iTRAQ.Ratio....117.114.	0.635	0.549

1 MVQLRFCVLG SIAGSVLRAS ATWTCVAGRA GRKGAGWECG GARSFSSAAV TMAPIK**V**GDT IPSVEVFEGE PGKKVNLAEI
 81 **F**KDKKGVLF**G** V**P**GA**F**TP**G**CS **K**TH**L**P**G**F**V**EQ **A**G**A**L**K**A**K**GAQ VVACLSVNDA FVTAEWGRAH Q**A**EG**K**V**Q**LL**A** D**P**T**G**A**F**G**K**ET
 161 **D**LL**L**DD**S**LV**S** L**F**GN**R**RL**K**RF SMVIDRGVVK ALNVEPDGTG LTCSLAPNIL SQL



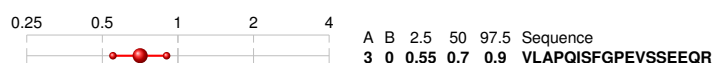
5.40 "NAD(P)H dehydrogenase, quinone 2 [Rattus norvegicus]"

Protein Accession	gi 51948400	
Mean Expression Ratio	0.756	
Median Expression Ratio	0.756	
Credible Interval	(0.595, 0.97)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.0779	

Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.808
Avg..iTRAQ.Ratio....116.114.	0.458
Avg..iTRAQ.Ratio....117.114.	0.521

```

1      MAGKKVLLVY AHQEPKSFNG SMKQVAVEEL SKQGCTVTVS DLYTMNFEPR ATRNDVTGAL SNPEVFKYGI EAYEAYKKA
81     LTSDILEEQR KVQEADLVIF QFPLYWFSVP AILKGWMDRV LCQGFADFVP GFYDSGFLKD KLALLSFTTG GTAEMYTRAG
161    VNGDFRYFLW FLQHGTLHFC GFKVLAPQIS FGPEVSSEEQ RKMVLAWSWQ RLKSIWKEEP IHCTPSWYFQ G
    
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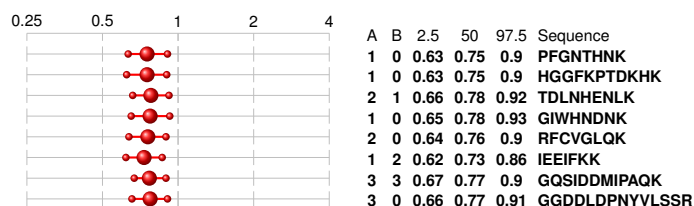


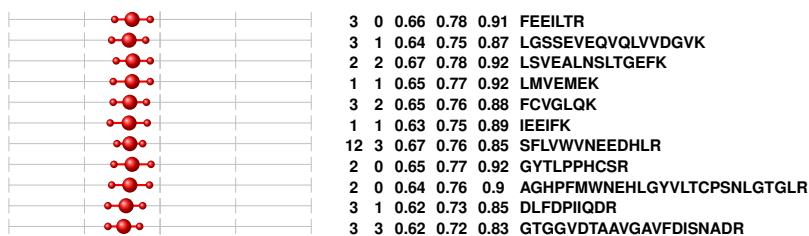
5.41 "creatine kinase, muscle [Rattus norvegicus]"

Protein Accession	gi 6978661	
Mean Expression Ratio	0.761	
Median Expression Ratio	0.76	
Credible Interval	(0.701, 0.828)	
Associated Peptides	19	
Associated Spectra	69	
Coverage	0.53	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.816	0.67
Avg..iTRAQ.Ratio....116.114.	0.83	0.656
Avg..iTRAQ.Ratio....117.114.	0.767	0.553

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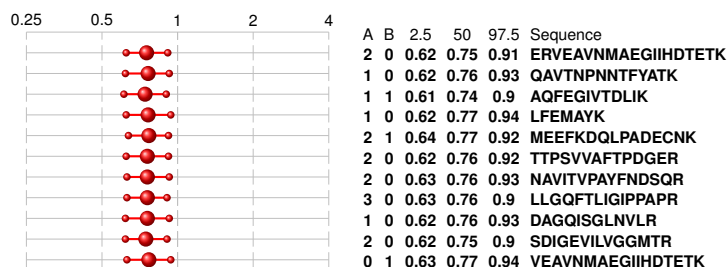
1      MPFGNTHNKF KLNYSQEEY PDLKHNHNM AKVLTDPDLYN KLRDKETPSG FTLDVVIQTG VDNPGHFFIM TVGCVAGDEE
81     SYTVFKDLFD PIIQDRHGGF KPTDKHKTDL NHENLKGDD LDPNYVLSSR VRTGRSIKGY TLPPhCSRGE RRAVEKLSVE
161    ALNSLTGEFK GKYYPLKSMT EQEQQLIDD HFLFDKPVSP LLLASGMARD WPDARGIWHN DNKSFLVWVN EEDHLRVISM
241    EKGGMKEVF RRFVGLQKI EEIFKRAGHP FMWNEHLGYV LTCPSNLGTG LRGVHVKLA NLSKHPKFE E ILTRLRLQKR
321    GTGGVDTAAV GAVFDISNAD RLGSSVEVQV QLVVDGKLM VEMEKKLEKQ QSIDDMIPAQ K
    
```





5.42 "PREDICTED: similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose regulated protein)"

Protein Accession	gij109507099	
Mean Expression Ratio	0.762	
Median Expression Ratio	0.763	
Credible Interval	(0.67, 0.867)	
Associated Peptides	11	
Associated Spectra	20	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.79	0.651
Avg..iTRAQ.Ratio....116.114.	0.742	0.74
Avg..iTRAQ.Ratio....117.114.	0.716	0.764



5.43 hypothetical protein LOC362946 [Rattus norvegicus]

Protein Accession	gij 56090401
Mean Expression Ratio	0.763
Median Expression Ratio	0.764
Credible Interval	(0.603, 0.96)
Associated Peptides	2
Associated Spectra	4
Coverage	0.138
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.792
Avg..iTRAQ.Ratio....116.114.	0.593
Avg..iTRAQ.Ratio....117.114.	0.582

```

1      MWPPCGAMRN LALVLARSQR ARACSGNERV SYTQGSPEP RTREYFYYVD HGGQLFLDDS KMKNFITCFK DLQFLVTFPS
81     RLRPNHSGRY EASFPFLSLC GRERNFLRCE DRPVVFTLL ASDSESPRLS YCGGGEALAI PFEPARLLPL AANGRLYHPA
161    PERAGGVGLV RSALAFELSA CFEYGPNSPT VPSHVQWQGR RIALTMDLAP LLLAAPP
  
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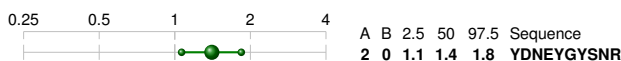


5.44 PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]

Protein Accession	gij 109467549
Mean Expression Ratio	1.31
Median Expression Ratio	1.31
Credible Interval	(1.00, 1.71)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0299
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.75
Avg..iTRAQ.Ratio....116.114.	1.70
Avg..iTRAQ.Ratio....117.114.	1.98

```

1      MVKISVNGFG HTGCLVTRAA FSSASGKVEI VSINDPFIDL NYTVYMFQYD FTHGKFNDTV KAENGLVTN GKPITVFQER
81     DPANIMWGDA GA EYVMESTG IFTTMEKAGA HLRGGAERVI ISTLSVDAPV FVMGVNHEKY DNSLKIIVSNA SCTTNCLTPL
161    AKVIHDNFGI VGGLMTTVHA ITATQKTVD C PSGKLWCDGR GAAQNIIPAS TGAAKAVGKV IPELRGKFTS TAFGVPTPSV
241    PVVDLTCCLE KPAKCDNIKK VVKQASEGPL KGILCYTEDQ VASCFNSNS HSSTFDAGAG IALDDNFVKL ISRYDNEYGY
321    SNRVVDLMVY TASKE
  
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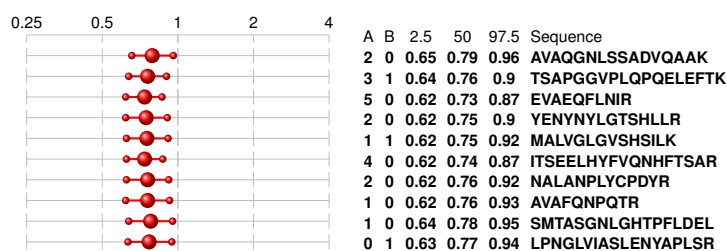


5.45 ubiquinol-cytochrome c reductase core protein II [Rattus norvegicus]

Protein Accession	gi 55741544	
Mean Expression Ratio	0.765	
Median Expression Ratio	0.765	
Credible Interval	(0.679, 0.864)	
Associated Peptides	10	
Associated Spectra	24	
Coverage	0.327	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.714	0.928
Avg..iTRAQ.Ratio....116.114.	0.856	0.498
Avg..iTRAQ.Ratio....117.114.	0.69	0.865

```

1   MKLLSRAGSF SRFYSLKVAP KLKTSAPGGV PLQPQLEFT KLPNGLVIAS LENYAPLSRI GLFIKAGSRY ENYNYLGTSH
81  LLRLASTLTT KGASSFKITR GIEAVGGKLS VTATRENMAY TVEGIRDDIE ILMEFLNVT TAPEFRRWEV AALRSQLKID
161 KAVAFQNPQT RIIENLHDVA YKNALANPLY CPDYRMGKIT SEELHYFVQN HFTSARMALV GLGVSHSILK EVAEQFLNIR
241 GGLGLAGAKA KYRGGEIREQ NGDNLVHAAI VAESAAIGNA EANAFSVLQH LLGAGPHIKR GNNTSLLSQ SVAKGSQQPF
321 DVSAFNASYS DSGLFGIYTV SQAAAAGDVI NAAYNQVKAV AQGNLSSADV QAAKNKLGAG YLMSVETSEG FLSEIGSQAL
401 ATGSYMPPT VLQQIDAVID ADVVKAARKF VSGKKSMTAS GNLGHTPFLD EL
    
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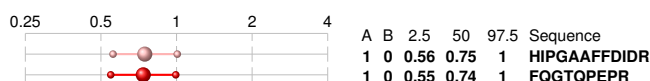
5.46 3-mercaptopyruvate sulfurtransferase [Rattus norvegicus]

Protein Accession	gi 20304123
Mean Expression Ratio	0.767
Median Expression Ratio	0.766
Credible Interval	(0.59, 1.00)

Associated Peptides	2
Associated Spectra	2
Coverage	0.0707
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.603
Avg..iTRAQ.Ratio....116.114.	0.464
Avg..iTRAQ.Ratio....117.114.	0.525

```

1      MAAFQLFRAL VSAQWVAEAL KSPRASQPLK LLDASWYLPK LGRDARREFE ERHIPGAAFF DIDRCS DHTS PYDHMLPSAT
81     HFADYAGSLG VSAATHVVIY DGSDQGLYSA PRVWMMFRAF GHHSVSLLDG GFRYWLSQNL PISSGKSPSE PAEFCAQLDP
161    SFIKTHEDIL ENLDARRFQV VDARAAGR FQ GTQPEPRDGI EPGHIPGSVN IPFTEFLTSE GLEKSPEEQI RLFQEKKVDL
241    SKPLVATCGS GVTACHVVLG AFLCGKPDVP VYDGSWVEWY MRAQPEHVIS QGRGKTL
  
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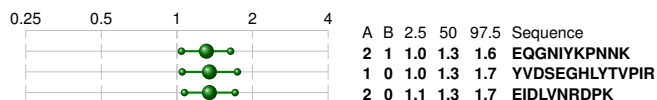


5.47 caveolin 1 alpha isoform [Rattus norvegicus]

Protein Accession	gi 19526761	
Mean Expression Ratio	1.31	
Median Expression Ratio	1.31	
Credible Interval	(1.07, 1.60)	
Associated Peptides	3	
Associated Spectra	6	
Coverage	0.197	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.26	1.14
Avg..iTRAQ.Ratio....116.114.	1.75	0.82
Avg..iTRAQ.Ratio....117.114.	2.01	1.27

```

1      MSGGKYVDSE GHLYTVPIRE QGNIYKPNK AMADEVNEKQ VYDAHTKEID LVNRDPKHLN DDVVKIDFED VIAEPEGTHS
81     FDGIWKASFT TFTVTKYWFY RLLSTIFGIP MALIWGIYFA ILSFLHIWAV VPCIKSFLIE IQCISRVYSI YVHTFCDFLF
161    EAIGKIFSNI RISTQE EI
  
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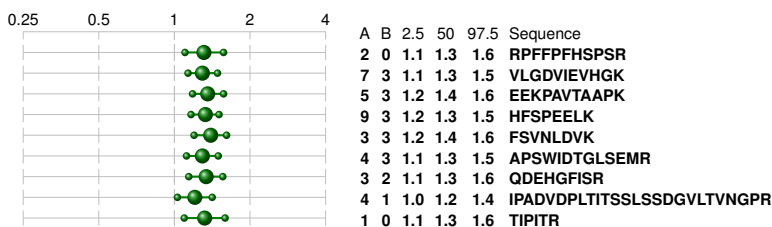


5.48 "crystallin, alpha B [Rattus norvegicus]"

Protein Accession	gij16905067	
Mean Expression Ratio	1.31	
Median Expression Ratio	1.30	
Credible Interval	(1.19, 1.43)	
Associated Peptides	9	
Associated Spectra	56	
Coverage	0.589	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	1.76
Avg..iTRAQ.Ratio....116.114.	1.29	1.44
Avg..iTRAQ.Ratio....117.114.	1.37	1.43

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1 MDIAIHHPWI RPPFFPFHSP SRLFDQFFGE HLESDFST ATSLSPFYLR PPSFLRAPSW IDTGLSEMRM EKDRFSVNL D
81 VKHFSPEELK VKVLGDVIEV HGKHEERQDE HGFISREFHR KYRIPADVDP LTITSSLSSD GVLTVNGPRK QASGPERTIP
161 ITREEKPAVT AAPKK
  
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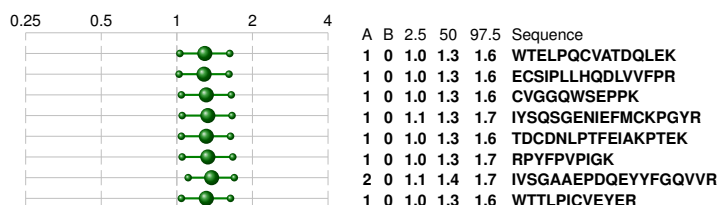
5.49 complement component factor H [Rattus norvegicus]

Protein Accession	gij77861917	
Mean Expression Ratio	1.30	
Median Expression Ratio	1.30	
Credible Interval	(1.10, 1.55)	
Associated Peptides	8	
Associated Spectra	9	
Coverage	0.0955	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.44	

Avg..iTRAQ.Ratio....116.114. 1.37
 Avg..iTRAQ.Ratio....117.114. 1.74

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1      MRLSARIWL  ILWTVCVAED  CKGPPPRENS  EILSGSWSEQ  LYSEGTQATY  KCRPGYRTL  TIVKVCKNGE  WVPSNPSRIC
81     RKRPCGHPG  TFFGSRFRAV  GSEFEFGAKV  VYTCDDEGYL  LGEIDYRECD  ADGWNTDIP  CEVVKCLPVT  ELENGRIVSG
161    AAEPDQEYF  GQVVRFECS  GFKIEGQKEM  HCSENGLWSN  EKPQCVESC  LPPRVENGDG  IYLKPVYKEN  ERFQYKCKQG
241    FVYKERGDAV  CTGSGWNPQP  SCEEMTCLTP  YIPNGIYTPH  RIKHRIDDEI  RYECCKNGFY  ATRSPVSKCT  ITGWIPAPRC
321    SLKPCDFPQF  KHGRLYEES  RRPYFPVPIG  KEYSYCDNG  FTTPSQSYWD  YLRCTVNGWE  PEVPCLRQCI  FHYVEYGESL
401    YWQRRYIEGQ  SAKVQCHSGY  SLPNGQDTIL  CTENGWSPPP  KCVRIKTCVS  SDIEIENGF  SESDYTYALN  RKTRYRCKQG
481    YVTNTGEISG  IITCLQDGWS  PRPSCIKSCD  MPVFENAMTK  NNNTWFKLND  KLDYECHIGY  ENEYKHTKGS  ITCTYDGWSS
561    TPCYERECES  IPLLHQDLVV  FPREVKYKVG  DSLSFSCRS  HRVGADLVQC  YHFGWSPNFP  TCEGQVKSCD  QPLEIPNGEI
641    KGTKKVEYSH  GDVVEYDCKP  RFLKGFNKI  QCVDGKWTTL  PICVEYERTC  GDLPALEHGS  VQLSVPPYHH  GDSVEFTCAE
721    TFTMIGHAVV  FCISGRWTEL  PQCVA TDQLE  KCKAPKSTGI  DAIHPNKNEF  NNFVSVSYRC  RQKQYEHSI  CINGRWDPPE
801    NCTRNEKRFC  PPPQPINAQ  VIETTVKYL  D  GERVSVLCQD  GYL TQGPEEM  VCKHGRWQSL  PRCTEKIPCS  QPPKIEHSGI
881    KSPRSSEERD  LIESSSYEHG  TFFSYVDDG  FRISEENRVT  CNMGKWSL  RCVGIPC  PSIPLGIVSH  ELESYQYGEE
961    VTYNCSEGFG  IDGPAFIKCV  GGQWSEPPK  IKTD  CDNLPT  FEIAKPT  KKSYSRSGEQV  TFRCP  DGSDIVTCVN
1041   TKWIGQPVCK  DNSCVNPPHV  PNATILTRHK  TKYPSGDKVR  YDCNKPFELF  GEVEVMCQNG  IWTEPPKCKD  STGCKGPPPP
1121   IDNGDITSL  LPVYAPLSSV  EYQCQNYLL  KGNKIVTCRN  GKWSQPPTCL  HACVIPEDIM  EKHNIVLRWR  ENAKIYSQSG
1201   ENIEFMCKPG  YRKRFRGSP  RTKCIEGHIN  YPTCV
    
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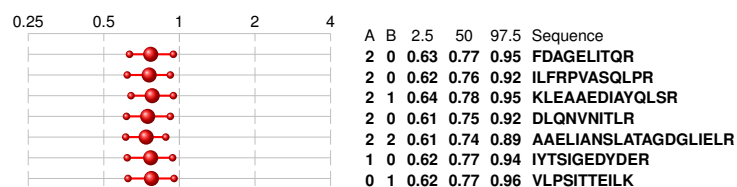


5.50 prohibitin [Rattus norvegicus]

Protein Accession	gi 13937353	
Mean Expression Ratio	0.769	
Median Expression Ratio	0.768	
Credible Interval	(0.663, 0.892)	
Associated Peptides	7	
Associated Spectra	15	
Coverage	0.327	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.785	0.563
Avg..iTRAQ.Ratio....116.114.	0.827	0.589
Avg..iTRAQ.Ratio....117.114.	0.718	0.607

```

1      MAAKFVESIG  KFGLALAVAG  GVVNSALYNV  DAGHRVIFD  RFRGVQDIVV  GEGTHFLIPW  VQKPIIFDCR  SRPRNPVIT
81     GSKDLQNVNI  TLRILFRPVA  SQLPRIYTSI  GEDYDERVLP  SITTEILKSV  VARFDAGELI  TQRELVSQV  SDDLTERAAT
161    FGLILDDVSL  THLTFGKEFT  EAVEARQVAQ  QEAERARFVV  EKAEQQKAA  IISAEGDSKA  AELIANSLAT  AGDGLIELRK
241    LEAAEDIAQ  LSRSRNITYL  PAGQSVLLQL  PQ
    
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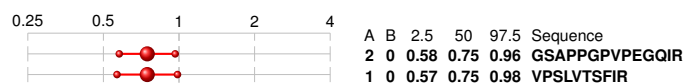


5.51 glutathione S-transferase omega 1 [Rattus norvegicus]

Protein Accession	gij56090550
Mean Expression Ratio	0.77
Median Expression Ratio	0.769
Credible Interval	(0.601, 0.987)
Associated Peptides	2
Associated Spectra	3
Coverage	0.0996
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.72
Avg..iTRAQ.Ratio....116.114.	0.461
Avg..iTRAQ.Ratio....117.114.	0.645

```

1   MSGASARSLG KGSAPPGPVP EGQIRVYSMR FCPFAQRTLM VLKAKGIRHE IININLKNKP EWFFEKNPFG LVPVLENTQG
81  HLITESVITC EYLDEAYPEK KLFPPDDPYEK ACQKMTFELF SKVPSLVTSF IRAKRKEDHP GIKEELKKEF SKLEEAMAKK
161 RTAFFGGNSL SMIDYLIWPW FQRLEALELN ECIDHTPKLK LWMATMQEDP VASSHFIDAK TYRDYLSLYL QDSPEACDYG
241 L
    
```



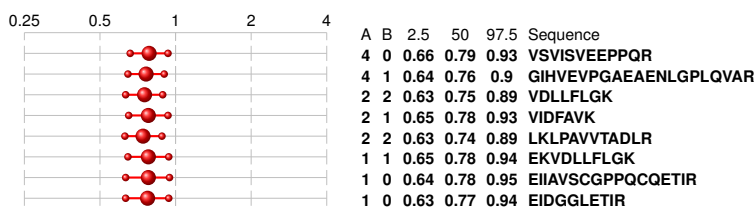
5.52 "electron-transfer-flavoprotein, beta polypeptide [Rattus norvegicus]"

Protein Accession	gij51948412
Mean Expression Ratio	0.775
Median Expression Ratio	0.775
Credible Interval	(0.685, 0.878)
Associated Peptides	8
Associated Spectra	24

Coverage	0.349	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.82	0.666
Avg..iTRAQ.Ratio....116.114.	0.831	0.705
Avg..iTRAQ.Ratio....117.114.	0.712	0.55

```

1 MAELRALVAV KRVIDFAVKI RVKPKDSGVV TDGVKHSMNP FCEIAVEEAV RLKEKLVKE IIAVSCGPPQ CQETIR TALA
81 MGADRGIHVE VPGAEEENLG PLQVARVLAK LAEKVKDLL FLGKQAIDDD CNQTGQMTAG LLDWPQGTFA SQVTLEGDKV
161 KVEREIDGGL ETIRLKLPAV VTADLRLNEP RYATLPNIMK AKKKKIEVIK AGDLGVDLTS KVSVISVEEP PQR LAGVKVE
241 TTEDLVAKLK EVGRI
    
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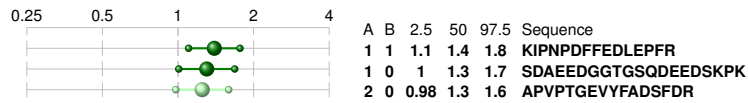


5.53 calnexin [Rattus norvegicus]

Protein Accession	gij25282419	
Mean Expression Ratio	1.29	
Median Expression Ratio	1.29	
Credible Interval	(1.03, 1.6)	
Associated Peptides	3	
Associated Spectra	5	
Coverage	0.0863	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.39	2.22
Avg..iTRAQ.Ratio....116.114.	1.12	2.11
Avg..iTRAQ.Ratio....117.114.	1.76	2.82

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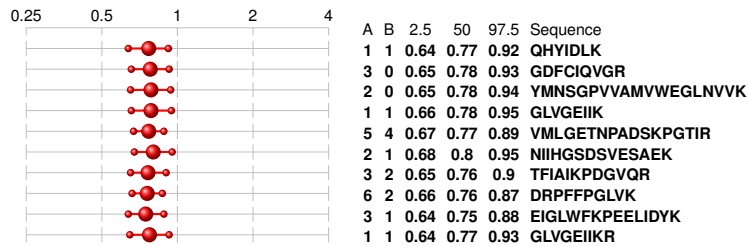
1 MEGKWLCLL LVLGTAAIQA HDGHDDMID IEDDLDDVIE EVEDSKSKSD TSTPPSPKVT YKAPVPTGEV YFADSFDFGS
81 LSGWILSKAK KDDTDDEIAK YDGKWEVDEM KETKLPQDKG LVLMsRAKHH AISAKLNKPF LFDTKPLIVQ YEVNFQNGIE
161 CGGAYVKLLS KTSELNLQDF HDKTPYTIMF GPKKCGEDYK LHFIFRHKNP KTGvYEEKHA KRPDADLKY FTDRKTHLYT
241 LILNPDNSFE ILVDQSVVNS GNLLNDMTTP VNPSREIEDP EDRKPEDWDE RPKIADPDVA KPDDWDEDAP SKIPDEEATK
321 PEGWLDDEPE YIPDPDAEKP EDWDEDMDGE WEAPQIANPK CESAPGCGVW QRPMIDNPNY KGKWKPPMID NPNYQGIWKP
401 RKIPNPDFFE DLEPFMRTPF SAIGLELWSM TSDIFFDNFI ISGDRRVVDD WANDGWGLKK AADGAAEPGV VQGMLEAAEE
481 RPWLWVVYIL TVALPVFLVI LFCCSGKKQS NAMEYKKTDA PQQPDVKDEEG KEEKKNKGE EEEEEKLEEK QKSDAEEDGG
561 TGSQDEEDSK PKAEDEILN RSPRNKRPRR E
    
```



5.54 expressed in non-metastatic cells 2 [Rattus norvegicus]

Protein Accession	gj 55926145	
Mean Expression Ratio	0.778	
Median Expression Ratio	0.778	
Credible Interval	(0.697, 0.868)	
Associated Peptides	10	
Associated Spectra	40	
Coverage	0.737	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.803	0.686
Avg..iTRAQ.Ratio....116.114.	0.839	0.726
Avg..iTRAQ.Ratio....117.114.	0.749	0.549

1 MANLERTFIA IKPDGVQRGL VGEIIKRFEQ KGFRLVAMKF LRASEEHLKQ HYIDLKDRPF FPGLVKYMNS GPVAMVWEG
 81 LNVVKTGRVM LGETNPADSK PGTIRGDFCI QVGRNIIHGS DSVESA EKEI GLWFKPEELI DYKSCAHDWV YE



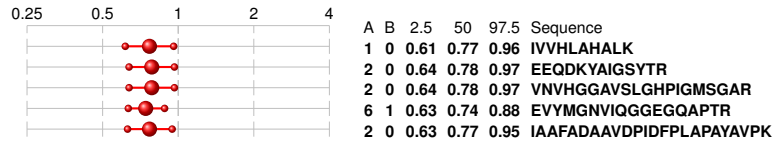
5.55 acetyl-coenzyme A acetyltransferase 1 [Rattus norvegicus]

Protein Accession	gj 8392836	
Mean Expression Ratio	0.779	
Median Expression Ratio	0.78	
Credible Interval	(0.665, 0.91)	

Associated Peptides	5	
Associated Spectra	14	
Coverage	0.200	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.884	0.662
Avg..iTRAQ.Ratio....116.114.	0.805	0.398
Avg..iTRAQ.Ratio....117.114.	0.72	0.214

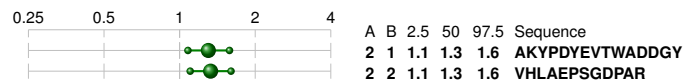
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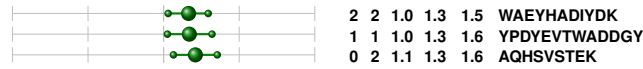
1      MAALAVLHGV VRRPLLRLGLL QEVRCLEGRSY ASKPTLNDVV IVSATRTPIG SFLGSLASQP ATKLGTTIAIQ GAIEKAGIPK
81     EEVKEVYMGV VIQGGEGQAP TRQATLGAGL PIATPCTTVN KVCASGMKAI MMASQSLMCG HQDVMVAGGM ETMSNVPYVM
161    SRGATPYGGV KLEDLIVKDG LTDVYNKIHM GNCAENTAKK LSISSEEQDK YAIGSYTRSK EAWDAGKFAN EITPITISVK
241    GKPDRVVKED EYKRVDFSK VPKLKTVPQK ENGTVTAANA STLNDGAAAV VLMTAEAAQR LKVKPLARIA AFADAAVDPI
321    DFPLAPAYAV PKVLKYAGLK KEDIAMWEVN EAFSVVVLAN IKMLEIDPQK VNVHGGAVSL GHPIGMSGAR IVVHLAHALK
401    QGEFGLASIC NGGGGASAVL IEKL
  
```



5.56 PREDICTED: similar to 14 kDa phosphohistidine phosphatase (Phosphohistidine phosphatase 1) [Rattus

Protein Accession	gi 109467870	
Mean Expression Ratio	1.28	
Median Expression Ratio	1.28	
Credible Interval	(1.11, 1.49)	
Associated Peptides	5	
Associated Spectra	15	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.26	1.19
Avg..iTRAQ.Ratio....116.114.	1.5	1.39
Avg..iTRAQ.Ratio....117.114.	1.17	1.38



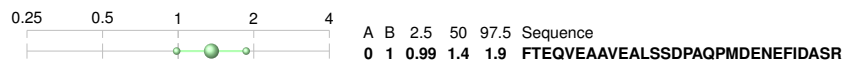


5.57 "catenin (cadherin-associated protein), alpha 1, 102kDa [Rattus norvegicus]"

Protein Accession	gi 55742755
Mean Expression Ratio	1.28
Median Expression Ratio	1.28
Credible Interval	(0.942, 1.72)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0330
Experiment	B
Avg..iTRAQ.Ratio....115.114.	2.11
Avg..iTRAQ.Ratio....116.114.	7.02
Avg..iTRAQ.Ratio....117.114.	1.37

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1      MTAVHTGNIN  FKWDPKSLEI  RTLAVERLLE  PLVTQVTTLV  NTNSKGPSNK  KRGRSKKAHV  LAASVEQATE  NFLEKGDKIA
81     KESQFLKEEL  VAAVDDVRRKQ  GDLMKSAAGE  FADDPCSSVK  RGNMVRARA  LLSAVTRLLI  LADMADVYKL  LVQLKVVEDG
161    ILKLRNAGNE  QDLGIQYRAL  KPEVDKLNIM  AAKRQQELKD  VGHDRQMAAA  RGILQKNVPI  LYTASQACLQ  HPDVAAYKAN
241    RDLIYKQLQQ  AVTGISNAAQ  ATASDDASQQ  QGGGGGGGEL  AYALNNFDKQ  IIVDPLSFSE  ERFRPSLEER  LESIISGAAL
321    MADSSCTRDD  RRERIVAECN  AVRQALQDLL  SEYMGNAGRK  ERSDALNSAI  DKMTKKTRDL  RRQLRKAVMD  HVSDSFLETN
401    VPLLVLEIAA  KNGNEKEVKE  YAQVFRHAN  KLIEVANLAC  SISNNEGVK  LVRMSASQLE  ALCPQVINAA  LALAAPQSK
481    LAQENMDLFK  EQWEKQVRVL  TDAVDDITSI  DDFLAVSENH  ILEDVNKCVI  ALQEKDVGDL  DRTAGAIRGR  AARVIHVVTS
561    EMDNYEPGVY  TEKVLEATKL  LSNTVMPRFT  EQVEAAVEAL  SDDPAQPMDE  NEFIDASRLV  YDGIRDIRKA  VLMIRTPPEL
641    DSDFFETEDF  DVRSRTSVQT  EDDQLIAGQS  ARAIMAQLPQ  EQKAKIAEQV  ASFQEEKSKL  DAEVSKWDDS  GNDIIVLAKQ
721    MCMIMMEMTD  FTRGKGPLKN  TSDVISAAKK  IAEAGSRMDK  LGRTIADHCP  DSACKQDLLA  YLQRIALYCH  QLNICKSVKA
801    EVQNLGGELV  VSGVDSAMSL  IQAAKNLMNA  VVQTVKASYV  ASTKYQKSQG  MASLNLPAVS  WKMKAPEKPP  LVKREKQDET
881    QTKIKRASQK  KHNPNVQALS  EFKAMDSI
    
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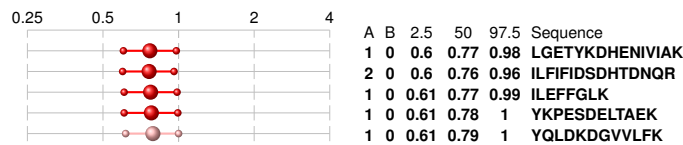
5.58 "prolyl 4-hydroxylase, beta polypeptide [Rattus norvegicus]"

Protein Accession	gi 6981324
Mean Expression Ratio	0.783
Median Expression Ratio	0.783

Credible Interval	(0.639, 0.956)
Associated Peptides	5
Associated Spectra	6
Coverage	0.122
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.846
Avg..iTRAQ.Ratio....116.114.	0.642
Avg..iTRAQ.Ratio....117.114.	0.675

```

1      MLSRALLCLA LAWAARVGAD ALEEDNVLV LKKSNEFAEPA AHNYLLVEFY APWCGHCKAL APEYAKAAK LKAEGSEIRL
81     AKVDATEESD LAQQYGVRGY PTIKFFKNGD TASPKEYTAG READDIVNWL KKRTGPAATT LSDTAAAESL VDSSEVTVIG
161    FFKDAGSDSA KQFLAAEAV DDIPFGITSN SDVFSK YQLD KDGVVLFK F DEGRNFEFE ITKEKLLDFI KHNQLPLVIE
241    FTEQTAPKIF GGEIKTHILL FLPKSVSDYD GKLSNFKKAA EGFKGKILFI FIDSDHTDNQ RILEFFGLKK EECPAVRLIT
321    LEEEMTRKYP ESEDLTAEKI TQFCHHFLEG KIKPHLMSQE LPEDWDKQPV KVLVGKNFEE VAFDEKKNVF VEFYAPWCGH
401    CKQLAPIWDK LGETYKDHEN IVIAKMDSTA NEVEAVKVHS FPTLKFFPAS ADRTVIDYNG ERTLDDGFKKF LESGGQDGAG
481    DNDDLDLEEA LEPDMEEDDD QKAVKDEL
  
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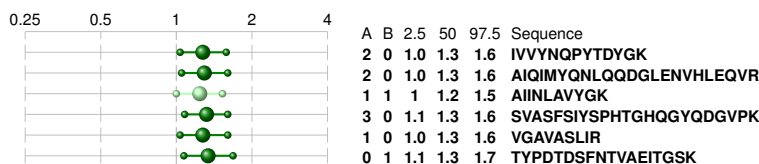


5.59 plasma glutamate carboxypeptidase [Rattus norvegicus]

Protein Accession	gij13928880	
Mean Expression Ratio	1.28	
Median Expression Ratio	1.28	
Credible Interval	(1.08, 1.50)	
Associated Peptides	6	
Associated Spectra	11	
Coverage	0.203	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.26	1.56
Avg..iTRAQ.Ratio....116.114.	1.40	1.24
Avg..iTRAQ.Ratio....117.114.	1.59	1.62

```

1      MRFLFFLFVA VVHLFSLGSG KAIYKSGVSQ RTFQEIKEEI ANYEDVAK AI INLAVYGKYQ NRSYERLGLL VDTVGPRLSG
81     SKNLEKAIQI MYQNLOQDGL ENVHLEQVRI PHWGRGEESA VMVVPRIHKL AILGLGGSIG TPPEGITAEV LVVASFVELQ
161    RRASEARGKI VVYNQPYTDY KTVQYRERG AVEAAKVGAV ASLIRSVASF SIYSPHTGHQ GYQDGVPKIP TACITIEDAE
241    MMSRMASRGD KIVIHLMKGA KTYPD TDSFN TVAEITGSKY PEEVVLVSGH LDSWDVQGA LDDGGGAFIS WEALSIVKDL
321    GLRPFKRTLRL VLWTAEEQGG VGASQYELH KANISKYSLV MEADSGTFLP TGLQFTGSDK ARAIMKEVMS LLQPLNITKV
401    FNDAEGTDIN FWIQAGVPGA SLRDDLYKYF FFHSHSGDTM TAMDPKQMNVA AAAVWAVVAY VVADMEEMLP RS
  
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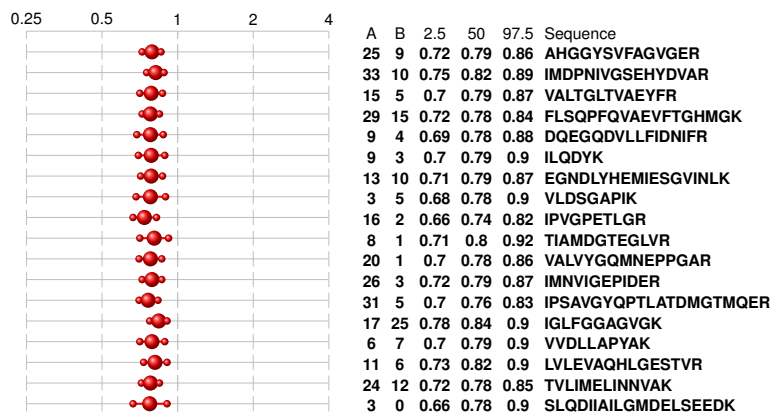



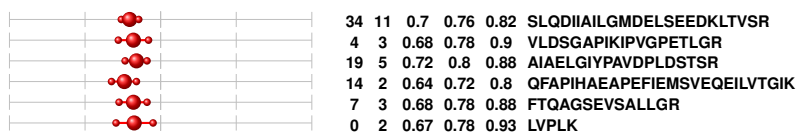
5.60 "ATP synthase, H+ transporting, mitochondrial F1 complex, beta subunit [Rattus norvegicus]"

Protein Accession	gij54792127	
Mean Expression Ratio	0.784	
Median Expression Ratio	0.785	
Credible Interval	(0.748, 0.822)	
Associated Peptides	24	
Associated Spectra	525	
Coverage	0.601	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.798	0.719
Avg..iTRAQ.Ratio....116.114.	0.88	0.589
Avg..iTRAQ.Ratio....117.114.	0.827	0.72

```

1      MSLVLVGRVAS ASASGALRGL NPLAALPQAH LLRTAPAGV HPARDYAAQS SAAPKAGTAT GQIVAVIGAV VDVQFDEGLP
81     PILNALEVQG RESRLVLEVA QHLGESTVRT IAMDGTEGLV RGQKVLDSGA PIKIPVGPET LGRIMNVIGE PIDERGP IKT
161    KQFAPIHAEA PEFIEMSVEQ EILVTGIKVV DLLAPYAKGG KIGLFGGAGV GKTVLIMELI NNVAKAHGGY SVFAGVGERT
241    REGNDLYHEM IESGVINLKD ATSKVALVYG QMNEPPGARA RVALTGLTVA EYFRDQEGQD VLLFIDNIFR FTQAGSEVSA
321    LLGRIPSAVG YQPTLATDMG TQERITTTK KGSITSVQAI YVPADDLTD P APATTFAHLD ATTVLSRAIA ELGIYPVAVDP
401    LDSTSRINDP NIVGSEHYDV ARGVQKILQD YKSLQDI IAI LGMDLSEED KLTVSRARKI QRFLSQPFQV AEVFTGHM GK
481    LVPLKETIKG FQQILAGDYD HLPEQAFYMW GPIEEAVAKA DKLAEHGS
    
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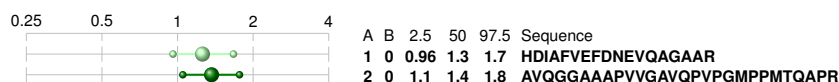


5.61 small nuclear ribonucleoprotein polypeptide A [Rattus norvegicus]

Protein Accession	gi 56605690
Mean Expression Ratio	1.27
Median Expression Ratio	1.27
Credible Interval	(0.996, 1.63)
Associated Peptides	2
Associated Spectra	3
Coverage	0.164
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.98
Avg..iTRAQ.Ratio....116.114.	1.34
Avg..iTRAQ.Ratio....117.114.	2.35

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1      MAVPETRPNH TIYINNLNEK IKKDELKKS L YAIFSQFGQI LDILVSRSLK MRGQAFVIFK EVSSATNALR SMQGFPPFYDK
81     PMRIQYAKTD SDIIAKMKGT FVERDRKREK RKPKSQETPA AKKAVQGGAA APVVGAVQPV PGMPPMTQAP RIMHHMPGQP
161    PYMPPPGMIP PPGLAPGQIP PGAMPPQQLM PGQMPPAQL SENPPNHILF LTNLPEETNE LMLSMLFNQF PGFKEVRLVP
241    GRHDIAPVEF DNEVQAGAAR DALQGFKITQ NNAMKISFAK K
    
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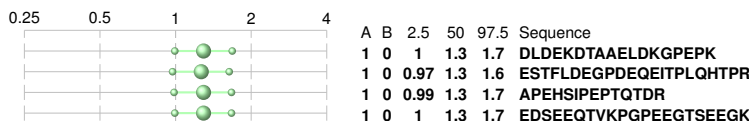
5.62 microtubule-associated protein 1 A [Rattus norvegicus]

Protein Accession	gi 13591886
Mean Expression Ratio	1.27
Median Expression Ratio	1.27
Credible Interval	(1.02, 1.59)
Associated Peptides	4
Associated Spectra	4
Coverage	0.0270
Experiment	A

Avg..iTRAQ.Ratio....115.114. 1.58
 Avg..iTRAQ.Ratio....116.114. 1.35
 Avg..iTRAQ.Ratio....117.114. 2.13

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1 MDGVAEFSEY VSETVDVPSF FDLLEPPTS GFLKLSKPC YIFPGGRGDS ALFAVNGFNI LVDGGSDRKS CFWKLVRHLD
81 RIDSVLLTHI GADNLPGING LLQRKVAELE EEQSQGSSSY SDWVKNLISP ELGVVFFNVP DKLRLPDASR KAKRSIEEAC
161 LTLQHLNRLG IQAEPLYRVV SNTIEPLTLF HKMGVGRDLM YVLNVPKDSK EMQFLMQKWA GNSKAKTGIV LANGKEAEIS
241 VPYLTSITAL VVWLPANPTE KIVRVLFPGN APQNKILEGL EKLRHLDFLR YPVATQKDLA AGAVPANLKP SKIKHRADSK
321 ESLKAAPKTA VSKLAKREEV LEEGAKREAR ELAKELAKTE KKAKEPSEKP PEKPSKSERV RGESEALKA EKRRLIKDKA
401 GKKHLKKEIS KLEEKKDKKE KEIKKERKEL KKEEGRKEEK KDAKKDEKRR DTKPEVKKLS KPDLPKPTPE VRKTLKAKA
481 PGRVKVDKGR AARGEKELSS EPRTTPAQKG AAPPAAVSGH RELALSSPED LTQDFEELKR EERGLLAEQR DTGLGEKPLP
561 ADATEQGHPS AAIQVTQPSG PVLEGEHVER EKEVVPDPSG DKGSTNRGPD SGAEVEKEKE TWEERKQREA ELGPENTAR
641 EESAEVKEK VIEKAELEEM EETHPSDEEG EETKAESFYQ KHTQEQALKAS PKSREALGGR DLGFQGKAPE KETASFLSSL
721 ATPAGATEHV SYIQDETIPG YSETEQTISD EEIHDEPDER PAPPFRFTST YDLSGPEGPG PFEASQAADS AVPASSSKTY
801 GAPETELTYP PNMVAAPLAE EEHVSAATSI TECDKLSSFA TSVAEQDQVA SLTAPQTEET GKSSLLLDTV TSIPSSRTEA
881 TQGLDYVPSA GTISPTSSLE EDKGFKSPPC EDFSVTGESE KKGETVGRGL SGEKAVGKEE KYVVTSEKLS GQYAAVFGAP
961 GHLLPPGEP A LGEVEERCLS PDDSTVKMAS PPPSGPPSAA HTPFHQSPVE DKSEPRDFQE DSWGETKHSV GVSKEDESEEG
1041 TVKPGPEEGT SEEGH GPPTR SPQAQDMPVS IAGGQTGCTI QLLPEQDKAI VFETGEAGSN LGAGTLPGEV RTSTEATEP
1121 QKDEVLRFTD QSLSPEDAES LSVLSVVSVD TTKQEATPRS PCSLKEQQPH KDLWPMVSPE DTQSLSFSEE SPSKETSLDI
1201 SSRQLSPESL GTLQFGELNL GKEERGPVMK AEDDSCHLAP VSIPEPHRAT VSPSTDETPA GTLPGGGFSH SALSVDRKHS
1281 PGEITGPGGH FMTSDSSSLTK SPESLSSPAM EDLAVWEGK APGKEKEPEL KSETRQKKGQ ILPEKVAVVE QDLI IHQKDG
1361 ALDEENKPGR QQDKTPEQKG RDLDEKDTAA ELDKGPEPEK KDLDRDQGG RAGPPAEKDK ASEQRDLDLQ QTQATEPRDR
1441 AQERRDSEK DKSLELRDRT PEEKDRILVQ EDRAPEHSIP EPTQTDRA PD RKGTTDKKQK EEASEEKEQV LEQKDWALGK
1521 EGETLDQEAR TAEQKDETLK EDKTQGGKSS FVEDKTTTSK ETVLDQKSAE KADSVQDQDQ AALEKTRALG LEESPAEGSK
1601 AREQEKKYWK EQDVVQGWRE TSPTRGEPVG GQKEPVPawe GKSPEQEVRY WRDRDITLQ DAYWRELSCD RKVWPFHLD
1681 GQGARRPYCE ERBESTFLDEG PDEQEITPLQ HTPRSPWTS FKFDFQEPLQ KGLEVERWLA ESPVGLPPEE EDKLTRSPFE
1761 IISPPASPE MTGQRVPSAP GQESPVPDTE STAPMRNEPT TPSWLAIEPP WVPKDRPLPP APLSPAPAPP TPAPPEPHTPV
1841 PFSWGLAEYD SVVAAVQEGA AELEGGYISP LGKDYRKAEG EREGEKGAGA PDSSSFSPKV PEAGESLATR DTEQTEPEQR
1921 EPTPYPDEERS FOYADIYEQM MLTGLGPACP TREPPLGASG DWPHLSTKE EAAGCNTSAE KETSSPASPO NLQSDTTPAFS
2001 YASLAGPAVP FRQEPDPGN VEPSITPPAV PPRAPISLSK DLSPLNGST VSCSPDRRTP SPKETGRGHV DDGTNDSLE
2081 KGAREQPEKE TRSPSPHPM PMGHSSLWPE TEAYSSLSDD SHLGSVRPSL DFPASAFGFS SLQPAPPQLP SPAEPRAPC
2161 GSLAFSDRA LALVPGTPTR TRHDEYLEVT KAPSLDSSLP QLPSPSSPGG PLLSNLPRPA SPALSEGSSS EATTPVIVSV
2241 AERFPPGLEA AEQSAEGLS GKESAAHSLW DLTPLSPAPS ASLDLAPAPA PAPAPAPGLP GDLGDGTLPC RPECTGELTK
2321 KPSPFLSPG DHEANGPGET SLNPPGFVNT TAEKEEAEP HAWERGSWE GAERSRPPD LLSSEQLLRP GKSSGGPPCS
2401 LSSEVEAGPQ GCATDRPHC GELSPSFLNP FLPPSTDSD LSTEARLAG KGRRRVGRP GATGGPCPMA DETPPTSASD
2481 SSSQSDSDV PPETECPESI TAEAAALDSE DGDFLPVDKA GGVSGTHHPR PGHDPPPTPL PDPRPSPRP DVCMDPEGL
2561 SSESGRVERL REKGRPGRRA PGRAPASPA RRLDIRGKRS PTPGKGPVDR TSRTVPRPRS TPSQVTSAAE KDGHSPPMSKG
2641 LVNGLKAGST ALGSKGSGSP PYYVDLAYIP NHCSSGKADQ DFFRRVRASY YVVSNDPAN GEPSRAVLDA LLEGKAQWGE
2721 NLQVTLIFTH DTEVTREWYQ QTHEQQQLN VLVLASSSTV VMQDESFPAC KIEF
    
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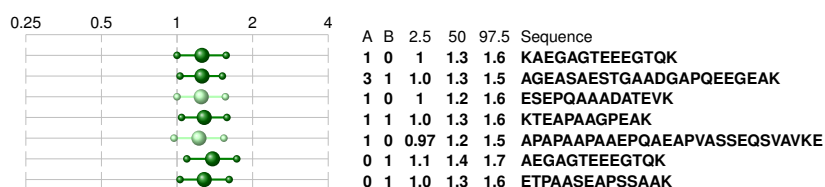
5.63 "brain abundant, membrane attached signal protein 1 [Rattus norvegicus]"

Protein Accession [gil11560135](#)
 Mean Expression Ratio 1.26
 Median Expression Ratio 1.27
 Credible Interval (1.07, 1.49)
 Associated Peptides 7
 Associated Spectra 11

Coverage	0.477	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.25	1.28
Avg..iTRAQ.Ratio....116.114.	1.03	1.35
Avg..iTRAQ.Ratio....117.114.	1.46	2.36

```

1      MGSKLSKSKK  GYVNVDEKAK  DKDKKAEGAG  TEEEGTQKES  EPQAAADATE  VRESAEKPK  DAADGEAKAE  EKEADKAAK
81     EEAPKAEPFK  SEGAAEEQPE  PAPAPEQEAA  APGPAAGGEA  PKAGESAES  TGAADGAPQE  EGEAKKTEAP  AAGPEAKSDA
161    APAASDSKPS  TEPAPSSKET  PAASEAPSSA  AKAPAPAAPA  AEPQAEAPVA  SSEQSVAVKE
    
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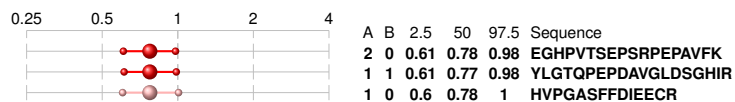


5.64 thiosulfate sulfurtransferase [Rattus norvegicus]

Protein Accession	gi 57528682	
Mean Expression Ratio	0.791	
Median Expression Ratio	0.791	
Credible Interval	(0.639, 0.977)	
Associated Peptides	3	
Associated Spectra	5	
Coverage	0.172	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.628	0.737
Avg..iTRAQ.Ratio....116.114.	0.776	0.63
Avg..iTRAQ.Ratio....117.114.	0.634	0.85

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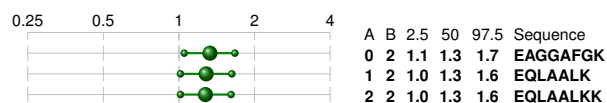
1      MVHQVLYRAL  VSTKWLAESI  RSGKVGPSLR  VLDASWYSPG  TRQARKEYQE  RHVPGASFFD  IEECRDTTSP  YEMMLPSEAH
81     FGDYVGNLGI  SNDTHVVVYD  GDDLGSFYAP  RVWWMFRVFG  HRTVSVLNGG  FRNWLKEGHP  VTSEPSRPEP  AVFKATLNRS
161    LLKTYEQVLE  NLQSKRFQLV  DSRAQGRYLG  TQPEPDAVGL  DSGHIRGSVN  VFFMNFLTED  GFEKSPEELR  AIFQDKKVDL
241    SQPLIATCRK  GVTACHIALA  AYLCGKPDVA  VYDGSWSEWF  RRAPPETRVS  QGKSGKA
    
```



5.65 ATPase inhibitory factor 1 [Rattus norvegicus]

Protein Accession	gi 77917528
Mean Expression Ratio	1.27
Median Expression Ratio	1.26
Credible Interval	(1.03, 1.55)
Associated Peptides	3
Associated Spectra	9
Coverage	0.150
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.54
Avg..iTRAQ.Ratio....116.114.	1.19
Avg..iTRAQ.Ratio....117.114.	1.12

1 MAGSALAVRA RLGWGMRLV QTRGFGSDSS ESMSGAGSI REAGGAFGKR EKAEDRYFR EKTRQLAAL KKHHEDEIDH
81 HSKEIERLQK QIERHKKIK YLKNSEH

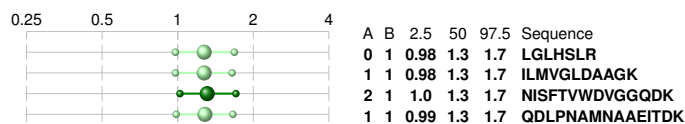


5.66 ADP-ribosylation factor 3 [Rattus norvegicus]

Protein Accession	gi 18266716
Mean Expression Ratio	1.26
Median Expression Ratio	1.26
Credible Interval	(1.01, 1.59)
Associated Peptides	4
Associated Spectra	8
Coverage	0.260
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.43
Avg..iTRAQ.Ratio....116.114.	1.30
Avg..iTRAQ.Ratio....117.114.	1.37

```

1      MGNIFGNLLK SLIGKKEMR L MVGLDAAGK TTILYKCLKG EIVTTIPTIG FNVETVEYKN ISFTVWDVGG QDKIRPLWRH
81     YFQNTQGLIF VVDSNDRERV NEAREELMRM LAEDELRLDAV LLVFANKQDL P NAMAAEIT DKLGLHSLRH RNWYIQATCA
161    TSGDGLYEGL DWLANQLKNK K
    
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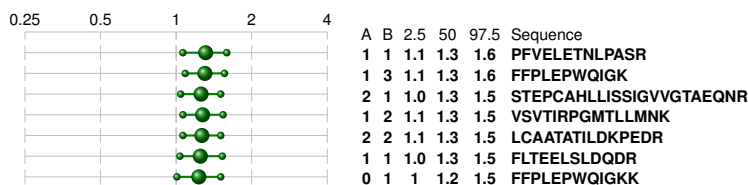


5.67 D-dopachrome tautomerase [Rattus norvegicus]

Protein Accession	gij13162287	
Mean Expression Ratio	1.26	
Median Expression Ratio	1.26	
Credible Interval	(1.1, 1.45)	
Associated Peptides	7	
Associated Spectra	19	
Coverage	0.763	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.33	1.02
Avg..iTRAQ.Ratio....116.114.	1.39	1.07
Avg..iTRAQ.Ratio....117.114.	1.72	1.26

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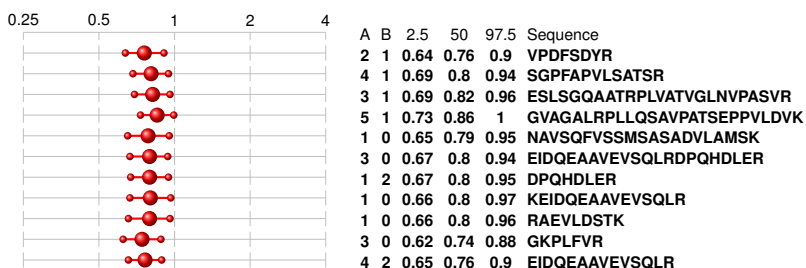
1      MPFVELETNL PASRIPAGLE NRLCAATATI LDKPEDRVSV TIRPGMTLLM NKSTEPCAHL LISSIGVVGT AEQNRSHSSS
81     FFKFLTEELS LDQDRIIIRF FPLEPWQIGK KGTVMTFL
    
```



5.68 "ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [Rattus norvegicus]"

Protein Accession	gi 57114330	
Mean Expression Ratio	0.796	
Median Expression Ratio	0.796	
Credible Interval	(0.716, 0.885)	
Associated Peptides	11	
Associated Spectra	36	
Coverage	0.482	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.775	0.794
Avg..iTRAQ.Ratio....116.114.	0.78	0.619
Avg..iTRAQ.Ratio....117.114.	0.797	1.06

1 M L S V A A R S G P F A P V L S A T S R G V A G A L R P L L Q S A V P A T S E P P V L D V K R P F L C R E S L S G Q A A T R P L V A T V G L N V P A S V R Y S H
81 T D I K V P D F S D Y R R A E V L D S T K S S K E S S E A R K G F S Y L V T A T T T V G V A Y A A K N A V S Q F V S S M S A S A D V L A M S K I E I K L S D I P
161 E G K N M A F K W R G K P L F V R H R T K K E I D Q E A A V E V S Q L R D P Q H D L E R V K K P E W V I L I G V C T H L G C V P I A N A G D F G G Y Y C P C H G
241 S H Y D A S G R I R K G P A P L N L E V P T Y E F T S G D V V V V G



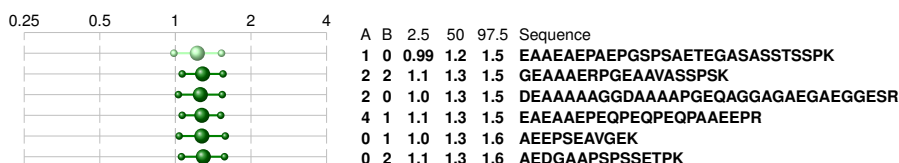
5.69 PREDICTED: similar to Myristoylated alanine-rich C-kinase substrate (MARCKS) (Protein kinase C subs

Protein Accession	gi 109510177
Mean Expression Ratio	1.25
Median Expression Ratio	1.25
Credible Interval	(1.08, 1.46)
Associated Peptides	6
Associated Spectra	15
Coverage	0.417

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.34	1.11
Avg..iTRAQ.Ratio....116.114.	1.27	1.23
Avg..iTRAQ.Ratio....117.114.	1.48	1.51

```

1      MGAQFSKTAA KGEAAAERPGEAAVASSPSK ANGQVNSTYR RKSDKSPKMA DPGQPPELXX XXXAPAADKE EPASGGAATP
81     AAADKDEAAA APESGAATAD KAAAEAEPAE PGSPSAETEG ASASSTSSPK AEDGAAPSPS SETPKKKKKR FSPKKSFKLS
161    GFSFKKSKKE AEGEGAEAGA TADGAKDEAA AAAGGDAAA PGEQAGGAGA EGAEGGESRE AEAAEPEQPE QPEQPAEEEP
241    RAEFPSEAVG EKAEFPAPGA TADDAPSAAG PEQEAPAAD EPAASAAPSA SFEPQECSP EAPPAPVAE
    
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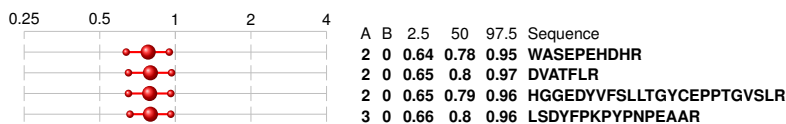


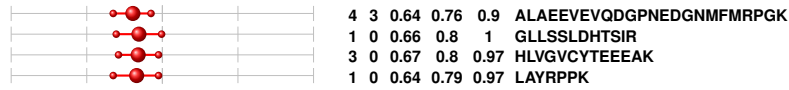
5.70 PREDICTED: similar to cytochrome c-1 [Rattus norvegicus]

Protein Accession	gij109482353
Mean Expression Ratio	0.799
Median Expression Ratio	0.799
Credible Interval	(0.698, 0.917)
Associated Peptides	8
Associated Spectra	21
Coverage	0.425
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.861
Avg..iTRAQ.Ratio....116.114.	0.654
Avg..iTRAQ.Ratio....117.114.	0.91

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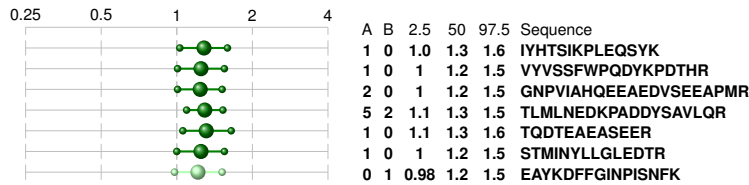
1      MLSALGMLAA GGAGLAVALH SAVSASDLEL HPPSYPWHR GLLSSLDHTS IRRGFQVYKQ VCSCHSMDY VAYRHLVGVC
81     YTEEEAKALA EEVEVDGPN EDGNMFMRPQ KLSDYFPKPY PNPEAARAAN NGALPPDLSY IVRARHGGED YVFSLLTGVC
161    EPPTGVSLRE GLYFNPFYFP QAIGMAPPYI TEVLEYDDGT PATMSQVAKD VATFLRWASE PEHDHRKRMG LKMLMMGLL
241    LPLTYAMKRH KWSVLKSRKL AYRPPK
    
```





5.71 PREDICTED: similar to sarcalumenin [Rattus norvegicus]

Protein Accession	gij109487785	
Mean Expression Ratio	1.25	
Median Expression Ratio	1.25	
Credible Interval	(1.07, 1.47)	
Associated Peptides	7	
Associated Spectra	14	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.43	1.15
Avg..iTRAQ.Ratio....116.114.	1.36	0.947
Avg..iTRAQ.Ratio....117.114.	1.62	1.18



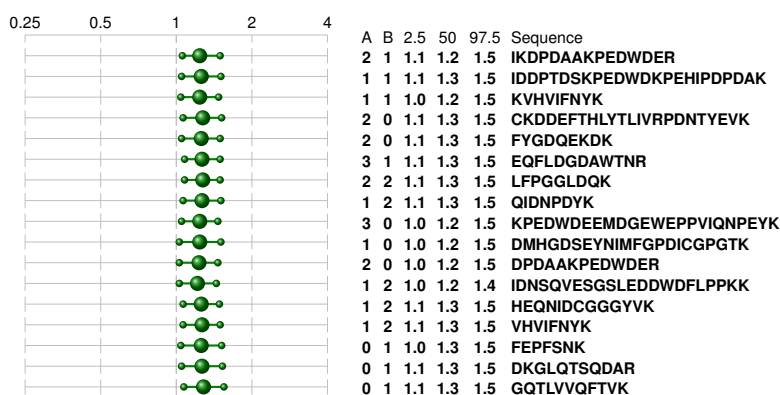
5.72 calreticulin [Rattus norvegicus]

Protein Accession	gij11693172	
Mean Expression Ratio	1.25	
Median Expression Ratio	1.25	
Credible Interval	(1.13, 1.38)	
Associated Peptides	17	
Associated Spectra	40	
Coverage	0.522	
Experiment	A	B

Avg..iTRAQ.Ratio....115.114.	1.24	1.36
Avg..iTRAQ.Ratio....116.114.	1.01	1.00
Avg..iTRAQ.Ratio....117.114.	1.32	1.73

```

1      MLLSVPLLLG LLGLAAADPA IYFKEQFLDG DAWTNRWVES KHKSDFGKFV LSSGKFYGDQ EKDKGLQTSQ DARFYALSAR
81     FEPFSNKGQT LVVQFTVKHE QNIDCGGGYV KLFPGGLDQK DMHGDSEYNI MFGPDICGPG TKKVHVIFNY KGKNVLINKD
161    IRCRDDEFTH LYTLIVRPDN TYEVKIDNSQ VESGSLEDDW DFLPPKKIKD PDAAKPEDWD ERAKIDDPD SKPEDWDKPE
241    HIPDPDAKKP EDWDEEMDGE WEPPVIQNPE YKGEWKPRQI DNPDYKGTWI HPEIDNPEYS PDANIYAYDS FAVLGLDLWQ
321    VKSGTIFDNF LITNDEAYAE EFGNETWGVV KAAEKQMKDK QDEEQRLKEE EEDKKRKEEE EAEDKKEDEDD RDEDEDEDEE
401    KEEDEEDATG QAKDEL
    
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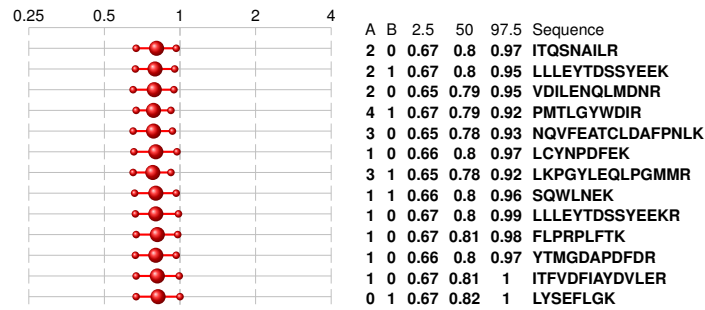


5.73 "glutathione S-transferase, mu type 3 [Rattus norvegicus]"

Protein Accession	gij13592152	
Mean Expression Ratio	0.802	
Median Expression Ratio	0.801	
Credible Interval	(0.714, 0.902)	
Associated Peptides	13	
Associated Spectra	27	
Coverage	0.61	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.799	0.825
Avg..iTRAQ.Ratio....116.114.	0.77	0.502
Avg..iTRAQ.Ratio....117.114.	0.782	1.19

```

1      MPMTLGYWDI RGLAHAIRLL LEYTDSSYEE KRYTMGDAPD FDRSQWLNEK FKLGLDFPNL PYLIDGSHKI TQSNAILRYL
81     GRKHNLGGET EEERIRVDIL ENQLMDNRMV LARLCYNPDF EKLPBGYLEQ LPGMMRLYSE FLGKRPFVAG DKITFVDFIA
161    YDVLERNQVF EATCLDAFFN LKDFIARFEG LKKISDYMKS SRFLPRPLFT KMAIWGSK
    
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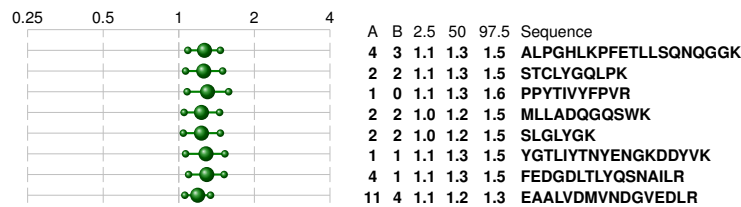


5.74 "glutathione S-transferase, pi [Rattus norvegicus]"

Protein Accession	gij25453420	
Mean Expression Ratio	1.25	
Median Expression Ratio	1.25	
Credible Interval	(1.12, 1.39)	
Associated Peptides	8	
Associated Spectra	42	
Coverage	0.519	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.16	1.11
Avg..iTRAQ.Ratio....116.114.	1.21	1.29
Avg..iTRAQ.Ratio....117.114.	1.28	1.48

```

1      MPPYTIYFYP VRGRCEATRM LLADQGQSWK EEVVTIDVWL QGSLKSTCLY GQLPKFEDGD LTLYQSNAIL RHLGRSLGLY
81     GKDQKEAALV DMVNDGVEDL RCKYGTLIYT NYENKDDYV KALPGHLKPF ETLLSQNGGG KAFIVGNQIS FADYNLLDLL
161    LVHQVLAPGC LDNFPLLSAY VARLSARPKI KAFLLSSPDHL NRPINGNGKQ
    
```



5.75 PREDICTED: similar to 60S ribosomal protein L38 isoform 1 [Rattus norvegicus]

Protein Accession	gij109484773
Mean Expression Ratio	1.25
Median Expression Ratio	1.25
Credible Interval	(0.92, 1.7)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0857
Experiment	A
Avg..iTRAQ.Ratio....115.114.	2.34
Avg..iTRAQ.Ratio....116.114.	3.39
Avg..iTRAQ.Ratio....117.114.	2.71

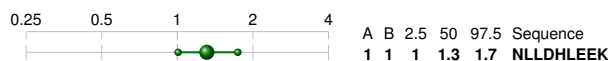
1 MPRKIEEIKD FLTARRKDA KSVKIKKND NVKFKVRCR YLYTLVITDK EKAELKQSL PPGLAVKELK



5.76 natriuretic peptide precursor type A [Rattus norvegicus]

Protein Accession	gij6981278	
Mean Expression Ratio	1.25	
Median Expression Ratio	1.25	
Credible Interval	(0.95, 1.62)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.0592	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.65	2.08
Avg..iTRAQ.Ratio....116.114.	1.12	1.8
Avg..iTRAQ.Ratio....117.114.	1.91	1.81

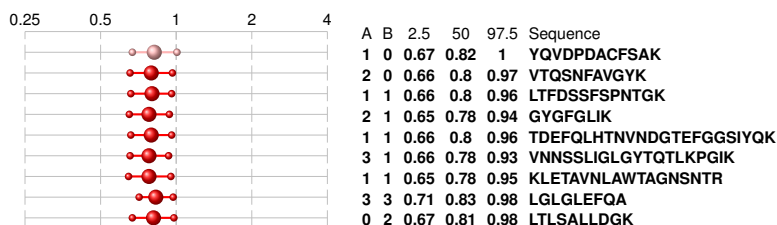
1 MGSFSITKGF FLFLAFWLPG HIGANPVYSA VSNTDLMDFK NLLDHLLEEKM PVEDEVMPQ ALSEQTDEAG AALSSLSEVP
81 PWTGEVNPSQ RDGGALGRGP WDFSDRSALL KSKLRALLAG PRSLRRSSCF GGRIDRIGAQ SGLGCNSFRY RR



5.77 voltage-dependent anion channel 1 [Rattus norvegicus]

Protein Accession	gij13786200	
Mean Expression Ratio	0.803	
Median Expression Ratio	0.803	
Credible Interval	(0.707, 0.908)	
Associated Peptides	9	
Associated Spectra	24	
Coverage	0.438	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.747	0.811
Avg..iTRAQ.Ratio....116.114.	0.886	0.583
Avg..iTRAQ.Ratio....117.114.	0.807	0.718

1 MAVPPTYADL GKSARDVFTK **GYGFGLIKLD** LKTKSENGLE FTSSGSANTE TTKVNGSLET KYRWTEYGLT FTEKWNTDNT
 81 LGTEITVEDQ LARGLK**LTFD** **SSFSPNTGKK** NAKIKTGYSR EHINLGCDVD FDIAGPSIRG ALVLGYEGWL AGYQMNPFETS
 161 KSRV**TQSNFA** **VGYKTDEFQL** HTNVNDGTEF **GGSIYQKVNK** **KLETAVNLAW** TAGNSNTRFG IAAKYQVDPD **ACFSAKVNNS**
 241 **SLIGLGYTQT** LKPGIKLTL**S** ALLDGKNVNA GGHKLG**LGLF** **FQA**



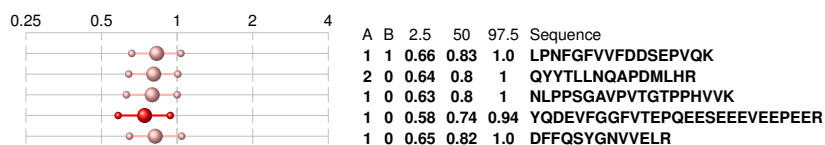
5.78 PREDICTED: similar to Ras-GTPase-activating protein binding protein 1 (ATP-dependent DNA helicase V)

Protein Accession	gij109488113	
Mean Expression Ratio	0.805	
Median Expression Ratio	0.805	
Credible Interval	(0.662, 0.971)	

Associated Peptides	5	
Associated Spectra	7	
Coverage	0.173	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.768	0.89
Avg..iTRAQ.Ratio....116.114.	0.703	0.887
Avg..iTRAQ.Ratio....117.114.	0.803	0.906

```

1      MGFTSPKTYG PTLWINRSCL DTRLVSGRRA RVPRHRARDA ATSSHAAALS SRSAQVEST KAMVMEKPS P LLVGREFVRQ
81     YYTLLNQAPD MLHR FYGKNS SYAHGGLDSN GKPADAVYGO KEIHRKVM SQ NFNCHTKIR HVDAAHATLND GVVVQVMGLL
161    SNNNQALRRF MQTFVLAPEG SVANKFYVHN DIFRYQDEVF GGFVTEPQEE SEEEVEEPEE RQQSPEVVAD DSGTFYDQTV
241    SNDLEEHL EE PVVEPEPEPE PEPEPEPVSD IQEDKPEPAL EEAAPEDVQK SASPAPADVA PAQEDLRTFS WASVTSK NLP
321    PSGAVPVVGT PPHVVKVPAS QPRPESKPDS QIPPQRPQRD QRAREQRINI PPQRGPRPIR EAGEPGDVPE RRMVHRPDSH
401    QLFIGNLPHE VDKSELKDFP QSYGNVVELR INSGGKLPNF GFFVFDSE P VQKVLNRRPI MFRGAVRLNV EEKTRAARE
481    GDRRDNRRLG PGGPRGGPSG GMRGPPRGGM VQKPGFVGR GITTPRQ
  
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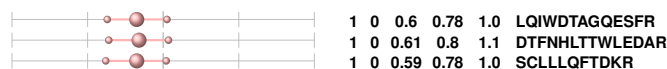
5.79 "RAB2, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gij13929006
Mean Expression Ratio	0.803
Median Expression Ratio	0.805
Credible Interval	(0.63, 1.03)
Associated Peptides	3
Associated Spectra	3
Coverage	0.179
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.637
Avg..iTRAQ.Ratio....116.114.	0.584
Avg..iTRAQ.Ratio....117.114.	0.773

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1      MAYAYLFKYI IIGDTGVGKS CLLLQFTDKR FQPVHDLTMG VEFGARMITI DGKQIKLQIW DTAGQESFRS ITRSYYRGAA
81     GALLVYDITR RDTFNHLTTW LEDAQHSNS NMVIMLIGNK SDLESRRVVK KEEGEAFARE HGLIFMETS A KTASNVEEAF
161    INTAKEIYEK IQEGVFDINN EANGIKIGPQ HAATNASHGG NQGGQQAGGG CC
  
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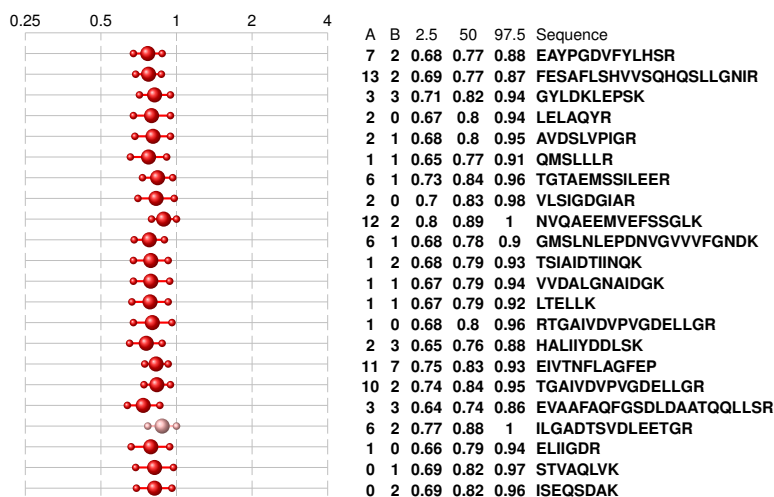


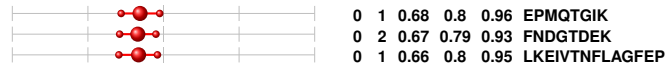
5.80 "ATP synthase, H⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Rattus norvegicu"

Protein Accession	gij40538742	
Mean Expression Ratio	0.805	
Median Expression Ratio	0.806	
Credible Interval	(0.753, 0.86)	
Associated Peptides	25	
Associated Spectra	132	
Coverage	0.495	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.843	0.728
Avg..iTRAQ.Ratio....116.114.	0.892	0.6
Avg..iTRAQ.Ratio....117.114.	0.862	0.744

```

1      M L S V R I A A A V  A R A L P R R A G L  V S K N A L G S S F  V G T R N L H A S N  T R L Q K T G T A E  M S S I L E E R I L  G A D T S V D L E E  T G R V L S I G D G
81     I A R V H G L R N V  Q A E E M V E F S S  G L K G M S L N L E  P D N V G V V V F G  N D K L I K E G D I  V K R T G A I V D V  P V G D E L L G R V  V D A L G N A I D G
161    K G P V G S K I R R  R V G L K A P G I I  P R I S V R E P M Q  T G I K A V D S L V  P I G R G Q R E L I  I G D R Q T G K T S  I A I D T I I N Q K  R F N D G T D E K K
241    K L Y C I Y V A I G  Q K R S T V A Q L V  K R L T D A D A M K  Y T I V V S A T A S  D A A P L Q Y L A P  Y S G C S M G E Y F  R D N G K H A L I I  Y D D L S K Q A V A
321    Y R Q M S L L L R R  F P G R E A Y P G D  V F Y L H S R L L E  R A A K M N D S F G  G G S L T A L P V I  E T Q A G D V S A Y  I P T N V I S I T D  G Q I F L E T E L F
401    Y K G I R P A I N V  G L S V S R V G S A  A Q T R A M K Q V A  G T M K L E L A Q Y  R E V A A F A Q F G  S D L D A A T Q Q L  L S R G V R L T E L  L K Q G Y S P M A
481    I E E Q V A V I Y A  G V R G Y L D K L E  P S K I T K F E S A  F L S H V V S Q H Q  S L L G N I R S D G  K I S E Q S D A K L  K E I V T N F L A G  F E P
    
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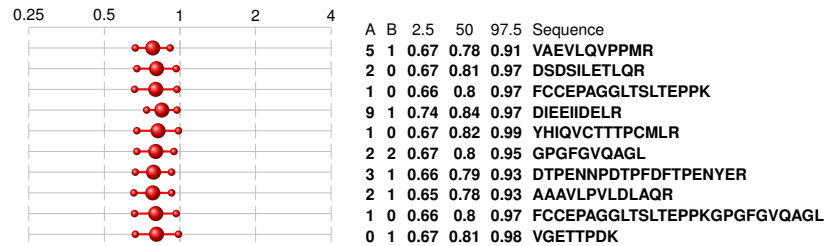




5.81 NADH dehydrogenase (ubiquinone) flavoprotein 2 [Rattus norvegicus]

Protein Accession	gj 51092268	
Mean Expression Ratio	0.806	
Median Expression Ratio	0.807	
Credible Interval	(0.721, 0.902)	
Associated Peptides	10	
Associated Spectra	33	
Coverage	0.46	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.86	0.657
Avg..iTRAQ.Ratio....116.114.	0.914	0.997
Avg..iTRAQ.Ratio....117.114.	0.695	0.616

1 MFSLALRARA SGLTAQWGRH ARNLHKTAVQ NGAGGALFVH RDTPENNDT PFDFTPENYE RIEAIVRNYP EGHRAAVLP
 81 VLDLAQRQNG WLPISAMNKV AEVLQVPPMR VYEVATFYTM YNRKPVGKYH IQVCTTPCM LRSDSILET LQRKLGKIVG
 161 ETPDKLFTL IEVECLGACV NAPMVQINDD YYEDLTPKDI EEIIDELRAG KVPKPGPRSG RFCCEPAGGL TSLTEPPKGP
 241 GFGVQAGL



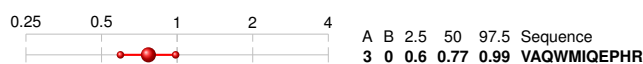
5.82 adenosine kinase [Rattus norvegicus]

Protein Accession	gj 52345435	
Mean Expression Ratio	0.808	
Median Expression Ratio	0.808	
Credible Interval	(0.629, 1.04)	
Associated Peptides	1	

Associated Spectra	3
Coverage	0.0305
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.785
Avg..iTRAQ.Ratio....116.114.	0.659
Avg..iTRAQ.Ratio....117.114.	0.555

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1      MAAADEPKPK KKKVEAPEAL SENVLFMGMN PLLDISAVVD KDFLDKYSLK PNDQILAEDK HKELFDELVK KFKVEYHAGG
81     STQNSMKVAQ WMIQEPHRAA TFFGCIGIDK FGEILKSKAA DAHVDAHYYE QNEQPTGTCA ACITGGNRSL VANLAAANCY
161    KKEKHLLEN NWMLVEKARV YYIAGFFLTV SPESVLKVAR YAAENNRFTT LNSAPFFISQ FFKEALMEVM PYVDILFGNE
241    TEAATFAREQ GFETKDIKEI ARKTQALPKV NSKRQRTVIF TQGRDDTIVA TGNDVTAFPV LDQNQEEIVD TNGAGDAFVG
321    GFLSQLVSNK PLTECIRAGH YAASVIIRRT GCTFPEKPNF H
  
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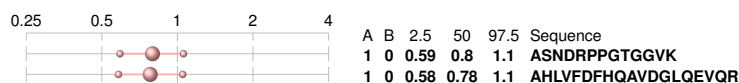


5.83 "PREDICTED: similar to Adenylosuccinate synthetase isozyme 1 (Adenylosuccinate synthetase, muscle is"

Protein Accession	gij109479986
Mean Expression Ratio	0.809
Median Expression Ratio	0.809
Credible Interval	(0.619, 1.05)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0816
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.547
Avg..iTRAQ.Ratio....116.114.	0.604
Avg..iTRAQ.Ratio....117.114.	0.614

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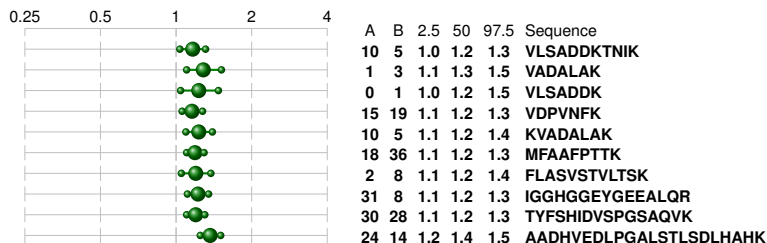
1      MSGTRASNDR PPGTGGVKRG RLQQEAAATG SRVTVVLGAQ WGDEGKGVV DLLATDADIV SRCQGGNAG HTVVVDGKEY
81     DFHLLPSGII NTKAVSFIGN GVVHLPGLF EEAENEKKG LKDWEKRLII SDRAHLVDFD HQAVDGLQEV QRQAQEGKNI
161    GTTKKGIGPT YSSKAARTGL RICDLLSDFD EFSARFKNLA HQHQSMFPTL EIDVEGQLKR LKGFAERIRP MVRDGVYFMY
241    EALHGPPKI LVEGANAALL DIDFGTYPFV TSSNCTVGGV CTGLGIPPQN IGDVYGVVKA YTRVVGIGAF PTEQINEIGD
321    LLQNRGHEWG VTTGRKRRCG WLDLMILRYA HMVNGFTALA LTKLDILDVL SEIKVGISYK LNGKRIPYFP GM
  
```



5.84 hemoglobin alpha 1 chain [Rattus norvegicus]

Protein Accession	gij 6981010	
Mean Expression Ratio	1.24	
Median Expression Ratio	1.24	
Credible Interval	(1.15, 1.33)	
Associated Peptides	10	
Associated Spectra	268	
Coverage	0.704	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.27	1.61
Avg..iTRAQ.Ratio....116.114.	1.15	1.09
Avg..iTRAQ.Ratio....117.114.	0.848	0.697

1 MVL SADDKTN IKNCWGKIGG HGGEYGEEAL QRMFAAFPTT KTYFSHIDVS PGSAQVKAHG KKVADALAKA ADHVEDLPGA
 81 LSTLSDLHAH KLRVDPVNFK FLSHCLLVTL ACHHPGDFTP AMHASLDKFL ASVSTVLTSK YR



5.85 PREDICTED: similar to tensin [Rattus norvegicus]

Protein Accession	gij 109487302	
Mean Expression Ratio	1.24	
Median Expression Ratio	1.23	
Credible Interval	(1.10, 1.38)	
Associated Peptides	14	
Associated Spectra	29	
Coverage	0.123	

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.40	2.19
Avg..iTRAQ.Ratio....116.114.	1.25	0.95
Avg..iTRAQ.Ratio....117.114.	1.36	1.82

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1      MSFSFTGLHQ  NYPPSTNSDK  YHYDSHSSCG  SQSLLTVAED  RQASVMVPRG  QRSRPLFDHH  WEKILPQQPN  IWGRAVPRRP
81     IATESVPKNV  VDVGEGDCRG  GSTPKNLEEA  VSMRRVGAKG  EPGEEQGVVL  AVGTVGAVDG  TRPYHLTAAW  PLGSMRVSPS
161    IQPQPQPQPQ  FIRYLAHGEG  VGYGHSCVPS  WILRLMLYSP  SERPGVGGPW  PSSLLSRNLS  VSRAMEDSCE  LDLVYITERI
241    IAVSFPS TAN  EENFRSNLRE  VAQMLKSKHG  GNYLLFNLSE  QRPDITKLHA  KVLEFGWDDL  HTPALEKICS  VCKAMD T WLN
321    ADPHNVVVLH  NKGNRGRIGV  VIAAYMHYSN  ISASADQALD  RFAMKR FYED  KIVPIGQPSQ  RRYVHYFSGL  LSGSIKMNNK
401    PFLPHHVIMH  GIPNFESKGG  CRPFLRIYQA  MQPVYTSGIY  NIPGDSQASI  CITIEPGLLL  KGDILLKCYH  KKFRSPARDV
481    IFRVQFH TCA  IHDLGVVFGK  EDLDEAFKDD  RFPDYGKVEF  VFSYGPEKIQ  GMEHLENGPS  VSVDYNTSDP  LIRWDSYDNF
561    NGHREDG MEE  VVGHTQGPLD  GSLYAKVKKK  DSLNGSSGPI  TTARPALSAT  PNHVEHTLSV  SSDSGNSTAS  TKTKDTDEPV
641    SGA AIAPAAL  SPQEKKELDR  LLSGFGVDRE  KQGAMYRAQQ  LRSHPGGGPT  VSSPGRHIVP  AQVHVNGGAL  ASERETDILD
721    DELPIQDQGS  GSGMGTLSL  DGVTTNTSEGG  YPETLSPLTN  GLDKPYPTPEP  ILNGGGYPYE  SANRVVPVHS  SHSAPIRPSY
801    SAQEGGLGGYQ  REGPHPAWSK  QVTSAHRGYD  PSGLFRSQSF  PDVEPQLPQA  PARGGSSREA  VQRGLNSWQQ  QQQQQQQQQQ
881    QQQQQQQQQP  HPPPRQQERS  PLQSLACSKP  SPHLSAETPI  PALPEFPRAA  SQQEIEQSIE  TLNMLMDLE  PASAAAPLHK
961    SQSVPGAWFG  ASPLSSQPLL  GSSCQSHPLT  QSRSGYIPSG  DTLGAPELLS  SGRSYSPYDY  QLHPAASNQS  FRPKSPASST
1041   FLPSPHSSAG  PQEPPASLPG  LIAEPQLPLK  ETTSDTSRTP  EEEPLNLEGL  VAHRVAGVQA  RERQPAEPPA  PLRRAASDGG
1121   QYENQSPEAT  SPRSPGVRSP  VQCVSPELAL  TIALNPGRRP  KEPHLHSYKE  AFEEMEGTSP  SSPPPSVARS  PPGLAKTPLS
1201   ALGLKPHNPA  DILLHPTGVA  RRLIQPEEDE  GEEVAKPPEE  PRSYVESVAR  TAVAGPRAQD  VEPKSF SAPA  THAYGHETPL
1281   RNGTHPGGSFV  SPSP LSTSSP  ILSADSTSVG  SFP SAGSSDQ  GPRTP IQPML  DSSIRSGSLG  QPSPAALSYQ  SSSPVVGGGS
1361   SYSSPDYSLQ  PFS SSPESQ  QPHFSAASVH  M VPGSPQARH  RTVGTNTPPS  PGFGRRALNP  TMAAPGSPSL  SHQVMG P SG
1441   PGFHGNV VSG  HPTSATVAPG  SP SLGRHPVG  SHQVPG LHS  VVTTPGSPSL  GRHPGAHQGN  LVSSSLHGNAV  ISPGSPSLGR
1521   HLGSGSVVVP  GSPSLDRHVA  YGGYSTPEDR  RPTLSRQSSA  SGYQAPSTPS  FVPVPAIYPG  LSSPATSPSP  DSAAFRQGSF
1601   TPALPEKRRM  SVGD RAGSLP  NYATINGKVS  SSPVANGMAS  PSGSSTVSFS  HTLPDFSKYS  MPDNSPETRA  KVKFVQDTSK
1681   YWYKPEISRE  QAIALLKDQE  PGAFIIRDSH  SFRGAYGLAM  KVSSPPPTIT  QQKKGDMTH  ELVRHFLIET  GPRGVKLGKC
1761   PNEPNFGLS  ALVYQHSVIP  LALPCKLVIP  SRDPTDESKD  SSGPANSTTD  LLKQGAACNV  LFINSVDMES  LTGPQAISKA
1841   TSETLAADPT  PAATVHFV  SAQGITLTDN  QRKLFRRHY  PLNTVTFCDL  DPQERKWMKT  EGGAPAKLFG  FVARKQGGST
1921   DNACHLFAEL  DPNQPASAI  V  NFVSKVMSLA  GQKR
  
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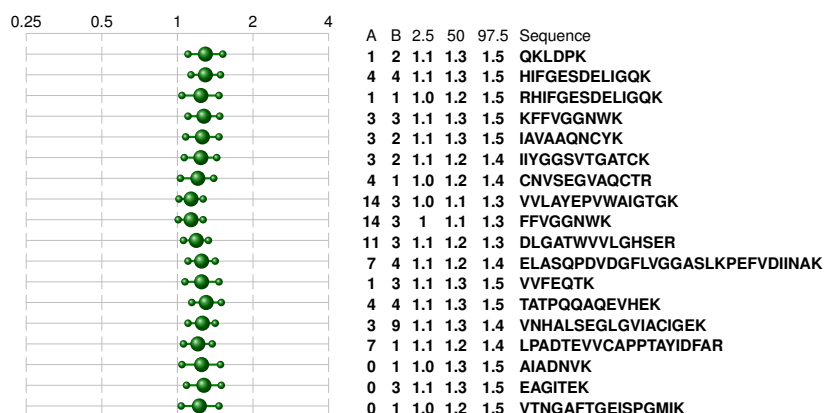
5.86 triosephosphate isomerase 1 [Rattus norvegicus]

Protein Accession	gi 117935064
Mean Expression Ratio	1.23
Median Expression Ratio	1.23
Credible Interval	(1.15, 1.32)

Associated Peptides	18	
Associated Spectra	130	
Coverage	0.843	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.11	1.4
Avg..iTRAQ.Ratio....116.114.	1.21	1.22
Avg..iTRAQ.Ratio....117.114.	1.17	1.15

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1      MAPSRKFFVG GNWKMNGRKK CLGELICTLN AAKLPADTEV VCAPPTAYID FARQKLDPKI AVAAQNCYKV TNGAFTGEIS
81     PGMIKDLGAT WVVLGHSERR HIFGESDELI GQKVNHALSE GLGVIACIGE KLDEREAGIT EKVVFEQTKA IADNVKDCK
161    VVLAYEPVWA IGTGKTATPQ QAQEVHEKLR GWLKC NVSEG VAQCTRIIYG GSVTGTATCKE LASQPDVDGF LVGGASLKPE
241    FVDIINAKQ
  
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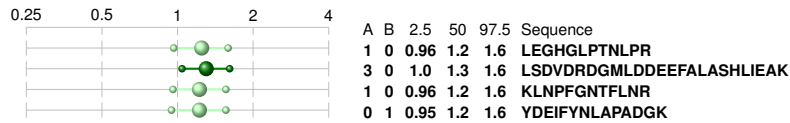


5.87 EH-domain containing 2 [Rattus norvegicus]

Protein Accession	gi 67846074	
Mean Expression Ratio	1.23	
Median Expression Ratio	1.23	
Credible Interval	(1.00, 1.51)	
Associated Peptides	4	
Associated Spectra	6	
Coverage	0.116	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.65	0.936
Avg..iTRAQ.Ratio....116.114.	1.19	0.995
Avg..iTRAQ.Ratio....117.114.	1.84	1.13

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1      MFSWLKKGGA  RGQRSEAIRT  VTSSLKELYR  TKLLPLEEHY  RFGSFHSPAL  EDADFDGKPM  VLVAGQYSTG  KTSFIQYLLE
81     QEVPGSRVGP  EPTTDCFVAV  MHGETEGTVP  GNALVVDPEK  PFRKLNPPGN  TFLNFMCAQ  LPNQVLESIS  IIDTPGILSG
161    AKQVRSRGYD  FPAVLRWFAB  RVDLIILLFD  AHKLEISDEF  SEAIGALRGH  EDKIRVVLNK  ADMVETQQLM  RVYGALMWAL
241    GKVVGTPEVL  RVIYIGSFSQ  PLLVPDNRRL  FELEEQDLFR  DIQGLPRHAA  LRKLNLDLVR  ARLVRVHAYI  ISYLKKEmps
321    VFGKENKKKQ  LIFKLPVIFA  KIQLHHHISP  GDFPDCQKMQ  ELLMAHDFTK  FHSCLKPKLE  ALDEMLTHDI  AKLMPLLRQE
401    ELESVEAGVQ  GGAFAEGTRM  PFVERGPDEA  IEDGEEGSED  DAEWVVTKDK  SKYDETFYNL  APADGKLSGS  KAKTWMVGTK
481    LPNSVLGRIW  KLSVDVRDGM  LDDEEFALAS  HLIKLEKLEGH  GLPTNLPRRL  VPPSKRRQKG  SAE
    
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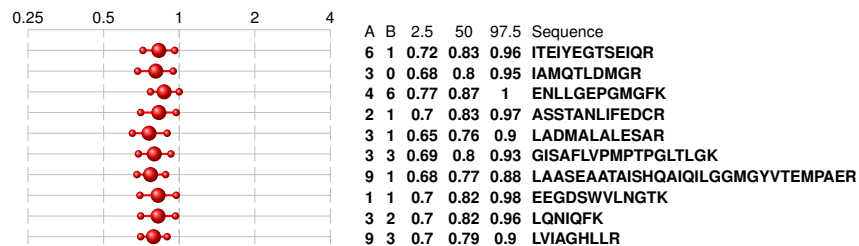


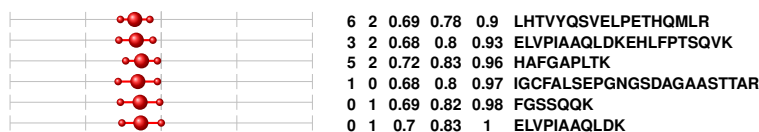
5.88 "acyl-coenzyme A dehydrogenase, short chain [Rattus norvegicus]"

Protein Accession	gij11968090	
Mean Expression Ratio	0.813	
Median Expression Ratio	0.813	
Credible Interval	(0.751, 0.879)	
Associated Peptides	16	
Associated Spectra	85	
Coverage	0.519	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.895	0.827
Avg..iTRAQ.Ratio....116.114.	0.792	0.687
Avg..iTRAQ.Ratio....117.114.	0.661	1.05

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1      MAMAAALLAR  AGGSLGRALR  ARDWRRLLHTV  YQSVELPETH  QMLRQTCRDF  AEKELVPIAA  QLDKEHLFPT  SQVKKMGEIG
81     LLAMDVPEEL  SGAGLDYLAY  SIALEEISRG  CASTGVIMSV  NNSLYLGPIL  KFGSSQKQKQ  WITPFTNGDK  IGCFALSEPG
161    NGS DAGAAS TAREEGDSWV  LNGTKAWITN  SWEASATVVF  ASTDRSRQNK  GISAFVPMPT  TPGLTLGKKE  DKLGIASST
241    ANLIFEDCRI  PKENLLGEPG  MGFKIAMQTL  DMGRIGIASQ  ALGIAQASLD  CAVKYAENRH  AFGAPLTKLQ  NIQFKLADMA
321    LALESARLLT  WRAAMLKDNK  KPFTKESAMA  KLAASEAATA  ISHQAIQILG  GMGYVTEMPA  ERYRDRARIT  EIYEGTSEIQ
401    RLVIAGHLLR  SYRS
    
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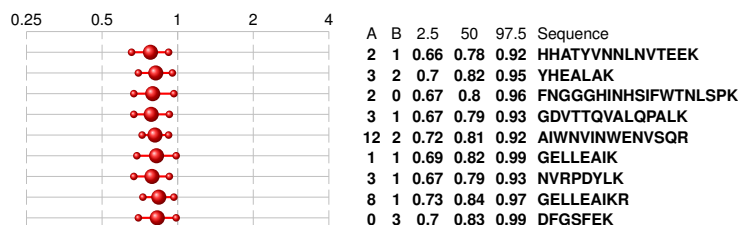


5.89 superoxide dismutase 2 [Rattus norvegicus]

Protein Accession	gij8394331	
Mean Expression Ratio	0.813	
Median Expression Ratio	0.813	
Credible Interval	(0.734, 0.9)	
Associated Peptides	9	
Associated Spectra	46	
Coverage	0	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.894	0.702
Avg..iTRAQ.Ratio....116.114.	0.867	0.814
Avg..iTRAQ.Ratio....117.114.	0.748	0.667

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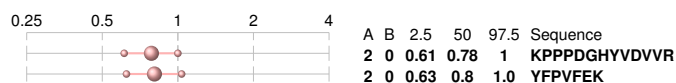
1      MSITPDTRVD LDRFWSTIEA SGEIGKGRPG GLSRLTLGDA DRDMRDLFRS WCEEAGLTVE VDAAGNIFGR RDGSDNDLPP
81     ILIGSHLDTQ INGGRFDGIA GVLAGLEVIR CLNDAGHVTK RPIVVVDWTN EEGARFSPPM VASGCFVGKY DIDWVHDLIG
161    DDGARFGDEL ERIGYNGERA CKAGEIDAYF ELHIEQGPIL DAEKRQVGIV TGGYPVRGMR ASFKGQTSHT GPTPMDLRKN
241    ALAAGARWLT AVDDIGWDFV VHDGKATAAR LTAWPNKPGI LSDTAEAVCD VRHPDPITTR AMAEKMRRL FESAARCGCE
321    AVIEDEWEWG GDIFDHMID GIRDEAIRMG FNWRDIESQA GHDAYFLATH CPTAMIFAPC ENGITHNNEE NCTPEDFVAG
401    LNILLHAVVK RADR
    
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5.90 PREDICTED: similar to Glutathione S-transferase alpha-4 (Glutathione S-transferase Yk) (GST Yk) (GS

Protein Accession [gij27720723](#)

Mean Expression Ratio	0.815
Median Expression Ratio	0.815
Credible Interval	(0.644, 1.02)
Associated Peptides	2
Associated Spectra	4
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.778
Avg..iTRAQ.Ratio....116.114.	0.772
Avg..iTRAQ.Ratio....117.114.	0.63



5.91 apolipoprotein C-I [Rattus norvegicus]

Protein Accession	gi 6978521
Mean Expression Ratio	0.818
Median Expression Ratio	0.817
Credible Interval	(0.637, 1.05)
Associated Peptides	2
Associated Spectra	3
Coverage	0.205
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.63
Avg..iTRAQ.Ratio....116.114.	1
Avg..iTRAQ.Ratio....117.114.	0.556

1 MRLFIALPVL IVVVAMALEG PAPAQAAPDF SSAMESLPDK LKEFGNTLED KARAIEHIK QKEIMIKTRN WFSETLNKMK
81 EKLKTTFA



5.92 cysteine-rich protein 3 [Rattus norvegicus]

Protein Accession	gij16924004	
Mean Expression Ratio	1.22	
Median Expression Ratio	1.22	
Credible Interval	(1.1, 1.36)	
Associated Peptides	10	
Associated Spectra	42	
Coverage	0.655	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.32	1.08
Avg..iTRAQ.Ratio....116.114.	1.15	1.26
Avg..iTRAQ.Ratio....117.114.	1.59	0.936

1 MPNWGGGAKC GACDKTVYHA EEIQCNRSF HKTCFHCMAC RKALDSTTVA AHSESIYCKV CYGRKYGPKG IGFQQGAGCL
 81 STDTGEHLGL QFOQSPKPAR AATTSNPSKF SAKFGESEKC PRCGKSVYAA EKVMGGGKPW HKTCFPKAIC GKSLESTNVT
 161 DKDGELYCKV CYAKNFGPTG IGFGLTHQV EKKE



5.93 PREDICTED: similar to Secretory carrier-associated membrane protein 3 (Secretory carrier membrane p

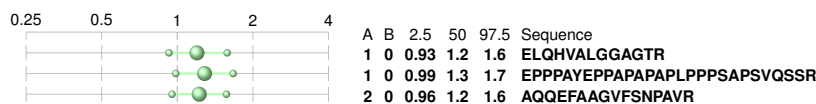
Protein Accession	gij109467015	
Mean Expression Ratio	1.22	
Median Expression Ratio	1.21	
Credible Interval	(0.969, 1.52)	
Associated Peptides	3	
Associated Spectra	4	
Coverage	0.163	

Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.43
Avg..iTRAQ.Ratio....116.114.	1.52
Avg..iTRAQ.Ratio....117.114.	1.60

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1      MAQNRDGGNP  FPDSGELDNP  FQDPAVIQHR  PSQQYATLDV  YNPFENREPP  PAYEPPAPAP  APLPPPSAPS  VQSSRKLSPA
81     EPKNYGSYST  QATAAAATAE  LLKKQEELNR  KAEBLDRRER  ELQHVALGGA  GTRQNNWPP  PSFCPVQPCF  FQDISMEIPQ
161    EFQKTVSTMY  YLWMCSTLAL  LLNFFACLAR  FCVDTGSGSG  FGLSMLWLLL  FTPCSFVCWY  RPMYKAFRSD  SSFNFFVFFF
241    IFFVQDVFV  LQAIGIPGW  FSGWVSALV  VGSNPAVAVL  MLLVALLFTG  IAVLGIVMLK  RIHSLYRQTG  ASFQAQQEF
321    AAGVFSNPAV  RTAAANAAAG  AAENAFRAP

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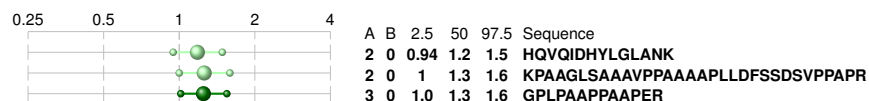
5.94 reticulon 4 [Rattus norvegicus]

Protein Accession	gi 13929188
Mean Expression Ratio	1.21
Median Expression Ratio	1.21
Credible Interval	(0.998, 1.47)
Associated Peptides	3
Associated Spectra	7
Coverage	0.0507
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.23
Avg..iTRAQ.Ratio....116.114.	1.38
Avg..iTRAQ.Ratio....117.114.	1.61

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1      MEDIDQSSLV  SSSDTPPPR  PPAFKYQFVT  EPEDEEDEEE  EDEEEEDDED  LEELEVLER  PAAGLSAAAV  PPAAAAPLLD
81     FSSDSVPPAP  RGPLPAAPPA  APERQPSWER  SPAAPAPSLP  PAAAVLPSKL  PEDDEPPARP  PPPPPAGASP  LAEPAAPPST
161    PAAPKRRGSG  SVDETLFALP  AASEPVISS  AEKIMDLMEQ  PGNTVSSGQE  DFPSVLLETA  ASLPSLSPLS  TVSRKEHGYL
241    GNLSAVSSSE  GTIETLNEA  SKELPERATN  PFVNRDLAEF  SELEYSEMGS  SFKGSPKGES  AILVENTKEE  VIVRSKDED
321    LVCSAALHSP  QESPVGKEDR  VVSPEKTMDI  FNEMQMSVVA  PVREYYADFK  PFEQAWEVKD  TYEGSRDVL  ARANVESKVD
401    RKCLEDSLQ  KSLGKDSEGR  NEDASFPSTP  EPVKDSSRAY  ITCASFTSAT  ESTTANTFPL  LEDHTSENKT  DEKKIEERKA
481    QIITEKTSKP  TSNPFLVAVQ  DSEADYVTTD  TLSKVTEAAV  SNMPEGLTPD  LVQEACESEL  NEATGTKIAY  ETKVDLVQTS
561    EAIQESLYPT  AQLCPSFEEA  EATPSPVLPD  IVMEAPLNSL  LPSAGASVVQ  PSVSPLEAPP  PVSYSIKLE  PENPPPYEEA
641    MNVALKALGT  KEGIKEPESE  NAAVQETEAP  YISIACDLIK  ETKLSTEPSP  DFSNYSEIAK  FEKSVPEHAE  LVEDSSPESE
721    PVDLFSDDSI  PEVPQTQEEA  VMLMKESLTE  VSETVAQHKE  ERLSASPQEL  GKPYLESFQP  NLHSTKDAAS  NDIPTLTRKE
801    KISLQMEEFN  TAIYSNDDL  SSKEDKIKES  ETFSDSSPIE  IIDEFFPTFVS  AKDDSPKLAK  EYTDLEVSDK  SEIANIQSGA
881    DSLPCLELPC  DLSFKNIYPK  DEVHVSDEFS  ENRSSVSKAS  ISPSNVSALE  PQTEMGSIK  SKSLTKEAEK  KLPDSTEKED
961    RSLSAVLSAE  LSKTSVVDLL  YWRDIKKTGV  VFGASLFLLL  SLTVFSIVSV  TAYIALALLS  VTISFRIYKG  VIQAIQKSD
1041   GHPFRAYLES  EVAISEELVQ  KYSNSALGHV  NSTIKELRRL  FLVDDLVDL  KFAVLMWVFT  YVGALFNGLT  LLILALISLF
1121   SIPVIYERHQ  VQIDHYLGLA  NFSVKDAMAK  IQAKIPGLKR  KAD

```



5.95 hypothetical protein LOC498174 [Rattus norvegicus]

Protein Accession	gi 62945328
Mean Expression Ratio	0.825
Median Expression Ratio	0.824
Credible Interval	(0.608, 1.11)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0569
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.658
Avg..iTRAQ.Ratio....116.114.	0.306
Avg..iTRAQ.Ratio....117.114.	0.567

1 MAARVLLARG GLLRPAAPGS FLPGLRRVTS SGHRAREDSW LKSLFVRKVD PRKDAHSNLL AKKETSSLYK LQFHNVKPEC
 81 LDAYNKICQE VLPKIHEDKQ YPCTLVGTWN TWYGEQDQAV HLWRYEGGYP ALTEVMNKLR ENQEFVSFRK ARSDMLLSRK
 161 NQLLLEFSFW NEPVPRSGPN IYELRSYQLR PGTMIWGN YWARAIRFRQD SNEAVGGFFS QIGQLYMHVH LWAYKDLQTR
 241 EDIRNAAWHK HGWEELVYYT VPLIQEMESR IMIPLKTSPL Q



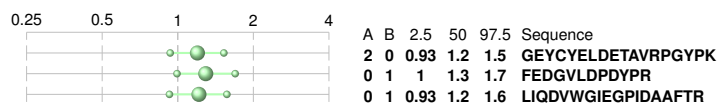
5.96 vitronectin [Rattus norvegicus]

Protein Accession	gi 9507241	
Mean Expression Ratio	1.21	
Median Expression Ratio	1.21	
Credible Interval	(0.964, 1.53)	
Associated Peptides	3	
Associated Spectra	4	
Coverage	0.100	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.16	1.16
Avg..iTRAQ.Ratio....116.114.	1.07	1.91

Avg..iTRAQ.Ratio....117.114. 1.25 2.4

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1 MASLRPFIL ALLALVSLAD QESCKGRCTQ GFMASKKCQC DELCTYYQSC CVDYMEQCKP QVTRGDVFTM PEDEYWSYDY
81 PEETKNSTNA GVQSENTSLH FNLKPRAEET IKPTTDPDQE QSNTQEPEVG QQGVAPRPDT TDEGTSEFPE EELCSGKPFD
161 AFTDLKNGSL FAFR GEYCYE LDEIAVRPGY PKLIQDVWGI EGPIDAAFR INCQGKTYLF KGSQYWR FED GVLDPDYPRN
241 ISEGFSGIPD NVDAALALPA HSYSGRERVY FFKGKQYWEY EFQQQPSQEE CEGSSLSAVF EHFALLQRDS WENIFELLFW
321 GRSSDGAKEP QFISRDWHGV PGKVDAAMAG RIYITGSTFR SVQAKKQKSG RRSRKRYSR RGRGHSRSRS RMSSSRRPSR
401 SVWFSLLSSE ESGLGTNYD YDMNWLIPT CEPIQSVYFF SGDKYYRVNL RTRRVDSVNP PYPRSIQYW LGCPTSEK
    
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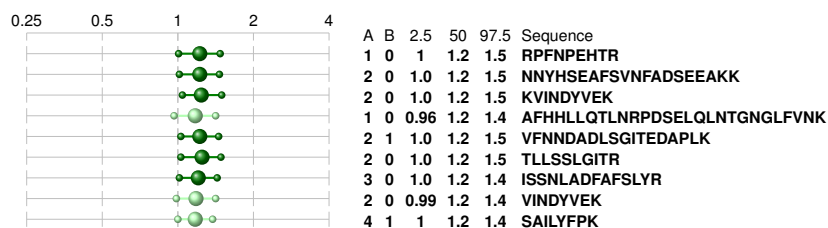


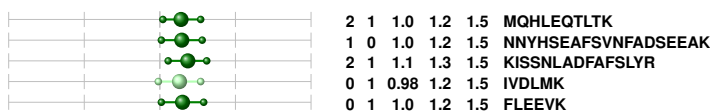
5.97 serine protease inhibitor alpha 1 [Rattus norvegicus]

Protein Accession	gi 51036655	
Mean Expression Ratio	1.21	
Median Expression Ratio	1.21	
Credible Interval	(1.09, 1.35)	
Associated Peptides	14	
Associated Spectra	30	
Coverage	0.336	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.27	1.31
Avg..iTRAQ.Ratio....116.114.	1.22	1.07
Avg..iTRAQ.Ratio....117.114.	1.46	0.879

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1 MAPSISRGLL LLAGLCCLAP SFLEADAQET DTSQQDQSPY YRKISSNLAD FAFSLYRELV HQSNTSNIFF SPMSITTAF
81 MLSLGSKGDY RKQILEGLEF NLQIPEADI HKAFHLLQTL LNRPDSELQL NTCNGLFVNK NLKLVKFLK EVKNNYHSEA
161 FSVNFADSEE AKKVINDIYE HGTQGRIVDL MKQLDEDIVF ALVNYIFFKG KWKRPFNPEH TRDADFHVVK STTVKVPMMN
241 RLGMFDMHYC STLSSWVLMY DYLGNATAIF LLPDDGRMQH LEQTLTKDLI SRFLNLRQTR SAILYFPKLS ISGTYNLRTL
321 LSSLGITRVF NNDADLSGIT EDAPLKLQA VHKAVLTIDE RGTEAAGATV VEAVPMSLPP QVKFDHPFIF MIVSETQSP
401 LFVKGVIDPT R
    
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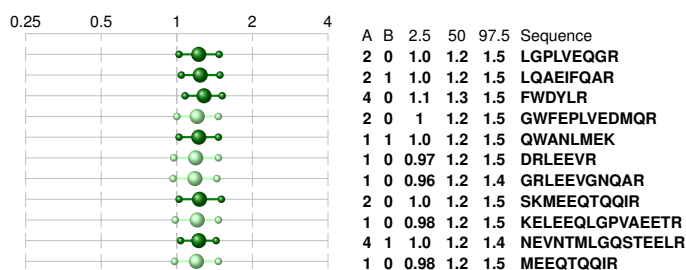




5.98 apolipoprotein E [Rattus norvegicus]

Protein Accession	gi 20301954	
Mean Expression Ratio	1.21	
Median Expression Ratio	1.21	
Credible Interval	(1.07, 1.37)	
Associated Peptides	11	
Associated Spectra	24	
Coverage	0.331	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.23	1.06
Avg..iTRAQ.Ratio....116.114.	1.54	1.28
Avg..iTRAQ.Ratio....117.114.	1.16	1.37

1 MKALWALLLV PLLTGCLAEG ELEVTDQLPG QSDQPWEQAL NRFWDYLRWV QTLSDQVQEE LQSSQVTQEL TVLMEDTMTE
 81 VKAYKKELEE QLGPVAEETR ARLTKEVQAA QARLGADMED LRNRLGQYRN EVNTMLGQST EELRSRLSTH LRKMRKRLMR
 161 DADDLQKRLA VYKAGAQEGA ERGVS AIRER LGPLVEQGRQ RTANLRWRRP APRDRAQALS DRIRGRLEEV GNQARDLLEE
 241 VREQMEEVRS KMEEQTQQIR LQAEIFQARI KGWFEPLVED MQRQWANLME KIQASVATNS IASTTVPLEN Q

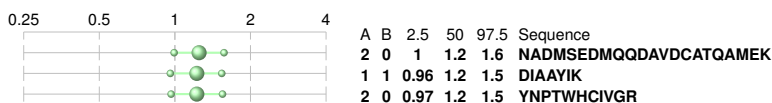


5.99 dynein light chain-2 [Rattus norvegicus]

Protein Accession	gi 18093106	
Mean Expression Ratio	1.21	
Median Expression Ratio	1.21	

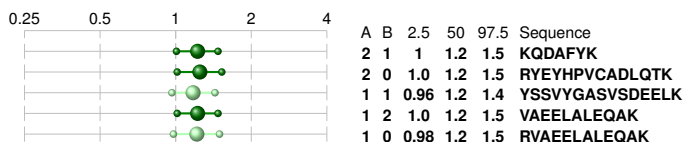
Credible Interval	(0.984, 1.48)	
Associated Peptides	3	
Associated Spectra	6	
Coverage	0.449	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.31	1.11
Avg..iTRAQ.Ratio....116.114.	1.28	1.38
Avg..iTRAQ.Ratio....117.114.	1.55	1.52

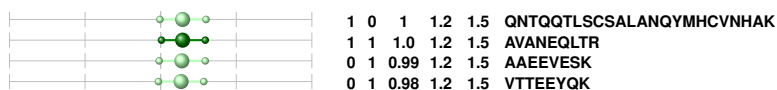
1 MSDRKAVIKN ADMSEDMQQD AVDCATQAME KYNIEKDIAA YIKREFDKKY NPTWHCIVGR NFGSYVTHET KHFIYFYLGQ
81 VAILLFKSG



5.100 PREDICTED: similar to coiled-coil-helix-coiled-coil-helix domain containing 3 [Rattus norvegicus]

Protein Accession	gij109471895	
Mean Expression Ratio	1.21	
Median Expression Ratio	1.21	
Credible Interval	(1.05, 1.40)	
Associated Peptides	9	
Associated Spectra	16	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.06	1.20
Avg..iTRAQ.Ratio....116.114.	1.66	1.03
Avg..iTRAQ.Ratio....117.114.	1.5	0.934

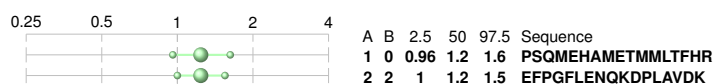




5.101 S100 calcium binding protein A10 [Rattus norvegicus]

Protein Accession	gi 13592079	
Mean Expression Ratio	1.21	
Median Expression Ratio	1.21	
Credible Interval	(0.98, 1.52)	
Associated Peptides	2	
Associated Spectra	5	
Coverage	0.358	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.23	1.02
Avg..iTRAQ.Ratio....116.114.	1.25	1.40
Avg..iTRAQ.Ratio....117.114.	1.76	1.46

1 MPSQMEHAME TMMLTFHFA GEKNYLTKED LRVLMER EFP GFLENQKDPL AVDKIMKDLD QCRDGVGFQ SFLSLVAGLI
81 IACNDYFVVH MKQKK



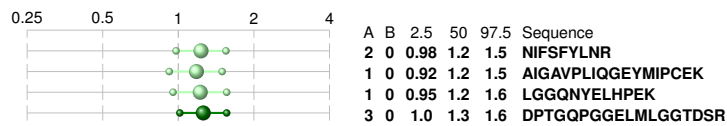
5.102 cathepsin D [Rattus norvegicus]

Protein Accession	gi 42476045	
Mean Expression Ratio	1.21	
Median Expression Ratio	1.21	
Credible Interval	(0.998, 1.46)	
Associated Peptides	4	
Associated Spectra	7	
Coverage	0.14	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.55	

Avg..iTRAQ.Ratio....116.114. 1.44
 Avg..iTRAQ.Ratio....117.114. 1.22

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1      MQTPGVLLLI LGLLAASSSA LIRIPLRKFT SIRRTMTEVG GSVEDLILKG PITKYSMQSS PRTKEPVSEL LKNYLDAQYY
81     GEIGIGTFPQ CFTVVFDTGS SNLWVPSIHC KLLDIACWVH HKYNSDKSST YVKNGTSTFDI HYGSGSLSGY LSQDTVSVPC
161    KSDLGGIKVE KQIFGEATKQ PGVVVIAAKF DGILGMGYPF ISVNNVLPVF DNLMKQKLE KNIFFSYLNR DPTGQPGGEL
241    MLGGTDSRYR HGELSYLNVT RKAYWQVHMD QLEVGSLETL CKGGCEAIVD TGTSLLVGPV DEVKELQKAI GAVPLIQGEY
321    MIPCEKVSSL PIITFKLGGQ NYELHPEKXI LKVSQAQKTI CLSGFMGMDI PPSGFLWIL GDVFIGCYT VFDREYNRVG
401    FAKAATL
    
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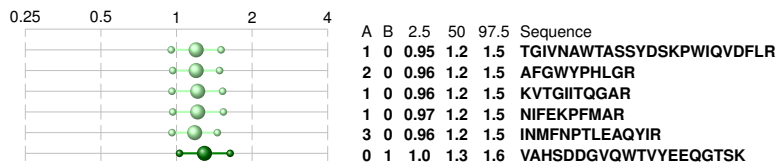


5.103 milk fat globule-EGF factor 8 isoform 1 precursor [Rattus norvegicus]

Protein Accession	gij93277126	
Mean Expression Ratio	1.21	
Median Expression Ratio	1.21	
Credible Interval	(1.01, 1.43)	
Associated Peptides	6	
Associated Spectra	9	
Coverage	0.184	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	2.82
Avg..iTRAQ.Ratio....116.114.	1.07	1.86
Avg..iTRAQ.Ratio....117.114.	1.63	3.86

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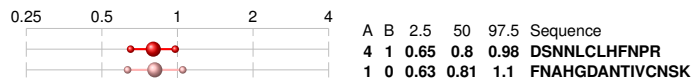
1      MQFSRVLAAL CGVLLCASGL FAASGDFCDS SLCNLGGTCL MGQDNDIYCL CPEGFTGLVC NETEKGPCSP NPCFHDACL
81     VTEDTQRGDI FTEYICQCPV GYSGIHCELE TTSYLDGEYL SSPAVPTTAV PTTAIPPTAV PTTAVPTTAV PTPAPNPDLS
161    NHLASRCSTK LGLEGGAIAD SQISASSVYM GFMGLQRWGP ELARLYRTGI VNAWTASSYD SKPWIQVDFL RKMRVSGVMT
241    QGASRAGRAE YLKTFFKVAIS LDGRRFFEFIQ DESGTGDFEF MGNQDNNSLK INMFNPTLEA QYIRLYPVSC HRGCTLRFEL
321    LGCELHGCSE FLGLKNNTIP DSQITASSSY KTWNLRAFGW YPHLGRRLDQ GKINAWTAQS NSAKEWLQVD LGTQKVTGI
401    ITQGARDFGH IQYVASYKVA HSDDGVQWTV YEEQGTSKVF QGNLDNNSHK KNIFEKPFMA RYVRVLPPLSW HNRITLRLLE
481    LGC
    
```



5.104 beta-galactoside-binding lectin [Rattus norvegicus]

Protein Accession	gij9845261	
Mean Expression Ratio	0.827	
Median Expression Ratio	0.829	
Credible Interval	(0.668, 1.02)	
Associated Peptides	2	
Associated Spectra	6	
Coverage	0.2	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.802	0.41
Avg..iTRAQ.Ratio....116.114.	0.705	1.23
Avg..iTRAQ.Ratio....117.114.	0.74	0.723

1 MACGLVASNL NLKPGECLKV RGELAPDAKS FVLNLGKDSN NLCLHFNPRF NAHGDANTIV CNSKDDGTWG TEQRETAPFF
 81 QPGSITEVCI TFDQADLTIK LPDGHEFKFP NRLNMEAINY MAADGDFRIK CVAFE



5.105 microtubule-associated protein 4 [Rattus norvegicus]

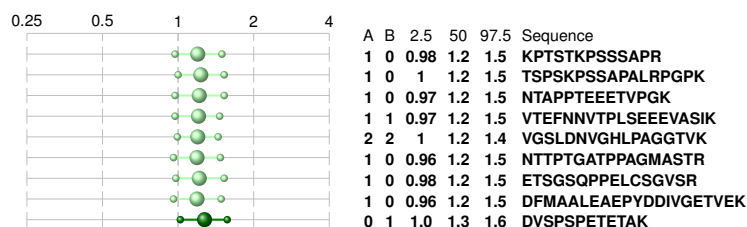
Protein Accession	gij66730360	
Mean Expression Ratio	1.21	
Median Expression Ratio	1.21	
Credible Interval	(1.03, 1.41)	
Associated Peptides	9	
Associated Spectra	13	
Coverage	0.138	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.24	1.19
Avg..iTRAQ.Ratio....116.114.	1.13	1.33
Avg..iTRAQ.Ratio....117.114.	1.28	1.64

NHLBI Zile/Grant, Aged Rat

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1      MADLSLVDAL TEPPEIEGE IKRDFMAALE AEPYDDIVGE TVEKTEFIPL LDGDEKSGNS ESKRKPQVDV SQVEDIPSSK
81     PTL LANGDHG VEGNNTGSP TDFLVENVYD EDYQNSQSWP EDASFQCFQPQ QVLDTNQADP FNVHHDDGLA DLLFVSSGPT
161    NASAFIEENN PLEDSYGVLP CDSFAPTAVV SQEWSVGAPD SPHSEPCVSP EVTIETAQPA TELSKAVDLE SVKEQLPAKA
241    LEMMAGQTTD AVPSKESEGS PDTDAAPGPD TDVTLTKDIE ESSSPDVISA NVTQPFTESD MFLTQEMELL IGTEAAQVKD
321    TMSVVEPDIS SAKNTAPPEE EETVPGKDMT FPKAEATALP IEMDLAPPED VALPKETELE LAPAAGTAPL SETEVALAKD
401    EEPSTGIPAA QEMLLSSETE VVLPSDSIMT LTKEVTVPLE AAGPLVSDMT AILETEMTLG GGTATPTETK LGKVKDMAPL
481    PESEVALGKD VVTLPETKVT EFNNTVPLSE EEVASIKDVS PSPETETAKN ADLHSGTELT LDNSMTPPSD PALPLETKVA
561    TVQIKDKETV QTQEELSEDS QLESVQLEGG SAVPPCTISP EPVKAADQKS TLPVDEGSPL EKLEQKETSQ SQPPELCSGV
641    SRQEEGKAAV GLTGNDIATP PNKELPPSPE KKAKPLATTQ PAKTSTSKAK IQPTSLPKQP APTSGGLNK KPMSLASGSV
721    PAAPHKRPA AATATARPSTL PARDLKPPI TETKVAEKRT SPSKPSAPL LRPGRKTTPT ISKATSPSTL VSTGSSSRSP
801    STTLPKRPTT TKTEGKPADV KRMTAKSATA DLSRSKTTSA SSVKRNTTPT GATPPAGMAS TRVKPMSAPC RSSVALSVDK
881    KPTSTKPSSS APRVSRLLAT VSAPDLKSVR SKVGSTENMK HQPGGGRVQI QNKKVDISKV SSKCGSKANI KHKPGGGDVK
961    IESQKLNFK EKAQAKVGLD NVGHLPAGGT VREGGGSEA PPCPGPPAGE EPAIPEAAPD AGAPTSASGL SGHTTSLSGG
1041   DQREPQTLDS QIQETSI

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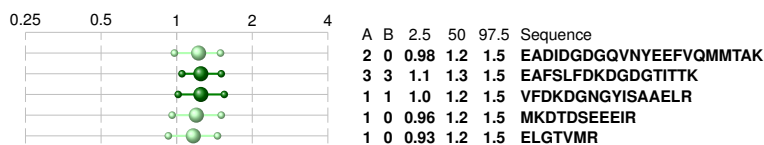
5.106 calmodulin 1 [Rattus norvegicus]

Protein Accession	gij14010863	
Mean Expression Ratio	1.20	
Median Expression Ratio	1.21	
Credible Interval	(1.02, 1.42)	
Associated Peptides	5	
Associated Spectra	12	
Coverage	0.49	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	1.04
Avg..iTRAQ.Ratio....116.114.	0.96	1.28
Avg..iTRAQ.Ratio....117.114.	1.71	2.06

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1      MADQLTEEQI AEFKEAFSLF DKDGDGTITT KELGTVMRSL GQNPTEAELQ DMINEVDADG NGTIDFPEFL TMMARKMKDT
81     DSEEEIEEAF RVFDRKDGNGY ISAAELRHVM TNLGEKLTDE EVDEMIREAD IDGDGQVNYE EFPQMMTAK

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5.107 PREDICTED: similar to Phosphoglycerate kinase 1 [Rattus norvegicus]

Protein Accession	gij62642907
Mean Expression Ratio	0.828
Median Expression Ratio	0.83
Credible Interval	(0.632, 1.08)
Associated Peptides	2
Associated Spectra	5
Coverage	0.0864
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.567
Avg..iTRAQ.Ratio....116.114.	0.56
Avg..iTRAQ.Ratio....117.114.	0.472

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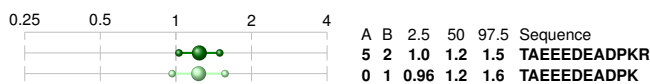
1      MSLSNKLTLD KLDVKGKQIV MRVDFSVPK NNQITNNQRI KAAVPSIKFC HPGRPDGVPM PDKYSLEPVA AELKSLGKD
81     VFLKDCVGS EVENACANPA ARTVILLENL HFHVEEKGK KDASGNKVK EPAKIDAFQA SLKLGDVVY NDAFGTAHRA
161    HSSMVGVNLP QKAGGFLMKK ELSYFTKALE SPERPFLAIL GGAVVEDKIQ LINNMLDKVN EMIIGGGIAS TFLKVLNNME
241    IGTSLCDEEG AKIVKELMVK AEKNGVKITL PVDFVTADKF DENARTGQAT VASGIPAGWL GLDCGTEGSE KYAETVARAK
321    QIVWNGPVGV FEWEAFARGT KSLVDEVVTA ASRGCITIIG GGNTATCCA WNTEDKVSHV STGGGASLEL LEGRVLPQVD
401    ALSNV
  
```



5.108 parathymosin [Rattus norvegicus]

Protein Accession	gij14010875	
Mean Expression Ratio	1.20	
Median Expression Ratio	1.21	
Credible Interval	(0.978, 1.48)	
Associated Peptides	2	
Associated Spectra	8	
Coverage	0.118	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.12	1.35
Avg..iTRAQ.Ratio....116.114.	1.03	1.34
Avg..iTRAQ.Ratio....117.114.	1.64	1.56

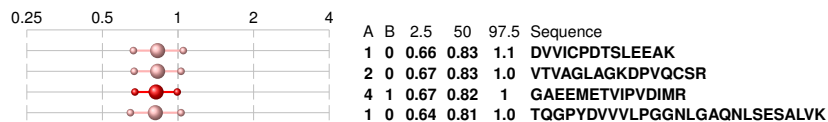
1 MSEKSV EAAA ELSAKDLKEK KDKVEEKAGR KERKKEVVEE EENGAE EEEEE ETAEDGEDDD EGDEE EEEEE EEEDEGPVRK
 81 RTAE E E E E A D P K R Q K T E N G A S A



5.109 DJ-1 protein [Rattus norvegicus]

Protein Accession	gij16924002	
Mean Expression Ratio	0.831	
Median Expression Ratio	0.83	
Credible Interval	(0.692, 0.998)	
Associated Peptides	4	
Associated Spectra	9	
Coverage	0.381	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.863	0.203
Avg..iTRAQ.Ratio....116.114.	0.837	1.29
Avg..iTRAQ.Ratio....117.114.	0.817	0.651

1 MASKRALVIL AKGA E E M E T V I P V D I M R R A G I K V T V A G L A G K D P V Q C S R D V V I C P D T S L E E A K T Q G P Y D V V V L P G G N L G A Q
 81 N L S E S A L V K E I L K E Q E N R R K L I A A I C A G P T A L L A H E V G F G C K V T S H P L A K D K M M N G S H Y S Y S E S R V E K D G L I L T S R G P G T
 161 S F E F A L A I V E A L S G K D M A N Q V K A P L V L K D



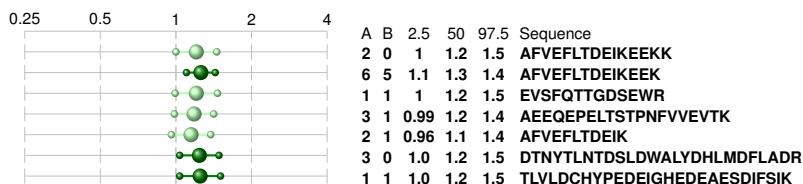
5.110 "complement component 1, q subcomponent binding protein [Rattus norvegicus]"

Protein Accession	gij48675371
Mean Expression Ratio	1.21

Median Expression Ratio	1.20	
Credible Interval	(1.07, 1.36)	
Associated Peptides	7	
Associated Spectra	27	
Coverage	0.362	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.15	1.27
Avg..iTRAQ.Ratio....116.114.	1.24	1.15
Avg..iTRAQ.Ratio....117.114.	1.38	1.27

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1      MPELLRCVPR ALGAAATGLR ASIPAPPLRH LLQPAPRCL RPFGLLSVRA GSARRSGLLQ PPVPCACGCG ALHTEGDKAF
81     VEFLTDEIKE EKKIQKHSL PKMSGDWELE VNGTEAKLLR KVAGEKITVT FNINNSIPPT FDGEEEPSQG QKAEFQEPFL
161    TSTPNFVVEV TKTDGKKTIV LDCHYPEDEI GHEDEAESDI FSIKEVSFQT TGDSEWRDTN YTLNTDSLWD ALYDHLMDFL
241    ADRGVDNTFA DELVELSTAL EHQEYITFLE DLKSFVKSQ
  
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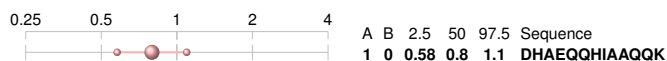


5.111 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gij109474981
Mean Expression Ratio	0.833
Median Expression Ratio	0.831
Credible Interval	(0.62, 1.13)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0565
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.283
Avg..iTRAQ.Ratio....116.114.	0.863
Avg..iTRAQ.Ratio....117.114.	0.824

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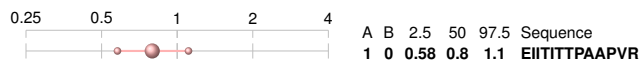
1      MLLLPGRMSF PEQHTADPWA KSPRSPAPTA LRPGSSATFP TARSPAPAEP LRARREGGTQ GGAGLKGGGG PPRPPPGRKC
81     AHRQLLPAAA ATVCQTRLLL KRGALHSRR VLRGRAPLHS GDWTARFLEV PRIPGFQNKV RVALIAELDK EKRRLLMQNQ
161    SSASHPGASI SLSRPSLSKD FRDHAEEQHT AAQQKAALQH AHAHSSGYFI TQDSAFGNLI LPVLPRLDPE
  
```



5.112 PREDICTED: similar to cell division cycle associated 5 [Rattus norvegicus]

Protein Accession	gij109463460
Mean Expression Ratio	0.834
Median Expression Ratio	0.833
Credible Interval	(0.613, 1.12)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0616
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.542
Avg..iTRAQ.Ratio....116.114.	0.475
Avg..iTRAQ.Ratio....117.114.	0.478

1 MIKIIITITT PAAPVRKAI I LKKIVPRAVE VPDVHTPVRR SPRISFILEK ENNPPLKVPT KEDLFKTCV PGTPSSSTPVL
 81 CAQNVKNSR EPEPDIRDLE MSQKRRSYS RLQSLHCAST STPGRRSFFG FERPEDLPGV SPVVRSKLME TPKVPVKHLV
 161 PDRTLPGISP PIVKEKRKKK VPEITRSELD KWAVAMNAEF EAAEQFELI E



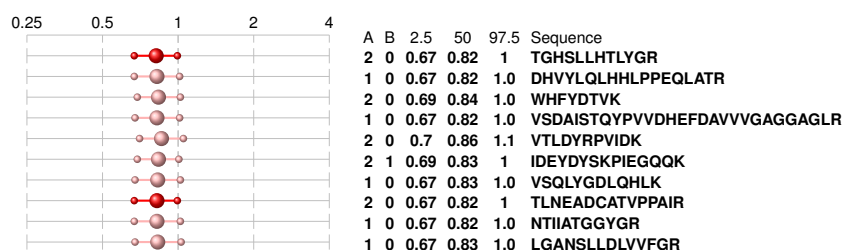
5.113 "succinate dehydrogenase complex, subunit A, flavoprotein (Fp) [Rattus norvegicus]"

Protein Accession	gij18426858	
Mean Expression Ratio	0.834	
Median Expression Ratio	0.833	
Credible Interval	(0.721, 0.965)	
Associated Peptides	10	
Associated Spectra	16	
Coverage	0.221	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.92	1.05
Avg..iTRAQ.Ratio....116.114.	0.795	0.75

Avg..iTRAQ.Ratio....117.114. 0.779 1.36

```

1   MAGVGAVSRL LRGRRLALAG ATRGFHFSVG ESKKASAKVS DAISTQYYPV DHEFDVAVVG AGGAGLFAAF GLSEAGFNTA
81  CLTKLFPTRS HTVAAQGGIN AALGNMEEDN WRNHFYDTVK GSDWLGDDA IHYMTEQAPA SVVELENYGM PFSRTEDGRI
161 YQRAFGGQSL KFGKGGQHR CCCVADR TGH SLLHTLYGRS LRYDTSYFVE YFALDLLMEN GECRGVIALC IEDGSIHRIR
241 AKNTIIATGG YGRTYFSCTS AHTSTGDGTA MVTRAGLPCQ DLEFVQFHPT GIYGAGCLIT EGCRGEGGIL INSQGERFME
321 RYAPVAKDLA SRDVVSRMT LEIREGRGCG PEKDHVYLQL HHLPPPEQLAT RLPGISSETAM IFAGVDVTK EPIPVLPTVHY
401 NMGGIPTNYK GQVLKHVNGQ DQIVPGLYAC GEACASVHG ANR LGANSLD DLVVFGGRACA LSAIESCRPG DKVPPIKANA
481 GEESVMNLDK LRFADGSVRT SELRLSMQKS MQSHAAVFRV GSVLQEGCEK VSQLYGDLQH LKTFDRGMVW NTDLVETLEL
561 QNLMLCALQT IYGAEARKES RGAHAREDYK VR IDEYDYSK PIEGQQK KPF AEHWRKHTLS YVDTKTGKVT LDYRPPVIDKT
641 LNEADCATVP PAIRSY
    
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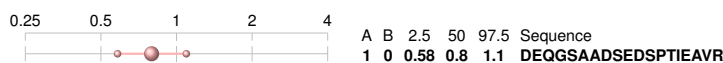


5.114 "aminolevulinatase, delta-, dehydratase [Rattus norvegicus]"

Protein Accession	gij6978483
Mean Expression Ratio	0.834
Median Expression Ratio	0.833
Credible Interval	(0.614, 1.13)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0576
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.705
Avg..iTRAQ.Ratio....116.114.	0.554
Avg..iTRAQ.Ratio....117.114.	0.431

```

1   MHHQSVLHSG YFHPLLRAWQ TTPSTVSATN LIYPIFVTDV PDDVQPIASL PGVARYGVNQ LEEMLRPLVE AGLRCVLIFG
81  VPSRVPKDEQ GSAADSEDSPT TIEAVL LRK TFPTLLVACD VCLCPYTSHG HCGLLSENGA FLAEESRQL AEVALAYAKA
161 GCQVVAPSDM MDGRVEAIIKA ALLKHGLGNR VSVMSYSAKF ASCFYGPFRD AAQSSPAFGD RRCYQLPPGA RGLALRAVAR
241 DIQEGADILM VKPGLPYLDM VQEVKDKHPE LPLAVYQVSG EFAMLWHGAK AGAFDLRTAV LESMTAFRA GADIIITYFA
321 PQLLKWLEKE
    
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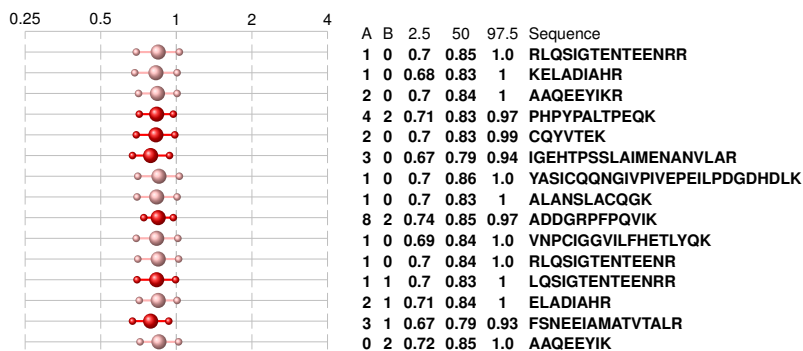


5.115 aldolase A [Rattus norvegicus]

Protein Accession	gij6978487	
Mean Expression Ratio	0.836	
Median Expression Ratio	0.836	
Credible Interval	(0.755, 0.927)	
Associated Peptides	15	
Associated Spectra	40	
Coverage	0.426	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.81	0.874
Avg..iTRAQ.Ratio....116.114.	0.852	0.716
Avg..iTRAQ.Ratio....117.114.	0.864	0.786

```

1      M P H P Y P A L T P E Q K K E L A D I A H F I V A P G K G I L A A D E S T G S I A K R L Q S I G T E N T E E N R R F Y R Q L L L T A D D R V N P C I G G V I L F
81     H E T L Y Q K A D D G R P F P Q V I K S K G G V V G I K V D K G V V P L A G T N G E T T Q G L D G L S E R C A Q Y K K D G A D F A K W R C V L K I G E H T P S
161    S L A I M E N A N V L A R Y A S I C Q Q N G I V P I V E P E I L P D G D H D L K R C Q Y V T E K V L A A V Y K A L S D H H V Y L E G T L L K P N M V T P G H A C
241    T Q K F S N E E I A M A T V T A L R R T V P P A V P G V T F L S G G Q S E E E A S I N L N A I N K C P L L K P W A L T F S Y G R A L Q A S A L K A W G G K K E N
321    L K A A Q E E Y I K R A L A N S L A C Q G Y T P S G Q S G A A A S E S L F I S N H A Y
    
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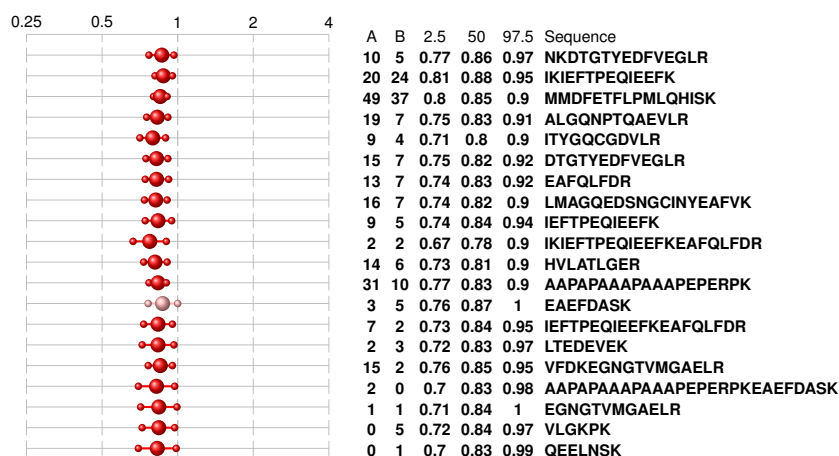


5.116 "myosin, light polypeptide 3 [Rattus norvegicus]"

Protein Accession	gij6981240	
Mean Expression Ratio	0.835	
Median Expression Ratio	0.836	
Credible Interval	(0.79, 0.885)	

Associated Peptides	20	
Associated Spectra	377	
Coverage	0.845	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.982	0.596
Avg..iTRAQ.Ratio....116.114.	0.774	1.20
Avg..iTRAQ.Ratio....117.114.	0.898	0.569

1 MAPKKPEPKK DDAKTAAPKA APAPAAAPAA APEPERPKEA EFDASKIKIE FTPEQIEEFK EAFQLFDRTP KGEMKITYGQ
 81 CGDVLRALGQ NPTQAEVLRV LGKPKQEELN SKMDDFETFL PMLQHSKKNK DTGTIEDFVE GLRVFDKEGN GTVMGAELRH
 161 VLATLGERLT EDEVEKLMAG QEDSNGCINY EAFVKHIMAS



5.117 PREDICTED: similar to androgen-induced prostate proliferative shutoff associated protein AS3 isoform

Protein Accession	gij109494992
Mean Expression Ratio	1.20
Median Expression Ratio	1.20
Credible Interval	(0.899, 1.62)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.68
Avg..iTRAQ.Ratio....116.114.	1.27

Avg..iTRAQ.Ratio....117.114. 3.07

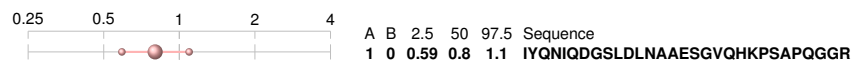


5.118 "RAB14, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gi 16758368
Mean Expression Ratio	0.838
Median Expression Ratio	0.836
Credible Interval	(0.624, 1.13)
Associated Peptides	1
Associated Spectra	1
Coverage	0.140
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.85
Avg..iTRAQ.Ratio....116.114.	0.733
Avg..iTRAQ.Ratio....117.114.	0.95

```

1   MATTPYNSY IFKYIIGDM GVGKSCLLHQ FTEKKFMADC PHTIGVEFGT RRIIEVSGQKI KLQIWDTAGQ ERFRAVTRSY
81  YRGAAGALMV YDITRRSTYN HLSSWLTDR NLTNPNTVII LIGNKADLEA QRDVTYEEAK QFAEENGLLF LEASAKTGEN
161 VEDAFLEAAK K IYQNIQDGS LDLNAAESGV QHRPSAPQGG RLTSEPQPQR EGCGC
  
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5.119 "PREDICTED: similar to Complex I intermediate-associated protein 30, mitochondrial precursor [Rattus"

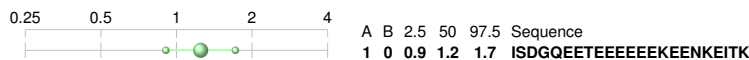
Protein Accession	gi 109470666
Mean Expression Ratio	0.836
Median Expression Ratio	0.837
Credible Interval	(0.637, 1.1)

Associated Peptides	1
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.651
Avg..iTRAQ.Ratio....116.114.	0.57
Avg..iTRAQ.Ratio....117.114.	0.773



5.120 PREDICTED: similar to PProtein Associated with Tlr4 [Rattus norvegicus]

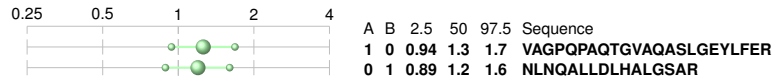
Protein Accession	gi 34871484
Mean Expression Ratio	1.20
Median Expression Ratio	1.19
Credible Interval	(0.902, 1.61)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	2.18
Avg..iTRAQ.Ratio....116.114.	1.63
Avg..iTRAQ.Ratio....117.114.	4.06



5.121 ferritin light chain 1 [Rattus norvegicus]

Protein Accession	gi 84000579	
Mean Expression Ratio	1.20	
Median Expression Ratio	1.19	
Credible Interval	(0.923, 1.57)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	0.213	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	2.5	1.15
Avg..iTRAQ.Ratio....116.114.	2.06	1.03
Avg..iTRAQ.Ratio....117.114.	2.7	1.03

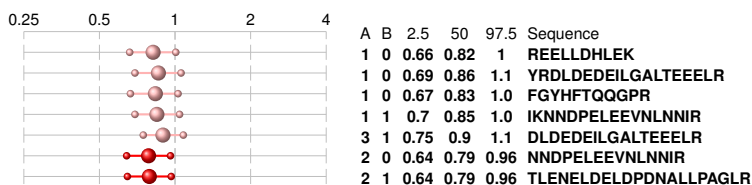
1 MTSQIRQNY S TEVEAAVNRL VNLHLRASY T YLSLGGFFDR DDVALEGVGH FFRELAEEKR EGAERLLKLO NERGGRALFQ
 81 DVQKPSQDEW GKTL EAMEAA LALEK NLNQ A LLDLHALGSA RTDPHLCDFL ESHFLDKEVK LIKKMGHLT NLR R VAGPQP
 161 AQTGVAQASL GEYLFERLTL KHD



5.122 tropomodulin 1 [Rattus norvegicus]

Protein Accession	gi 48675841	
Mean Expression Ratio	0.837	
Median Expression Ratio	0.837	
Credible Interval	(0.72, 0.973)	
Associated Peptides	7	
Associated Spectra	14	
Coverage	0.217	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.912	0.747
Avg..iTRAQ.Ratio....116.114.	0.674	1.2
Avg..iTRAQ.Ratio....117.114.	0.768	1.09

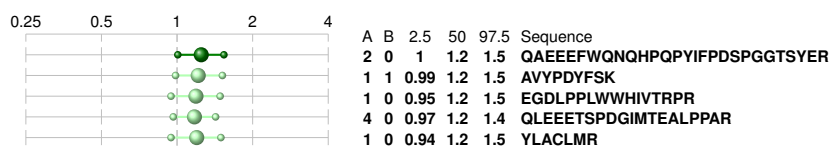
1 MSYRRELEKY RDLDEDEILG ALTEEELRTL ENELDELDPD NALLPAGLRQ KDQTTKAPTG PFKREELLDH LEKQAKEFKD
 81 REDLVPYTG E KRGKIWVPKQ KPMDFVLESV TLEPELEEAL ANASDAELCD IAAILGMHTL MSNQYYQAL GSSSIVNKEG
 161 LNSVIKPTQY KPVPDEEPNS TDVEETLER KNNDPLEEV NLNNIRNIP I PTLKAYAEAL KENSIVKFFS IVGTRSNDPV
 241 AFALAEMLV NKVLKTLNVE SNFISGAGIL CLVEALPHNT SLVELKIDNQ SQPLGNKVEM EIVNMLEKNT TLLKFGYHFT
 321 QQGPRLRASN AMMNNDLVR KRRLADLTGP IIPKCRSGV



5.123 "PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 [Rattus norvegicus]"

Protein Accession	gij109482288	
Mean Expression Ratio	1.19	
Median Expression Ratio	1.19	
Credible Interval	(1.00, 1.42)	
Associated Peptides	5	
Associated Spectra	10	
Coverage	0.447	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.19	1.25
Avg..iTRAQ.Ratio....116.114.	1.45	1.09
Avg..iTRAQ.Ratio....117.114.	1.38	1.32

1 MAFCAPPAYL THRQKVLRLY KRALRHLESW CVHRDKYR^{YL} ACLM^RARFEE HKNEKDMKA TQLLRQ^AE^EE^E FWQ^NQHP^QPY
 81 IFP^DSPGG^TS YERYECYKVP EWCLDYWHPS EKAVY^PDY^FS KREQW^KLRM ESWDREVK^{QL} EE^TSPD^GIM TEAL^PPA^KE
 161 GDL^PPL^WWHI VTR^PERPT

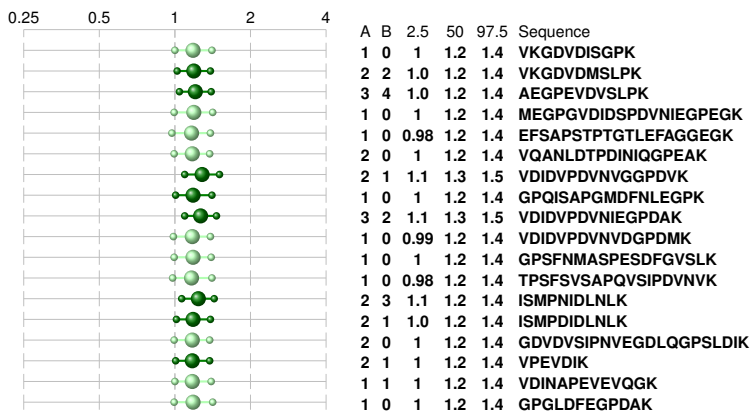


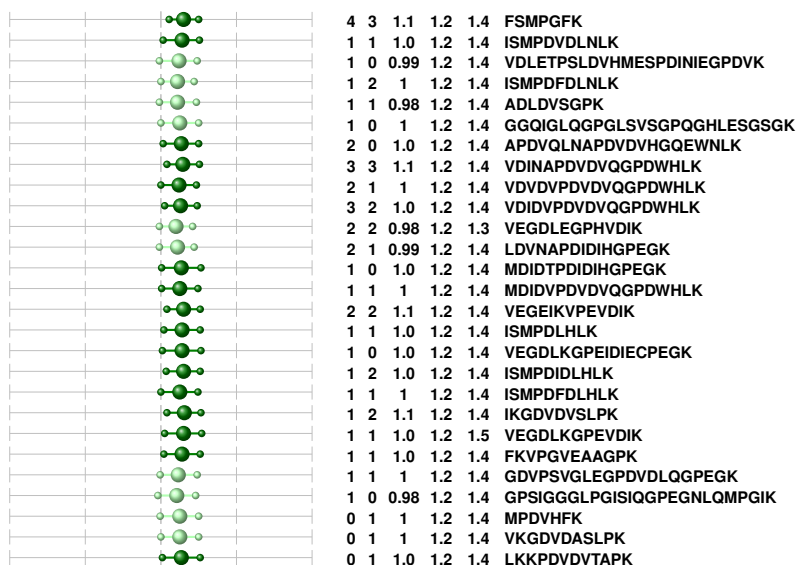
5.124 PREDICTED: similar to AHNAK nucleoprotein isoform 1 isoform 5 [Rattus norvegicus]

Protein Accession	gij109463547
Mean Expression Ratio	1.19

Median Expression Ratio	1.19	
Credible Interval	(1.12, 1.27)	
Associated Peptides	45	
Associated Spectra	111	
Coverage	0.273	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.06	1.16
Avg..iTRAQ.Ratio....116.114.	1.08	1.09
Avg..iTRAQ.Ratio....117.114.	1.33	1.45

1	MPDLNLNLK	PNVKGDVDV	IPNVEGDLQ	PSLDIKSPKL	DVNAPDIDIH	GPEGNLKGPK	LKMPDMHVNM	PKISMPDIDL
81	NLKGSKVRGD	VDISGPKLEG	DIKTPKVDVK	GPELDISASK	VNIDAKGKKS	RFKLPKFNF	GSKVQTEVD	VKLKKPDVDV
161	TAPKVDINAP	EVEVQGVKVG	PKFKMPFLSI	SSPKVSPMPD	ELNLKGPKVK	GELDATVPL	EGDFKSPKVD	IKAPDVQLNA
241	PDVDVHGQEW	NLKMHKMKMP	KFSVSVGKAE	GPDVAVDLPK	GDINIEGPM	NIEGPELNVE	CPEGLKGP	FKMPEMNIKA
321	PKISMPNIDL	NLKGPKVKGD	VDVSLPKVEG	DLKGPEVDIK	GPKMIDVDP	VQVQGDWHL	KMPKVKMPKF	SMGFKAEKP
401	EVDVLSKAD	LDVSGPKVDI	DVPDVIIEGP	DAKLGPKFK	MPEMNIKAPK	ISMPDIDLHL	KGPKIKGDVD	VSLPKVEGDL
481	EGPHVDIKGP	KVDINAPD	VQGDWHLKM	PKMKMPKFSM	PGFKAEGPEV	DVSLPKADLD	VSGPKVDIDV	PDVNIIEGPA
561	KLKGPKFKMP	EMNIKAPKIS	MPNIDLNLK	PKVKGVDVMS	LPKVEGEIKV	PEVDIKGPKV	DINAPD	VPDVKMPK
641	VKMPKFSMPG	FKAEGPEVDV	SLPKADLDV	GPKVDIDVDP	VNIEGPDAL	KGPKFKMPEM	NIKAPKISMP	NIDLNLKGPK
721	VKGDVMSLP	KVEGEIKVPE	VDIKGPKVDI	DVPDVIIEGP	DWHLKMPKVK	MPKFSMPGFK	AEGPEVDVSL	PKADLDVSGP
801	KVDIDVDPVN	IEGPDALKLG	PKFKMPEMNI	KAPKISMPDL	HLKGPVKIKG	VDVSLPKVEG	EIKVPEVDIK	GPKVDIDVDP
881	VDVQGDWHL	KMPKMKMPKF	SMPGFKAEKP	EVDVSLPKAD	LDVTGPKVDI	DVPDVIIEGP	DVKVKGPKFK	MPEMNIKAPK
961	ISMPDIDLHL	KGPKVKGDVD	ASLPKMEGPG	VDIDSPDVI	EGPEGKLGPK	KFKMPDMHIK	APKISMPD	LNLGSKVKG
1041	DVDLSLPKVE	GDLKGEIDI	ECPEGKLGPK	KFKMPDVEFK	TPQISMSDID	LNMKGPKVK	DMDISVPKLE	GDLKGTKVDV
1121	KGPKMIDITP	DIDIHGPEGK	LKGPFKMPD	LHLKAPKISM	PDVDLNLKGP	KVKGVDVSL	PKVEGDLKGP	EVDIKGPKVD
1201	INAPD	VQGDWHLKMPK	KMPKFSMPG	KAEGPEVDV	LPKADLDVSG	PKVDIDVDP	NIEGPDALK	GPKFKMPEM
1281	IKAPKISMPD	IDLNLKGPVK	KGDVMSLPK	VAGEIKVPEV	DIKGPKVDV	VQVQGDWHL	WHLKMPKVKM	PKFSMPGKA
1361	EGPEVDVSLP	KADLDVSGPK	VDIDVDPVN	DGPDMLKVK	KFKMPEINIK	APKISMPD	LELKGPKVK	AFDGSVPKIE
1441	GTLKGPEIDM	KGGGLDFEGP	DAKLSGPNLK	MPSLEVPVK	ISGPDANVHL	KTPNVGISGP	KLGGGEVDLR	GPKVDLETPS
1521	LDVMSPEPDI	NIEGPDVVP	KFKKPKFGFG	AKSPKADIKT	PTVDVTPPEA	ELSVETPEIN	IGGKGGKSKF	KMPRIHMSGP
1601	KVKTKKQGF	LNVPGGEIDA	SLKVPD	VAGPDAALKA	EVKSPKVKKT	MFGKMYFPD	EFDIKSPKFK	AEAALPSPKL
1681	EGEIKVPD	ISSPGVNVEA	PDIHVKAPKF	KVPGVEAAGP	KIEGNLKGPK	VQANLDTPI	NIQGP	TPSFSVSAQ
1761	VSI	PDVNVKLG	KGNPKGDV	SVGLEGPD	LQGEPIKIF	PKFSLPKISA	PGVKMGGS	ETHAQMP
1841	EGPGVSLKGP	GVDLPSVDL	LPKVS	GDLDLNLK	GPPSLK	DVAASSPMK	LHAPGLDMK	VAGKVQIGAD
1921	AALSVGAPDV	TLKGS	SLQGD	LAVSGDIKCP	KVSVGTPEVS	VEALEGGVRL	PQMKLPQFGI	STPGSDLDIN
2001	QGS	TDVNLK	GPQISAPGMD	FNLEGP	KVRS	SLGATGELK	PSIGGGLPGI	SIQGP
2081	PEIKGDLKGS	GIGLHGAVPD	LSVKGPSFNM	ASPESSDFGVS	LKGPVKVGGV	DVSGGVSVPD	INLGEHMNV	KPFGGEWRGP
2161	QVSSVNLDT	TKLVGNLHFS	GPKIEGDVK	GQIGLQGPGL	SVSGPQGHLE	SGSGVTFPK	MKIPKFTFSG	RELTGREVGV
2241	DVNFNPVEAN	VQAGAGEGEL	EESAVLKKKS	KIRKMPKFTS	KPKKGGVVTG	SPEASVSGSK	GDLKSSKASL	GSLEGEAEAE
2321	TSSPKGKFSL	FKSKKPRNRS	NSFSDER	EFSSAPSTPTGTLE	FAGGEGKXKH	GKLFKFTFGG	LGSKSKGHYE	VTGSDDAEAG
2401	LQSGSVSLAS	KKSRLSSSSS	NDSGTLGIQ	LPEVEISVST	KKE			



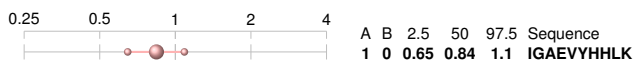


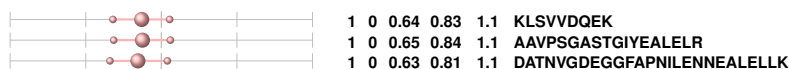
5.125 "enolase 3, beta [Rattus norvegicus]"

Protein Accession	gij126723393
Mean Expression Ratio	0.839
Median Expression Ratio	0.839
Credible Interval	(0.669, 1.04)
Associated Peptides	4
Associated Spectra	4
Coverage	0.145
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.794
Avg..iTRAQ.Ratio....116.114.	0.744
Avg..iTRAQ.Ratio....117.114.	0.81

```

1      MAMQKIFARE ILDSRGNPTV EVDLHTAKGR FRAAVPSGAS TGIYEALELR DGDKSRYL GK GVLKAVEHIN KTLGPALLEK
81     KLSVVDQEKV DKFMIELDGT ENKSKFGANA ILGVSLAVCK AGAAEKGVPL YRHIADLAGN PDLVLPVPAF NVINGGSHAG
161    NKLAMQEFMI LPVGASSFK EAMRIGAEVYH HLLGVIRAKY GKDATNVGDE GGFAPNILEN NEALELLKTA IQAAGYDPKV
241    VIGMDVAASE FYRNGKYDLD FKSPDDPARH ISGKELGELY KSFIKNYPVV SIEDPFDQDD WATWTSFLSG VDIQIVGDDL
321    TVTNPKRIAQ AVEKACNCL LLKVNQIGSV TESIQAACKLA QSNGWGMVVS HRSGETEDTF IADLVVGLCT GQIKTGAPCR
401    SERLAKYNQL MRIEEALGDK AVFAGRKFRN PKAK
    
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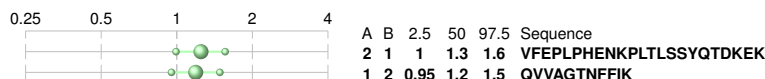




5.126 cystatin B [Rattus norvegicus]

Protein Accession	gi 6978715	
Mean Expression Ratio	1.19	
Median Expression Ratio	1.19	
Credible Interval	(0.972, 1.48)	
Associated Peptides	2	
Associated Spectra	6	
Coverage	0.347	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.06	1.55
Avg..iTRAQ.Ratio....116.114.	0.98	1.58
Avg..iTRAQ.Ratio....117.114.	1.24	1.55

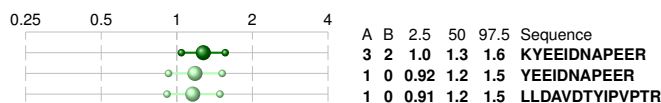
1 MMCGAPSATM PATTETQEIA DKVKSQLEEK ANQKFDVFKA ISFRRQVVAG TNFFIKVDVG EEKCVHLRVF EPLPHENKPL
81 TLSSYQTDKE RHEDELYF



5.127 "PREDICTED: similar to Tu translation elongation factor, mitochondrial [Rattus norvegicus]"

Protein Accession	gi 109459347	
Mean Expression Ratio	1.19	
Median Expression Ratio	1.19	
Credible Interval	(0.974, 1.45)	
Associated Peptides	3	
Associated Spectra	7	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.34	1.83

Avg..iTRAQ.Ratio....116.114.	1.06	1.18
Avg..iTRAQ.Ratio....117.114.	1.20	2.37

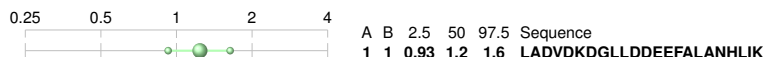


5.128 PREDICTED: similar to EH-domain-containing protein 1 (mPAST1) [Rattus norvegicus]

Protein Accession	gj 109463451	
Mean Expression Ratio	1.19	
Median Expression Ratio	1.19	
Credible Interval	(0.897, 1.54)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.0431	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.67	2.28
Avg..iTRAQ.Ratio....116.114.	1.00	1.25
Avg..iTRAQ.Ratio....117.114.	1.85	1.46

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1      MFSWVSKDAR RKKEPELFQT VAEGLRQLYA QKLLPLEEHY RFHEFHSPAL EDADFDNKPM VLLVGQYSTG KTFIRHLIE
81     QDFPGMRIGP EPTTDSFIAV MHGPTTEGVVP GNALVVDPFR PFRKLNAFGN AFLNRFMCAQ LPNPVLDNIS IIDTPGILSG
161    EKQRISRGYD FAAVLEWFAE RVDRIILLFD AHKLDISDEF SEVIKALKNH EDKIRVVLNK ADQIETQQLM RVYGALMWSL
241    GKIINTPEVV RVYIGSFWSH PLLIPDNRKL FEABEQDLFK DIQSLPRNAA LRKLNLIKR ARLAKVHAYI ISSLKKEMPN
321    VFGKESKKE LVNNLGEIYQ KIEREHQISS GDFPSLRKMQ ELLQTQDFSK FQALKPKLLD TVDDMLANDI ARLMVMVRQE
401    ESLMPSQAVK GGAFDGTMNG PFGHGYGEGA GEGIDDVWV VGKDKPTYDE IFYTLSPVNG KITGANAKKE MVKSKLPNTV
481    LGKIWKLADV DKDGLLDDEE FALANHLIKV KLEGHELPAD LPPHLIPPSK RRHE
    
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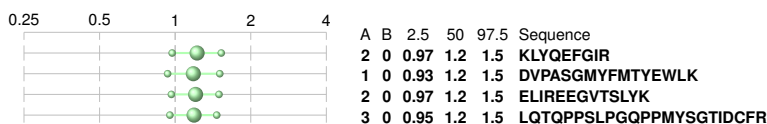


5.129 "solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 [Rattus norvegicus]"

Protein Accession	gij 52138624
Mean Expression Ratio	1.19
Median Expression Ratio	1.19
Credible Interval	(0.985, 1.43)
Associated Peptides	4
Associated Spectra	8
Coverage	0.203
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.41
Avg..iTRAQ.Ratio....117.114.	1.58

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1   MAEEPKPISP LKNLLAGGFG GVCLVFVGHF LDTVKVRLQT QPPSLPGQPP MYSGTIDCFR KTLFREGITG LYRGMAAPII
81  GVTPMFAVCF FGFGLGKRLQ QKSPDELTY PQLFTAGMLS GVFTTGIMTP GERIKCLLQI QASSGKNKYS GTLDCAKKLY
161 QEPGIRGFYK GTVLTLMRDV PASGMYFMTY EWLKLNFTPO GKSVHDLSP RVLVAGGFAG IFNWVVAIPP DVLKSRFQTA
241 PPGKYPNGFR DVLRSLIREE GVTSLYKGFN AVMIRAFPAN AACFLGFEIA MKILNWIAPN L
    
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5.130 "myosin heavy chain, polypeptide 6 [Rattus norvegicus]"

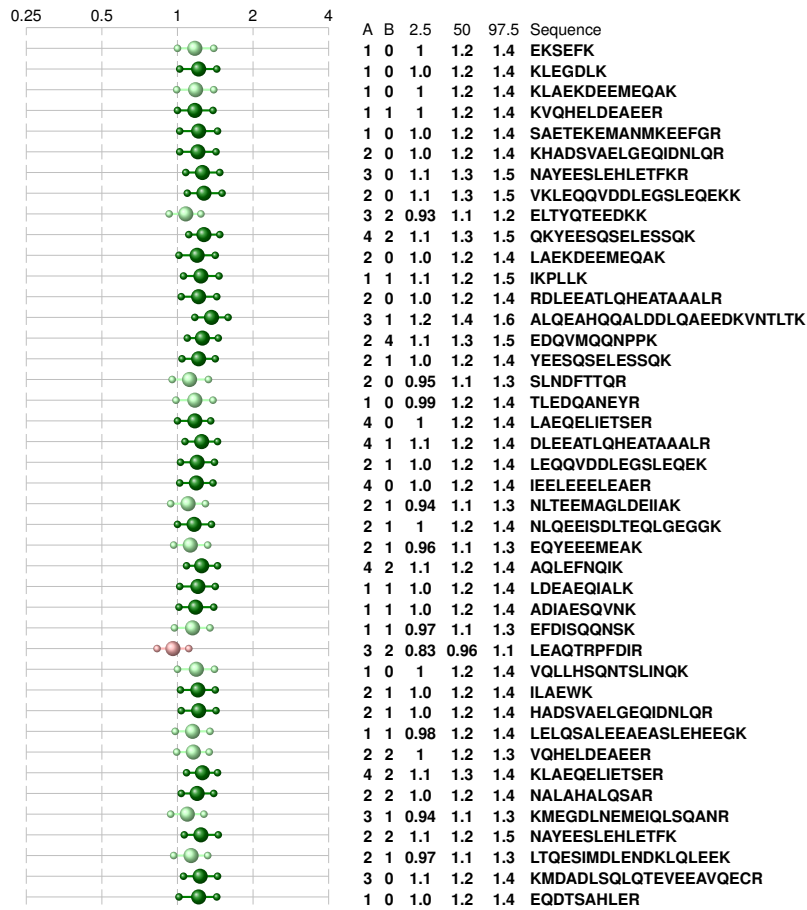
Protein Accession	gij 8393804	
Mean Expression Ratio	1.19	
Median Expression Ratio	1.19	
Credible Interval	(1.13, 1.25)	
Associated Peptides	74	
Associated Spectra	201	
Coverage	0.38	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.978	1.07
Avg..iTRAQ.Ratio....116.114.	1.13	0.896
Avg..iTRAQ.Ratio....117.114.	1.64	1.49

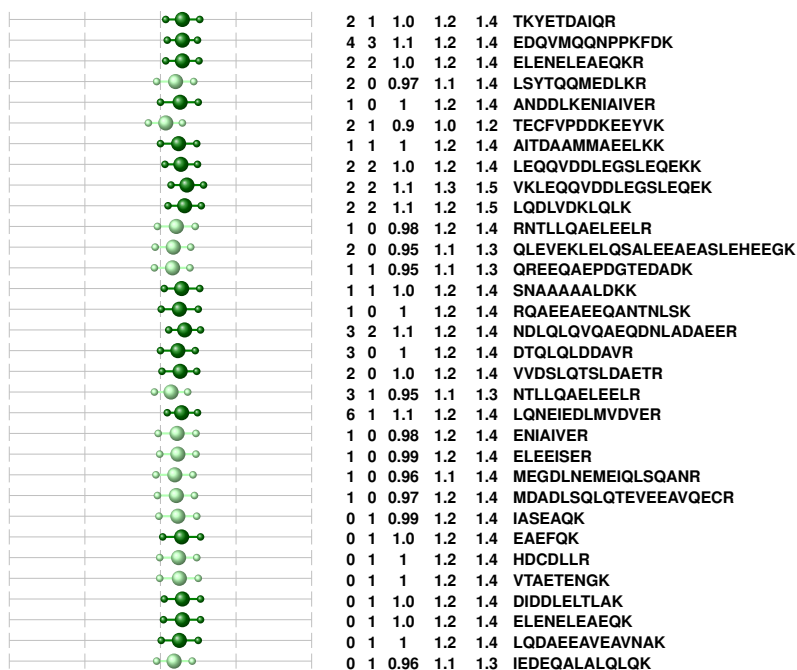
NHLBI Zile/Grant, Aged Rat

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1      MTDQMADFG AARYLRKSEK ERLEAQRFP DIRTECFVPD DKEEYVAKI VSREGGKVTG ETENGTVTV KEDQVMQQNP
81     PKFDKIEDMA MLTFLHEPAV LYNLKERYAA WMIYTYSGLF CVTVNPKYKL PVYNAEVVAA YRGKKRSEAP PHIFSISDNA
161    YQYMLTDREN QSILITGESG AGKTVTNTRV IQYFASIAAI GDRSKKDNPN ANKGTLEDQI IQANPALEAF GNAKTVRNDN
241    SSRFGKFIRI HFGATGKLAS ADIETYLLEK SRVIFQLKAE RNYHIFYQIL SNKKPELDDM LLVTNNPYDY AFVSOGEVSV
321    ASIDDSELLL ATDSAFDVLG FTAEEKAGVY KLTGAIMHYG NMKFKQKQRE RQAEEDGTEB ADF SAYLMGL NSADLLKGLC
401    HPRVKVGNFY VTKGQSVQVQ YYSIGALAKS VYEKMFNWMV TRINATLETQ QPRQYFIGVL DIAGFEIFDF NSFELCINF
481    TNEKLQFFN HHMFVLEQEE YKKEGIEWEF IDFGMDLQAC IDLIEKPMGI MSILEEECMF PKATDMTFKA KLYDNHLGKS
561    NNFQKPRNVK GKQEAHFSLV HYAGTVDYNI LGWLEKNKDP LNETVVGLYQ KSSLKLMATL FSTYASADTG DSGKGGKGGK
641    KGSFQTVSA LHRENLNKLM TNLRTTHPHF VRCIIPNERK APGVMDNPLV MHQLRCNGVL EGRICRKGKFN PNRILYGFDR
721    QRYRILNPAA IPEGQFIDSG KGAEKLLGSL DIDHNQYKFG HTKVFVKAGL LGLLEEMRDE RLSRIITRIQ AQARGQLMRI
801    EFKKMEVERRD ALLVIQWNIR AFMGVKNWPW MKLYFKIKPL LKSAETEKEM ANMKEEFGRV KDALEKSEAR RKELEKMSV
881    LLQEKNDLQL QVQAEQDNLA DAEERCDQLI KNKIQLEAKV KEMTERLEDE EEMNAELTAK KRKLEDECSE LKKDIDDLLEL
961    TLAKVEKEKH ATENKVNLT EEMAGLDEII AKLTKEKAL QEAHQALDD LQAEEDKVNT LTKSKVKLEQ QVDDLEGSLE
1041   QEKKVRMDLE RAKRLEGLD KLTQESIMDL ENDKLQLEEK LKKKFDISQ QNSKIEDEQA LALQLQK KKL ENQARIELE
1121   EELAEARTAR AKVEKLRSDL TRLEEISER LEEAGGATSQ QIEMNKKREA EFQKMRDLE EATLQHEATA AALRKKHADS
1201   VAELEGEIDN LQRVQKLEK EKSEFPLELD DVTSHMEQII KAKANLEKVS RLEDDQANEY RVLKEEQRS LNDFTTQAK
1281   LQTENGLAR QLEEKALIW QLTRGKLSYF QQMEDLRFQL BEEGKAKNAL AHALQSARHD CDLLREQYEE EMEAKAELQR
1361   VLSKANSEVA QWRTKYETDA IQRTELEEA KKKLAQLRQD AEEAVEAVNA KCSSLEKTKH RLQNEIEDLM VDVERSNAAA
1441   AALDKKQRFN DKILAEWKQK YEESQSELES SQKEARSLST ELFKLKNAYE ESLEHLETFK RENKNLQEEI SDLTEQLGEG
1521   GKNVHELEKI RKQLEVEKLE LQSALEEAEA SLEHEEGKIL RAQLEFNQIK AEIER LAEK DEEMEQAARN HLRVVDSLQT
1601   SLDAETRSRN EALRVKCKME GDLNEMEIQL SQANRIASEA QKHLKNAQAH LKDTQLQLDD AVRANDDLKE NIAIVERRNT
1681   LLQAELEELR AVVEQTERTS KLAEQELIET SERVQLBHSQ NTSLINQK MKADLSQLOT EVEEAVQEQR NAEKAKKAI
1761   TDAAMMAEEL KKEQDTSABL ERMKNMEQT IKDLQHRLDE AEQIALKGGK KQLQKLEARV RELENELEAE QKRNAESVKG
1841   MRKSERRIKE LTYQTEEDKK NLVRLQDLVD KLQLKVKAYK RQAEAEAEQA NTNLSKFRKV QHELDEAEER ADIAESQVNK
1921   LRAKSRDIGA KQKMHDEE

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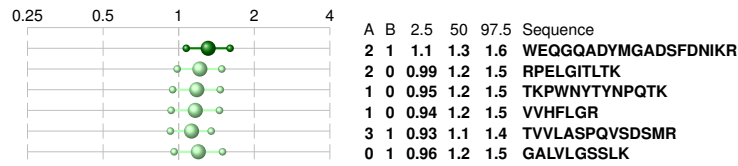


5.131 glycogenin 1 [Rattus norvegicus]

Protein Accession	gi 13591969	
Mean Expression Ratio	1.19	
Median Expression Ratio	1.19	
Credible Interval	(1.02, 1.40)	
Associated Peptides	6	
Associated Spectra	12	
Coverage	0.219	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.18	1.58
Avg..iTRAQ.Ratio....116.114.	1.24	0.784
Avg..iTRAQ.Ratio....117.114.	1.44	1.19

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1      MTDQAFVILT TNDAYAKGAL VLGSSSLKQHR TTRRTVVLAS POVSDSMKV LETVFDEVIM VDVLDSGDSA HLTLMKRPEL
81     GITLTKLHCW SLTQYSKCVF MDADTLVLSN IDDLFEREEL SAAPDPGWD CFNSGVFVYQ PSJETYNQLL HLASEQGSFD
161    GGDQGLLNTY FSGWATTDIT KHLPFVYNLS SLSIYSYLPFA FKAFGKNAK VBFGLRITKPW NYFYNPQTKS VKCESQDPFV
241    SHPEFLNLWW DTFTTNVLP LQHHGLVKDA GSYLMMEHVT GALSDLSFGE APPASQPSSL SEERKERWEQ GQADYMGADS
321    FDNIKRRLDT YLQ
  
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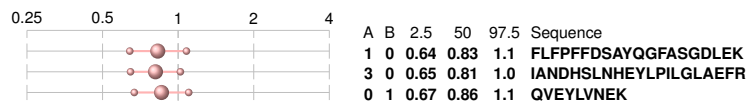


5.132 glutamate oxaloacetate transaminase 1 [Rattus norvegicus]

Protein Accession	gj 6980970	
Mean Expression Ratio	0.844	
Median Expression Ratio	0.844	
Credible Interval	(0.684, 1.05)	
Associated Peptides	3	
Associated Spectra	5	
Coverage	0.121	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.794	0.864
Avg..iTRAQ.Ratio....116.114.	0.7	0.753
Avg..iTRAQ.Ratio....117.114.	0.727	1.00

```

1      MAPPSFFAQV  PQAPPVLVFK  LIADFRDDPD  PRKVN LGVGA  YRTDDSQPWV  LPVVTKVEQK  IANDHSLNHE  YLPILGLAEF
81     RSCASQLVLG  DNSPALRENG  VGGVQSLGAT  GALRIGADFL  ARWYNGTDNK  NTFVYVSSPT  WENHNGVFSA  AGFKDIRSYR
161    YWDAEKRRGLD  LQGFNDLLEN  APEFSIFVLH  ACAHNPTGTD  PTEEEWKQIA  AVMKRRFLFP  FFDSEYQGFPA  SGDLEKDAWA
241    IRYFVSEGF  LFCPQSF  SKN  FGLYNERVGN  LTVVGKEHDS  VLRVLSQMEK  IVRITWSNPP  AQQGARIVATT  LSNPELFKEW
321    KGNVKTADR  ILTMRSELRA  RLEALRTPGT  WSHITEQIGM  FSFTGLNPKQ  VEYLVNEKHI  YLMPSGRINM  CGLTTKNLDY
401    VATSINEAVT  KFQ
    
```



5.133 PREDICTED: similar to tumor protein D52 isoform 1 [Rattus norvegicus]

Protein Accession	gj 109466311	
Mean Expression Ratio	1.18	
Median Expression Ratio	1.18	
Credible Interval	(0.875, 1.59)	
Associated Peptides	1	

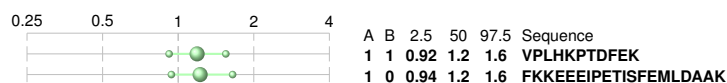
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.92
Avg..iTRAQ.Ratio....116.114.	1.80
Avg..iTRAQ.Ratio....117.114.	1.64



5.134 growth and transformation-dependent protein [Rattus norvegicus]

Protein Accession	gi 71361663	
Mean Expression Ratio	1.18	
Median Expression Ratio	1.18	
Credible Interval	(0.928, 1.53)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	0.174	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.45	1.28
Avg..iTRAQ.Ratio....116.114.	1.48	0.916
Avg..iTRAQ.Ratio....117.114.	1.75	1.51

1 MWSLRGLRLA AGHCFRLCER NVSSPLRLTR NTDLKRINGF CTKPQESPKA PTQSYRHRVP LHKPTDFEKK ILLWSGRFKK
 81 EESTPEPTISF EMLDAAKXNKI RVKVSYLMI A LTVAGCVYMV IEGKKLEPRK ESPSERGGSY EGQSGLDVVFV LDLEKPGIFQ
 161 KPSPSGKAIE RERDTVQG

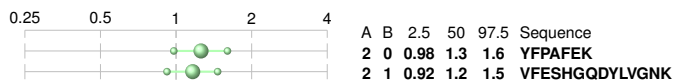


5.135 hypothetical protein LOC501110 [Rattus norvegicus]

Protein Accession	gi 66730521	
Mean Expression Ratio	1.18	
Median Expression Ratio	1.18	
Credible Interval	(0.948, 1.48)	
Associated Peptides	2	
Associated Spectra	5	
Coverage	0.0946	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.27	1.03
Avg..iTRAQ.Ratio....116.114.	1.41	0.851
Avg..iTRAQ.Ratio....117.114.	1.46	1.40

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1      MAEKPLFHYD EARGRMESVR WLLAAAGVEY EEKFIHTNED LEKLRSDGVL MFQQVPMVEV DGMKLVQTRA IMNYFSSKYN
81     LYGKDMKERA LIDMYSEGLA DLNEMFILYP FDPFGVKKEAN IALMKEKATN RYFPAFEKVF ESHGQDYLVG NKLSKADVHL
161    VEMIYNMEEL DTNILANFPL LQALKTRISD MPTIKKFLQP GSQRQPPVDE KSIQKTRKIF KF
  
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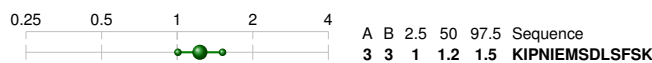


5.136 beta-2-microglobulin [Rattus norvegicus]

Protein Accession	gi 7549746	
Mean Expression Ratio	1.18	
Median Expression Ratio	1.18	
Credible Interval	(0.945, 1.48)	
Associated Peptides	1	
Associated Spectra	6	
Coverage	0.118	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.10	1.39
Avg..iTRAQ.Ratio....116.114.	1.09	1.05
Avg..iTRAQ.Ratio....117.114.	1.40	1.62

```

1      MARSVTVIFL VLVSLAVVLA IQKTPQIQVY SRHPPENGKP NFLNCYVSQF HPPQIEIELL KNGKKIPNIE MSDLSFSKDW
81     SFYILAHTEF TPTETDVYAC RVKHVTLKEP KTVTWDRDM
  
```



5.137 PREDICTED: similar to CD34 antigen [Rattus norvegicus]

Protein Accession	gij109498401
Mean Expression Ratio	1.18
Median Expression Ratio	1.18
Credible Interval	(0.905, 1.54)
Associated Peptides	1
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.28
Avg..iTRAQ.Ratio....116.114.	1.64
Avg..iTRAQ.Ratio....117.114.	2.02

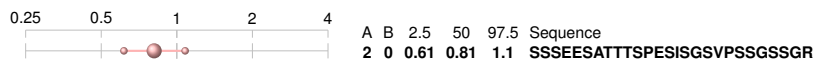


5.138 RAD23a homolog [Rattus norvegicus]

Protein Accession	gij61557236
Mean Expression Ratio	0.845
Median Expression Ratio	0.847
Credible Interval	(0.643, 1.11)
Associated Peptides	1
Associated Spectra	2
Coverage	0.077
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1
Avg..iTRAQ.Ratio....116.114.	0.978
Avg..iTRAQ.Ratio....117.114.	0.397

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1   MAVTITLKTLL QQQTFKIRME PDETVKVLKE KIEAEKGRDA FVAVGQKLIY AGKILSDDDIP IKEYHIDEKN FVVVMVTRAK
81  AGQGTAPPE ASPTAAPEPS TFFPPAPASG MSHPPPSNRE DKSSSEESAT TTSPEISGS VPSSGSSGRE EDAASTLVTG
161 SEYETMLTEI MSMGYERERV VAALRASYNH PHRAVEYLLT GIPGSPEPEH GSVQESQAPE QPATEAGENP LEFLRDQPFQF
241 QNMRQVIQQN FALLPALLQQ LGQENPQLLQ QISRHQEQFI QMLNEPPGEL ADISDVEGEV GALGEEAPQM NYIQVTPQEK
321 EAIERSPACP KLLARFGSDR WAPFLGCPSS L
    
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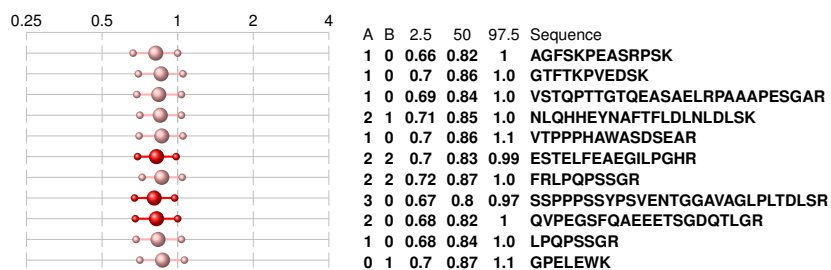


5.139 NADH dehydrogenase (ubiquinone) flavoprotein 3-like [Rattus norvegicus]

Protein Accession	gij12018282	
Mean Expression Ratio	0.848	
Median Expression Ratio	0.848	
Credible Interval	(0.743, 0.972)	
Associated Peptides	11	
Associated Spectra	22	
Coverage	0.369	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.836	0.75
Avg..iTRAQ.Ratio....116.114.	0.94	0.681
Avg..iTRAQ.Ratio....117.114.	0.835	0.781

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1   MAVSLLLRRG RIRALKAALL EAKVFRGELA STVPLSTESE NNKKAAGPTS KTESVFKDVV GAEERAKLLD THTAAALSKS
81  SPPSSSYPSV ENTGGAVAGL PLTDLSRKTLL VAFPQKVTPP PHAWASDSEA FRHVQKVTKD SSSSSSSSSS DSDSDGEEHG
161 SDIGPRVASK SKAGFSKPEA SRPSKNGAPK ITVFAKEKAK VQKPHTDVTY PEKPLQPKKK GTFTKPVEDS KEIRSKLMTS
241 KPQSSEVLEQ KMKEKQHQGK RRPDKTGKES TELFEAEGIL PGHRKARVST QPTTGTQEAS AELRPAAAPE SGAPQEAKEP
321 ELEWK TASPL VRKESLEKQV PEGSFQAEAE TSGDQTLGRY SKTVPVVEKN TFGERAGPQL EGTFAQPAGE APPTDAGPPQ
401 EAPGDTQEPT LVPSSDSTTT YK NLQHHEYNAFTFLDLNLD LSKFRLPQPS SGRESFRH
    
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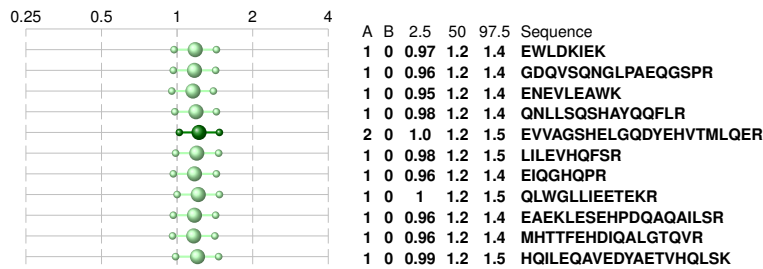


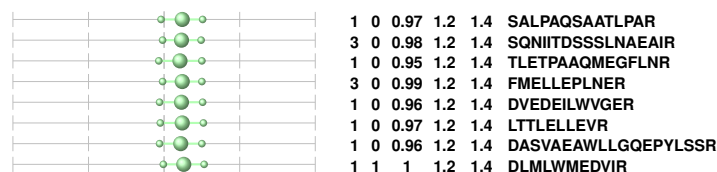
5.140 spectrin beta 2 [Rattus norvegicus]

Protein Accession	gi 61557085	
Mean Expression Ratio	1.18	
Median Expression Ratio	1.18	
Credible Interval	(1.05, 1.33)	
Associated Peptides	19	
Associated Spectra	25	
Coverage	0.113	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.17	0.402
Avg..iTRAQ.Ratio....116.114.	1.12	2.09
Avg..iTRAQ.Ratio....117.114.	1.55	2.62

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1      MTTT VATDYD NIEIQQQYSD VNNRWDVDDV DNESSARLF ERSRIKALAD EREAVQKKT FTKWVNSHLAR VSCRITDLYT
81     DLRDGRMLIK LLEVLSGERL PKPTKGRMRI HCLENVDKAL QFLKEQRVHL ENMGSHDIVD GNHRLTLGLI WTII LRFQIQ
161    DISVETEDNK EKKSADKALL LWCQMTAGY PNVNIHNFTT SWRDGMAFNA LIHKHRPDLI DFDKLLKSNA HYNLQNAFNL
241    AEQHLGLTKL LDPEDISVDH PDEKSIITYV VTYHYHFSKM KALAVEGKRI GKVLDNAIET EKMIKEYESL ASDLLEWIEQ
321    TIIILNNRKF ANSLVGVQQQ LQAFNTYRTV EKPPKFTKKG NLEVLLFTIQ SKMRRANNQKV YMPREGKLIS DINKAWERLE
401    KAEHERELEL RNELIRQEKL EQLARRFDRK AAMRETWLESE NQRLVSDNF GFDDLPAVEAA TKKHEAIEDT IAAYEERVQA
481    VVAVARELEA ESYHDIKRIT ARKDNVIRLW EYLLELRLAR RQRLEMNLGL QKIFQEMLYI MDWMDEMVKV LLSQDYGKHL
561    LGVEDLLQKH ALVEADIAIQ AERVGVNAS AQKFATDGEQ YKPCDPPQVIR DRVAHMEFCY QELCQLAAER RARLEESRRL
641    WKFFWEMAE EGWIREKEKI LSDDYQKDL TSMRLLSKH RAFEDEMSGR SGHFEQAIKE GEDMIAEEHF GSEKIRERIS
721    YIREQWANLE QLSAIRKKRL EASLLHQFQ ADADDIDAWM LDILKIVSSN DVGHDYESTQ SLVKKHKDVA EEISNYRPTI
801    DTLHEQAGAL PQAHAESPDV KGRLAGIEER YKEVAELTRL RKQALQDTLA LYKMFSEADA CELWIDEKEQ WLNMQIPEK
881    LEDLEVIQHR FESLEPEMNN QASRVAVVNO IARQLMHSQH PSEKEIRAQQ DKLNRWSQF RELVDRKKDA LLSALSIOQY
961    HLECNETKSW IREKTKVIES TQDLGNDLAG VMA LQRKLTG MERDLVAIEA KLSDLQKBAE KLESEHPDQA QAILSR LAEI
1041   SDVWEEMKTT LKNREASLGE ASKLQQLFRD LDDFQSWLSR TQTAIASEDM PNTL TEAEKL LTQHENIKNE IDNYBEDYQK
1121   MRDMGEMVTQ GQTD AQYMF L RQRLQALDTG WNELHKMWEN RQNL LSQSHA YQQFLFDTKQ AEAFLNNQEQ VLAHTEMPPT
1201   LEGAEAAIKK QEDFMTTMDA NEEKINAVVE TGRRLVSDGN INSDRIQEKV DSIDDRHRKN REAASELLMR LKDNRD LQKF
1281   LQDCQELSLW INEKMLTAQD MSYDEARNLH SKWLKHQAFM AELASNKENL DKIEBEGMQL ISEKPEAVL VKEKLTGLHK
1361   MWEVLESTQ TKAQR LFDAN KAELFTQSCA DLDKWLHGLE SQIQSDDYGK DLTTSAQNKV LDGASVFLM YSCP PRCWRI
1441   RKKRGRAQMR VDSKRLTVQT K MELLEPLN ERKHNLLASK EIHQFNROVE DEILWVGERM PLATSTDPHG NLQTVQLLIK
1521   KNQTLQK TIQ GHQP I IDIF ER SQNIITDS SSLNAEAI RQ RLADLQQLWG LLIEETEKR H RRLEEAHKAQ QYF DAAEAE
1601   AWMSEQELYM MSEKAKDEQ SAVSMLKKHQ ILEQAVEDYA ETVHQLS TS RALVADSHPE SERISMRQSK VDKLYAGLKD
1681   LAEERRGKLD ERHRLFQLNR EVDDLEQWIA EREV VAGSHE LGQDYEHVTM LQERFPREFAR DTGNIGQERV DTVNHMADDL
1761   INSGHSDAAT IAERKDG LNE AWADLLELID TRTQILAASY ELHKFYHDAK EIFGRIQDKH KKLPEELGRD QNTVETLQRM
1841   HTTFEHDIAQ LGTQVRQLQE DAARLQAAYA GDKADDIQR ENEVLEAWKS LLDACEGRRV RLVDTGDKFR FFSMVRDLML
1921   WMEDVIQIE AQEKPRDVSS VELLMNHHQG IKA EIDARN D SFTACIELG ALLARKHYAS EEIKKLLQL TEKRKEMIDK
2001   WEDRWELRL ILEVHQFSRD ASVAEAWLLG QEPYLSREI GQSVDEVEKL IKRHEAFEKS AATWDERFSA LER LTTLELL
2081   EVLRQEEEEE RKRPPSPPEP SAKVSEEAES QQWDTSKGDQ VSQNGLPAAEQ GSPRMAGTME TSEMVGAAE QRTSSKESP
2161   VPSPTS DRKA K SALPAQSA TLPARTLETP AAQMEGFLNR KHEWEAHNKK ASSRSWHNVY CVINNQEMGF YKDAKSAASG
2241   VPHYSEVPVS LKEAICEVAL DYKKKHHVFK LRLSDGNEYL FQAKDDDEM N TWIQAITS AI SSDKHDTSAS TQSTPASSRA
2321   QTLPTS SVVTI TSESSPGKRE KDKEKDKER FSLFGKXK
    
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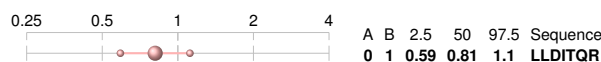


5.141 PREDICTED: similar to DC-STAMP domain containing 1 [Rattus norvegicus]

Protein Accession	gij109467025
Mean Expression Ratio	0.847
Median Expression Ratio	0.848
Credible Interval	(0.631, 1.15)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00954
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.496
Avg..iTRAQ.Ratio....116.114.	0.48
Avg..iTRAQ.Ratio....117.114.	0.443

```

1      MSFLSSTFHS LGIFEKISGI KEALKNRLLD ITQRQYRAGG QQRKRPHITII QGLLRWGLPV SWSRFLWRQP GEFVPTAFLL
81     GTGTGGLLAI GLFQLLVNPM NIYEEQKVVA LYGLTSLGAI GWGISPHIRC ASLLLLVPKML GKEGRLFIMG YALASIYKGP
161    VANLQYNINE VIASLGCTVE LQINNTRSAW RVSTAPLRV FKDMLSSKDS LKTEIANVST SFEDLDAQVE SNIGYSPEDK
241    DMDTAPGTKA LGTGTSRARL HLTQMVYEL KTKLRCSHVV NKAILSCYRW FDKKHQRQCMQ RIQVPLLSL LCLPMKFKFF
321    CNIKVMEIW  CHKRIPEVGN FGQTYDSVNO SIHLSGEFS ANIDIKEQKQ SAVVGLSTNW EHVSVVEVRDY ARQBEARLQW
401    AVGLMHVLLS CTFLLVFHA  FSYMDNWNWD IRFDNIYIST YFYQIDARRK KLGKQSLPL RKAEKTSVIF PLKATIQATE
481    MRNVIRELLE TLPILLLLIV LFAIDWVLYS IPDITGHHSF VQYSFRSSHK LEINVEGDSI LARLLRKTIG ALNTTSDTEM
561    ETNNMPCLPR AVGLSAGGYF RASLPTCLLM CVCLAQAFGY RLRRVIAAFY FPKREKRVL FLYNELLRKR SAFTKLRRAA
641    IVRRARQQT  PRPPVVDALY RRCPLLRRLT RRCVVCQAL ETPESYVCPT PDCKALYCRS CWDDMQRQCP VCTPREELSS
721    SAHSDSNDT  VYGE
    
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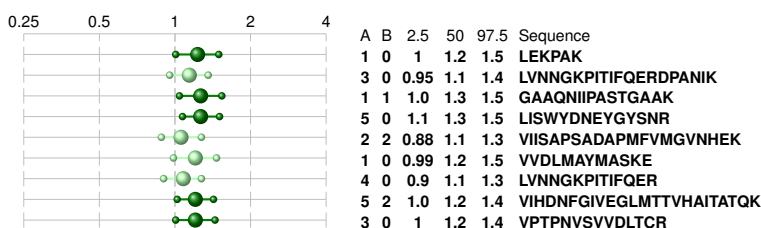
5.142 PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]

Protein Accession	gij62653546
Mean Expression Ratio	1.18

Median Expression Ratio	1.18
Credible Interval	(1.04, 1.34)
Associated Peptides	9
Associated Spectra	30
Coverage	0.378
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.34
Avg..iTRAQ.Ratio....116.114.	0.987
Avg..iTRAQ.Ratio....117.114.	1.51

```

1      MVKVGVNGFG RIGRLVTRAA FSCDKVDIVA INDPFDLNY MVYMSQYGSP HGKFNSTVKA ENGLVNNGK PITIFOERDP
81     ANIHWGDAGA EYVMESTGIF TTMEKAG AHL KGGAKRVIIS APSADAPMFV MGVNHEKYDN SLKIVSNASC TTNCLAPLAK
161    VIHDNFGIVE GLMTTVHAIT ATQKTVDGPS GKLWRDGRGA AQNIIPASTG AAKAVGKVIP ELNGKLTGMA FRVPTPNVSV
241    VDLTCRLEKP AKYDDIKKVV KQAAEGPLKG ILGYTEDQVV SCDFNNSHNS STFDAGAGIA LNDNFVKLIS WYDNEYGYSN
321    RVVDLMAYMA SKE
  
```



5.143 clusterin [Rattus norvegicus]

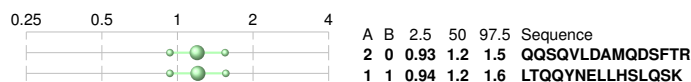
Protein Accession	gij46048420	
Mean Expression Ratio	1.18	
Median Expression Ratio	1.18	
Credible Interval	(0.932, 1.49)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.0671	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.31	1.76
Avg..iTRAQ.Ratio....116.114.	1.25	1.45
Avg..iTRAQ.Ratio....117.114.	1.37	1.23

NHLBI Zile/Grant, Aged Rat

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1      MKILLLCVAL LLTWDNGMVL GEQEFSDNEL QELSTQGSRY VNKEIQNAVQ GVKHIKTLLIE KTNAERKSLI NSLEBAKSKK
81     EGALDDTRDS EMKLFKAFPEV CNETMMALWE ECKPCLKHTC MKFYARVCRS GSGLVGRQLE EFLNQSSPFY FWMNGDRIDS
161    LLESDRQQSQ VLDAMQDSFT PASGIIHTLF QDRFFTHEPQ DIHHFSPMGF PHKRPFLYP KSLRVRSLMP LSHYGPLSFH
241    NMFQFFFDMI HQAQQAMDVQ LHSPALQFPD VDFLKEGEDD PTVCKEIRHN STGCLKMKGQ CEKCQEILSV DCSTNNPQA
321    NLRQELNDSL QVAERLTQQY NELLHSLQSK MLNTSSLLEQ LNDQFTWVSQ LANLTQGDQ YLRVSTVTHH SSDSEVPSRV
401    TEVVVKLFDS DPITVVLPPE VSKDNPKFM DVAEKALQEY RRKSRME

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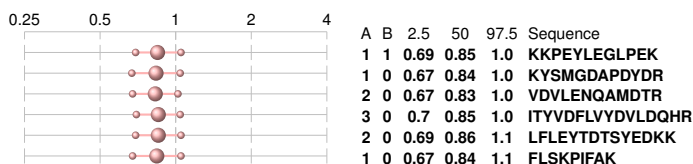
5.144 "glutathione S-transferase, mu 2 [Rattus norvegicus]"

Protein Accession	gi 28933457	
Mean Expression Ratio	0.849	
Median Expression Ratio	0.85	
Credible Interval	(0.721, 1)	
Associated Peptides	6	
Associated Spectra	11	
Coverage	0.339	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.789	0.752
Avg..iTRAQ.Ratio....116.114.	0.786	0.696
Avg..iTRAQ.Ratio....117.114.	0.83	1.34

```

1      MPMTLGYWDI RGLAHAIRLF LEYTDTSYED KKYSMGDAPD YDRSQWLSEK FKLGLDFPNL PYLIDGSHKI TQSNAILRYL
81     GRKHNLGGET EEERIRVDVL ENQAMDTRLQ LAMVCYSPDF ERKKPEYLEG LPEKMKLYSE FLGKQPWFAG NKITYVDPLV
161    YDVLQHRIF EPKCLDAFPN LKDFVARFEG LKKISIDYMK SGRFLSKPIFA MAFWNP

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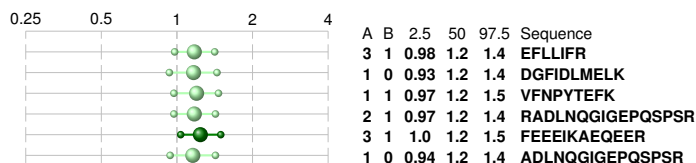
5.145 EF hand domain containing 2 [Rattus norvegicus]

Protein Accession	gi 72255531
Mean Expression Ratio	1.18

Median Expression Ratio	1.18	
Credible Interval	(1.01, 1.37)	
Associated Peptides	6	
Associated Spectra	15	
Coverage	0.226	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	1.43
Avg..iTRAQ.Ratio....116.114.	1.11	1.16
Avg..iTRAQ.Ratio....117.114.	1.38	1.51

```

1   MATDELASKL SRRLQMEDEG GEATEQPGLN GAAAAAAEAP DETAQALGSA DDELSAKLLR RADLNQIGIG PQSPSRRVFN
81  EYTFEFKEFSR KQIKDMEKMF KQYDAGK DGF IDLMELI LMM EKLGAPOQTHL GLKSMIQEVD EDFDSKLSFR EFLLIFFKAA
161 AGELQEDSGL HVLARLSEID VSTEGVKGAK NFFEAKVQAI NVSSRFEEEI KAEQERKKQ AEEVKQRKAA FKELQSTFK
  
```



5.146 PREDICTED: similar to ubiquitin-conjugating enzyme E2O [Rattus norvegicus]

Protein Accession	gij109492276
Mean Expression Ratio	0.85
Median Expression Ratio	0.85
Credible Interval	(0.625, 1.14)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00686
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.607
Avg..iTRAQ.Ratio....116.114.	0.483
Avg..iTRAQ.Ratio....117.114.	0.61

NHLBI Zile/Grant, Aged Rat

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1      MTSCFLVRAA LRPASVLP PPQASSASPS DRAAAPSNI PAAAAATAAA VAAAAARDSR RAVMADPAAP APAPAPAQAQ
81     AAAAPTAAA PAAAPPPAPA TDSASGPSSD SEDGRGSSGC SEAGGAGHEE GRASPLRRGY VRVQWYPEGV KQHVKETLKL
161    LEDRSVVRPD VVRHMRSTDS QCGTVIDVNI DCAVKLIGTN CIIYPVNSKD LQHIWFFMYG DYIAYDCWLG KVDLKNQII
241    LKLSNGARCS MNTEDGAKLY DVCPHVSDSG LFFDSDYGFY PGQVLIGPAK IFSSVQWLSG VKPVLSTKSK FRVVVEEVQV
321    VELKVTWITK SFCPGGTDV SPPPSVIAQE NLGRVKRLGC FDHAQRQLGE RCLYVFPKAV EPAKIAWECF EKNCAQGEES
401    MAKVKRLLK KQVVRIMSCT PDAQCSRDA MEDPDKKGEA RAGSEVGSAS PEEQLDGSAS PVEMQDEGSE ELHETGEPLP
481    PFLKEGGDE GLHSAEQDAD DEAADTDDT SSVTSSASST TSSQSGSGTG RKKSIPLSIK NLKRKHKRKK NKITRDFKPG
561    DRVAVEVVT MTSADVWQD GSVECNIRSN DLFPVHHLN NEFCPGDFVV DKRVQSCPDP AVYGVVQSGD HVGRTCMVKW
641    FKLRFSGDDV ELIGEEEDVS VYDIADHPDF RFRTTDIVIR IGNTEDGALP KEDEPSVGQV ARVDVSSKVE VVWADNSKTI
721    ILPQHLYNIE SEIEESDYDS VEGSTSGASS DEWEDDSDSW ETDNGLVDDE HPKIEDLAAI LPTEQPAAPE EDKGVVISEE
801    AATAAIQAV AMAAPVAGLM EKAGKDGPPK SFRELKAIK ILESKNMTV EQLLTGSPTS PTVPEKPTR EKKFLDDIKK
881    LQENLKKTLN NVAIAEEEMK EAVPDTERKE DKPEVQSPVK AEWPSVETPV CQQCGRPGV TFTAAGKEVF SVLEFAPSNI
961    SFKKIEFQPP EAKKFFSTVR KEMALLATSL PDGIMVKTFE DRMDLFSALI KGPTRTPYED GLYLFDIQLP NIYPVAVPHF
1041   CYLSQCSGRL NPNLYDNGKV CVSLLGTVIG KGTERRWTSKS SLLQVLISIQ GLILVNEPEY NEAGFDSDRG LQEGYENSRC
1121   YNEMALIRVY QSMTQLVRRP PEVFEQEIRQ HFSVGGWRLV NRIESWLETH VVLERAQALP NGVPKDSSSL EPQAAELSD
1201   SGREPEPDVG MTPGEASQGS DSEGGAQGPA SASREHPQT ETAPDASAPP SVRPKRRRKS YRSFLPEKSG YPDIGFPLFP
1281   LSKGFIKSIR GVLTFRAAL LEAGMPESTE DK

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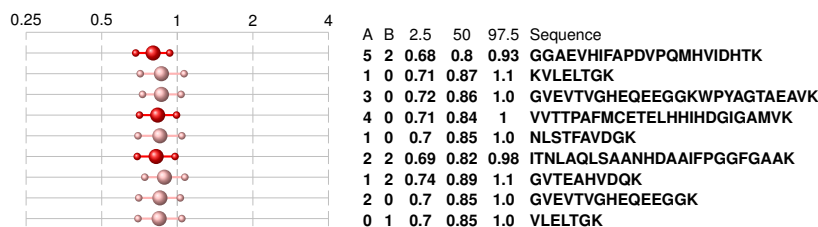
5.147 es1 protein [Rattus norvegicus]

Protein Accession	gi 51948422	
Mean Expression Ratio	0.852	
Median Expression Ratio	0.85	
Credible Interval	(0.756, 0.964)	
Associated Peptides	9	
Associated Spectra	26	
Coverage	0.474	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.962	0.599
Avg..iTRAQ.Ratio....116.114.	0.744	0.883
Avg..iTRAQ.Ratio....117.114.	0.844	0.935

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1      MAAVRVLVSP RLASALLPLS GRHRTTSQRA AIHSSAPRPR ARVALVLVSGC GYVDGTEIHE ASAILVHLSR GGAEVHIFAP
81     DVPQMVIDH TKGEPSEKES RNVLAESARI ARGKITNLAQ LSAANHDAAI FPGGFGAAKN LSTFAVDGKD CKVNKEVERV
161    LKFPHGAKKP IGLCCIAFVL AAKVIK GVEV TVGHEQEEGG KWPYAGTAEA VVALGAKHCV KGVTEAHVDQ KNKVVTTTAP
241    MCETELHHIH DGIGAMVKKV LELTGG

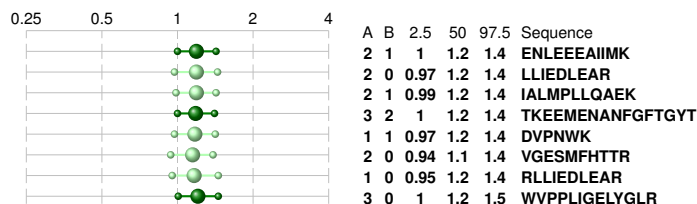
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5.148 "PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 [Rattus norvegicus]"

Protein Accession	gi 109481899	
Mean Expression Ratio	1.17	
Median Expression Ratio	1.17	
Credible Interval	(1.03, 1.34)	
Associated Peptides	8	
Associated Spectra	21	
Coverage	0.535	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	1.37
Avg..iTRAQ.Ratio....116.114.	1.35	0.901
Avg..iTRAQ.Ratio....117.114.	1.21	1.53

1 MASKVKQDMP PPRGYGPIDY KRNLPRRRGL SGYSMFALGI GALIFGYWRI MRWNRERRL LIEDELEARIA LMPLLQAEKD
 81 RRRLQILREN LEEEAIIIMK VPNWKVGESM FHTTRWVPL IGELYGLRTE EEMENANFGF TGYT



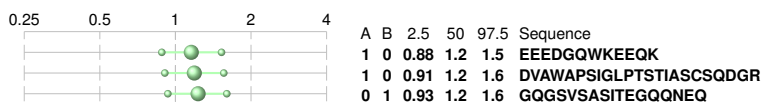
5.149 SEC13-like 1 [Rattus norvegicus]

Protein Accession	gi 55741774	
Mean Expression Ratio	1.18	
Median Expression Ratio	1.17	
Credible Interval	(0.926, 1.50)	
Associated Peptides	3	
Associated Spectra	3	
Coverage	0.161	

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.21	1.06
Avg..iTRAQ.Ratio....116.114.	1.38	1.86
Avg..iTRAQ.Ratio....117.114.	1.14	2.95

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1      M V S V I N T V D T   S H E D M I H D A Q   M D Y Y G T R L A T   C S S D R S V K I F   D V R N G G Q I L I   A D L R G H E G P V   W Q V A W A H P M Y   G N I L A S C S Y D
81     R K V I I W K E E N   G T W E K T H E H S   G H D S S V N S V C   W A P H D Y G L I L   A C G S S D G A I S   L L T Y T G E G Q W   E V K K I N N A H T   I G C N A V S W A P
161    A V V P G S L I D Q   P S G Q K P N Y I K   K F A S G G C D N L   I K L W R E E E D G   Q W K E E Q K L E A   H S D W V R D V A W   A P S I G L P T S T   I A S C S Q D G R V
241    F I W T C D D A S G   N M W S P K L L H K   F N D V V W H V S W   S I T A N I L A V S   G G D N K V T L W K   E S V D G Q W V C I   S D V N K G Q G S V   S A S I T E G Q Q N
321    E Q
    
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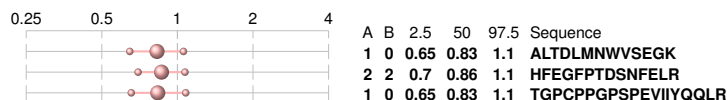


5.150 leukotriene B4 12-hydroxydehydrogenase [Rattus norvegicus]

Protein Accession	gi 20302022	
Mean Expression Ratio	0.853	
Median Expression Ratio	0.852	
Credible Interval	(0.691, 1.04)	
Associated Peptides	3	
Associated Spectra	6	
Coverage	0.140	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.808	0.874
Avg..iTRAQ.Ratio....116.114.	0.638	0.719
Avg..iTRAQ.Ratio....117.114.	0.65	1.43

```

1      M V Q A K T W T L K   K H F E G F P T D S   N F E L R T T E L P   P L N N G E V L L E   A L F L S V D P Y M   R V A A K K L K E G   D S M M G E Q V A R   V V E S K N S A F P
81     T G T I V A L L G   W T S H S I S D G N   G L R K L P A E W P   D K L P L S L A L G   T V G M P G L T A Y   F G L L D I C G L K   G G E T V L V N A A   A G A V G S V V G Q
161    I A R L K G C K V V   G T A G S D E K V A   Y L K K L G F D V A   F N Y K T V K S L E   E A L R T A S P D G   Y D C Y F D N V G G   E F S N T V I L Q M   K T F G R I A I C G
241    A I S Q Y N R T G P   C P P G P S P E V I   I Y Q Q L R M E G F   I V T R W Q G E V R   Q K A L T D L M N W   V S E G K I R Y H E   Y I T E G F E K M P   A A F M G M L K G D
321    N L G K T I V K A
    
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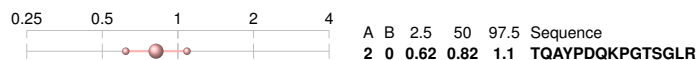


5.151 phosphoglucomutase 1 [Rattus norvegicus]

Protein Accession	gi 77627971
Mean Expression Ratio	0.853
Median Expression Ratio	0.853
Credible Interval	(0.649, 1.13)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0267
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.815
Avg..iTRAQ.Ratio....116.114.	0.584
Avg..iTRAQ.Ratio....117.114.	0.653

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1      MVKIVTVKTQ AYPDQKPGTS GLRKRKVFQ GNANYAENFI QSIYSTVEPA LRQEATLVVG GDGRFYMTEA IQLIVRIAAA
81     NGIGRLVIGQ NGILSTPAVS CIIRKKAIG GIILTASHNP GGPNGDFGIK FNISNGGPAP EAITDKIFQI SKTIEEYAIC
161    PDLKVDLSVL GKQQFDLENK FKPFTVEIVD SVEAYATMLR NIFDFNALKE LLSGPNRLKI RIDAMHGVVG PYVKKILCEE
241    LGAPANSAVN CVPLEDFGGH HPDPNLTAAA DLVETMKSGE HDFGAAFDGD GDRNMILGKH GFFVNPDSVS AVIAANIFSI
321    PPFQQTGVRG FARSMPTSGA LDRVANATKI ALYETPTGWK FFGNLMDSK LSLCGEESFG TGSDHIREKD GLWAVLAWLS
401    ILATRKQSV E DILKDHQKF GRNFFTRYDY EEVEAEGANK MMKDLEALML DRSFVGGQFS ANDKVYTV EK ADNFEYSDPV
481    DGSISKNQGL RLIFADGSR I FRLSGTGSA GATIRLYIDS YEKDAAKINQ DPQVMLAPLI SIALKVSQ LQ ERTGRTAPT V
561    IT
  
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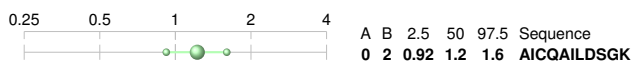


5.152 PREDICTED: similar to LanC lantibiotic synthetase component C-like 3 [Rattus norvegicus]

Protein Accession	gi 109511543
Mean Expression Ratio	1.17
Median Expression Ratio	1.17
Credible Interval	(0.887, 1.52)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0428
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.19
Avg..iTRAQ.Ratio....116.114.	1.18
Avg..iTRAQ.Ratio....117.114.	1.63

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1      MRVGCILHEF RVGKSLRRTV VNAEEDLSVL TPAQIKAICG AILDSGKQYA LKRRKPFPLM YSYYGTEYLG AAHGLSSILQ
81     MLLSYHEHLK PSDRELWQS VDFLMEQEQN CNWPPPELGET IERENELVHW CHGAPGIAYL FAKAYLISKK PQYLDTCIRC
161    GELTWQKGLL KKGPGICHGV AGSAYVFLLL YRLTGNSKYI YRAQRFAQFL FTEEFKAGSR VLESIYSLYE GFSGTVCFLI
241    DLLQPNQAEF PLFSVVFV
    
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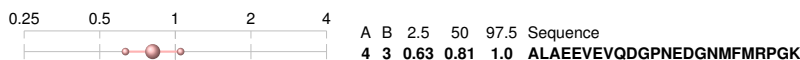


5.153 PREDICTED: similar to cytochrome c-1 [Rattus norvegicus]

Protein Accession	gij109480910
Mean Expression Ratio	0.852
Median Expression Ratio	0.855
Credible Interval	(0.659, 1.09)
Associated Peptides	1
Associated Spectra	7
Coverage	0.0902
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.712
Avg..iTRAQ.Ratio....116.114.	0.376
Avg..iTRAQ.Ratio....117.114.	1.06

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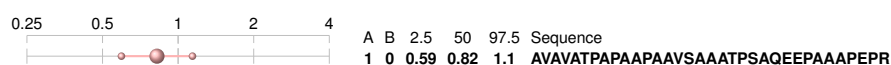
1      MLSALGMLAA GGAGLAVALH SAVSASDLEL HPSPYPWSHR GLLSSLDHTS IRRGFQVYKQ VCSSCHSMDY VAYRHLVGVG
81     YTEEEAKALA EVEVQDGNP EDGNMFMRPPG KLSDYFPKPY PNPEAARAAN NGALPPDLSY IVRARHGGED YVFSLLTGVC
161    EPPTGVSRLR GLYFNPFYFP QAIGMAPPYI TEVLEYDDGT PATMSQVAKD VATFLRWASE PEHDKRMRG LKMLMMGGLL
241    LPLTYAMKRH KWSVLKSRKL AYRPPK
    
```



5.154 PREDICTED: similar to Ser/Arg-related nuclear matrix protein [Rattus norvegicus]

Protein Accession	gij109477501
Mean Expression Ratio	0.854
Median Expression Ratio	0.855
Credible Interval	(0.63, 1.16)

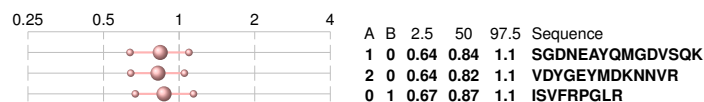
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.644
Avg..iTRAQ.Ratio....116.114.	0.445
Avg..iTRAQ.Ratio....117.114.	0.945



5.155 single-stranded DNA binding protein 1 [Rattus norvegicus]

Protein Accession	gj 34328536	
Mean Expression Ratio	0.855	
Median Expression Ratio	0.855	
Credible Interval	(0.68, 1.08)	
Associated Peptides	3	
Associated Spectra	4	
Coverage	0.245	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.721	1.17
Avg..iTRAQ.Ratio....116.114.	0.658	1
Avg..iTRAQ.Ratio....117.114.	0.659	0.782

1 MFRRPVLQVF RQFVRQESEV ASSLVLERSL NRVQLLGRVG QDPVMRQVEG KNPVTIFSLA TNEMWRSGDN EAYQMGDVSQ
 81 KTTWHRISVF RPGLFDVAYQ YVKKGARIFV EGKVDYGEYM DKNNVRRQAT TIIADNIIFL SDQAREKPLN G



5.156 PREDICTED: similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M) [Rattus

Protein Accession	gij62653460
Mean Expression Ratio	0.854
Median Expression Ratio	0.855
Credible Interval	(0.649, 1.11)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0482
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.863
Avg..iTRAQ.Ratio....116.114.	0.563
Avg..iTRAQ.Ratio....117.114.	0.641

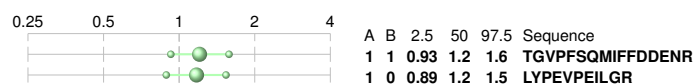
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1      MAALKEQLIV  NLKKEEQVPQ  NKITVVGVGA  VGMACAISIL  MKDLADELAL  VDVIEDKLG  EMDLQHGSL  FLKTPKIVSS
81     KDYSVTANSK  LVIITSGARQ  QEGESQLNLV  QRNVNIFKFI  IPNVVKYSPQ  CKLLIVSNPV  DILTYVAWKI  SGFPKNRVIG
161    SGCNLSARF  RYLMGERLGV  HPLSCHGWVL  GEHGSSVPV  WSGVNVTVGS  LKSLNPOLGT  DADKEQWKDV  HKQVVD SAYE
241    VIKLKGYTSW  AIGLSVADLA  ESIMKNLRRV  HPISTMIKSL  YGIKEDVFLS  VPCILGQNGI  SDVVKVTLTP  DEEARLKKSA
321    DTLWGIQKEL  QF
    
```



5.157 PREDICTED: similar to magnesium-dependent phosphatase-1 [Rattus norvegicus]

Protein Accession	gij27700106	
Mean Expression Ratio	1.17	
Median Expression Ratio	1.17	
Credible Interval	(0.91, 1.50)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.17	1.91
Avg..iTRAQ.Ratio....116.114.	1.27	1.9
Avg..iTRAQ.Ratio....117.114.	1.28	1.49



5.158 PREDICTED: similar to AKT1 substrate 1 (proline-rich) [Rattus norvegicus]

Protein Accession	gij109458687
Mean Expression Ratio	0.857
Median Expression Ratio	0.857
Credible Interval	(0.67, 1.10)
Associated Peptides	2
Associated Spectra	3
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.93
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	0.515

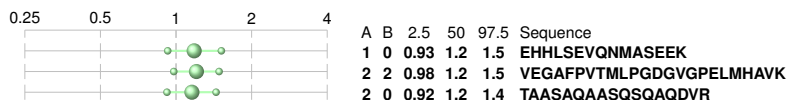


5.159 isocitrate dehydrogenase 3 (NAD+) beta [Rattus norvegicus]

Protein Accession	gij55926203	
Mean Expression Ratio	1.17	
Median Expression Ratio	1.17	
Credible Interval	(0.96, 1.42)	
Associated Peptides	3	
Associated Spectra	7	
Coverage	0.145	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.38	1.44
Avg..iTRAQ.Ratio....116.114.	1.19	1.20
Avg..iTRAQ.Ratio....117.114.	1.37	1.18

```

1      MAALSNVRWL TRAVLGARNS GAWRGLRTAA SAQAASQSQQA QDVRVEGAFP VTMLPGDGVG PELMHAVKEV FKAAAVPVEF
81     KEHHLSEVQN MASEEKLEQV LSSMKENKVA IIGKIYTPME YKGE LASYDM QLRRKLDLFA NVVHVKSLPG YKTRHNNLDL
161    VIIREQTEGE YSSLEHESAR GVIECLKIVT RTKSQRIAKF AFDYATKKGR SKVTAVHKAN IMKLGDLFL QCCEEVAELY
241    PKIKFETMII DNCCMQLVQN PYQFDVLVMP NLYGNIIDNL AAGLVGGAGV VPGESYSAEY AVFETGARHP FAQAVGRNIA
321    NPTAMLLSAS NMLRHLNLEY HSSMIADAVK KVIKVGKVRT RDMGGYSTTT DFIKSVIGHL HPHGG
  
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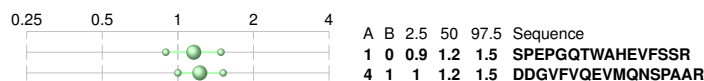


5.160 PREDICTED: similar to AHNAK nucleoprotein isoform 2 isoform 2 [Rattus norvegicus]

Protein Accession	gij109463561	
Mean Expression Ratio	1.17	
Median Expression Ratio	1.17	
Credible Interval	(0.945, 1.44)	
Associated Peptides	2	
Associated Spectra	6	
Coverage	0.22	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.21	0.874
Avg..iTRAQ.Ratio....116.114.	1.22	2.49
Avg..iTRAQ.Ratio....117.114.	1.39	3.5

```

1      MEKEEETTRE LLLPNWQGS GSHGLTIAQRD DGVFVQEVMQ NSPAARTGVV KEGDQIVGAT IYFDNLQSGE VTQLLNTMGH
81     HTVGLKLRK GDRSPEPGQT WAHEVFSSRS SEVVLSTARP SSLDGNQNK HKEAINKTGA ASGSTPDAGL
  
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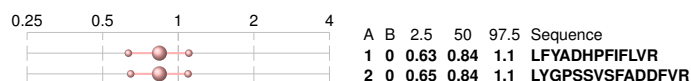


5.161 "serine (or cysteine) proteinase inhibitor, clade H, member 1 [Rattus norvegicus]"

Protein Accession	gij8393057
Mean Expression Ratio	0.856
Median Expression Ratio	0.858
Credible Interval	(0.668, 1.09)
Associated Peptides	2
Associated Spectra	3
Coverage	0.0671
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.786
Avg..iTRAQ.Ratio....116.114.	0.748
Avg..iTRAQ.Ratio....117.114.	0.763

```

1      MRSLLLGTLCLLAVALAAEVKKPVEAAAPGTAEKLSSKATTLAERSTGLA  FSLYQAMAKDQAVENILLSP  LVVASSLGLV
81     SLGGKATTASQAKAVLSAEKLRDEEVHTGLGELVRSLSNSTARNVTWKLGSRLYGPSSVS  FADDFVSSK  QHYNCEHSKI
161    NFRDKRSALQSINEWASQTDGKLPVETKDVERTDGALLV  NAMFFKPHWD  EKFHMKVDN  RGFVTRSYT  VGVMMHRTG
241    LYNYYDDEKEKLQLVEMPLAHKLSSLILM  PHHVEPLERL  EKLLTKEQLK  TWMGKMQKKA  VAISLPKGVV  EVTHDLQKHL
321    AGLGLTEAIDKKNADLSRMSGKKDLYLASV  FHATAFEWDT  EGNPFDQDIY  GREELRSPK  L  FYADHPFIFL  VRDNQSGSLL
401    FIGRLVRPKG  DKMRDEL
  
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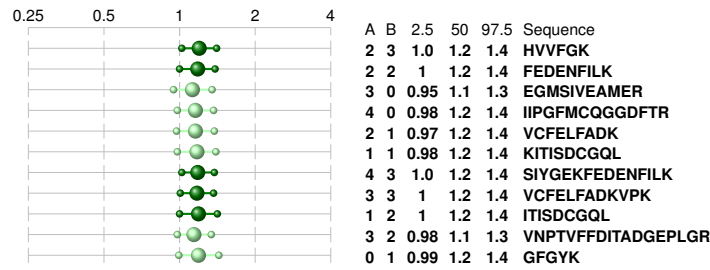


5.162 peptidylprolyl isomerase A [Rattus norvegicus]

Protein Accession	gij8394009	
Mean Expression Ratio	1.17	
Median Expression Ratio	1.16	
Credible Interval	(1.05, 1.29)	
Associated Peptides	11	
Associated Spectra	43	
Coverage	0.555	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.26
Avg..iTRAQ.Ratio....116.114.	1.02	0.92
Avg..iTRAQ.Ratio....117.114.	1.29	1.50

```

1      MVNPTVFEDI  TADGEPLGRV  CFELFADKVP  KTAENFRALS  TGEKGFQYK  SSFHR  IIPGF  MCQGGDFTRH  NGTGGKSIYG
81     EKFEDEFIL  KHTGPGILSM  ANAGPNTNGS  QFFICTAKTE  WLDGKHVVF  G  KVKEGMSIVE  AMERFGSRNG  KTSK  ITISD
161    CGQL
  
```



5.163 "REX2, RNA exonuclease 2 homolog [Rattus norvegicus]"

Protein Accession	gi 56605730	
Mean Expression Ratio	1.16	
Median Expression Ratio	1.16	
Credible Interval	(0.886, 1.51)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.076	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.11	1.53
Avg..iTRAQ.Ratio....116.114.	1.14	1.75
Avg..iTRAQ.Ratio....117.114.	1.11	2.84

1 MLGVSLGARL LRGVGGRRGQ FGARGVSEGS AAMAAGESMA QRMVWVDLEM TGLDIEKDQI IEMACLITDS DLNILAEGPN
 81 LIIKQPDELL DSMSDWCKEH HGKSGLTAKV KESTVTLQQA EYEFLSFVR QTPPGLCPLA GNSVHADKKF LDKHMPQFMK
 161 HLHYRIIDVS TVKELCRRWY PEDYEFAPKK AASHRALDDI SESIKELQFY RNNIFKKKT D EKRKKIENG ENKPVV



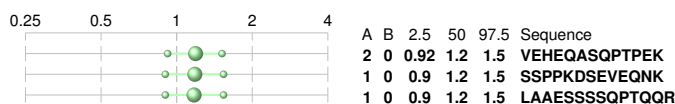
5.164 PREDICTED: similar to dystrobrevin alpha isoform 1 isoform 8 [Rattus norvegicus]

Protein Accession	gi 109507009	
Mean Expression Ratio	1.16	
Median Expression Ratio	1.16	

Credible Interval	(0.925, 1.46)
Associated Peptides	3
Associated Spectra	4
Coverage	0.0511
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.48
Avg..iTRAQ.Ratio....116.114.	1.29
Avg..iTRAQ.Ratio....117.114.	1.40

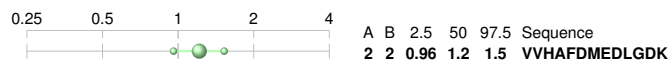
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1      MIEDSGKRGN TMAERRQLFA EMRAQDLDR I RLSTYRTACK LRFVQKKCNL HLVDIWNVIE ALRENALNNL DPNIELNVAR
81     LEAVLSTMFY QLNKRMPSTH QIHVEQSISL LLNFLLAAFD PEGHGKISVF AVKMALATLC GPKIMDKLRY IFSMISDSSG
161    VMVYGRYDQF LREVLKLPFTA VFEGPSFGYT EQSARSCFSQ QKKVTLNGFL DILMSDPPPQ CLVWLP LLHR LANVENVFHP
241    VECSYCHSES MMGFRYRCQQ CHNYQLCQDC FWRGHAGGSH SNQHQMKEYT SWKSPAKKLT NALSKSLSCA SSREPLHPMF
321    PDQPEKPLNL AHIVDTWPPR PVTSMNDTLF SHSVSSSGSP FITR S SPPKD SEVEQNKILA RAAPAF LK GK GIHYS LNVA D
401    RLAD EHV LIG LYVNM LRNNP SCMLESSNRL DEEHLIARY AAR LAAESSS SQPTQQRSAP DVSFTIDANK QQRQLIAELE
481    NKNREILQEI QRLR VEHBCA SQPTPEKAQQ NP TLLAELRL LRQRKDELEQ RMSALQESRR ELMVQLEGLM KLLKTQGAGS
561    PRSSPSHTIS RPIPMPIRST SACSTPAYTP QDSL TGVGGD VQEAF AQSKC SLLYCVLLVP AKSFTNTFSS HYK YISEDVA
641    SETESTVDSE FSRTQFEDLV PSPTSEKSF L AQIHARKPGY IHGGATSTMH GDMVPEDGDP YPQPEDGNYE NESVRQLENE
721    LQMEEYLKQK LQDEAYQRHV STETRLKHPC PVTETKWRVL FWG FVIVGGF LSLALQIYFW GLF
    
```



5.165 PREDICTED: similar to Protein C10orf70 [Rattus norvegicus]

Protein Accession	gij109509802	
Mean Expression Ratio	1.16	
Median Expression Ratio	1.16	
Credible Interval	(0.918, 1.48)	
Associated Peptides	1	
Associated Spectra	4	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.16	1.18
Avg..iTRAQ.Ratio....116.114.	1.34	0.911
Avg..iTRAQ.Ratio....117.114.	1.28	2.12

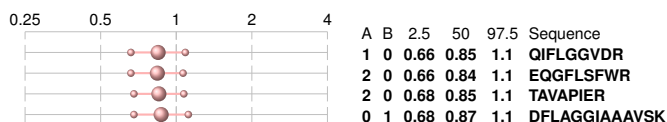


5.166 "solute carrier family 25, member 4 [Rattus norvegicus]"

Protein Accession	gij32189355	
Mean Expression Ratio	0.86	
Median Expression Ratio	0.86	
Credible Interval	(0.701, 1.06)	
Associated Peptides	4	
Associated Spectra	6	
Coverage	0.131	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.903	0.873
Avg..iTRAQ.Ratio....116.114.	0.82	0.81
Avg..iTRAQ.Ratio....117.114.	0.673	1.02

```

1   MGDQALSFLK DFLAGGIAAA VSKTAVAPIE RVKLLLVQVH ASKQISA EKQ YKGIIDCVVR IPKEQGFLSF WRGNLANVIR
81  YFPTQALNFA FKDKYKQIFL GGVDRHKQFW RYFAGNLASG GAAGATSLCF VYPLDFARTR LAADVKGSS QREFNGLGDC
161 LTKIFKSDGL KGLYQGFSVS VQGIIIRYAA YFGVYDTAKG MLPDPKNVHI IVSWMIAQSV TAVAGLVSYF FDTVRRRMMM
241 QSGRKGADIM YTGTVDCWRK IAKDEGRKAF FKGAWSNVLR GMGGAFVLVL YDEIKKYV
    
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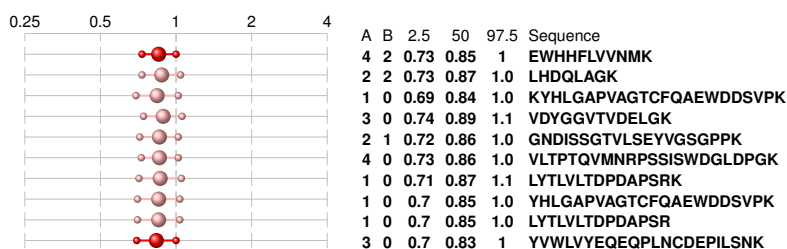


5.167 phosphatidylethanolamine binding protein [Rattus norvegicus]

Protein Accession	gij8393910	
Mean Expression Ratio	0.861	
Median Expression Ratio	0.861	
Credible Interval	(0.766, 0.972)	
Associated Peptides	10	
Associated Spectra	27	
Coverage	0.722	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.9	0.902
Avg..iTRAQ.Ratio....116.114.	0.919	0.81
Avg..iTRAQ.Ratio....117.114.	0.826	0.707

```

1      MAADISQWAG PLSLQEVDEP PQHALRVDYG GVTVDLQKV LTPTQVMNRP SSISWDGLDP GKLYTLVLTG PDAPSRKDPK
81     FREWHHFLV NMKGNDISSG TVLSEYVSGG PPFDTGLHRY VWLVYEQQP LNCDEPILSN KSGDNRGKFK VESFRKKYHL
161    GAPVAGTCFQ AEWDDSVPKL HDQLAGK
    
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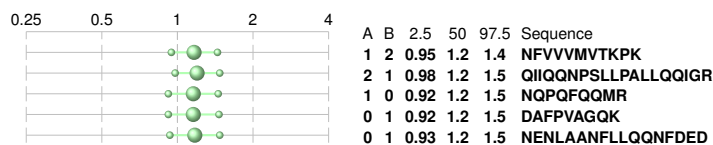


5.168 RAD23b homolog [Rattus norvegicus]

Protein Accession	gi 70778952	
Mean Expression Ratio	1.16	
Median Expression Ratio	1.16	
Credible Interval	(0.973, 1.39)	
Associated Peptides	5	
Associated Spectra	9	
Coverage	0.157	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.18	1.13
Avg..iTRAQ.Ratio....116.114.	1.12	1.05
Avg..iTRAQ.Ratio....117.114.	1.31	1.37

```

1      MQVTLKTLQQ QTFKIDIDPE ETVKALKEKI ESEKGDAFP VAGQRLIYAG KILSDDTALK EYKIDKENV VVMVTKPFAV
81     TSAVPATFQQ SSSPSTTTVS SSPAAAVAQA PAPTPALAPT STPASTTPAS TTASSEPAAT GATQPEKPAE KPAQTPVLTS
161    PAPADSTPGD SSRSNLFEDA TSALVTGQSY ENMVTEIMSM GYEREQVIAA LRASFNNPDR AVEYLLMGIP GDRESQAVVD
241    PPPQAVSTGT PQSPAVAAAA ATTTATTTTT SGGHPLEFLR NQPQFQQMRQ IQQNPSLLP ALLQQIGREN PQLLQQISQH
321    QEHFIQMLNE FVQEAGGQGG GGGGGGGGGG GGGGIAEAGS GHMNYIQVTP QEKEAIERLK ALGFPEGLVI QAYFACEKNE
401    NLAANFLLQQ NFDED
    
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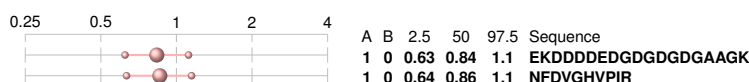


5.169 initiation factor 2 associated 67 kDa protein [Rattus norvegicus]

Protein Accession	gi 11993954
Mean Expression Ratio	0.86
Median Expression Ratio	0.863
Credible Interval	(0.658, 1.12)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0604
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.878
Avg..iTRAQ.Ratio....116.114.	0.753
Avg..iTRAQ.Ratio....117.114.	0.608

```

1   MAGVEEASSF GGHLNRDLDP DDREECTSST AEEAAKKKRR KKKKGGKAVS AGQQELDKEG GTSVDEVAKQ LERQALEEK
81  KDDDDDEDGG DGGGAAGK KKKKKRGRPR VQTDPPSPVI CDLYPNGVFP KGQCEYPPPT QDGRATAAWRT TSEKKALDQ
161 ASEEIWNDFR EAAEAHRQVR KYVMSWIKPG MTMIEICEKL EDCSRKLIKE NGLNAGLAFQ TGC SLNNCAA HYTPNAGDTT
241 VLQYDDICKI DFGTHISGRI IDCAFTVTFN PKYDILLKAV KDATNTGIKC AGIDVRLCDV GEAIQEVMS YEVEIDGKTY
321 QVKPIRNLNG HSIQPYRIHA GKTVPVIVKGG EATRMEEGEV YAIETFGSTG KGVVHDDMEC SHYMKNFDVG HVPVIRLPRTK
401 HLLNVINENF GTLAFCCRWL DRLGESKYLK ALKNLCLDGI VDPYPLCDI KGSYTAQFEH TILCAQPVKK LSAEEMTIKT
    
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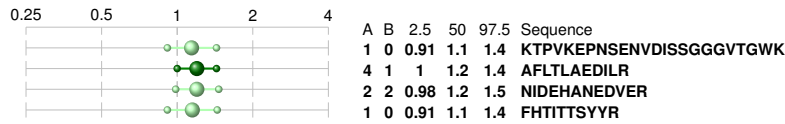
5.170 "RAB10, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gi 61889071	
Mean Expression Ratio	1.16	
Median Expression Ratio	1.16	
Credible Interval	(0.976, 1.38)	
Associated Peptides	4	
Associated Spectra	11	
Coverage	0.285	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	1.42
Avg..iTRAQ.Ratio....116.114.	1.17	1.5
Avg..iTRAQ.Ratio....117.114.	1.18	1.45

NHLBI Zile/Grant, Aged Rat

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1      MAKKTYDLLF KLLIGDSGV GKTCVLFRRS DDAFNNTTFFIS TIGIDFKIKT VELQGKKIKL QIWDTAGQER FHTITTSYYR
81     GAMGIMLVYD ITNGKSFENI SKWLRNIDEH ANEDVEIMLL GNKCDMDDKR VVPKKGKEQI AREHGIRFFE TSAKANINIE
161    KAFLTLAEDI LRKTPVKEPN SENVDISSGG GVTGWKSKCC
  
```



5.171 hypothetical protein LOC498332 [Rattus norvegicus]

Protein Accession	gij112984196
Mean Expression Ratio	0.864
Median Expression Ratio	0.864
Credible Interval	(0.646, 1.17)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0187
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.494
Avg..iTRAQ.Ratio....116.114.	0.745
Avg..iTRAQ.Ratio....117.114.	0.793

```

1      MLRLGGAGLV RGLRVVSPAW LRPGGGLPLA LARTTGTSGA RDRRAPASGT QRGRALSLSA AAVVNSAPRP LQPYLRMLRL
81     DKPIGTWLLY LPCTWSIGLA ADPGCFPDWY MSLFLGTGAI LMRGAGCTIN DMWDRDFDKK VERTANRPIA AGDISAFQSF
161    VFLGAQLTLA LGVLLHLNYY SIAMGAASLL LVVTYPLMKR VTFWPQLALG LTFNWGALLG WSAVKGSCDP AVCCLPLYFSG
241    VMWFLIYDTI YAHQDKKDDA LIGLKSTALL FRENTKQWLS GFGVAMVGAL SLVGASSGQT LPYYAAVAAV GAHLAHQIYT
321    VDIHRAEDCW EKFTSNRTVG LLLFLGIVLG NLYKDKPDET KGVDAVGEES ERTS
  
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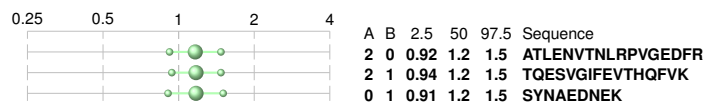


5.172 PREDICTED: similar to CG4646-PA isoform 2 [Rattus norvegicus]

Protein Accession	gij109476873
Mean Expression Ratio	1.16
Median Expression Ratio	1.16
Credible Interval	(0.94, 1.43)
Associated Peptides	3

Associated Spectra	6	
Coverage	0.263	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.16	1.19
Avg..iTRAQ.Ratio....116.114.	1.11	1.37
Avg..iTRAQ.Ratio....117.114.	1.31	1.74

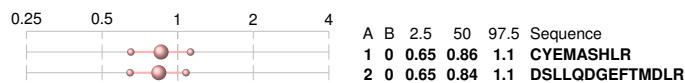
1 MGKIALQLKA TLENVTNLRP VGEDF¹WYLK MKCGNCGEIS EKWQYIRLMD SVALKGGGRGS ASMVQKCKLC ARENSIEILS
 81 STIKSYNAED NEKFKTIVEF ECRGLEPVD²F QPQAGFAAEG VESGTVFSDI NLQEKDWDY DEK³TQESVGI FEVTHQFVKC



5.173 profilin 1 [Rattus norvegicus]

Protein Accession	gi 42476144
Mean Expression Ratio	0.862
Median Expression Ratio	0.864
Credible Interval	(0.677, 1.1)
Associated Peptides	2
Associated Spectra	3
Coverage	0.164
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.74
Avg..iTRAQ.Ratio....116.114.	0.839
Avg..iTRAQ.Ratio....117.114.	0.752

1 MAGWNAYIDS LMADGTCQDA AIVGYKDS¹PS VWAAVPGKTF VSITPAEVGV LVGKDRSSFF VNGLTGGQK CSVIR²DSLLQ
 81 DGEFTMDLRT KSTGGAPTFN VTVTMTAKTL VLLMGKEGVH GGLINKK³CYE MASHLFRSQY

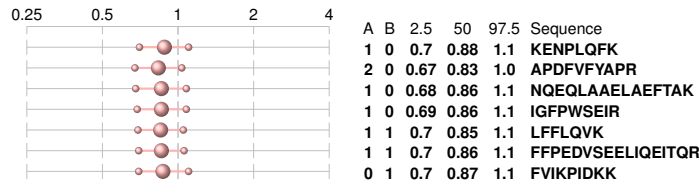


5.174 radixin [Rattus norvegicus]

Protein Accession	gj 56799432	
Mean Expression Ratio	0.864	
Median Expression Ratio	0.864	
Credible Interval	(0.732, 1.02)	
Associated Peptides	7	
Associated Spectra	10	
Coverage	0.129	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.909	0.799
Avg..iTRAQ.Ratio....116.114.	0.796	0.76
Avg..iTRAQ.Ratio....117.114.	0.815	0.745

```

1      MPKPINVRVT  TMDAELEFAI  QPNTTGKQLF  DQVVKTVGLR  EVWFFGLQYV  DSKGYSTWLK  LNKKVTQQDV  KKENPLQFKF
81     RAKFFPEDVS  EELIQEITQR  LFFLQVKEAI  LNDEIYCPEE  TAVLLASYAV  QAKYGDYNKE  IHKPGYLAND  RLLPQRVLEQ
161    HKLTKEQWEE  RIQNWHEEHR  GMLREDSMME  YLKIAQDLEM  YGVNYFEIKN  KKGTELWLGV  DALGLNIYEH  DDKLTPKIGF
241    PWSEIRNISF  NDKKFVIKPI  DKKAPDFVfy  APFLRINKRI  LALCMGNHEL  YMRRRKPDIT  EVQQMKQAR  EEKHQKQLER
321    AQLENEKKKR  EIAEKEKERI  EREKEELMER  LRQIEEQTMK  AQKELEEQTR  KALELEQERQ  RAKEEAERLD  RERRAAEEAK
401    SAIAKQAADQ  MKNORQLAAB  LAEFTAKIAL  LEEAKKKEE  EATEWQHKA  AAQEDLEKTK  EELKTVMCAP  PPPPPAVVP
481    PTENEHDEQD  EHSAEASAE  SSEGVTNHR  EEERVTEQK  NERVKKQLQA  LSSELAQARD  ETKKTQNDVL  HAENVKAGR
561    KYKTLRQIRQ  GNTKQRIDEF  EAM
  
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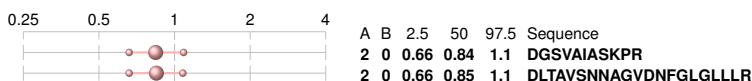
5.175 PREDICTED: similar to 3-oxoacid CoA transferase 1 isoform 2 [Rattus norvegicus]

Protein Accession	gj 109466092	
Mean Expression Ratio	0.863	
Median Expression Ratio	0.864	
Credible Interval	(0.687, 1.08)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.0615	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.788	

Avg..iTRAQ.Ratio....116.114. 0.732
 Avg..iTRAQ.Ratio....117.114. 0.869

```

1      MAALKLLSSG LRLCASARNS RGALHKGCAC YFSVSTRHHT KFYTDPVEAV KDIPNGATLL VGGFGLCGIP ENLIGALLKT
81     GVKDLTAVSN NAGVDNFGGLG LLLRSKQIKR MISSYVGENA EFERQFLSGE LEVELTPQGT LAERIRAGGA GVPAFYTSTG
161    YGTLVQEGGS PIKYNKDGSV AIASKPREVR EFRGQHFILE EAITGDFALV KAWKADRAGN VIFRKSARNF NLPCKKAAGT
241    TVVEVEEIVD IGSFAPEDIH IPKIYVHRLI KGEKYEKRIE RLSLRKEGEG KAKSGKPGED VRERIIKRAA LEFEDGMYAN
321    LGIGIPLLAS NFISPNMTVH LQSENGVLGL GPYPLKDEAD ADLINAGKET VTVLPGASF SDESFSAMIR GGHVNLMLG
401    AMQVSKYGLD ANWMIPGKMV KGMGGAMDLV SSSKTKVVVT MEHSAKNAH KIMEKCTLPL TGKQCVNRII TEKGVFVDVK
481    KNGLTLIELW EGLTVDDIRK STGCDFAVSP NLMPMQQIST
    
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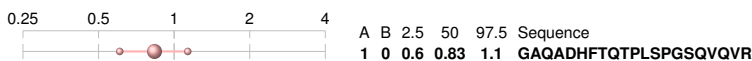


5.176 hypothetical protein LOC619440 [Rattus norvegicus]

Protein Accession	gi 77627733
Mean Expression Ratio	0.863
Median Expression Ratio	0.865
Credible Interval	(0.648, 1.16)
Associated Peptides	1
Associated Spectra	1
Coverage	0.051
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.717
Avg..iTRAQ.Ratio....116.114.	0.529
Avg..iTRAQ.Ratio....117.114.	0.554

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1      MAFLCQRDSY AREFTTTVVS CCPAELQTDG NGSKKEVLSG FQVVLEDTLL FPEGGGQPDD RGTINDISVL RVTRRGAQAD
81     HFTQTPLSPG SQVQVRVDWE RRFDMQQHS GQHLITAVAD LLFGLKTTSW ELGKLCRVIE LDSPSVTAEQ VAAIEQSVNQ
161    KIRDRLPVSV RELSLDDPEV EQVRGRGLPD DHAGPIRVVT IEGVDSNMCC GTHVNNISDL QVIKILGTEK GKKNKSNLIF
241    LAGNRVLKWM ERSHGSEKAL TSLKCGAED HVEAVKKLQN ATKLLQKNNL NLLRDLAVHT AHTLRSSPAW GGVVTLHRKE
321    GDSEFMNIIA NEIGSEETLL FLTVDGKGA GLFLLAGPTE AVETLGRVA EVLEGGKAGK KGRFQKATK MSRRAEVQAL
401    LQDYVSTQSA EE
    
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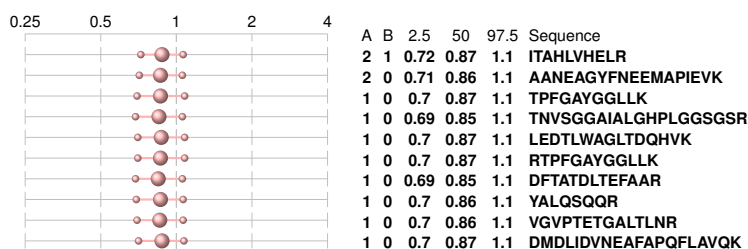


5.177 acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Rattus norvegicus]

Protein Accession	gj 18426866	
Mean Expression Ratio	0.866	
Median Expression Ratio	0.865	
Credible Interval	(0.746, 1.01)	
Associated Peptides	10	
Associated Spectra	13	
Coverage	0.327	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.01	0.942
Avg..iTRAQ.Ratio....116.114.	0.802	0.708
Avg..iTRAQ.Ratio....117.114.	0.794	1.11

```

1      MALLRGVFIV AAKRTPFGAY GLLKDFAT DLTEFAARAA LSAGKVPPE IDSVIVGNVM QSSSDAAYLA RHVGLRVGVP
81     TETGALTLNR LCGSGFQSIY SGCQEICSKD AEVVLCGGTE SMSQSPYSVR NVRFGTKFGL DLKLEDTLWA GLTDQHVLPL
161    MGMTAENLAA KYNISREDCD RYALQSQQRW KAANEAGYFN EEMAPIEVKT KKGKQTMQVD EHARPQTLE QLQNLPPVFK
241    KEGTVTAGNA SGMSDGAGVV IASEDAVKK HNFPLARVV GYFVSGCDPA IMGIGVPAI TGALKKAGLS LKDMDLIDVN
321    EAFAPQFLAV QKSLDLDPK TNVSGGAIAL GHPLGGSGSR ITAHLVHELRRRGKYAVGS ACIGGGGGIS LIIQNTA
  
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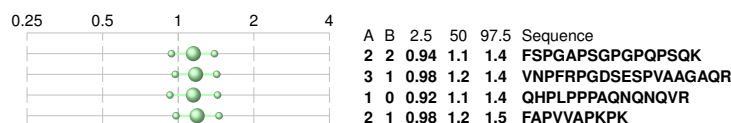
5.178 PREDICTED: similar to zyxin [Rattus norvegicus]

Protein Accession	gj 109473414	
Mean Expression Ratio	1.15	
Median Expression Ratio	1.16	
Credible Interval	(0.974, 1.36)	
Associated Peptides	4	
Associated Spectra	12	
Coverage	0.09	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.16	1.01

Avg..iTRAQ.Ratio....116.114.	1.14	0.864
Avg..iTRAQ.Ratio....117.114.	1.46	1.50

```

1      MRREAAGGPL  QSLRPRAGPG  PLPGGVSCPA  LPPRPLPAPS  PGRSLYGLGA  ALSPPPPSLP  LRVVPPRLAR  SCSGPGRVR
81     GLGAEAVIRD  AALTLLPAQP  GLTMAAPRPP  PAISVSVSAP  AFYAPQKKFA  PVVAPKPKVN  PFRPGDSESP  VAAGAQRQM
161    GRVGEIPPPP  PEDFPLPPP  VIGEGDDEG  ALGGAFFFFP  PPLIEEFPFP  APLEEDIFPS  PPPPLEEGG  PEAPTQLPPQ
241    PREKVSSIDL  EIDSLSSLLD  DMTKNDFFKA  RVSSGYVPPP  VATPFVVKPS  TKPAPVGTAP  LPPWKAPSSS  QPPPQPQAKP
321    QVQLHAQPQA  KPHVQPQSVS  SANTQPRGPL  SQAPTPAPKF  APVAPKFTPV  ASKFSFGAPS  GPGFPQPSQKS  VPLEAPSSVG
401    TGSFPQPPSFT  YAQQKEKPLV  QEKQHPLEPP  AQNQNQVRS  GGGPGLTLKE  VEELEQLTQQ  LMQDMEHPQR  QSVAVNESCG
481    KCSQPLARAQ  PAVRALGQLF  HITCFTCHQC  QQQLQGQFY  SLEGAPYCEG  CYDTLEKCN  TCGQPITDRM  LRATGKAYHP
561    HCFTCVVCAC  PLEGTSFIVD  QANQPHCVPD  YHKQYAPRCS  VCSEFIMPEP  GRDETVRVVA  LDRNFHMKCY  KCEDCGKALS
641    IEADDNGCFP  LDGHVLCRKC  HSARAQT
  
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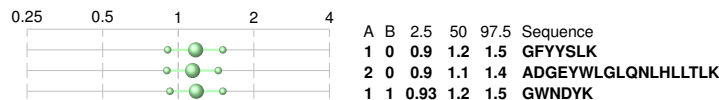


5.179 microfibrillar-associated protein 4 [Rattus norvegicus]

Protein Accession	gi 77627994	
Mean Expression Ratio	1.15	
Median Expression Ratio	1.15	
Credible Interval	(0.927, 1.42)	
Associated Peptides	3	
Associated Spectra	5	
Coverage	0.120	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.29	1.20
Avg..iTRAQ.Ratio....116.114.	1.21	1.08
Avg..iTRAQ.Ratio....117.114.	1.38	1.47

```

1      MKTLSGLPLL  LLLLLSTPPP  CAPQASGIRG  DALEKSCLQQ  PLDCDDIYMQ  GYQEDGVYLI  YPYGPSVPPV  VFCDMTTEGG
81     KWTVFQKRFN  GSVSFFRGWN  DYKLGFGRAD  GEYWLGLQNL  HLLTLKQKYE  LRVLDLDFEN  NTAYAKYVDF  SISPNAVSAE
161    EDGYTLYVAG  FEDGGAGDSL  SYHSGQKFST  FDRDQDLFVQ  NCAALSSGAF  WFRSCHFANL  NGFYLGGSHL  SYANGINWAQ
241    WKGFYSLKR  TEMKIRRA
  
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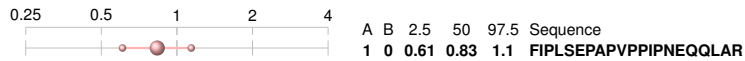


5.180 "COP9 (constitutive photomorphogenic) homolog, subunit 8 [Rattus norvegicus]"

Protein Accession	gij61557351
Mean Expression Ratio	0.866
Median Expression Ratio	0.867
Credible Interval	(0.636, 1.16)
Associated Peptides	1
Associated Spectra	1
Coverage	0.100
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.523
Avg..iTRAQ.Ratio....116.114.	0.798
Avg..iTRAQ.Ratio....117.114.	0.603

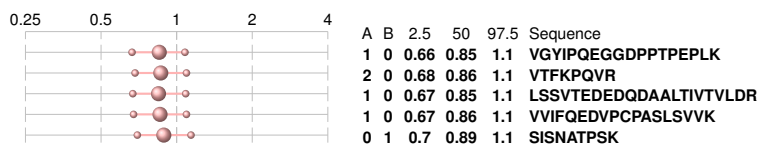
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1      MPVAVMADNA FSRKLLDQC ENQELEAPGG IATPPVYGQL LALYLLQNDM NNARYLWKRI PPAIKSANSE LGGIWSVGQR
81     IWQRDFPGIY TTINAHQWSE TVQPIMEALR DATRRRAFAL VSQAYTSIIA DDFAAFVGLP VEEAVKGVLE QGWQADSTTR
161    MVLPRKPPAG ALDVSLNRFI PLSEPAVPPP IPNEQQLARL TDYVAFLEN
    
```



5.181 PREDICTED: similar to serum deprivation response protein [Rattus norvegicus]

Protein Accession	gij27714505	
Mean Expression Ratio	0.869	
Median Expression Ratio	0.868	
Credible Interval	(0.71, 1.06)	
Associated Peptides	5	
Associated Spectra	6	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.85	0.964
Avg..iTRAQ.Ratio....116.114.	0.754	0.899
Avg..iTRAQ.Ratio....117.114.	0.795	1.07



5.182 glutathione S-transferase A5 [Rattus norvegicus]

Protein Accession	gij13928688
Mean Expression Ratio	1.15
Median Expression Ratio	1.15
Credible Interval	(0.88, 1.51)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0498
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.51
Avg..iTRAQ.Ratio....116.114.	1.64
Avg..iTRAQ.Ratio....117.114.	1.75

1 MPGKPVLYHF DGRGRMEPIR WLLAAAGVEF EEQFLKTRDD LARLRNDGSL MFQQVPMVEI DGMKLVQTRA ILNYIATKYN
 81 LYGKDMKERA LIDMYAEGVA DLDEIVLHYP YIPPGEKEAS LAKIKDKARN RYFPAFKVL KSHGQDYLVG NRLSRADVYL
 161 VQVLYHVEEL DPSALANFPL LKALRTRVSN LPTVKKFLQP GSQRKPLEDE KCVESAVKIF S

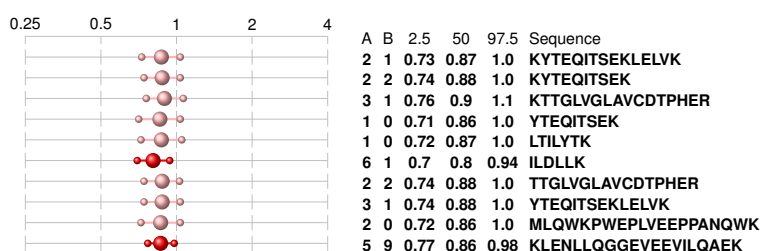


5.183 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5 [Rattus norvegicus]

Protein Accession	gij6981260
Mean Expression Ratio	0.869
Median Expression Ratio	0.868
Credible Interval	(0.785, 0.963)
Associated Peptides	10
Associated Spectra	44

Coverage	0.733	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.826	0.757
Avg..iTRAQ.Ratio....116.114.	0.937	0.823
Avg..iTRAQ.Ratio....117.114.	0.901	0.717

1 MAGLVKKTG LVGLAVCDTP HERLTILYTK ILDLLKHFPK HAAYRKYTEQ ITSEKLELVK LEPDVKKLEN LLQGGEVEEV
 81 ILQAEKELSL ARKMLQWKWP EPLVEEPPAN QWFWPI

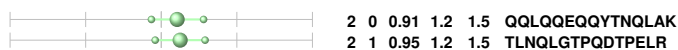


5.184 syntaxin 7 [Rattus norvegicus]

Protein Accession	gi 55741787	
Mean Expression Ratio	1.15	
Median Expression Ratio	1.15	
Credible Interval	(0.922, 1.43)	
Associated Peptides	2	
Associated Spectra	5	
Coverage	0.115	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.23	4.15
Avg..iTRAQ.Ratio....116.114.	1.24	0.467
Avg..iTRAQ.Ratio....117.114.	1.28	2.28

1 MSYTPGIGGD PAQLAQRIS NIQKITQCSA EIQRILNQLG TPQDTPELRQ QLQQEQQYTN QLAKETDKYI KEFGFLPTTP
 81 SEQRQRKIQK DRLVAEFTTA LTNFQKVQRQ AAEREKEFVA RVRASSRVSG GPPEDSSKEK NFVSWESQTQ PQVQVQDEEI
 161 TEDDLRLIHE RESSIRQLEA DIMDINEIFK DLGMMIHEQG DVIDSIEANV ESAEVHVQQA NQQLSRAANY QRKSRKTLCI
 241 IILILVGVIV IIFFIVWGLK G



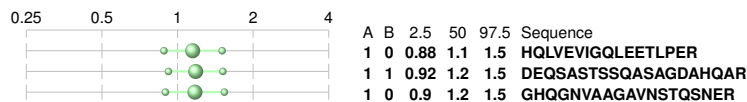


5.185 PREDICTED: similar to desmuslin isoform H isoform 1 [Rattus norvegicus]

Protein Accession	gj 109458882	
Mean Expression Ratio	1.15	
Median Expression Ratio	1.15	
Credible Interval	(0.915, 1.45)	
Associated Peptides	3	
Associated Spectra	4	
Coverage	0.036	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.49	1.81
Avg..iTRAQ.Ratio....116.114.	1.20	1.33
Avg..iTRAQ.Ratio....117.114.	1.45	0.85

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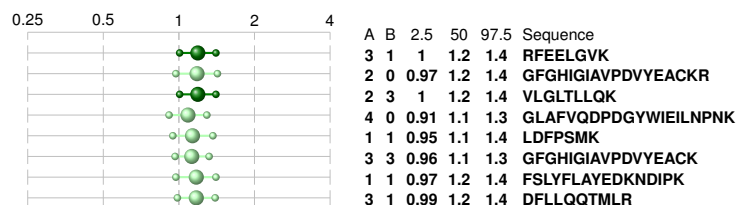
1      MLSWRLQTSS  EKAEQLQELNA  RLYEYVCRVR  ELERENLLE  EELRSRLSRE  DRWAEDQALY  AEEARSLRQQ  LDELSWSTAL
81     AEGERDALRR  ELLDLQREGL  EASTARGRLD  AELEAQRREL  EEALGARAAL  EALLGRLEAE  RRDLDAAHER  QVRELRRARAS
161    SLTMHFRARA  TGPAAPPPRL  RDVHDSYALL  VAESWRESMQ  LYDEVVRELE  QALRRGQESR  LQAEDEARLC  AQEADALRNQ
241    ALELEQLRAR  LEDELRLMRE  EYGMQABERQ  RVIDSLEDEK  DALPLAMADR  LREYQELLQV  KTGLSLEVAT  YRALLEGESN
321    PEILIWTEINI  ENVPRESRNT  SYRYTDSVLQ  RKNEKNLFFR  RKTPWAAVNH  SSTLYSNGPG  HLDSTTTAV  GNAARRGFLT
401    SCYSSSATTS  QQKPLEKTVS  SQASLRPVIP  THGFLRNTDA  QVKTFSHGPK  AEGMGDTLTR  RATESVITRE  SYR GHQGNVA
481    AGAVNSTQSN  ERTVILGKKL  ETQATKEQER  DRSGVVKLLP  EEKMFDSKEK  ASEERNLRWE  ELTKLDARER  ESQHLRNEAK
561    GKETLTGRSR  KEREVPISE  VSRGSKSEVS  TIHLQSSGRK  DSANSREREV  KTKETKFHLD  GKDTAGSLQS  DSTTETIAEN
641    IVTTILKQFT  QSPGAENVVS  SLPDTRVYYL  DRKEFPGRDK  TKTEIVMESK  LTEDVDVSDE  AGLDYLKSKD  VKEVGLKSKS
721    TETVIGEMIN  LGLKGREGRA  KVVNVEIVVE  PMSYVGGGKV  EFSTPFQVEE  VDDVSPSPKG  FIEEEEGEGE  THMAFSMHQR
801    QRTNQPPQNV  PHVEEVTEAG  DSEGEQSYFV  STPDEYPPGH  DREDDGSVYG  QIHIEEESTI  RYSWQDEIAQ  GTWRRKARGD
881    TGEKHKMKVL  EVPSASLGGA  FGSADVKEEA  SGELHAEPTI  IEKEIKIPHE  FHTSIKGVFS  SEPRHQLVEV  IGQLEETLPE
961    RMKEELSALT  RQSQGEPPSV  SVDVKKVQSS  AGGSVTLMAE  VNLSQTVDAD  QLDLEELSRD  EAGEIEKAVE  SVVRESLTKR
1041   SSPVPRSPDR  EDGEAPAGG  FLFKRWATRE  LYSFSGEKDD  TDRVFHSSDQ  RVTQGPVSAT  VEVTSPTFGV  QSHVLEDVSQ
1121   SVRHVKLGPT  EMWRTEQVSY  GGPTSPVVEV  SEDFSEAVSS  EGASRSVRHV  TLGPRQNRVS  TEVIFRGSVP  TGQETGDTGE
1201   PDPAAALSVEA  DISGSRMPG  SQAANEKET  PFPGPISGAA  QVGNFSTEG  SVGTQTFVRH  LQLGSREGFR  EEIQFIAPIP
1281   DRAEWGEEDS  GYTRVSLGRS  TSIQHIDIVP  QRYQASKQVA  PQTLGFRDSE  GVVLVERSAG  MTQATHNFTS  DREILKKEEN
1361   TFORVISGSP  PDSVGDGTAE  VTENISRSFR  HIQIGTPEED  PSEYIVTSGP  LSKTFVLDS  VASPPGGGA  DGSSTPCHIA
1441   LGPKETSFTF  QMGVSDTRAI  RSWTRDTGSE  VEAHSVSHHG  GWRVAHSRDE  QSASTSSQAS  AGDAHQARGE  KGTEQAGFDK
1521   TVQLQRMVDQ  RSVASDEKKV  ALLYLDNEEE  EEEGEGWF
    
```



5.186 glyoxylase 1 [Rattus norvegicus]

Protein Accession	gj 46485429	
Mean Expression Ratio	1.15	
Median Expression Ratio	1.15	
Credible Interval	(1.02, 1.29)	
Associated Peptides	8	
Associated Spectra	29	
Coverage	0.473	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.11	1.22
Avg..iTRAQ.Ratio....116.114.	1.16	1.09
Avg..iTRAQ.Ratio....117.114.	1.22	1.19

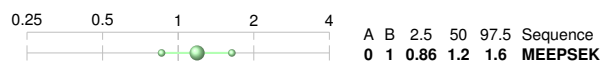
1 MAEPQPASSG LTDEAALSCC SDPDPSTKDF LLQQTMLRIK DPKKSLDFYT RVLGLTLLQK LDFPSMKFSL YFLAYEDKND
 81 IPIDKTERTA WAFSRKATLE LTHNWGTEDD ETQSYHNGNS DPRGFGHIGI AVPDVYEACK RFEELGVKFV KKPDDGKMKG
 161 LAFVQDDPGY WIEILNPNFM ATII



5.187 PREDICTED: similar to developmental pluripotency-associated 3 [Rattus norvegicus]

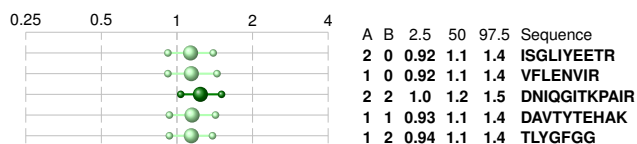
Protein Accession	gj 109483527	
Mean Expression Ratio	1.15	
Median Expression Ratio	1.15	
Credible Interval	(0.853, 1.55)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0467	
Experiment	B	
Avg..iTRAQ.Ratio....115.114.	1.40	
Avg..iTRAQ.Ratio....116.114.	1.66	
Avg..iTRAQ.Ratio....117.114.	1.4	

1 MEEPSEK VNP VVDPETPQMK DEEGSSDDSE VPQPETLVQV MKTTLNPSA NQSAHRISLR HRIGSSPVEN GSERILREVQ
 81 SAFFKRKVRT LLLVLKDPFA RMRRFVQIEQ RQKRLEGNEY KWNTPEFFRCP CTFCHYQRWD PSENAKTRKN



5.188 PREDICTED: similar to germinal histone H4 gene [Rattus norvegicus]

Protein Accession	gi 109504929	
Mean Expression Ratio	1.15	
Median Expression Ratio	1.15	
Credible Interval	(0.976, 1.36)	
Associated Peptides	5	
Associated Spectra	12	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.29	1.12
Avg..iTRAQ.Ratio....116.114.	0.977	1.12
Avg..iTRAQ.Ratio....117.114.	1.20	1.52

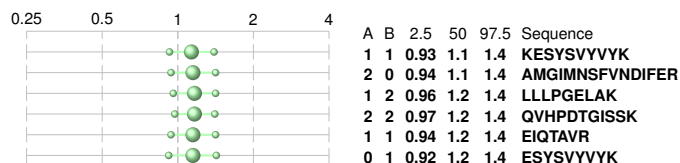


5.189 PREDICTED: similar to Histone H2B 291B isoform 2 [Rattus norvegicus]

Protein Accession	gi 109467201	
Mean Expression Ratio	1.15	
Median Expression Ratio	1.15	
Credible Interval	(0.984, 1.34)	
Associated Peptides	6	

Associated Spectra	14	
Coverage	0.413	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.26	1.06
Avg..iTRAQ.Ratio....116.114.	0.981	0.98
Avg..iTRAQ.Ratio....117.114.	1.25	1.33

1 MPDPAKSAPA P K K G S K K A V T K V Q K K D G K K R K R S R K E S Y S V Y V Y I V L K Q V H P D T G I S S K A M G I M N S F V N D I F E R I A G E A S R
 81 L A H Y N K R S T I T S R E I Q T A V R L L L P G E L A K H A V S E G T R A V T K Y T S S K



5.190 PREDICTED: similar to transforming growth factor beta 1 induced transcript 4 isoform 1 isoform 1 [R

Protein Accession	gij109502739
Mean Expression Ratio	1.15
Median Expression Ratio	1.15
Credible Interval	(0.854, 1.55)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.64
Avg..iTRAQ.Ratio....116.114.	1.18
Avg..iTRAQ.Ratio....117.114.	1.8

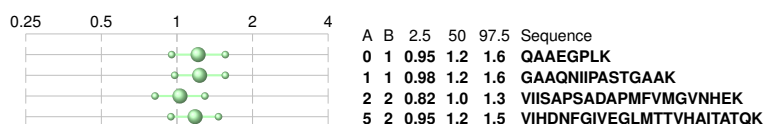


5.191 PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]

Protein Accession	gij109475159
Mean Expression Ratio	1.15
Median Expression Ratio	1.15
Credible Interval	(0.946, 1.40)
Associated Peptides	4
Associated Spectra	14
Coverage	0.204
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.23
Avg..iTRAQ.Ratio....116.114.	1.30
Avg..iTRAQ.Ratio....117.114.	0.848

```

1      MVKVGVNGFG RIGRLVTRAA FSCDKVDIVA INDPFDLNY MVYMFQYDST HGKFNGTVKA ENGKLVINGK PITIFQERDP
81     ANIKWGDAGA EYVVESTGVF TMEKAG AHL KGGAKRVIIS APSADAPMFV MGVNHEKYDN SLKIVSNASC TTNCLAPLAK
161    VIHDFGIVE GLMTTVHAIT ATQKTVDGPS GKLWRDGRGA AONIIPASTG AAKAVGKVIP ELNGKLTGMA FRVPTPNVSV
241    VDLTCRLEKP AKYDDIKKVV KQAAEGPLKG ILGYTEDQVV SCDFNNSHS STFDAGAGIA LNDNFVKLIS WYDNEYGYSN
321    RVVDLMAYMA SKE
    
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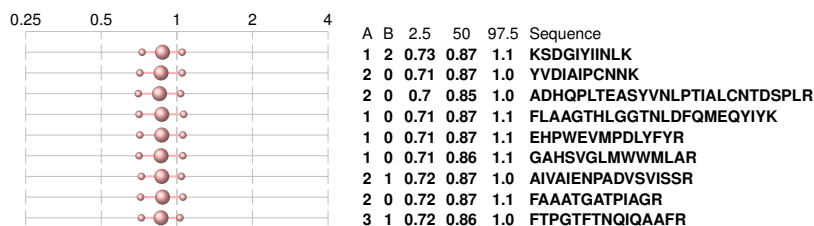


5.192 laminin receptor 1 [Rattus norvegicus]

Protein Accession	gij8393693	
Mean Expression Ratio	0.87	
Median Expression Ratio	0.872	
Credible Interval	(0.761, 0.992)	
Associated Peptides	9	
Associated Spectra	19	
Coverage	0.492	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.987	0.843
Avg..iTRAQ.Ratio....116.114.	0.86	0.975
Avg..iTRAQ.Ratio....117.114.	0.761	0.726

```

1      MSGGLDVLQM KEEDVLKFLA AGTHLGGTNL DFQMEQYIYK RKS DGIYIIN LKRTWEKLLL AAR AIVAIEN PADVSVISSR
81     NTGQRAVLKF AAATGATPIA GRFTPGFTFN QIQAAFREPR LLVVTDPRA D HQPLTEASYV NLPTIALCNT DSPLRYVDIA
161    IPCNNKGAHS VGLMWMLAR EVLRMRGTIS REHPWEVMPD LYFYR DPEEI EKEEQAAAEK AVTKEEFQGE WTAPAPEFTA
241    AQPEVADWSE GVQVPSVPIQ QFPTEDWSAQ PATEDWSAAP TAQATEWVGA TTEWS
    
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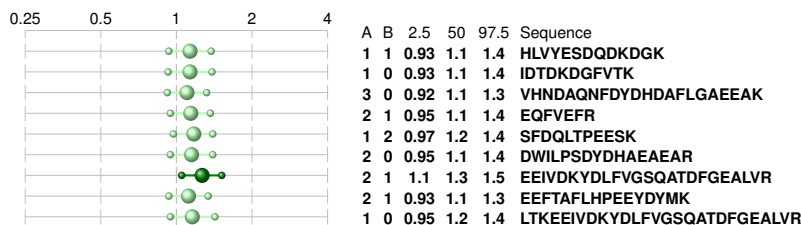


5.193 hypothetical protein LOC360380 [Rattus norvegicus]

Protein Accession	gij76559925	
Mean Expression Ratio	1.15	
Median Expression Ratio	1.15	
Credible Interval	(1.01, 1.30)	
Associated Peptides	9	
Associated Spectra	21	
Coverage	0.390	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.99	1.36
Avg..iTRAQ.Ratio....116.114.	1.09	1.26
Avg..iTRAQ.Ratio....117.114.	1.23	1.70

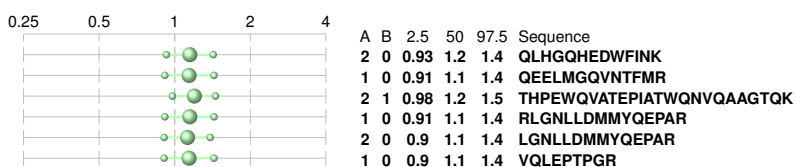
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1      MDLRQFLMCL SLCTAFALSK PTEKKDRVHH EPQLSDK VHN DAQNFYDHD AFLGAEAAKS FDQLTPPEESK ERLGMIVDKI
81     DTDKDCGVTK GELKSWIKHA QKXYIDNVE NQWQEFDMNQ DGLISWDEYR NVTYGTYLDD PDPDDGFNYK QMMVRDERRF
161    KMADKGDLI ATKEEFTAF L HPEEYDYMKD IVVQETMEDI DKNADGFIDL EEYIGDMYSH DGNADPEPW KTER QFVEF
241    RDKNRDGMKD KEETK DWILP SDYDHAEAEA RHLVYESDQD KDGLTKKEI VDKYDLFVGS QATDFGEALV RHDEF
    
```



5.194 "PREDICTED: similar to Deoxyguanosine kinase, mitochondrial precursor (dGK) [Rattus norvegicus]"

Protein Accession	gij34856307	
Mean Expression Ratio	1.14	
Median Expression Ratio	1.15	
Credible Interval	(0.963, 1.35)	
Associated Peptides	6	
Associated Spectra	10	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.12	1.93
Avg..iTRAQ.Ratio....116.114.	1.21	1.76
Avg..iTRAQ.Ratio....117.114.	1.23	2.74



5.195 "mitochondrial trifunctional protein, beta subunit [Rattus norvegicus]"

Protein Accession	gij19424338
Mean Expression Ratio	0.872
Median Expression Ratio	0.872
Credible Interval	(0.653, 1.17)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0189
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.715
Avg..iTRAQ.Ratio....116.114.	0.616
Avg..iTRAQ.Ratio....117.114.	0.589

```

1      MTTILTSTFR NLSTTSKWAL RFSVRPLSCS SQVQSAPAVQ TKSCKTLAKP NLKNIIVVVEG VRIPFLLSGT SYKDLMPHDL
81     ARAALSGLLY RTNIPKDVDV YIIFGTVIQE VKTSNVAREA ALGAGFSDKT PAHTVTMACI SSNQAMTAV GLIASGQCDV
161    VVAGGVELMS DVPIRHSRNM RKMMLDLNKA KTLAQRSLSL TKFRLNFLSP ELPVAEAFST NETMGHSADR LAAAFVSRM
241    EQDKYALRSH SLAKKAQDEG HLSDIVPFKV PGKDTVSKDN GIRPSSLEQM AKLKPAFIKP YGTVTAANSS FLTDGASAML
321    IMSEDRALAM GYKPKAYLRD FIYVSQDPKD QLLLGPTYAT PKVLEKAGLT MNDIDAFEFH EAFSGQILAN FKAMDSDFWA
401    QNYMGRKTKV GAPPLEKFN I WGGSLSLGHP FGATGCRLVM AAANRLRKG D GQYALVAACA AGGQGHAMIV EAYPK
    
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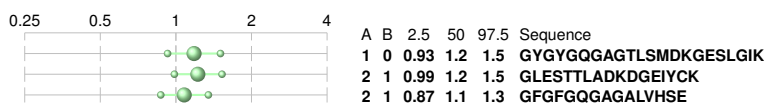


5.196 cysteine and glycine-rich protein 1 [Rattus norvegicus]

Protein Accession	gi 8393206	
Mean Expression Ratio	1.15	
Median Expression Ratio	1.14	
Credible Interval	(0.943, 1.41)	
Associated Peptides	3	
Associated Spectra	7	
Coverage	0.28	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.13	0.94
Avg..iTRAQ.Ratio....116.114.	1.17	1.28
Avg..iTRAQ.Ratio....117.114.	1.96	0.725

```

1      MPNWGGGKCC GVCQKTVYFA EEVQCEGNSF HKSCFLCMVC KKNLDSTTVA VHGEIYCKS CYGKKYGPKE YGYGQGAGTL
81     SMDRGESLGI HHEEAPGHRP TTNPNASKFA QKIGGSERCP RCSQAVYAAE KVIGAGKSWH KSCFRCAKCG KLESTTLAD
161    KDGEIYCKGC YAKNFGPKGF GFGQGAGALV HSE
    
```



5.197 xanthine dehydrogenase [Rattus norvegicus]

Protein Accession	gi 8394544
Mean Expression Ratio	0.874
Median Expression Ratio	0.874

Credible Interval	(0.646, 1.18)
Associated Peptides	1
Associated Spectra	1
Coverage	0
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.704
Avg..iTRAQ.Ratio....116.114.	0.524
Avg..iTRAQ.Ratio....117.114.	0.587

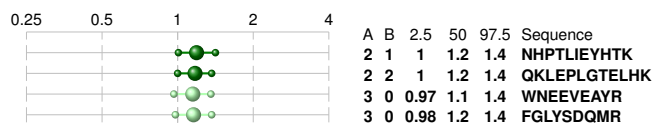
1 MMSPHVILRV VSKVLIPLII VYGFYVHFHG EYSPGGGFQA GVVLASAIL YALIFGLDEA RRVFPPYWAR VGMALGGFIY
 81 ASVGFVSLMM GGFLEYAVL HPDVSHGTGQ HGIIIAVEIG VLTTVTCVMI AIFYAFAGRT PEISDEDW

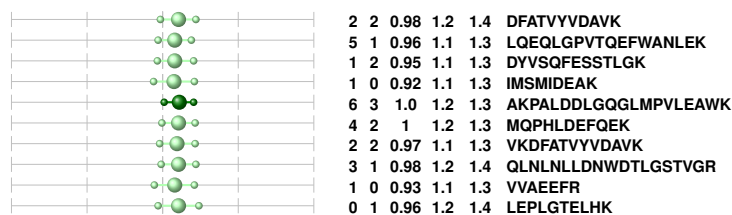


5.198 apolipoprotein A-I [Rattus norvegicus]

Protein Accession	gi 6978515	
Mean Expression Ratio	1.14	
Median Expression Ratio	1.14	
Credible Interval	(1.04, 1.26)	
Associated Peptides	14	
Associated Spectra	52	
Coverage	0.583	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.25
Avg..iTRAQ.Ratio....116.114.	1.28	1.06
Avg..iTRAQ.Ratio....117.114.	1.09	1.24

1 MKA AVLAVL VFLTGCQAW EFWQDEPQSQ WDRV KDFATV YVDAVKD SGR DYVSQFESST LGKQLNLNLL DNWDTLGSTV
 81 GRLQEQLGPV TQEFWANLEK ETDWLRNEMN KDLENVKQKM QPHLDEFQEK WNEEVEAYRQ KLEPLGTELH KNAKEMQRHL
 161 KVVAE EFPDR MRVNADALRA K FGLYSDQMR ENLAQRLTEI KNHPTLIEYH TKASDHLKTL GEKAKPALDD LGQGLMPVLE
 241 AWKAKIMSMI DEAKK LNA

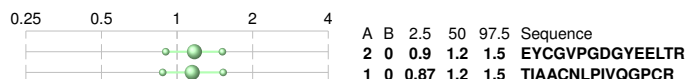




5.199 alpha 1 microglobulin/bikunin [Rattus norvegicus]

Protein Accession	gij6978497
Mean Expression Ratio	1.14
Median Expression Ratio	1.14
Credible Interval	(0.892, 1.45)
Associated Peptides	2
Associated Spectra	3
Coverage	0.086
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.47
Avg..iTRAQ.Ratio....116.114.	1.20
Avg..iTRAQ.Ratio....117.114.	1.54

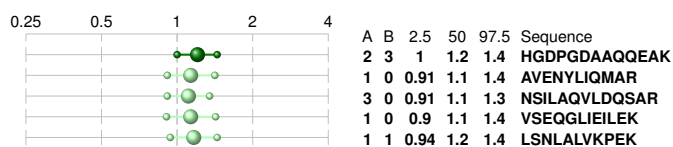
1 MQGLGALFLL LTACLTLKAD NVPTLPDIQV QENFNARIY GKWFNLAVGS TCPWLRRIKN KMSVSTLVLQ EGATEAEISV
 81 TSTQWRKGYC EEISGVYQKT DIDGKFLYHK SKWNATLESY VVHTNYDEYA IFLTKKFSHR HGPTITAKLY GREPQLRDSL
 161 LQEFREVALS VGIPENSIVF MADRGECVPG DREVETSFA RARRAVLPQE NEGSGSEPLI TGTLKKEDSC QLNyseGPCI
 241 GMQKYYNYG ASMACETFQY GGCLGNNGNF ASEKECLQTC R**TIAACNLPI** **VGGPCFAFAE** LWAFDAAQ GK CIQFIYGGCK
 321 GNGNKFYSEK ECK**EYCGVPG** **DGYEELTR**S



5.200 PREDICTED: similar to Programmed cell death protein 5 (TFAR19 protein) (TF-1 cell apoptosis related)

Protein Accession	gij109461756
Mean Expression Ratio	1.14
Median Expression Ratio	1.14
Credible Interval	(0.974, 1.34)

Associated Peptides	5	
Associated Spectra	12	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	1.47
Avg..iTRAQ.Ratio....116.114.	1.13	1.17
Avg..iTRAQ.Ratio....117.114.	1.08	1.53

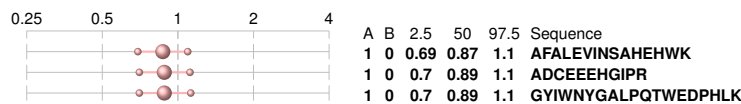


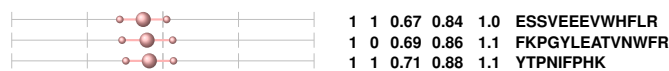
5.201 PREDICTED: similar to inorganic pyrophosphatase 2 [Rattus norvegicus]

Protein Accession	gij109465582	
Mean Expression Ratio	0.876	
Median Expression Ratio	0.875	
Credible Interval	(0.735, 1.04)	
Associated Peptides	6	
Associated Spectra	8	
Coverage	0.245	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.966	0.672
Avg..iTRAQ.Ratio....116.114.	0.92	0.645
Avg..iTRAQ.Ratio....117.114.	0.842	0.535

```

1      MRALLPLLSV GRGWRVGAAA LPPRRVMSLY RTEELGHPRS KDYRLFFKHV AGHYISPFHD IPLKADCEEE HGIPRKKARN
81     DEYKASFNMV VEIPRWTNAK MEIATEEPLN PIKQDTKNGR LRYTPNIFPH KGYIWNYGAL PQTWEDPHLK DKSTNCCGDN
161    DPIDVCEIGS KVL SRGDVVH VKILGTLALI DQSETDWKII AINVNDPEAE KFHDIDDVKK FKPGYLEATV NWFPLYKVFD
241    GKPENKFAFN GEFKNAFAL EVINSAHEHW KEMVMKRC DK GAI SCVNVHI CDSPFHCTTE EARSLVESIP TPMSKESV
321    EEEVWHFLRN
    
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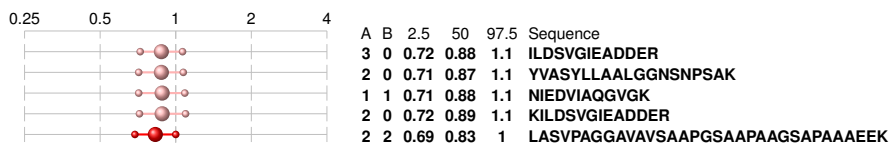




5.202 "ribosomal protein, large P2 [Rattus norvegicus]"

Protein Accession	gj 71795613	
Mean Expression Ratio	0.875	
Median Expression Ratio	0.876	
Credible Interval	(0.75, 1.02)	
Associated Peptides	5	
Associated Spectra	13	
Coverage	0.678	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.838	1.70
Avg..iTRAQ.Ratio....116.114.	0.959	1.13
Avg..iTRAQ.Ratio....117.114.	0.878	0.851

1 MR YVASYLLA ALGGNSNPSA KDIKKILDSV GIEADDERLN KVISELNGKN IEDVIAQGVG KLASVPAGGA VAVSAAPGSA
81 APAAGSAPAA AEEKKDEKKE ESEESDDDMG FGLFD



5.203 PREDICTED: similar to RuvB-like 2 (p47 protein) [Rattus norvegicus]

Protein Accession	gj 109499390	
Mean Expression Ratio	1.14	
Median Expression Ratio	1.14	
Credible Interval	(0.85, 1.52)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0714	
Experiment	B	
Avg..iTRAQ.Ratio....115.114.	1.38	

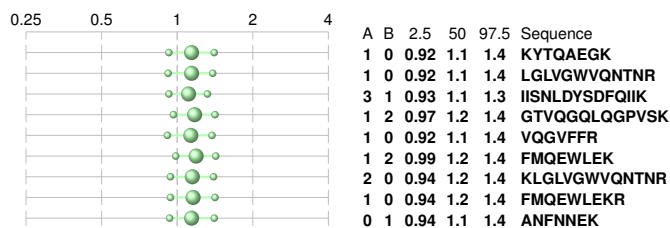
Avg..iTRAQ.Ratio....116.114. 1.09
 Avg..iTRAQ.Ratio....117.114. 2.12

1 MGMVQALGPD TQFTAIAGSE IFSLEMSKTE ALTKAFCSI GVSIKEETEI IEGDVVEIQI DRPATCTGFK VGKLTlKTME
 81 METIYDLCTK MIESLTKDKV QAGDVITIDK ATGKISKLRR SFTRARDYDG SQTkFVPGRR AAKTQGGGAH RVVP



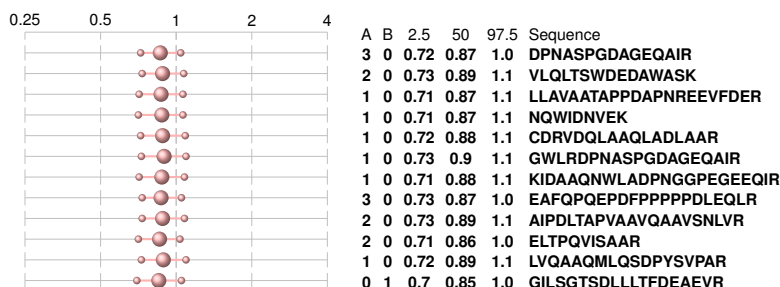
5.204 "PREDICTED: similar to acylphosphatase 1, erythrocyte (common) type [Rattus norvegicus]"

Protein Accession	gi 109479686	
Mean Expression Ratio	1.14	
Median Expression Ratio	1.14	
Credible Interval	(0.995, 1.31)	
Associated Peptides	9	
Associated Spectra	17	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.10	1.14
Avg..iTRAQ.Ratio....116.114.	1.14	1.06
Avg..iTRAQ.Ratio....117.114.	1.2	1.37



5.205 PREDICTED: similar to Vinculin (Metavinculin) [Rattus norvegicus]

Protein Accession	gij109501157	
Mean Expression Ratio	0.878	
Median Expression Ratio	0.877	
Credible Interval	(0.767, 1.00)	
Associated Peptides	12	
Associated Spectra	19	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.985	0.456
Avg..iTRAQ.Ratio....116.114.	0.907	0.621
Avg..iTRAQ.Ratio....117.114.	0.879	0.814



5.206 "PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 [Rattus norvegicus]"

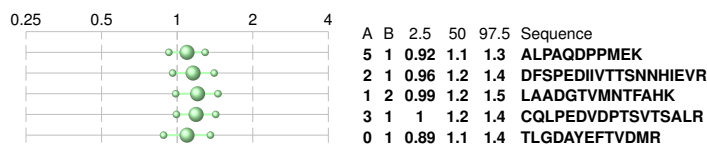
Protein Accession	gij109507159	
Mean Expression Ratio	0.875	
Median Expression Ratio	0.877	
Credible Interval	(0.669, 1.14)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	NA	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.775	
Avg..iTRAQ.Ratio....116.114.	0.925	

Avg..iTRAQ.Ratio....117.114. 0.654



5.207 "PREDICTED: similar to heat shock protein family, member 7 (cardiovascular) [Rattus norvegicus]"

Protein Accession	gij109477617	
Mean Expression Ratio	1.14	
Median Expression Ratio	1.14	
Credible Interval	(0.984, 1.32)	
Associated Peptides	5	
Associated Spectra	17	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	1.13
Avg..iTRAQ.Ratio....116.114.	1.10	1.20
Avg..iTRAQ.Ratio....117.114.	1.29	1.26



5.208 cell division cycle 5-like [Rattus norvegicus]

Protein Accession	gij16758290	
Mean Expression Ratio	1.14	
Median Expression Ratio	1.14	

Credible Interval	(0.886, 1.46)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.00748	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.27	0.832
Avg..iTRAQ.Ratio....116.114.	1.14	0.802
Avg..iTRAQ.Ratio....117.114.	1.53	1.12

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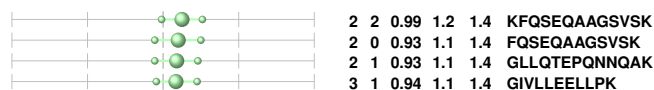
1      MPRIMIKGGV WRNTEDEILK AAVMKYKGNQ WSRIASLLHR KSAKQCKARW YEWLDPSIKK TEWSREEEEK LLHLAKLMPT
81     QWRTIAPIIG RTAAQCLEHY EFLLDKTAQR DNEEETDDP RKLLPGEIDP NPETKPARPD PIDMDEDELE MLSEARARLA
161    NTQGKKAKRK AREKQLEEAR RLAALQKRRE LRAAGIEIQK KRKKKRGVDY NAEIPFEKKP ALGFYDTSEE NYQALDADFR
241    KLRQQDL DGE LRSEKEGRDR KKDKQHLKRR KESDLPSAIL QTSQVSEFTK KRSLVLPAP QISDAELQEV VKVGQASEVA
321    RQTAEESGIT NSASSTLLSE YNVTNNSIAL RTPRTPASQD RILQEAQNLN ALTNVDTPLK GGLNTP LHES DFSGVTPPQRQ
401    VVQTPNTVLS TPFRTPSNGA EGLTPRSGTT PKPVTNATPG RTPLRDKLN I NPEDEGMADYS DPSYVKQMER ESREHLRLGL
481    LGLPAPKNDF EIVLPENAEK ELEEREMDDT YIEDAADVDA RKQAIRDAER VKEMKRMHKA VQKDLPRPSE VNETILRPLN
561    VEPPLTDLQK SEELIKKEMI TMLHYDLLHH PYEPSGNKKG KNVGFATNNS EHITYLEHSP YEKFSKEDLK KAQDVLVQEM
641    EVVKQGM SHG ELSSEAYNQV WEECYSQVLY LPAQSR YTRA NLASKKDRIE SLEKRLEINR GHMTTEAKRA AKMEKKMKIL
721    LGGYQSRAMG LLKQLNDLWD QIEQAHLELR TFEELK KHE D SAIPRRLECL KEDVQRQQR EKELQQR YAD LLMEKETLQA
801    KF
    
```



5.209 PREDICTED: similar to tetratricopeptide repeat domain 11 [Rattus norvegicus]

Protein Accession	gij27664028	
Mean Expression Ratio	1.14	
Median Expression Ratio	1.14	
Credible Interval	(0.97, 1.33)	
Associated Peptides	4	
Associated Spectra	13	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.13
Avg..iTRAQ.Ratio....116.114.	1.24	1.15
Avg..iTRAQ.Ratio....117.114.	1.20	1.38



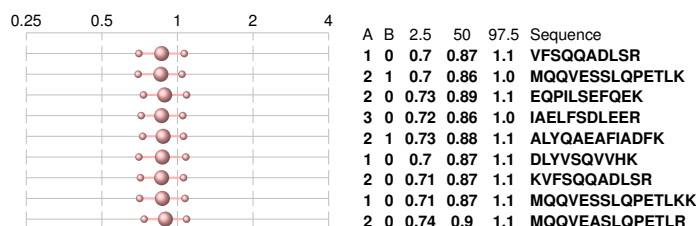


5.210 serine protease inhibitor 2a [Rattus norvegicus]

Protein Accession	gi 32563565	
Mean Expression Ratio	0.878	
Median Expression Ratio	0.879	
Credible Interval	(0.766, 1.01)	
Associated Peptides	9	
Associated Spectra	18	
Coverage	0.139	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.901	0.696
Avg..iTRAQ.Ratio....116.114.	0.807	0.702
Avg..iTRAQ.Ratio....117.114.	0.985	0.75

```

1    MAHWGRDTLS HEDHGKGRQL HSLTLASSNT DFALSPLYKKL ALRNPDKNVV FSPLSISAAL TILSLGAKDS TMEIILEGLK
81   FNLTEITEEE IHQGFHLLQ RLSQPEDQVE INTGSALFID KEQPILSEFQ ERTRALYQAE AFIADFFQPN EAKKLINDYV
161  SNQTQGK IAE LFSDLLEERTS MVLVNYLLFK GKMQQVESSL QPETLKKWKD SLIPRIINDL RMPKFSISTD YSLKEVLPFL
241  GIKKVFSQQA DLSRITGTKD LYVSQVVHKA VLDVDEGTGE ATAATGVATV IRRQPRTLNF NRPFMVVITD MDSQSILFVA
321  KITNPKRPVK VPMMKLEDLT TPYVQDEELN CTVVVELKYTG NASALFILPD QGKMQQVEAS LQPETLLEWK DSLRPSMIDE
401  LYPPKFSISA DYSVEECRAP SNGEQRVLYS KGLFPPEESC RMSFLLARRW ARDVGCETEE VLPPELGIKEV FSTQADLSGI
481  TGDKDLTVSQ EAGAGGMLNP PLAASILAVP SEDVEKLPVR KLLPLPTAIL QFVVVHKAVL DVAETGT EAA AATGVKLVPM
561  SAKLDPLIIV FNRPLIIMS DTETEIAPFW PRYLTPNEIR TSQGLTLLPR H
    
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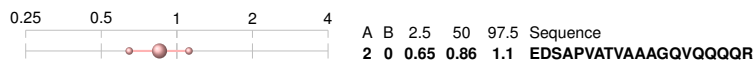


5.211 "protein phosphatase 1, regulatory (inhibitor) subunit 14C [Rattus norvegicus]"

Protein Accession	gi 19173802
Mean Expression Ratio	0.879
Median Expression Ratio	0.88
Credible Interval	(0.667, 1.14)
Associated Peptides	1
Associated Spectra	2
Coverage	0.122
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.679
Avg..iTRAQ.Ratio....116.114.	0.851
Avg..iTRAQ.Ratio....117.114.	0.784

```

1      MSVVTGGGGEA AGGTSGGGAR VFFQSPRGGT GGSRESSSHS GSSREDSAPV ATVAAAGQVQ QQQRRHQQGT VTKYDRKEL
81     RKRLVLEEWI  VEQLGQLYGC EEEEMPVDEI DIDDLLDADS EEERASKLQE ALVDCYKPT E F IRELLSRI  RGMRKLSPPQ
161    KKSVM
  
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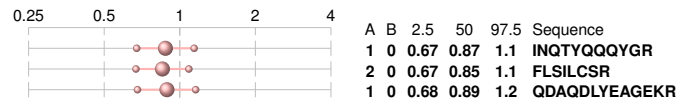


5.212 annexin A4 [Rattus norvegicus]

Protein Accession	gi 55742832
Mean Expression Ratio	0.881
Median Expression Ratio	0.881
Credible Interval	(0.7, 1.10)
Associated Peptides	3
Associated Spectra	4
Coverage	0.100
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.909
Avg..iTRAQ.Ratio....116.114.	0.83
Avg..iTRAQ.Ratio....117.114.	0.758

```

1      METKGGTVKA ASGFNATEDA QVLRKAMKGL GTDEDIIGV LACRNTAQRQ EIRTAYKSTI GRDLLEDLKS ELSSNFEQVI
81     LGMPTPTVLY DVQELRRAMK GAGTDEGCLI EILASRNPEE IRRINQTYQQ OYGRSLEEDI CSDTSFMFQR VLVSLTAGGR
161    DEGNYLDDAL VKQDAQDLYE AGEKRWGTDE VKFLSILCSR NRNHLLHVED EYKRISQKDI EQSIKSETSG SPEDALLAIV
241    KCMRNKPAYF AERLYKSMRG LGTDDSTLIR VMVSRAEIDM LDIRANFKRL YGKSLSYFIK GDTSGDYRKV LLILCGGDD
  
```



5.213 PREDICTED: similar to sorting nexin associated golgi protein 1 [Rattus norvegicus]

Protein Accession	gij109466059
Mean Expression Ratio	1.14
Median Expression Ratio	1.13
Credible Interval	(0.866, 1.48)
Associated Peptides	1
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.52
Avg..iTRAQ.Ratio....116.114.	1.26
Avg..iTRAQ.Ratio....117.114.	1.83



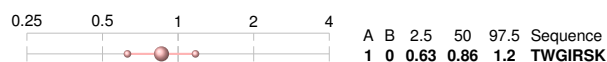
5.214 unc-13 homolog C [Rattus norvegicus]

Protein Accession	gij49248545
Mean Expression Ratio	0.88
Median Expression Ratio	0.882
Credible Interval	(0.654, 1.18)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00318
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.94
Avg..iTRAQ.Ratio....116.114.	0.459
Avg..iTRAQ.Ratio....117.114.	0.562


```

1      MVASLFKSLI LAYIHKLCCK MFTKKLGNTT KKKENRQQNK DQDFPTAGHT KPPKLSNALK STVKKIAKCS STRNFSVEDE
81     EGHKDFSLSP TFSYRVAIAN GLQTAVTNSD EDLLQELSSI ESSYSESFNE LRSSTENQVQ STHTMPVRRN RKSSSSSLAPS
161    EGSSDGERL  HTLKLGLARL LRKWKKSQEC VSSDSELSTV KKTWGIRKFS LDRTARNPKT NVLEPGFSSS GCISQTHDVM
241    EMIFKELQGI SQIETELSEL RGHVNALKYS IDEISSSVEV VQSEIEQLRT GFVQARRETR DIHDYIKHLG HMGSKVSLRF
321    LNVPEERHEY VESVYQIILV DKMGFSDVNP AIKIEFAQRI GQQRDCPNAK PRPILVYFET PQQRDSVLKK SYKLGKTGIA
401    ISTDILTYDI RERKEKGVLP SSQTYESMDM KLSTPEPKAK KNAWLSPNDS DRELESLSR SSYADSPAKG SSSKSSSKSH
481    SARSKNKAAN SRTSQKSDYN KRPSKPPASE KPTPHYVEAT PLWHSQSDFF TPKLSRSED FSKLCQSYSE DFSESQFFCR
561    TNGSSLLSS  DRELWQRKQE GMTALYHSPQ DQGLDGNIPT VPGQGEIENT ETVDSGMSNS VVCASGDRSN YSGQLSLHE
641    DLSFWKEWNQ AGHGTDLGDS STQEPFDYDT NSLSDQLDM SSKDLDDLK CHSDLDQDSE SYDLTQDDNS SPCGGLDNEP
721    QGQWVGQYDS YQKTNNSNDLY PNQSHPSMMY RSQSELQSD SEAAQPKSWH SRLSIDLSDK TFFKPKFGST LQRAKSALEV
801    VWNKSTQSLG CEDSGSSSLM GRFRTLSQST ANESSTLDS DIYTEPYYYK AEEEEEDYCEP VADSETDYVE VMEQVLAKLE
881    NRSTVTEVDE HIKEYDHPSY ETPYETPQDE GYDQADDII SEGELETLNE PAVEMELVED ESQNLPEVPP EVMKPKRIRP
961    SFKEAALRAY KQMAELEEK ILAGDSSSDV EKARIVSGND LDASKFSALQ VFGGAGRGLY GIDSMPLRR KKTLPVIRDV
1041   AMTLAARKSG  LSLAMVIRTS LNNEELKMHV FRKTLQALIY PISSTPHNF EVWTATPTY CYECEGLLWG IARQGMKCLE
1121   CGVKCHEKQC DLLNADCLQR AAEKSSKHGA EDKTQTIITA MKERMKIRER NRPEVFEVIQ EMFQISKEDF VQYTKAAKQS
1201   VLDGTSKWSA KITITVVSQA GLQAKDKTGS SDPYVTVQVG KNKRRTKTIF GNINPVWDEK FYFECHNSTD RIKVRVWDED
1281   DDIKSRVKQH FKKESDDFLG QTIVEVRTLS GEMDVWYMLE KRTDKSAVSG AIRLKNVEI KGEKVPAPYH IQYTCLHENL
1361   FHYLTEVKN  GSVKIPEVKG DEAWKVFDD ASQEIIVDEFA MRYGVESIQ AMTHFSCLSS KYMCPGVPV MSALLANINA
1441   FYAHTTVSTN VQVSASDRFA ATNFGREKFI KLLDQLHNSL RIDLSKYREN FPASNSERLQ DLKSTVLLT SITFFRMKVL
1521   ELQSPPKASA VVKDCVRACL DSTYKYIFDN CHELYSLQID PSKKQDVPRE EQGPTTKNLD FWFQLITLMV TIIDEDKTAY
1601   TPVLNQFPQE LNMKGISAEI MWSLFALDMK YALEEHEKQR LCKSTDMNL HFKVKWFYNE YVRELPAFKD AVPEYSLWFE
1681   PFVMQWLDEN EDVSMFLHG ALGRDKKDG  QQTS DHALFS CSVVDVFAQL NQSFEIKKL ECPNPEALSH LMRRFAKTIN
1761   KVLVQYAAIV SDFSSYCDK  ETVPCILMNN IQQLRVQLEK MFESMGKEL DPEASTILKE LQIKLNGVLD ALSVTYGESF
1841   QLVIEECIKQ MGAELNQRA NGNSAANKNN AAMD AEIVLR PLMDFLDKIL SLSAKICEKT VLKRVLKELEW KLVLNKIEKQ
1921   IVLPLPLDQT GPQMFIAAK  ELGQLSKLKE HMRDDAKGL TPRC AIMEV VLATIKQYFH AGGNGLKKNF LEKSPDLHSL
2001   RYALSPLYQT  TDALIKKFI  EQGSQSRSSK DAVGQISVHV DVTTTPGTGE HKVTVKVIAI NDLNMQTTM FRPFVEVCML
2081   GPSLGDKKRK QGTTKSNNTW SPKYNETFQF  ILGNENRPGA YELHLSVKDY CFAREDRIIG MTVIQLQIA EKSYGAWYP
2161   LLKNLSMET  GLTIILRILS  RTSDDVAKEF VRLKSETRSI  DESA

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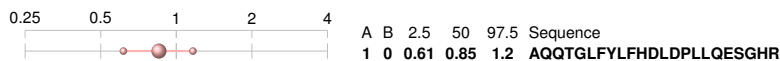
5.215 PREDICTED: similar to Nucleoside diphosphate linked moiety X motif 13 (Nudix motif 13) [Rattus norv

Protein Accession	gij109502118
Mean Expression Ratio	0.88
Median Expression Ratio	0.882
Credible Interval	(0.651, 1.18)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0653
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.691
Avg..iTRAQ.Ratio....116.114.	0.626
Avg..iTRAQ.Ratio....117.114.	0.565

NHLBI Zile/Grant, Aged Rat

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1      MSLYCGTFFR RKSFGCYRLL STYVTRARYL FELKEDDEAC RKAQQTGLFY LFHDLDPLLQ ESGHRYLVPR LSRAELEGLL
81     GKFGQDSQRI EDSVLVGCSN EQEAWFALDL GLKSASSVRA SLPKSEMEAE LGGSFVKLRQ ALLQLNSVDS SLLFTAQALL
161    RWHDGHQFCS KSGQPTQKNM AGSKRVCPSN NIIYYPQMAP VVITLVSDGA RCLLARQSSF PRGLYSALAG FCDIGERVEE
241    AVHREVAAEV GLEVENIQYS ASQHWPFPNS SLMIACHATV KPGHTEIQVN LKELEAAAWF SLDEVATALR RKGSFAQQQR
321    EASPLMLPPK LAVAHMIKE WVEKQSRSSL AA
  
```



5.216 PREDICTED: similar to Acyl-CoA thioesterase 4 (Peroxisomal acyl coenzyme A thioester hydrolase lb)

Protein Accession	gij109479629
Mean Expression Ratio	0.883
Median Expression Ratio	0.882
Credible Interval	(0.69, 1.14)
Associated Peptides	1
Associated Spectra	3
Coverage	0.0447
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.963
Avg..iTRAQ.Ratio....116.114.	0.83
Avg..iTRAQ.Ratio....117.114.	0.645

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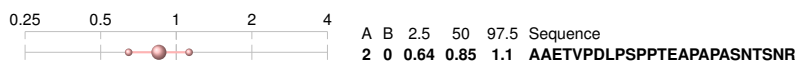
1      MAATLSLEPA GRSCWDEPLS ITVRGLAPEQ PVTLRAALRD EKGALFRAHA RYHADSHGML DLARAPALGG SFAGLEPMGL
81     LWAMEPERPF WRLIKRDVQT PFVVELEVLD GHEPDGGQRL ARAVHERHFM APGVRVPVR EGRVRATLFL PPGQGFPPGI
161    IDVYGVGGGL LEYRASLLAG HGFATLALAF YGFEDLPKEF NVIEVDYFEE AVCYMLQHPK VLLVCFIHSV SLGTSLYRGG
241    LLHQLY
  
```



5.217 PREDICTED: similar to target of myb1-like 2 isoform 2 [Rattus norvegicus]

Protein Accession	gij109490844
Mean Expression Ratio	0.881
Median Expression Ratio	0.883
Credible Interval	(0.675, 1.16)
Associated Peptides	1

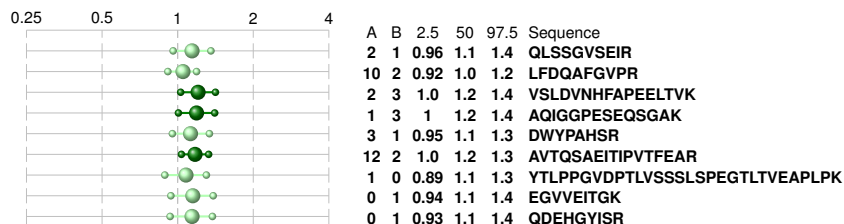
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.585
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	0.863



5.218 heat shock 27kDa protein 1 [Rattus norvegicus]

Protein Accession	gij94400790	
Mean Expression Ratio	1.13	
Median Expression Ratio	1.13	
Credible Interval	(1.02, 1.26)	
Associated Peptides	9	
Associated Spectra	45	
Coverage	0.6	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	1.22
Avg..iTRAQ.Ratio....116.114.	1.11	1.13
Avg..iTRAQ.Ratio....117.114.	1.17	1.25

1 MTERRVPFSL LRSPSWEPFR DWYPAHSRLF DQAFGVPRFP DEWSQWFSSA GWPGYVRPLP AATAEGPAAV TLARPFSTRAL
 81 NRQLSSGVSE IRQTADRWRV SLDVNHFAPE ELTVKTRGV VEITGKHEER QDEHGYISR C FTRKYTLPPG VDPFLVSSSL
 161 SPEGLTLVEA PLPRAVTQSA EITIPVTFEA RAQIGPPESE QSGAK

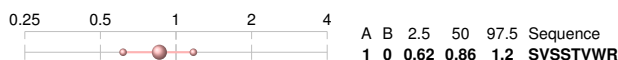


5.219 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gij109503724
Mean Expression Ratio	0.883
Median Expression Ratio	0.883
Credible Interval	(0.656, 1.20)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0147
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.711
Avg..iTRAQ.Ratio....116.114.	0.695
Avg..iTRAQ.Ratio....117.114.	0.53

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1   MAPFRDPLGS AGSAAGCTAA GLDSVRLHIG AGHLWRPLEQ RFRFPVVRPW RQADPETHSA HLAPEGVSKP SQSGSGSGST
81  LSGLELSMAA MSSHPEPGA REPQSPRPQP LSQSSSSLLC EGREQRPELR KSVSSTVWR A QQAEASTGPR TLQEEGCQME
161 STEQAQTANP PSQAAAGGHW RSSTVGNVST MGIGDLCRLQ APSVAAVQRS HSDLVHSTQT RGHGSVQKPS LSCSALGISP
241 VHRAHLQPGG VAGQGGPTPA PLPSDSSLED GTSKSACTLG ESQVWVPTIE LEDTTGLLIG SQGEPQATGQ PSTTFCHALP
321 PATLLCTVGE AVPGSTCHAL PAKGILAFPK LVASVSESL QAQCCKMFKC QLSGGISGRA HCCVHPWGPT GLATESGSRT
401 KDVWTMTSAT DLALGVASAQ DAGVQAAPVA ACKAVATSPS LEAPKTLNIF PEVMLGPGLE EASSPVREVR WDAEGMTWEV
481 YGASVDPEVL GIATQKHLEM QFEQLQQAPA SEDSLSTEGR RGPLRAVMQS LRRPSCCGCS GAAP
  
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5.220 translocase of inner mitochondrial membrane 8 homolog b [Rattus norvegicus]

Protein Accession	gij11968134
Mean Expression Ratio	0.882
Median Expression Ratio	0.883
Credible Interval	(0.694, 1.12)
Associated Peptides	2
Associated Spectra	3
Coverage	0.217
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.798
Avg..iTRAQ.Ratio....116.114.	0.941
Avg..iTRAQ.Ratio....117.114.	0.722

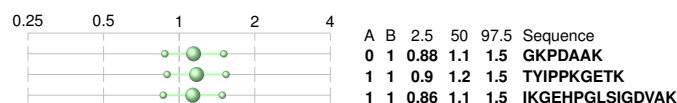
1 MAELGEADEA ELQRLVAAEQ QKAQFTAQVH HFMELCWDKC VEKPGSRLDS RTENCLSSCV DRFIDTTLAI TGRFAQIVQK
 81 GGQ



5.221 PREDICTED: similar to High mobility group protein 1 (HMG-1) (High mobility group protein B1) (Ampho

Protein Accession	gij109474683
Mean Expression Ratio	1.13
Median Expression Ratio	1.13
Credible Interval	(0.89, 1.44)
Associated Peptides	3
Associated Spectra	5
Coverage	0.149
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.09
Avg..iTRAQ.Ratio....116.114.	1.21
Avg..iTRAQ.Ratio....117.114.	1.15

1 MGKGDPPKLR GKSSSYAFFV QTCREEHKKK HPDASVNFSE FSKKCSERWK TMSAKEKGF EDMAKADKAR YEREMKTYIP
 81 PKGETKKKFK DPNAKRPFS AFFLCSEYH PKIKGEHPGL SIGDVAKKLG EMWNNTAADD KQPCEKKAAL LKEKYEKIDIA
 161 AYRAKGPDA AKKGVVKAEL SKKKKEEEDD EDEDEDEEEE EEEEEDEEEE DDDDE



5.222 eukaryotic translation elongation factor 1 delta [Rattus norvegicus]

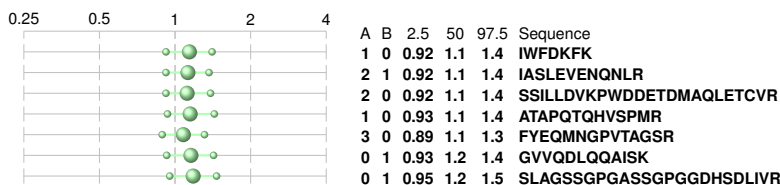
Protein Accession	gij61556967
Mean Expression Ratio	1.13

Median Expression Ratio	1.13	
Credible Interval	(0.968, 1.32)	
Associated Peptides	7	
Associated Spectra	12	
Coverage	0.163	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.09
Avg..iTRAQ.Ratio....116.114.	1.16	1.62
Avg..iTRAQ.Ratio....117.114.	1.07	1.68

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1   M R S G K A S C A L   E T V W E D K H K Y   E E A E R R F H E H   E A T Q A A A A S V   Q Q L L A E V P A V   N G P S S Q E D A E   D T D E A E T P N T   S S R S D P R K S H
81  E C K K P L Q K K R   K R S P K S W L G Q   A D L A L V G L S A   D H V W L D K P L F   D Q A E S S Y R Q R   L A D V A A Q A A Q   S P A L A P R G P C   T H G S H V A C H H
161 V T W G I W V N K S   C F D Q A E R A F V   E W S Q A L L L A A   E G S H R E G T P D   T G Q Q A V T P D L   A L A C Q P C P P A   N G Q P P L G S L Q   A L V R E V W L E K
241 P R Y D A A E R G F   Y E A L F D G H P P   G K V R L Q E R A S   Q A E G T R R G R R   D R R S R N T V G N   K R A G S K R A D G   E A P S A L P Y W Y   F L H K D A E A P W
321 L S K P T Y D S A E   C R H H A A E A L R   I A W R L E A A S L   A H R P T P R S G P   S M S S L R P K K M   A T N F L M H E K   I   W F D K F K   Y D D A   E R R   F Y E Q M N G
401 P V T A G S S Q E N   G A S V I L R D I A   R A R E N I Q K S L   A G S S G P G A S S   G P G G D H S D L I   V R I A S L E V E N   Q N L R G V V Q D L   Q Q A I S K L E V R
481 L S T L E K S S P T   H R A T A P Q T Q H   V S P M R Q V E P P   A K K G A T P A E D   D E D N D I D L F G   S D E E E D K E A   A R L R E E R L R Q   Y A E K K A K K P T
561 L V A K S S I L L D   V K P W D D E T D M   A Q L E T C V R S I   Q L D G L V W G A S   K L V P V G Y G I R   K L Q I Q C V V E D   D K V G T D L L E E   E I T K F E E H V Q
641 S V D I A A F N K I

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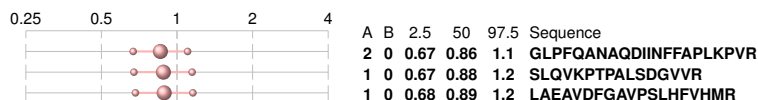
5.223 PREDICTED: similar to G-rich sequence factor 1 (GRSF-1) [Rattus norvegicus]

Protein Accession	gij109499565
Mean Expression Ratio	0.884
Median Expression Ratio	0.885
Credible Interval	(0.704, 1.11)
Associated Peptides	3
Associated Spectra	4
Coverage	0.0843
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.881
Avg..iTRAQ.Ratio....116.114.	0.85
Avg..iTRAQ.Ratio....117.114.	0.793

NHLBI Zile/Grant, Aged Rat

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1      MYYTHIQSQY FRSKQSWPSA RTSRLTVSTP PSASSQNVLE LGITFLETS SGRPADLSSN LSRRRAWEGFH FEQSQVTFPT
81     PLRGEKPRPQ GGAQAEPFAL LRLRASSQPR VRAAHVPGSP SPALDSTSPF LAPQRQSPGP APPPEPMAGT RWVLGALLRG
161    CGCNCSSCRP TGAACLFPYS AAGTFPSGVS GRRRLLLLLG AAAAAASQTR GLQLGPAAG RLAGTTLRAR DPRRPRARVL
241    LSASASRARP GIRGTHRTPA SLPLRPPIGH RNKGRSPGPG SSPCFVPSES GRLVSVSVAG VNVEALFPAG PMESKTTYLE
321    DLPLLPEYEL SPSKLGEEVD DYLIRAQGL PWSCTVEDVL SFFSDCRIRN SENGIFLLN RDGKRRGDAL IEMESEQDVQ
401    KALEKHRMYM GQRYVEVYEI NNEDVDALMK SLQVKPTPAL SDGVVRLRGL PYSCNEKDIV DFFAGLNIVD ITFVMDYRGR
481    RKTGEAYVQF EPEEMANQAL LKHREIIGNR YIEIFPSRRN EVRTHVGSBK GKMMVSPPT KYITEPEVVF EEHEVNEDAR
561    PMTAFESEKE IELPKEMSDK LAEAVDFGAV PSLHFVHMRG LPFQANAQDI INFFAPLKPV RITMEYSSSG KATGEADVHF
641    DTHEDAVAAM LKDRSHVRKS GPLFLSRCCV CIWELA
  
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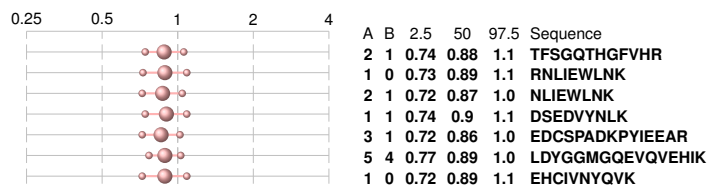


5.224 hypothetical protein LOC310201 [Rattus norvegicus]

Protein Accession	gj 56912206	
Mean Expression Ratio	0.885	
Median Expression Ratio	0.885	
Credible Interval	(0.778, 1.01)	
Associated Peptides	7	
Associated Spectra	23	
Coverage	0.29	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.89	0.94
Avg..iTRAQ.Ratio....116.114.	0.943	0.895
Avg..iTRAQ.Ratio....117.114.	0.683	0.923

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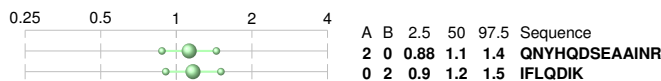
1      MANEANPCPC DIGHRLDYGG MGQEVQVEHI KAYVTRSPVD AGKAVIVVQD IFGWQLSNTR YMADMIAGNG YTTIVPDFV
81     GQEPWDPAGD WSTFPPEWLS RNARKINREV DAVLRYLKQQ CHAQRIGIVG FCWGGIVVHH VMTTYPEVRA GVSVYGIIRD
161    SEDVYNLNP TLFIFAENDA VIPLEQVSIL IQKLKEHCIV NYQVTFSGQ THGFVHRKR EDCSPADKPYI EEARRNLIEW
241    LNKYI
  
```



5.225 "ferritin, heavy polypeptide 1 [Rattus norvegicus]"

Protein Accession	gj 6978859	
Mean Expression Ratio	1.13	
Median Expression Ratio	1.13	
Credible Interval	(0.896, 1.43)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.110	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	0.984
Avg..iTRAQ.Ratio....116.114.	1.27	1.12
Avg..iTRAQ.Ratio....117.114.	1.16	1.72

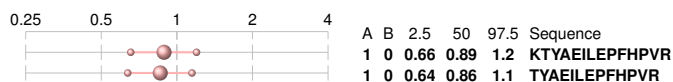
1 MTTASPSQVR QNYHQDSEAA INRQINLELY ASYVYLSMSC YFDRDDVALK NFAKYFLHQ S HEEREHAEKL MKLQNQRGGR
 81 IFLQDIK KPD RDDWESGLNA MECALHLEKS VNQSLLLELHK LATDKNDPHL CDFIETHYLN EQVKSIKELG DHVTNLRKMG
 161 APESGMAEYL FDKHTLGHGD ES



5.226 "NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 [Rattus norvegicus]"

Protein Accession	gj 57164133	
Mean Expression Ratio	0.886	
Median Expression Ratio	0.886	
Credible Interval	(0.674, 1.16)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	0.117	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.742	
Avg..iTRAQ.Ratio....116.114.	0.845	
Avg..iTRAQ.Ratio....117.114.	0.709	

1 MMNGRPGHEP LRFLPDEARR LPPPKLNDPR LVIYIGFLGYC TGLMDNMMRM RPVMKAGLHR QLLYVTSFFF AGYFYLKRQN
 81 YLYAVRDHDM FGYIKLHPED FPEKERKTYA EILEPFHPVR

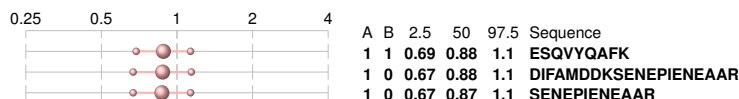


5.227 "PREDICTED: similar to succinate-Coenzyme A ligase, GDP-forming, beta subunit isoform 3 [Rattus norv"]

Protein Accession	gij109473906	
Mean Expression Ratio	0.887	
Median Expression Ratio	0.886	
Credible Interval	(0.707, 1.12)	
Associated Peptides	3	
Associated Spectra	4	
Coverage	0.0668	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.93	0.891
Avg..iTRAQ.Ratio....116.114.	0.733	0.78
Avg..iTRAQ.Ratio....117.114.	0.77	0.946

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1   MASAVAIAAQ AGKLLRERSL RPRL LAVRSQ AGHLT PRRWL NLQ EYQSKKL MSEHGVRVQR FVASTAKEA QEA AKRLNAK
81  EIVLKAQILA GGRGKGVFDS GLKGGVHLTK DPKVVGQLAQ QMIGYNLATK QTPKEGVKVN KVMVAEALDI SRETYLA ILM
161 DRSHNGPVLV GSPQGGVDIE EVAASSPELI FKEQIDIFEG IKDSQAQRMA ENLGF LGS LK NQAADQIKKL YHLFLKIDAT
241 QVEVNPFA CA SFSGFVCFDA KINFDDNAEF RQK DIFAMDD KSENEPIENE AARYDLKYIG LDGNIACFVN GAGLAMATCD
321 IIFLNGGKPA NFLDLGGGVK ESQVYQAFKL LTSDPKVEAI LVNIFGGIVN CAIIANGITK ACQELELKVP LVVRLEG TNV
401 QEAQNILKSS GLPITSAVDL EDAAKKAVAS VAKK
    
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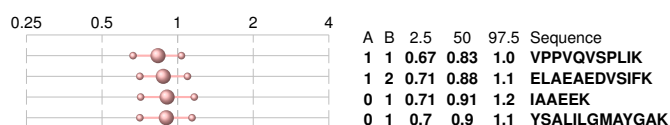


5.228 "ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E [Rattus norvegicus]"

Protein Accession	gij17978459	
Mean Expression Ratio	0.886	
Median Expression Ratio	0.887	
Credible Interval	(0.728, 1.08)	
Associated Peptides	4	

Associated Spectra	7	
Coverage	0.592	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.678	0.784
Avg..iTRAQ.Ratio....116.114.	0.802	0.612
Avg..iTRAQ.Ratio....117.114.	0.677	1.02

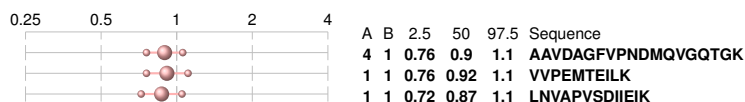
1 MVPPVQVSPL IKFGRYSALI LGMAYGAKRY SYLKPRAEER RRIAAEEKKR LDELKRIERE LAEAEVDSIF K

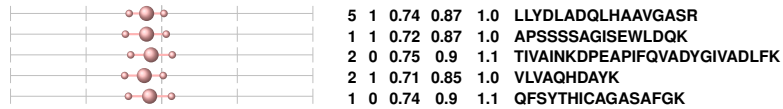


5.229 alpha-ETF [Rattus norvegicus]

Protein Accession	gi 57527204	
Mean Expression Ratio	0.887	
Median Expression Ratio	0.888	
Credible Interval	(0.779, 1.01)	
Associated Peptides	8	
Associated Spectra	23	
Coverage	0.384	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.95	0.793
Avg..iTRAQ.Ratio....116.114.	0.869	0.801
Avg..iTRAQ.Ratio....117.114.	0.912	0.712

1 MFRAAAPGQL RRAASLLRFQ STLVIAEHAN DSLAPITLNT ITAAGR LGGE VSCLVAGTKC DKVVQDLCKV AGVAKVLVAQ
 81 HDAYKGLLPE ELTPLILETQ KQFSYTHICA GASAFGNLL PRVAAKLNVA PVSDIIEIKS PDTFVRTIYA GNALCTVKCD
 161 EKVKVFSVRG TSFEAAAASG GSASSEKAPS SSSAGISEWL DQKLTKSDRP ELTGAKVVVS GGRGLKSGEN FKLLYDLADQ
 241 LHAAVGASRA AVDAGFVPND MQVGQTGKIV APELYIAVGI SGAIQHLAGM KDSKTIVAIN KDPEAPIFQV ADYGIVADLF
 321 KVVPEMTEIL KKK



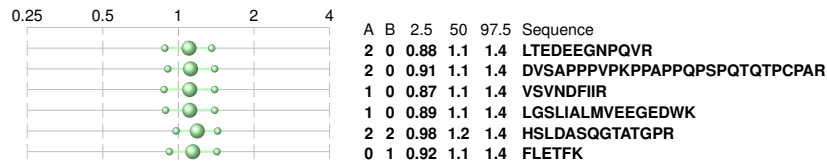


5.230 hypothetical protein LOC311254 [Rattus norvegicus]

Protein Accession	gi 113205496	
Mean Expression Ratio	1.12	
Median Expression Ratio	1.12	
Credible Interval	(0.949, 1.32)	
Associated Peptides	6	
Associated Spectra	11	
Coverage	0.158	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	1.48
Avg..iTRAQ.Ratio....116.114.	1.11	1.22
Avg..iTRAQ.Ratio....117.114.	1.19	1.28

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1      MQVEEGAKNI KLGSLIALMV EGEDWKHVE IPKDVSAAPP VPKPPAPPQ SPQTQTPCPA RKERTVGTTP RLRLSPAARN
81     ILEKHSLDAS QGTATGPRGV FTKEYELSPI KVQQRLLRWA VTCVKSSQQC VTPVLRVRLTV VLEVLGSSQA GGWCDSRSDQ
161    RTTARATVSL EKSTGSELVF RFHVKTEVVL QVHVQQKHS EDALRLVELK QMGKIAEFRP APGPPSTLSA PVPPQPTAGL
241    SYPRPMIPPV SIPGQPNAAG TFTEIPASNI RKVIKRLTE SKSTVPHAYA TANCDLGAVL KVRRLVKDD IKVSVNDFII
321    RAAAVTLQOM PGVNVTDGGE GPKHLPVSDI SVAVATDKGL ITPIIKDAAA KDIREDIADAV KPHLLYFLFW PCVTVEALQL
401    RIEQWFGNS YDIYMCAGRH VLWPLSSIAE GSVLKYANLI GTMPPSAVFS FLSSISNLGM FGIDEFTAVI NPPQACILAV
481    GRFRPVLKIT EDEEGNPQVR QHQLITVTMS SDSRMVDEL ATKFLETFFA NLENPMRLA
  
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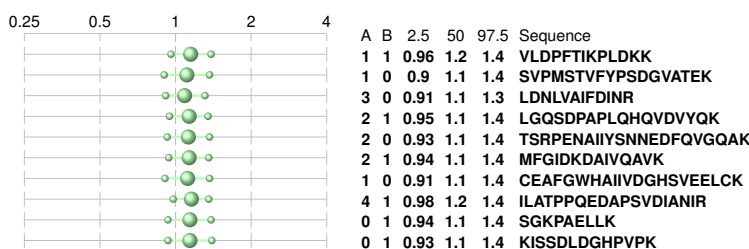
5.231 transketolase [Rattus norvegicus]

Protein Accession	gi 12018252	
Mean Expression Ratio	1.12	
Median Expression Ratio	1.12	
Credible Interval	(0.992, 1.28)	
Associated Peptides	10	

Associated Spectra	22	
Coverage	0.243	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	1.47
Avg..iTRAQ.Ratio....116.114.	0.987	1.35
Avg..iTRAQ.Ratio....117.114.	1.12	1.63

```

1      MDPVRIQCD REGKRFPFLS APPASTSSPD RAMEGYHKPD QQKLQALKDT ANRLRISSIQ ATTAAGSGHP TSCCSAAEIM
81     AVLFFHTMRY KALDPRNPHN DRFVLSKGHA APILYAVWAE AGFLPEAEEL NLRKISSDDL GHPVPKQAFD DVATGSLGQG
161    LGAACGMAYT GKYPDKASYR VYCM LGDGEV SEGSVWEAMA FAGIYKLDNL VAIFDINRLG QSDPAPLQHQ VDVYQKRCEA
241    FGWHAIIVDG HSVEELCRAF GQAKHQPTAI IAKTFKGRGI TGIEDKEAWH GKPLPKNMAE QIIQEIYSQV QSKKKILATP
321    PQEDAPSVDI ANIMPTPPN YKVGDKIATR KAYGLALAKL GHASDRRIAL DGDTKNSTFS ELFKKEHPDR FIECYIAEQN
401    MVSIAVGCAT RDRTVPFCST FAAFFTRAFD QIRMAAISES NINLCGSHCG VSIAGEDGPSQ MALEDLAMFR SVPMTSTVFP
481    SDGVATEKAV ELAANTKGC FIRTSRPENA IISNNEDFO VGOAKVVLKS KDDQVTVIGA GVTLHEALAA AEMLKKEKIG
561    VRVLDPFTIK PLDKK LILDC ARATKGRILT VEDHYEYGGI GEAVSAVVVG EPGVTVTRLA VSQVPRSGKP AEELKMFQID
641    KDAIVQAVKG LVTKG
  
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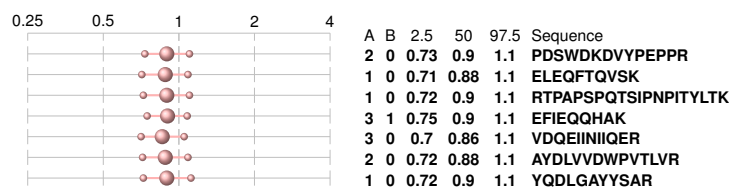


5.232 PREDICTED: similar to NADH-ubiquinone oxidoreductase PDSW subunit (Complex I-PDSW) isoform

Protein Accession	gij109490345	
Mean Expression Ratio	0.89	
Median Expression Ratio	0.889	
Credible Interval	(0.764, 1.03)	
Associated Peptides	7	
Associated Spectra	14	
Coverage	0.511	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.812	1.11
Avg..iTRAQ.Ratio....116.114.	0.897	0.944
Avg..iTRAQ.Ratio....117.114.	0.952	0.936

NHLBI Zile/Grant, Aged Rat

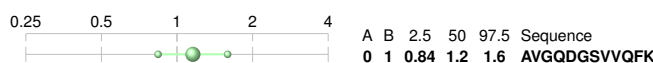
1 MPDSWDKDVY PEPPRRTPAP SPQTSIPNPI TYLTKAYDLV VDWPVTLVRE FIEQQHAKNR TYYHRQYRR VPDITECKEG
 81 DVICIYEAE M QWRRDFKVDQ EIINIIQERL KACQQREGES ALQNCAKELE QFTQVSKAYQ DRYQDLGAYY SAR KCLAKQK
 161 QRMLEERKAA KETAAA



5.233 PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 isoform 1 [Rattus norvegicus]

Protein Accession	gij109476002
Mean Expression Ratio	1.13
Median Expression Ratio	1.12
Credible Interval	(0.836, 1.51)
Associated Peptides	1
Associated Spectra	1
Coverage	0.158
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.06
Avg..iTRAQ.Ratio....116.114.	0.933
Avg..iTRAQ.Ratio....117.114.	1.16

1 MADEKPKKEGV K TENNDHINL KAVGQDGSVV QFEIKRHPTL SKLMKAYCER QDTPAQLEME DEDTIDVFRQ QTGGVY



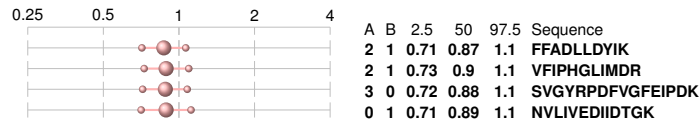
5.234 hypoxanthine guanine phosphoribosyl transferase [Rattus norvegicus]

Protein Accession	gij51092266
Mean Expression Ratio	0.89

Median Expression Ratio	0.89	
Credible Interval	(0.746, 1.06)	
Associated Peptides	4	
Associated Spectra	10	
Coverage	0.229	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.954	0.886
Avg..iTRAQ.Ratio....116.114.	0.82	0.61
Avg..iTRAQ.Ratio....117.114.	0.907	0.843

```

1   MSTLSPSVVI SDDEPGYDLD LFCIPNHYAE DLEKVFIPHG LIMDRTERLA RDVMKEMGGH HIVALCVLKG GYKFFADLLD
81  YIFALNRNSD RSIPMTVDFI RLKSYCNDQS TGDIKVIGGD DLSTLTGKVV NLVEDIIDTG KTMQTLLSLV KQYSPKMKVQ
161 ASLLVKRTR SVGYRPDFVG FEIPDFVVG YALDYNHFR DLNHVCVISE SGKAKYKA
    
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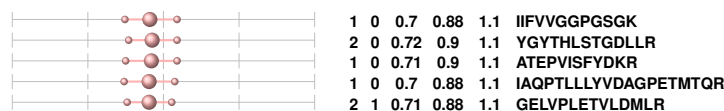
5.235 adenylate kinase 1 [Rattus norvegicus]

Protein Accession	gi 61889092	
Mean Expression Ratio	0.892	
Median Expression Ratio	0.891	
Credible Interval	(0.744, 1.08)	
Associated Peptides	5	
Associated Spectra	8	
Coverage	0.366	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.895	0.871
Avg..iTRAQ.Ratio....116.114.	0.992	0.902
Avg..iTRAQ.Ratio....117.114.	0.785	0.656

```

1   MEDKLRKAKI IFVVGPPGSG KGTQCEKIVQ KYGYTHLSTG DLLFAEVSSG SSRGKMLSSI MEKGELVPLE TVLDMLRDAM
81  LARVDSSNGF LIDGYPREVK QGEEFERKIA QPTLLLYVDA GPETMTQRL KRGETSGRVD DNEETIKRRL ETTYKATEPV
161 ISFYDKRGIV RKNVAEGSVD TVFSQVCTYL DSLK
    
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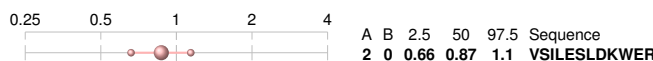


5.236 "protein kinase, cAMP dependent regulatory, type I, alpha [Rattus norvegicus]"

Protein Accession	gij6981396
Mean Expression Ratio	0.892
Median Expression Ratio	0.891
Credible Interval	(0.684, 1.17)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0315
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.713
Avg..iTRAQ.Ratio....116.114.	0.799
Avg..iTRAQ.Ratio....117.114.	0.796

```

1   MASGSMAASE EERSLRECEL YVQKHNIQAL LKDSIVQLCT ARPERPMAFL REYFERLEKE EARQIQSLQK SGIRTDSDRED
81  EISPPPPNPV VKGRRRRGAI SAEVYTEEDA ASYVRKVIPK DYKTMAALAK AIEKNVLFSD LDDNERSDIF DAMFPVSFIA
161 GETVIQQGDE GDNFYVIDQG EMDVYVNNW ATSVGEGGSF GELALIYGTP RAATVKAKTN VKLWGIDRDS YRRILMGSTL
241 RKRKMYEFL SKVSIESLD KWERLTVADA LEPVQFEDGQ KIVVQGEPGD EFFIILEGTA AVLQRRSENE EFVEVGRGLGP
321 SDYFGEIALL MNRPRAATVV ARGPLKCVKL DRPRFERVLG PCSDILKRNI QQYNSFVSLV V
    
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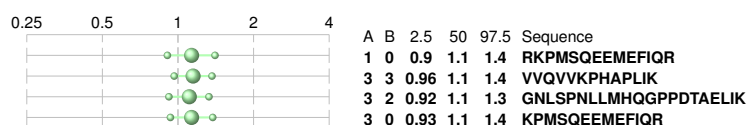
5.237 PREDICTED: similar to mitochondrial ribosomal protein S36 [Rattus norvegicus]

Protein Accession	gij109465995
Mean Expression Ratio	1.12
Median Expression Ratio	1.12
Credible Interval	(0.957, 1.31)
Associated Peptides	4
Associated Spectra	15

Coverage	0.262	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	1.38
Avg..iTRAQ.Ratio....116.114.	1.30	0.986
Avg..iTRAQ.Ratio....117.114.	1.21	0.972

```

1      MLSNTELGQS  TRLRQGRAPE  GCQCLAQLYS  QRGKSLSTQ  EIQLGQKSCN  IVLNRLRPTL  PTLDTSAARL  RFGSCPYSKV
81     MMGSKMASAT  RVVQVVKPHA  PLEKFPNRRD  KPKLSASDTL  RSAALPSHSS  VISQHSKGNL  SPNLLMHQGP  PDTAELIISL
161    PQKYRKKPMS  QEEMEFIQEG  GPE
  
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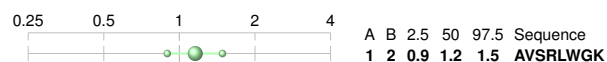


5.238 E74-like factor 1 [Rattus norvegicus]

Protein Accession	gi 59710101	
Mean Expression Ratio	1.12	
Median Expression Ratio	1.12	
Credible Interval	(0.873, 1.42)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.013	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.26	1.18
Avg..iTRAQ.Ratio....116.114.	1.16	0.94
Avg..iTRAQ.Ratio....117.114.	0.81	0.89

```

1      MAAVVQQNDL  VFDFASNVM  DEQQLGDPAI  FPAVIVEHVP  GADILNGYAG  LACVEEPNDM  ITESSLDVAE  EEIEDDDDD
81     ITLTVASCH  NGDETIETI  AAEALLNMD  S  PGPVLDEKRI  NNNIFSSSED  DIVAPITHVS  VTLDGIPVEM  ETQQVQESNA
161    DSPGASSPEQ  PKRKKGRKT  PPRPDSPAT  T  PNISVKKKSK  DGKGNITYLW  EFLALLQDK  ATCPKYIKWT  QREKGIFKLV
241    DSKAVSRLWG  KHKNKPMNY  ETMGRALRY  Y  YQRGILAKVE  GQRLVYQFKE  MPKDLYIDD  EGPSSSTESS  DQSLSTTTS
321    SRNQANRTRM  SSSPGIKGGA  TTILKPGNPK  V  VARPDKTVEV  GQPSEVLRTV  QPSQAPYPTQ  LFRTVHVVQP  VQAIPEEATI
401    TSTMQEEAAG  SSVQGIRTI  ASTQVPVVVS  P  PGNQQQLHTVT  LQTVPLTTVI  ASTDPSSGAG  PQKFILQAIP  SSQPMTVLKE
481    NVLLQSQKPG  SPPSIVFSPT  PVQQVLTGSV  Q  QSLGNGAVSM  ASPPNFSATA  PVVTFSSRSQ  LAAHPPGTVI  TSVIKAQETK
561    TPRAEVEKKA  EGHNLNDP  EE  IEQQQPQYVM  VVSSSNGFSS  QVAITQNEL  L  EPSSF
  
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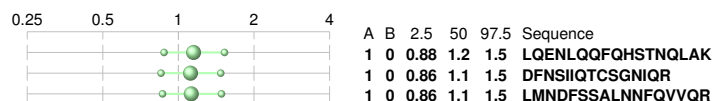


5.239 syntaxin 12 [Rattus norvegicus]

Protein Accession	gi 77695930
Mean Expression Ratio	1.12
Median Expression Ratio	1.12
Credible Interval	(0.884, 1.43)
Associated Peptides	3
Associated Spectra	3
Coverage	0.179
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.24
Avg..iTRAQ.Ratio....116.114.	1.49
Avg..iTRAQ.Ratio....117.114.	1.28

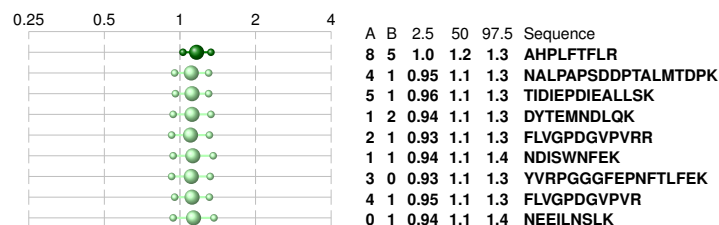
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1      MSYGPLDMYR  NPGPSGPQPR  DFNSIIQTCS  GNIQRISQAT  AQIKNLMSQL  GTKQDSSKLO  ENLQQFQHST  NQLAKETNEL
81     LKELGSLPLP  LSASEQRQOK  LQKERLMNDF  SSALNNFQVV  QRKVSEKEKE  SIARARAGSR  LSAEDRQREE  QLVSFDSHEE
161    WNMQSQEEE  AAITEQDLEL  IKERETAIQQ  LEADILDVNQ  IFKDLAMMIH  DQGDLIDSIE  ANVESSEVHV  ERASDQLQRA
241    AYYQKSRKK  MCILVLVLSV  IVTVLVVVIW  VASK
  
```



5.240 glutathione peroxidase 1 [Rattus norvegicus]

Protein Accession	gi 30520381	
Mean Expression Ratio	1.12	
Median Expression Ratio	1.12	
Credible Interval	(1.01, 1.25)	
Associated Peptides	9	
Associated Spectra	41	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.30
Avg..iTRAQ.Ratio....116.114.	1.13	1.16
Avg..iTRAQ.Ratio....117.114.	1.06	1.31

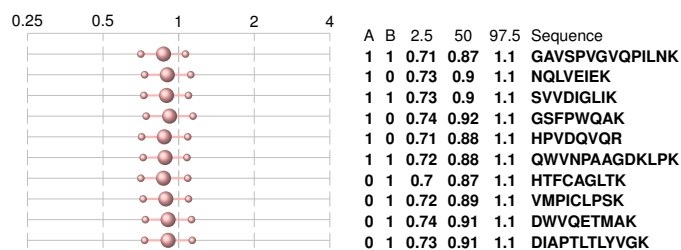


5.241 haptoglobin [Rattus norvegicus]

Protein Accession	gij60097941	
Mean Expression Ratio	0.894	
Median Expression Ratio	0.893	
Credible Interval	(0.767, 1.04)	
Associated Peptides	10	
Associated Spectra	13	
Coverage	0.285	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.63	0.577
Avg..iTRAQ.Ratio....116.114.	0.89	0.668
Avg..iTRAQ.Ratio....117.114.	1.34	1.15

```

1      MRALGAVVTL LLWGQLFAVE LGNDATDIED DSCPFPPEIA NGYVEHLVRY RCRQFYKLTQ EGDGIYTLNS EKQVNPAAAG
81     DKLPKCEAVC GKPKHPVDQV QEIIGGSMDA KGSFPWQAKM ISRHGLTTGA TLISDQWLLT TAQNLFNLHS ENATAKDIAIP
161    TLTLYVGKNQ LVEIEKVVVH PERSVVDIGL IKLKQKVLVT EKVMPICLPS NDYVAPGRMG YVSGWGRNVN FRFTERLKYYV
241    MLPVADQKEC ELHYEKSTVP EKKGAVSPVG VQPILNKHTF CAGLTKYEED TCYGDAGSAF AVHDEEDTW YAAGILSFDK
321    SCAVAEYGVY VRATDLKDWV QETMAFN
    
```



5.242 PREDICTED: similar to Cysteine-rich protein 1 (Cysteine-rich intestinal protein) (CRIP) [Rattus nor

Protein Accession	gij109480057
Mean Expression Ratio	1.12
Median Expression Ratio	1.12
Credible Interval	(0.878, 1.41)
Associated Peptides	2
Associated Spectra	3
Coverage	0.130
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.17
Avg..iTRAQ.Ratio....116.114.	1.18
Avg..iTRAQ.Ratio....117.114.	1.59

1 MPKCPK**CDKE** **VYFA**ERVTSL GKDWRPCLK CEKCGKTLTS GGHAHEGKP YCNHPCYSAM FGPKGFGRRG AESHTFK



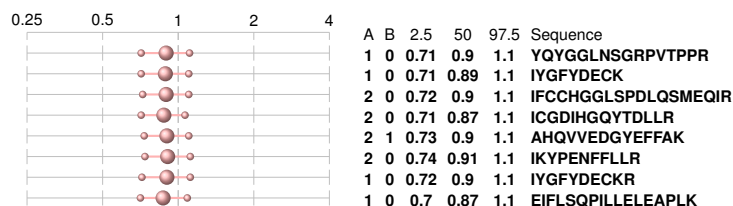
5.243 "protein phosphatase 1, catalytic subunit, beta [Rattus norvegicus]"

Protein Accession	gij6981388
Mean Expression Ratio	0.893
Median Expression Ratio	0.893
Credible Interval	(0.76, 1.04)
Associated Peptides	8
Associated Spectra	13
Coverage	0.309
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.957
Avg..iTRAQ.Ratio....116.114.	0.908
Avg..iTRAQ.Ratio....117.114.	0.854

NHLBI Zile/Grant, Aged Rat

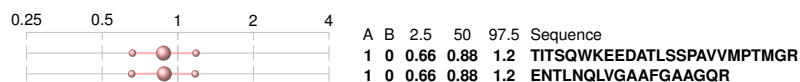
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1      MADGELNVDS LITRLLLEVRG CRPGKIVQMT EAEVRGLCIK SREIFLSQPI LLELEAPLKI CGDIHGQYTD LLRLFYGGF
81     PPEANYLFLG DYVDRGKQSL ETICLLLAYK IKYPENFFLL RGNHECASIN RIYGFYDECK RRFNIKLWKT FTDCFNCLPI
161    AAIVDEK LFC CHGGLSPDLQ SMEQIR RIMR PTDVDPDTGLL CDLLWSDPDK DVQGWGENDR GVSFTFGADV VSKFLNRHDL
241    DLICRAHQVV EDGYEFFAAR QLVTLFSAPN YCGEFDNAGG MMSVDETLMC SFQILKPSEK KAKYQYGLN SGRPVTTPR
321    ANPPKKR
  
```



5.244 "aldehyde dehydrogenase family 6, subfamily A1 [Rattus norvegicus]"

Protein Accession	gij13591997
Mean Expression Ratio	0.893
Median Expression Ratio	0.894
Credible Interval	(0.681, 1.17)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.826
Avg..iTRAQ.Ratio....116.114.	0.779
Avg..iTRAQ.Ratio....117.114.	0.783

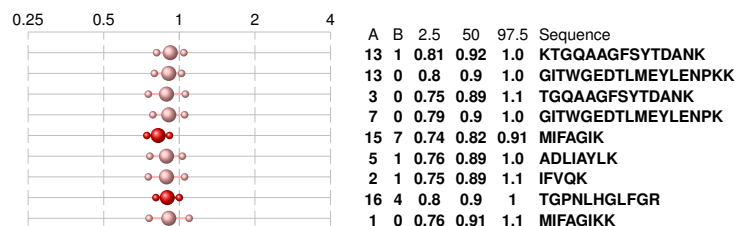


5.245 "PREDICTED: similar to Cytochrome c, somatic [Rattus norvegicus]"

Protein Accession	gij109490661
Mean Expression Ratio	0.894
Median Expression Ratio	0.894

Credible Interval	(0.82, 0.975)	
Associated Peptides	9	
Associated Spectra	89	
Coverage	0.619	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.865	0.961
Avg..iTRAQ.Ratio....116.114.	1.10	0.857
Avg..iTRAQ.Ratio....117.114.	0.77	0.844

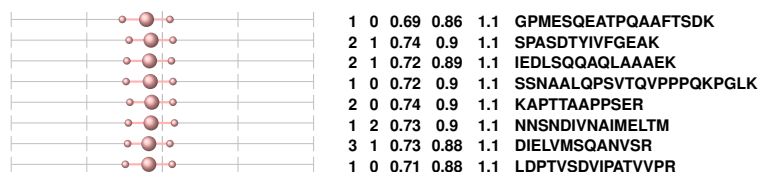
1 MGDVEKGGKI FVQKCAQCHT VEKGGKHKTG PNLHGLFGRK TGQAAGFSYT DANKNKGITW GEDTLMEYLE NPKIYIPGK
 81 MIFAGIKKKG ERADLIAYLK KTTNE



5.246 "PREDICTED: similar to Nascent polypeptide-associated complex alpha subunit, muscle-specific form (A)"

Protein Accession	gij109480121
Mean Expression Ratio	0.894
Median Expression Ratio	0.894
Credible Interval	(0.765, 1.04)
Associated Peptides	8
Associated Spectra	18
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.927
Avg..iTRAQ.Ratio....116.114.	0.875
Avg..iTRAQ.Ratio....117.114.	0.923

0.25 0.5 1 2 4 A B 2.5 50 97.5 Sequence



5.247 similar to TSC22 domain family protein 4 (TSC22-related-inducible leucine zipper protein 2) [Rattus

Protein Accession	gij112983956	
Mean Expression Ratio	0.895	
Median Expression Ratio	0.894	
Credible Interval	(0.708, 1.13)	
Associated Peptides	1	
Associated Spectra	4	
Coverage	0.0465	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.78	0.797
Avg..iTRAQ.Ratio....116.114.	0.915	0.9
Avg..iTRAQ.Ratio....117.114.	0.729	1.4

```

1   MSGGKKKSSF QITSVTDDYE GPGSPGASDP PAPPAPAGPP PRLPNGEPPN DPGGRGTPRN GSPPPGAPAS RFRVVKLPQG
81  LGEFYRRGRW TCVDVYERDL EPPSFGRLLE GIRGASGGTG GRSLDSRLEL ASLGISTPIP QPGLSQGPTS WLRPPPTSPG
161 PQARSFTGGL QLAGPGKAK VETPPLSASP PQRPPGPGT GDSAQTLPSL RVEVESGGLA AGTPPLSRRR DGAVLRMEL
241 VAPEETGKVP PIDSRPNSPA LYFDASLVHK SPDFFGAAA QSLSLARSM L A ISGHLDSDD DSGSGSLVGI DNKIEQAMD L
321 VKSHLMFAVR EEVEVLKEQI RDLAERNAAL EQENGLLRAL ASPEQLAQLP SSGLPFLGPS APNGPSI
    
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5.248 "PREDICTED: similar to aldehyde dehydrogenase family 7, member A1 [Rattus norvegicus]"

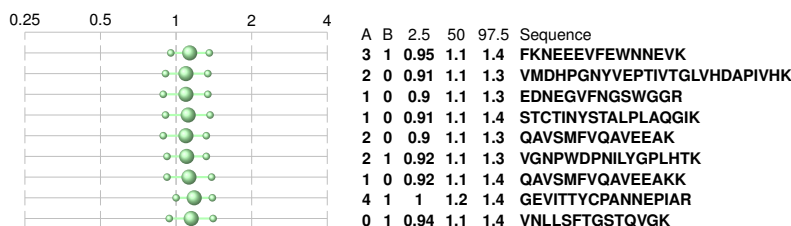
Protein Accession	gij62664437	
Mean Expression Ratio	1.12	
Median Expression Ratio	1.12	
Credible Interval	(0.98, 1.28)	

Associated Peptides	9	
Associated Spectra	20	
Coverage	0.252	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	1.38
Avg..iTRAQ.Ratio....116.114.	1.13	1.39
Avg..iTRAQ.Ratio....117.114.	1.10	1.67

```

1      MLRLARPLCV QTVKASKLSR LWSRPAALMS TLLIHPQYA WLQDLGLRED NEGVFNGSWG GRGEVITYC PANNEPIARV
81     RQASMKDYEE TIGKAKKAWN IWADIPAPKR GEIVRKIGDA LREKIQLLGR LVSLEMGKIL VEGIGEVQEY VDVCDYAAGL
161    SRMIGGPTLP SERPGHALME QWNPLGLVGI ITAFNFPVAV FGWNNAIALI TGNVCLWKA PTTSLVSIIV TKIIAKVLED
241    NLLPGAICSL TCGGADMGTA MARDERVNLL SPTGSTQVGK QVALMVQERF GKSLLELGGN NAIIFEDAD LSLVLPSALF
321    AAVGTAGQRC TTVRRLFLHE SIHDEVVDRL KNAYSQIRVG NPWDPNILYG PLHTRQAVSM FVQAVEEAKK EGGTVVYGGK
401    VMDHPGNYVE PTIVTGLVHD APIVHETFA PILYVFKTKN EEEVFEWNNE VKQGLSSSIF TKDLGRIFRW LGPKGSDCGI
481    VNVNIPTSGA EIGGAFGGEK HTGGGRESGS DAWKQYMRRS TCTINYSTAL PLAQQIKFQ

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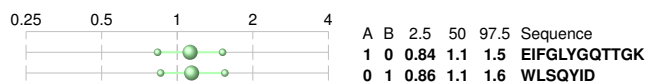
5.249 SAR1a gene homolog 1 [Rattus norvegicus]

Protein Accession	gij56090263	
Mean Expression Ratio	1.12	
Median Expression Ratio	1.12	
Credible Interval	(0.87, 1.47)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	0.096	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.15	1.15
Avg..iTRAQ.Ratio....116.114.	1.08	1.60
Avg..iTRAQ.Ratio....117.114.	1.20	1.62

```

1      MSFIFEWIYN GFSSVLQFLG LYKKSGLVF LGLDNAGKTT LLHMLKDDRL GQHVPTLHPT SEELTIAGMT FTFDLGGHE
81     QARRVWKNYL PAINGIVFLV DCADHSRLME SKVELNALMT DETISNVPII ILGNKIDRTD AISEEKLEI FGLYQTTGK
161    GNVTLKELNA RPMEVFMCSV LKRQGYGEGF RWLSQYID

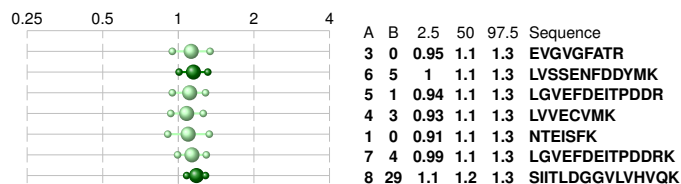
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5.250 fatty acid binding protein 4 [Rattus norvegicus]

Protein Accession	gi 16758094	
Mean Expression Ratio	1.12	
Median Expression Ratio	1.12	
Credible Interval	(1.01, 1.23)	
Associated Peptides	7	
Associated Spectra	76	
Coverage	0.433	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.11	1.03
Avg..iTRAQ.Ratio....116.114.	1.06	1.19
Avg..iTRAQ.Ratio....117.114.	0.987	1.2

1 MCDAFVGTWK LVSSSEFDDY MKEVGVGFAT RKVAGMAKPN LIISVEGDLV VIRSESTFKN TEISFKLQVE FDEITPDDRK
 81 VKSIITLDGG VLVHVQKWDG KSTTIKRRXD GDKLVVECVK KGVSTTRVYX RAXAKGRGPG LKFASNSTIT



5.251 ribosomal protein S15 [Rattus norvegicus]

Protein Accession	gi 8394212	
Mean Expression Ratio	1.12	
Median Expression Ratio	1.12	
Credible Interval	(0.874, 1.44)	
Associated Peptides	1	
Associated Spectra	3	

Coverage	0	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	1.49
Avg..iTRAQ.Ratio....116.114.	1.09	1.14
Avg..iTRAQ.Ratio....117.114.	1.39	1.48

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1      MSINSFGHLF RVTTWGESHG PALGATVDGC PPGVTITEEM IQHWMDKRRP GQNKYTTQRR EADEVRILSG VFEGVTTGTP
81     IQLMIENDQ  RSKDYGDIKD KFRFGHADIT YFQYGIIRDY RGGGRSSARE TASRVAAGGL AREAIKAIAP NVQITGYMVQ
161    MGPBKIDRDA FDWDQIEQNP FWVPDAKAAE EWAAYLDGLR KSGSSVGAII EVTARGVPAG LGAPVYKGLD TDLAAMMSI
241    NAVKVEIGE  GMSAAMLTEG LNADEISMGP DGPVYSSNHA GGILGGISTG QDIVLRFVAVK PTSSILTRK TITKTGEDTE
321    IITKGRHDPC VGIRAVPVGE AMMACVLLDH MLLHRGQVGE NRGIIIG
    
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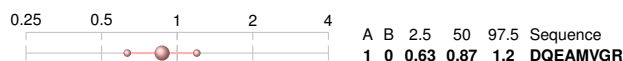


5.252 PREDICTED: similar to ring finger protein 186 [Rattus norvegicus]

Protein Accession	gij109477570
Mean Expression Ratio	0.895
Median Expression Ratio	0.895
Credible Interval	(0.661, 1.20)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0285
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.8
Avg..iTRAQ.Ratio....116.114.	0.738
Avg..iTRAQ.Ratio....117.114.	0.554

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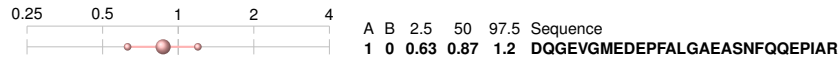
1      MPDIRCQQVP AESRKEAGSV PTGPEPMQVP AAPADIACGC PCAEQPHPPS SVPRVSCTEA PQPIPAGATT TNTIIALGPT
81     GRLSISVEGD LECLVCREPY NCARSPKLLS CQHTFCAVCL KLLLYVQEDT WSIPCPLCRK VTAVPGLLIC SLRQQEAMVG
161    RLLALPCPEVR LCPQRLVGP AASAAHPANR TGEDEQDVVS VNRVAARRLA VHLLLLALLI VLILPFIYPG VIRVLAFAVI
241    ALALLMSTLF CCHPQSQSSN WPCPRTLFCR EQRQTQITSI A
    
```



5.253 synaptopodin [Rattus norvegicus]

Protein Accession	gi 11067429
Mean Expression Ratio	0.895
Median Expression Ratio	0.895
Credible Interval	(0.657, 1.22)
Associated Peptides	1
Associated Spectra	1
Coverage	0
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.985
Avg..iTRAQ.Ratio....116.114.	0.464
Avg..iTRAQ.Ratio....117.114.	0.889

1 MIKVKNLKKS YKNLEVLKDV NMEVKQGEVV VIIGPSGSGK STFLRCLNLY ESPDKGEIQV GHVKVNAEKI SKKEINDLRK
 81 QSAMVFQHYN LFNKNTVLQN VTEALIVVEK MDKKAEEIA LENLKKVGMV DKKDNYPTL SGGQKQVSI ARAMAINPNV
 161 TLFDEPTSAL DPELVAEVLV VIKDLAKEHK TMIIVTHEMS FARDVADRNV FMDGGIVLEE GTPPEEIFKNP KNERTKQFLE
 241 RFIVN



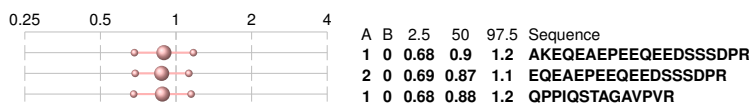
5.254 PREDICTED: similar to microfibrillar-associated protein 1 [Rattus norvegicus]

Protein Accession	gi 62645675
Mean Expression Ratio	0.894
Median Expression Ratio	0.895
Credible Interval	(0.712, 1.13)
Associated Peptides	3
Associated Spectra	4
Coverage	0.0774
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.938
Avg..iTRAQ.Ratio....116.114.	0.878
Avg..iTRAQ.Ratio....117.114.	0.835

NHLBI Zile/Grant, Aged Rat

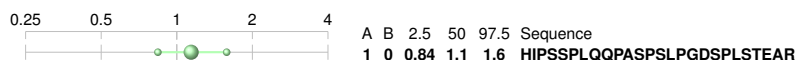
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1      MSVPSALMKQ PPIQSTAGAV PVRNEKGEIS MEKVVKRYV SGKRPDYAPM ESSDEEDEF QFIKKAKEQE AEPEEQEEDS
81     SSDPRLRLRQ NRISEDVEER LARHRKIVEP EVVGESDSEV EGDAWRLERE DSSEEEEEEEI DDEEIERRRG MMRQRAQERK
161    NEEEMVMEVE DEGRSGEESA SESEYEEYTD SEDEMPEPLK PVFIRKKDRV TVQEREAEAL RQKELEQEAQ RMAEERRKYT
241    LKIVEEETKK ELEENKRSLA ALDALNTDDE NDEEYEAWK VRELKRIKRD REDREALEKE KAEIERMNL TEEERRAELR
321    ANGKVI TNKA VKGKYKFLQK YHRGAFFMD EDEEVYKRF SAPTLEDHFN KTILPKVMQV KNFGRSGRTK YTHLVDQDTT
401    SFDSAWGQES AQNTKFFKQK AAGVRDVFER PSAKRRKTT
  
```



5.255 PREDICTED: similar to supervillin isoform 1 [Rattus norvegicus]

Protein Accession	gij109505025
Mean Expression Ratio	1.12
Median Expression Ratio	1.12
Credible Interval	(0.832, 1.50)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.74
Avg..iTRAQ.Ratio....116.114.	1.42
Avg..iTRAQ.Ratio....117.114.	1.89



5.256 PREDICTED: similar to glycerol-3-phosphate dehydrogenase 1-like [Rattus norvegicus]

Protein Accession	gij109485458
Mean Expression Ratio	0.895
Median Expression Ratio	0.895
Credible Interval	(0.667, 1.20)
Associated Peptides	1

Associated Spectra	1
Coverage	0.0342
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.734
Avg..iTRAQ.Ratio....116.114.	0.398
Avg..iTRAQ.Ratio....117.114.	0.98

```

1      MAAAPLKVCI VSGSNWGS AV AKIIGSNVKN LQKFSSTVKM WVFEETVNGR KLTDIINNDH ENVKYLPGHK LPENVVAVPN
81     LGEAVQDADL LVFVIPHQFI HKICDEITGR VPKKAVGITLL IKGIDEGPDG LKLISDIIRE KMGIDISVLM GANIASEVAA
161    EKFCETTIGS KVLQNGLLFK ELLQTPNFRI TVVDDADTVE LCGALKNIVA VGAGFCDGLC CGDNTKAAVI RLGLMEMIAF
241    AKIFCKGQVS TATFLESCGV ADLITTCYGG RNRKVAEAF A RTGKTIEELE KELLNGQKLQ GPQTSAEVYR ILKQKGLLDK
321    FPLFTAVYQI CYEGRPVTQM LSCLQSHPEH I
  
```



5.257 PREDICTED: similar to glutaredoxin 5 [Rattus norvegicus]

Protein Accession	gij109478609	
Mean Expression Ratio	0.895	
Median Expression Ratio	0.895	
Credible Interval	(0.74, 1.08)	
Associated Peptides	2	
Associated Spectra	9	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.871	1.48
Avg..iTRAQ.Ratio....116.114.	0.946	1.19
Avg..iTRAQ.Ratio....117.114.	0.78	0.698

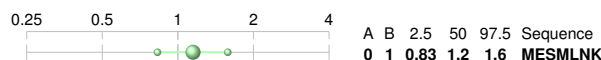


5.258 PREDICTED: similar to D10Ert802e protein [Rattus norvegicus]

Protein Accession	gij109481746
Mean Expression Ratio	1.12
Median Expression Ratio	1.12
Credible Interval	(0.832, 1.50)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00753
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.21
Avg..iTRAQ.Ratio....116.114.	1.16
Avg..iTRAQ.Ratio....117.114.	1.49

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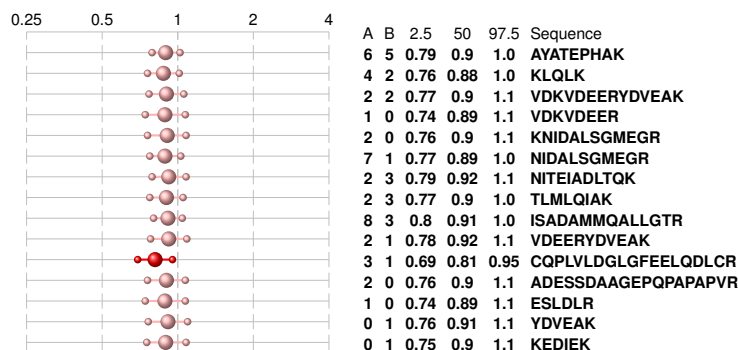
1      MESMLNK LKS TVTKVTADVT SAVMGNPVTR EFDVGRHIAS GGNGLAWKIF NGTKKSTKQE VAVFVFDKKL IDKYQKFEKD
81     QIIDS LKRGV QQLTRLRHRP LLTVQHPLEE SRDCLAFCTE PVFASLANVL GNWENLPSSI SPD IKDYKLY DVETKYGLLQ
161    VSEGLSFLHS SVKMVHGNTV PENIILNKSG AWKIMGDFDC VSSSNPSEQE PKFPCKEWDN NLP SLCLPNP EYLAPEYILS
241    VSCETASDMY SLGAVMYAVF NKGRPIFEVN KQDIYKFSR QLDQLSRLGS SSLTSIPEEV REHVKLLNV TPTVRPDADQ
321    MTKIPFFDDV GAVTLQYFDT LFQDNLQKS QFFKGLPKVL PKLPKRVIQV RILPCLTSEF VNPDMVPFVL PNVLLIAEEC
401    TKEEYIKLIL PELGPVFKQQ EPIQILLIFL QKMDLLTKT PPDEIKNSVL PMVYRALEAP SIQIQELCLN IIPTFANLID
481    YPSMKNALIP RIKNAQLQTS SLAVRVNSLV CLGKILEYLD KWFVLDLILP FLQQIPSKPEP AVLMGILGIY KCTFTHKKLG
561    ITKEQLAGKV LPHLIPLSIE NNLNLNQFSS FIAVIKEMLS RLESEHRTKL EQLHIMQEQQ RSLDIGNQMS TSEETKVTPS
641    GTQQIDKVFN NIGADLLSGG ESENREDGLQ GKQKRGSLTL EEKQKLAKEQ EQAQKLSQQ PLKPQVHTPI APVRQTKDLT
721    DTLMENMSSL TSLSVSTPKI SASSTFTSVP STGLSMMFST PIDNTRNLT NGLNANMGFQ TSGFNMPVNP NQNFSGTST
801    AGVTMTLGA PPTMSNFSP L SIPPASVKQT QQRPPDMSAL NNLFQPKFK VSMNQLSQQK PNQWLNQFVP PQGSPGMGSA
881    AMGTQVNVMG QAAFQMGQNP FFPNQSFQAP PPTTMTSSSS ASNDLKDLFG
  
```



5.259 "troponin 1, type 3 [Rattus norvegicus]"

Protein Accession	gij8394469	
Mean Expression Ratio	0.896	
Median Expression Ratio	0.896	
Credible Interval	(0.82, 0.979)	
Associated Peptides	15	
Associated Spectra	65	
Coverage	0	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.962	0.73
Avg..iTRAQ.Ratio....116.114.	0.813	0.88
Avg..iTRAQ.Ratio....117.114.	0.895	0.97

1 MAQAAPAAGT AYRKWLCITC GHIYDEALGD EHEGFPPGTL FSQIPDDWCC PDCGATKEDY VLYEEK

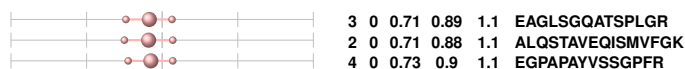


5.260 "chaperone, ABC1 activity of bc1 complex like [Rattus norvegicus]"

Protein Accession	gi 61557218
Mean Expression Ratio	0.897
Median Expression Ratio	0.896
Credible Interval	(0.749, 1.07)
Associated Peptides	3
Associated Spectra	9
Coverage	0.0678
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.868
Avg..iTRAQ.Ratio....116.114.	0.982
Avg..iTRAQ.Ratio....117.114.	0.831

1 MAAMLGDAIM VAKGLAKLTQ AAVETHLQNL GLGGELILAA RALQSTAVEQ ISMVFGKVQG QDKHEDSYAT ENFEDLEAEV
 81 QFSTPQAAGS SPDFSTASSL DQPLSSSLGH AHRGGPAPAY VSSGPFREAG LSGQATSPLG RVNGRLFVDC RDLFLANSIQ
 161 RRFHQDQAP VGGLTAEDIE KARQAKARPE SKPHKQMLSE RARERKVPVT RIGRLANFGG LAVGLGFGAL AEVAKKSLRS
 241 ENSTGKKAVL DSSPFLSEAN AERIVSTLCK VRGAALKLGO MLSIQDDAFI NPHLAKIFER VRQSADFMP LKQMTKTLNND
 321 LGPHWRDKLE YFEERPFAAA SIGQVHLARL KGGREVAMKI QYPGVAQSIN SDVNNLMAVL NMSNMLPEGL FPEHLIDVLR
 401 RELTLECDYQ REAAYAKKFR ELLKDHPPFY VPEIVDELCS PHVLTTELIT GFPLDQAEGL SQEVRNEICY NILVLCLEL
 481 FEFHVMQTD P NWSNFFYDPQ QHKVALLD F G ATREYDRSFT DLYIQVIRAA ADQDREAVLK KSIEMKFLTG YEVKAMEDAH
 561 LDAILLILGEA FASEEPFDG TQSTTEKIHN LIPIMLKHRL IPPPEETYS L HRKMGGSFLI CSKCLKACFPC KAMFEEAYS N
 641 YCRMKSLQ

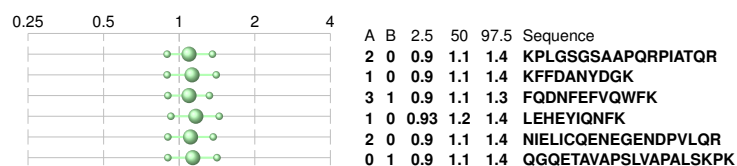




5.261 "microtubule-associated protein, RP/EB family, member 1 [Rattus norvegicus]"

Protein Accession	gij78097100	
Mean Expression Ratio	1.11	
Median Expression Ratio	1.12	
Credible Interval	(0.945, 1.31)	
Associated Peptides	6	
Associated Spectra	11	
Coverage	0.332	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.14	1.34
Avg..iTRAQ.Ratio....116.114.	1.14	1.09
Avg..iTRAQ.Ratio....117.114.	1.16	1.38

1 MAVNVYSTSV TSDNLSRHDM LAWINESLQL NLTKIEQLCS GAAYCQFMDM LFPGSIALKK VKFQAKLEHE YIQNFKILQA
 81 GFKRMGVDKI IPVDKLVK GK FQDNFEFVQW FKRPFEDANYD GKEYDPVAAR QGQETAVAPS LVAPALSKPK KPLGSGSAAF
 161 QRPIATQRTT AAPKAGPGMV RKNPGMGNGD DEAAELMQQV KVLKLTVEDL EKERDFYFGK LR NIELICQE NEGENDPVLQ
 241 RIVDILYATD EGFVIPDEGG PQEEQEYY



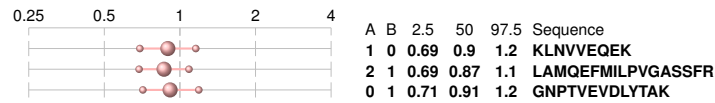
5.262 PREDICTED: similar to Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)

Protein Accession	gij109468300	
Mean Expression Ratio	0.899	
Median Expression Ratio	0.897	
Credible Interval	(0.723, 1.13)	
Associated Peptides	3	

Associated Spectra	5	
Coverage	0.0788	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.916	0.832
Avg..iTRAQ.Ratio....116.114.	0.802	0.517
Avg..iTRAQ.Ratio....117.114.	0.917	1.04

```

1      MVLELTLP  ESLEKYEHT  STPNLSLSD  LPVILKNI  PSVSPGPS  PPQRSYCN  TMSILKIH  EIFDSRGN
81     VEVLDLYT  LFRAAVPS  STGIYEAL  RDNDKTRF  KGVSKAVE  NKTIAPAL  KKLNVVEQ  IDQLMIEM
161    TENKSKFG  AILGVSLA  KAGAVEKG  LYRHIADL  NPEVILPV  FNVINGGS  GNKLAMQE  ILPVGASS
241    EAMRIGAE  HNLKNVIK  YGKDATNV  EGGFAPNI  NKEALELL  AIKAGYTD  VVIGMDVA  EFYRAGKY
321    DFKSPDDA  YITPDQLA  YKSFIDYP  VSIEDPFD  DWDAWQKF  TAGIQVVG  LTVTNPKR  KAAGEKSC
401    LLLKVNQI  VTESLQAC  AQSNGWGM  SHRSGETE  FIADLVVGL  TGQIKTGA  RSECLAKY  ILRIEELG
481    KAKFAGRS  NPLAK
    
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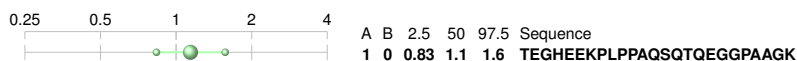


5.263 microtubule-associated protein 6 [Rattus norvegicus]

Protein Accession	gi 8850229
Mean Expression Ratio	1.11
Median Expression Ratio	1.11
Credible Interval	(0.828, 1.49)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0263
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.86
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	2.2

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1      MAWPCITR  CIARFVNQ  KADIAVPL  TKYSEATE  GAPPQPPA  QPGLAPPS  VAJETQPA  ESDAVARA
81     PAPGPSGD  TAAAPGR  GLGAASGS  GSGPADSV  QDYRAWKV  PEPSCRPR  YQPSDAP  ETQYQKDF
161    WPLPFRGD  WIPKPVQ  TSQPSPPV  MPKRRPQS  RGPQLSAD  RDPEGAGG  VPAAGKAS  DQRDTRRK
241    PAWMVTR  FEG  HEEKPLPP  SQTQEGGP  ASGADQR  TRRKAGPA  VTRTEGH  PLPPAQSQ
321    GADQRDTR  AGPAWMV  EGHEETPL  AQSQTQEG  AAGKASGA  RDTRRKAG  WMVTRTE  ETPLPQAQ
401    TQEGGPA  ASGADER  RKAGPAWM  RSEGHEQT  AHAQGTGP  GKGRAVAD  NRQIREE  TVSSSYRN
481    RAWTDIK  PIKAKPQ  PDDKMVHE  YSAQFKGE  KPTTADNK  DRRRIRSL  EPFKESP  KPSVQSSK
561    KTSTSQK  KAKDKQV  QAAKKKTT  PSATKPD  QSKEMNN  EAKESRV  SDKNQGP  EPHKDGQV
641    PGLPKGG  VQEP LK  MVPGLPKD  FVVPGLK  SPTAPGPP  QGAVLLGP  DLGVPVAP  KDQDHMAS
721    LKNKDSV  PAKAQSP  EPLKNQSP  PARAKDQS  APAPTPL  GPVIEPE  GAPMVP  DQNASIMA
801    KNEAPVA  VKNQGL  PAKDTGT  GHGSVVF  KSQGPVV  TKGQDF  LAKDQGP  EPPKNQGP
881    VLGPIKN  VIPVPL  PVVVPAP  GPTAPDPL  QGPRGP  VSPSPVM  TVPHEA  YIEG SP
    
```

5.264 "serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4 "

Protein Accession	gi 56961650
Mean Expression Ratio	1.12
Median Expression Ratio	1.11
Credible Interval	(0.818, 1.50)
Associated Peptides	1
Associated Spectra	1
Coverage	0.026
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.37
Avg..iTRAQ.Ratio....116.114.	1.60
Avg..iTRAQ.Ratio....117.114.	1.45

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1      MHYTRCLLLL LAGLLELSHS QPDQEEPNT TNQTYRQFSQ QNISSYQIAS GNANFAFRLY HLIASQNSEK NIFFSPLSIS
81     VSLAILSTGA GGD TQAQILE GLGFNLTKLS LPEIHEGFRS LQHTIARPFT EPQISVGSAL ILSQNLQILS EFVSAIETSY
161    NSKVLHANFR DKEAAVQLIN NYVKQNTQGK IKNLVSDLSP DVKMVLVNYI FFQGLWKKPF PSSRVSTSDF YVDENTVVKI
241    PMMLQDKEDH WYLED RRVPC TVLRMDYRGD AVAFFILPDQ GKMNEVEQVL SPGM L LRWKR LLQNRFFYRK LILQLPKFSI
321    SNSYELDEIL PDLGFQDLFT P N ANFSNISK KEKLYLSKVF HKT VLDVNEV GTKAAAATGS FATFFSAQPK KRYLIFNRPF
401    LVILYSTSSQ DILFMGKVVN PTA
    
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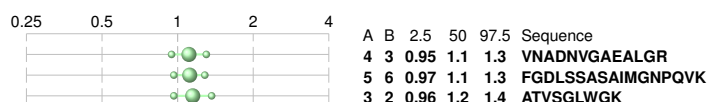


5.265 PREDICTED: similar to Hemoglobin beta-2 subunit (Hemoglobin beta-2 chain) (Beta-2-globin) (Hemoglobin)

Protein Accession	gi 109462578
Mean Expression Ratio	1.11
Median Expression Ratio	1.11
Credible Interval	(0.965, 1.29)
Associated Peptides	3
Associated Spectra	23
Coverage	0.265

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.34	1.68
Avg..iTRAQ.Ratio....116.114.	1.27	1.06
Avg..iTRAQ.Ratio....117.114.	0.811	0.56

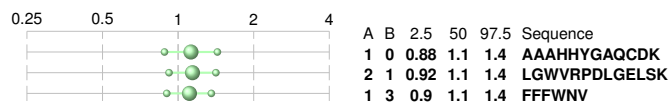
1 MVHLTDAEKA TVSGLWGKVN ADNVGAEALG RLLVVYPWTQ RYFSKFGDLS SASAIMGNPO VNAHGKKVIN AFNDGLKHLD
 81 NLKGTFAHLS ELHCDKLHVD PENFRLGNM IVIVLGHHLG KEFTPCAQAA FQKVVAGVAS ALAHKYH



5.266 "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 [Rattus norvegicus]"

Protein Accession	gij114145517	
Mean Expression Ratio	1.11	
Median Expression Ratio	1.11	
Credible Interval	(0.922, 1.35)	
Associated Peptides	3	
Associated Spectra	8	
Coverage	0.164	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.23	0.973
Avg..iTRAQ.Ratio....116.114.	1.6	0.899
Avg..iTRAQ.Ratio....117.114.	1.30	1.00

1 MLDEFERELP DFIGYEEAGE GTRLPLRSL LSLVMKVSSA VLKAAAHHYG AQCDKTNKEF MLCRWE EKDP RRCLKEGKLV
 81 NGCALNFFRQ IKSHCAEPFT EYWTCLDYSS MQLFRHCRKQ QAKFDECULD KLGWVRPDLG ELSKVTVKKT DRPLPENPYH
 161 SRPRPEPSPV IEGDLKPAKH GSRFFWNV

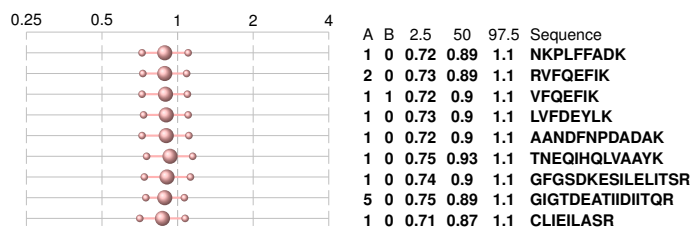


5.267 annexin A6 [Rattus norvegicus]

Protein Accession	gi 130502086	
Mean Expression Ratio	0.9	
Median Expression Ratio	0.898	
Credible Interval	(0.777, 1.04)	
Associated Peptides	9	
Associated Spectra	15	
Coverage	0.135	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.885	0.844
Avg..iTRAQ.Ratio....116.114.	0.98	0.758
Avg..iTRAQ.Ratio....117.114.	0.869	0.868

```

1   MAKIAQGAMY RGSVHDFADF DANQDAEALY TAMKGFGSDK ESILELITSR SNKQRQEICQ SYKSLYGKDL IADLKYELTG
81  KFERLIVNLM RPLAYCDAKE IKDAISGIGT DEKCLIEILA SRTNEQIHQL VAAYKDAYER DLESDIIGDT SGHFQKMLVV
161 LLQGTRENDV VVSEDLVQQD VQDLYEAGEL KWTDEAQFI YILGNRSKQH LRLVFDEYLK TTGKPIEASI RGEKSGDFEK
241 LMLAVVKCIR STPEYFAERL FKAMKGLGTR DNTLIRIMVS RSELDMLDIR EIFRTKYEKS LYSMIKNDTS GEYKALLKLL
321 CGGDDDAAGQ FFPEAAQVAY QMWELSAVSR VELKGTVRA NDFNPDADAK ALRKAMKGIG TDEATIIDII TORSNAQRQQ
401 IRQTFKSHFG RDLMDLTKSE ISGDLARLIL GLMPPPAHYD AKQLKKAMEG AGTDEKALIE ILATRTRNAEI RAINEAYKED
481 YHKSLEDALS SDTSGHFKRI LISLATGNRE EGGENRDQAQ EDAQVAEIL EIADTPSGDK TSLETRFMFTV LCTRSYPHLR
561 RVFQEFIKKT NYDIEHVIKK EMSGDVKDAF VAIVQSVKNK PLFFADKLYK SMKAGAGTDEK TLRTRVMVSR EIDLLNIRRE
641 FIEKYDKSLH QAIEGDTSGD FMKALLALCG GED
    
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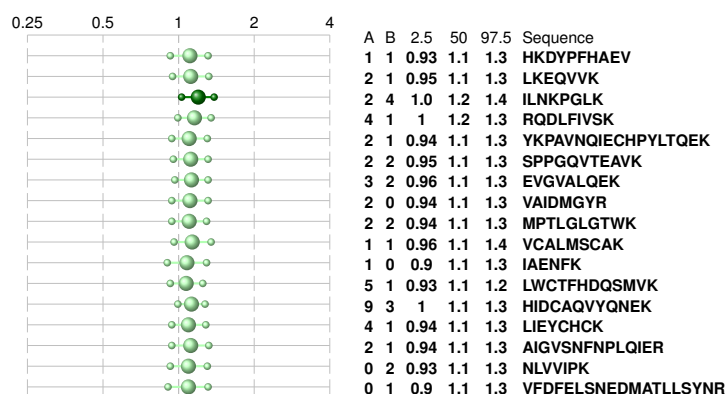
5.268 aldehyde reductase 1 [Rattus norvegicus]

Protein Accession	gi 6978491
Mean Expression Ratio	1.11
Median Expression Ratio	1.11
Credible Interval	(1.02, 1.21)
Associated Peptides	17
Associated Spectra	66
Coverage	0.56

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.10	1.29
Avg..iTRAQ.Ratio....116.114.	1.16	1.04
Avg..iTRAQ.Ratio....117.114.	1.08	1.00

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1      MASHLELNNG TKMPTLGLGT WKSPPGQVTE AVKVAIDMGY RHIDCAQVYQ NEKEVGVALQ EKLKEQVVKR QDLFIVSKLW
81     CTFHDQSMVK GACQKTLSDL QLDYLDLYLI HWPTGFKPGP DYFPLDASGN VIPSDTDFVD TWTAMEQLVD EGLVKAIGVS
161    NFNPLQIERI LNKPGLKYKP AVNQIECHPY LTQEKLI EYC HCKGIVVTAY SPLGSPDRPW AKPEDPSLLE DPRIKEIAAK
241    YNKTTAQVLI RFPIQRNLVV IPKSVTPARI AENFKVDFE LSNEDEMATLL SYNRNWRVCA LMSCAKHKDY PFHAEV
    
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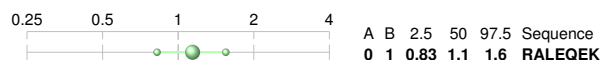
5.269 PREDICTED: similar to Spingomyelin phosphodiesterase 3 (Neutral sphingomyelinase 2) (Neutral sphin

Protein Accession	gij62652640
Mean Expression Ratio	1.11
Median Expression Ratio	1.11
Credible Interval	(0.827, 1.49)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0137
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.21
Avg..iTRAQ.Ratio....116.114.	1.17
Avg..iTRAQ.Ratio....117.114.	1.51

NHLBI Zile/Grant, Aged Rat

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1      MNLPDVPRLR SPVPQEPSFG WPQTPDLRPP SPFPNPVLQT LYSLSRMLLF PAYWSDLRLL GCWAPVSRSG SLRWLKVLAG
81     SGAALLPLVV VGLPLALVGL VLWLPLQLCR RPFQYQPPPS CWVWFQPPWRP PAERQRCFVF LTANLCLFPH GLAHFNLSN
161    SQQRADAVGA VLLDGLRSSQ YGVTEPRQPL PKVPGGVLKA TLPMLGLDFVC LQEVFDLRAA RRLVRIIVPN LGPVLYDVGT
241    FGLVAGPYIK VLGSGLLLAS RYPLLRATFR CFPNARREDA MASKGLLSVQ AQLGILDGRR IVGYLHCTHL QAPLEDGHIR
321    CKQLTLLLEW VEEFEAESRQ SGEAVAFSVL LGDLNFDNCS QGNELGRVEP GHPALPTKKR FSSTDHAKAQ GHKFFSCFKD
401    PCRLGPCQEQ FWALGTILNN STLHQSIISS PEMLRRALEQ EKGRRLLYLAG PLHGNYSASQ WKGRRLDYIT YRGVFGSRLS
481    PEAEQVTFST AFAGLTDHLA MGLKLVVCS
  
```



5.270 hypothetical protein LOC288683 [Rattus norvegicus]

Protein Accession	gi 112984424
Mean Expression Ratio	0.9
Median Expression Ratio	0.9
Credible Interval	(0.67, 1.20)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0543
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.655
Avg..iTRAQ.Ratio....116.114.	0.742
Avg..iTRAQ.Ratio....117.114.	0.595

```

1      MQALHLQHRN PRSYRVKARA SYVDETLFGS PTGTRPTLPD FDPWPVQNCN RSRGVSPGPP KVSLAKRDCE SPSSRGSTPN
81     LTPRKNKYR LIGHTPSYCD ESLFGSRPQG TSKERSRTAV EDAAKLRTLF WTPPATPRGS HSPRPRETPL RAIHPTGPPR
161    TEPRVATGSQ MVS RDGLDAP RSLGQRRSYS LTHLAVPSTG HPASTAPQTN GPWSPRPYTS GATVQSP LVT RKVCSGSVSG
241    PTTPTQRGACP QKPKPPWK
  
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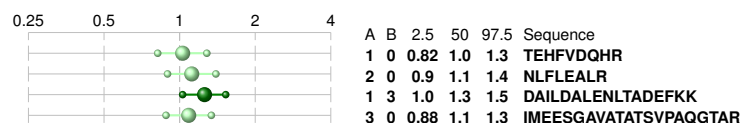
5.271 PYD and CARD domain containing [Rattus norvegicus]

Protein Accession	gi 27229294
Mean Expression Ratio	1.11
Median Expression Ratio	1.11
Credible Interval	(0.928, 1.32)
Associated Peptides	4

NHLBI Zile/Grant, Aged Rat

Associated Spectra	10	
Coverage	0.285	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.906	1.96
Avg..iTRAQ.Ratio....116.114.	0.964	1.56
Avg..iTRAQ.Ratio....117.114.	1.21	1.89

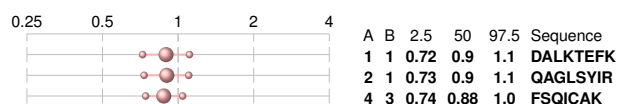
1 MGRARDAILD ALENLTADEF KFKMKLLTA PVREGYGRIP RGALLQMDPI DLTDKLVSY LEGYGLELTM SVLRDMGIQE
 81 LAEQLQK ME ESGAVATATS VPAQQTARTE HFVDQHR QAL IARVTKVDGL LDALYGNVLT EGQYQAVRAE TPNQNKMRKL
 161 FSPAPAWNLT CKNLFLEALR QTQPYLVTDL EQS



5.272 "ATP synthase, H⁺ transporting, mitochondrial F1 complex, epsilon subunit [Rattus norvegicus]"

Protein Accession	gij20806139	
Mean Expression Ratio	0.9	
Median Expression Ratio	0.9	
Credible Interval	(0.759, 1.07)	
Associated Peptides	3	
Associated Spectra	12	
Coverage	0.451	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.856	0.823
Avg..iTRAQ.Ratio....116.114.	1.10	0.895
Avg..iTRAQ.Ratio....117.114.	0.778	0.56

1 MVAYWRQAGL SYIRFSQICA KAVRDALKTE FKANAERTSG TSIRTVKIKK E



5.273 afadin [Rattus norvegicus]

Protein Accession	gi 6978469
Mean Expression Ratio	0.9
Median Expression Ratio	0.9
Credible Interval	(0.703, 1.15)
Associated Peptides	2
Associated Spectra	3
Coverage	0.0197
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.839
Avg..iTRAQ.Ratio....116.114.	0.86
Avg..iTRAQ.Ratio....117.114.	0.91

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1 MSAGGRDEER RKLADIHHW NANRLDLFEI SQPTEDLEFH GVMRFYFQDK AAGNFATKCI RVSSSTATQD VIETLAEKFR
81 PDMRMLSSPK YSLYEVHVS ERRLDIDEKP LVVQLNWNKD DREGRFVLKN ENDAIPAKKA QSNNGPEKQEK EGVIQNFKRT
161 LSKKKEKKEK KREKEALRQA SDKEERPSQG DDENSRLAA EVYKDMPEFS FRTTISNPEV VMKRRRQKQL EKRMQEFRSS
241 DGRPDSGRTL RIYADSLKPN IPYKTTLLST TDPADFAVAE SLEKYGLEKE NFKDYCIARV MLPPGAQHS D ERGAKIILD
321 DDECPLQIFR EWPSDKGILV FQLKRRPPDY IPKKMKKHVE GKPLKGDRA DGSGYGSALP PEKLPYLVEL SPGRRNHFAY
401 YSYHTYEDGS DSRDKPKLYR LQLSVTEVGT EKFDNSIQL FGPGIQPHHC DLTNMDGVVT VTPRSMDAET YVDGQRISSET
481 TMLQSGMRLQ FGTSHVFKFV DP IQDHVLSK RSV DGGMLVK GPRHKPGAVQ ETTFFLGGDI HSGTALPASR STTRLDSDRV
561 SSASSTAERG MVKPMIRLDQ EQDYRRRESR TQDAAGPELM LPASIEFRES SEDSFLSAI NYTNSSTVHF KLSPTYVLYM
641 ACRYVLSQHP RDISPTERT HKAIVVNMK VSMMEGVQIE VDQVDQKQKN IAGALAFWMA NASELLNFIK QDRDLSRITL
721 DAQDVLAHLV QMAFKYLHVC LQSELNMYMP AFLDDPEENS LQRPKIDVVL HTLTGAMSL RRCRVNAALT IQLFSQLFHF
801 INMWLFNRLV TDPDGLCSH YWGAIIRQQL GHIEAWAEKQ GLELAADCHL SRIVQATTLL TMDKYVDDI PNINSTCFKL
881 NSLQLQALLQ NYHCAPDEPF IPTDLIENVV AVAENTADEL ARSDGRDVL EEDDDLQLPF LLPEDGYSCD VVRNIPNGLQ
961 EFLDPLCQRG FCRLVPHTRS PGTWTIYFEG ADYESHLMRE NTELTQPLRK EPEVITVTLK KQNGMGLSIV AAKGAGQDKL
1041 GIYKSVVVKG GAADV DGRLA AGDQLLSVDG RSLVGLSQER AAELMTRTSS VVTLEVAKQG AIYHGLATLL NQPSMMQRI
1121 SDRRGSGKPR PKSEGFELYN NSAQNGSPES PQMPWTEYSE PPKLPGDDR L MKNRADHRSS PNVANQPPSP GSKSPYTSGT
1201 AAKITSVSTG NLCTEEQTPP PRPEAYPIPT QTYTREYFTF PASKSQDRMA PVQNQWPNYE EKPHMHTESD HASIAIQVVT
1281 RSQEELREEK VYQLERHRVE SGMDRKCDS MWLNQSSSVE SSTSSEHLN HSSKSVTPAS TLTKSGPGRW KTPAAVLPPTP
1361 VAVSQPIR TD LPPPPPPPPA HTSDFDGIS MDLPLPPPPA NQAAPQSAQV AAAERKKRE HQRWYEKKA RLEEERERKR
1441 REQERKLGQM RTQSLNPASF SPLATQAKPE KPSTLQRPQE TVIRELQPPQ QPRTIERRDL QYITISKEEL SSGDSLSPDP
1521 WRDAREKLE KQQQMHIVDM LSKEIHELQN KGDRTAESD RLRLMLEWQ FQKRLQESKQ KDEDDDEED DDVDTMLIMQ
1601 RLEAERRARL QDEERRRQQQ LEEMRKREVE DRVRQEDGR HQEEERVKRD AEEKRQEEG YSRLEAERP RQHEEAARRL
1681 LEPEEPGLSR PPLPQDYEPF SQSSAPSAPP PPPQRNASYL KTQVLSPPSL FTAKFVAYDD DDEENYVPA GPNSYSGSAG
1761 TTAGTYDAPR DTREKLSR SQ DADLPGSSGA PENLTF ERQ RLFSGQDVS DKVKASRKL T ELENELNTK
    
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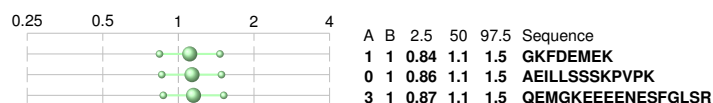
5.274 nexilin isoform s [Rattus norvegicus]

Protein Accession	gi 40538878
Mean Expression Ratio	1.11
Median Expression Ratio	1.11
Credible Interval	(0.865, 1.43)
Associated Peptides	3
Associated Spectra	7
Coverage	0.0579
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.06
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	1.18

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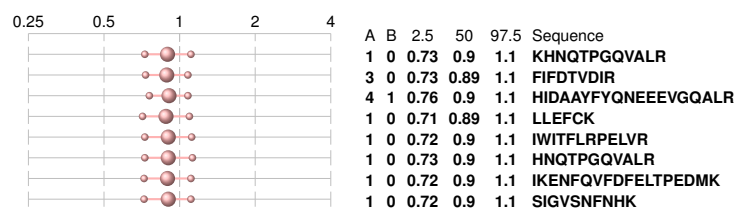
1      MNDVSQKAEI LLSSSKPVPK SYVPKLGKGD VKDKFEAMQR AREERNQRRS RDEKQRRKEQ YIREREWNRR KQEIKDMLAS
81     DEEEEPSKVE KAYVPKLTGT VKGKFDMEK HRQEEQRKRT EERKRRIEQ DLEKRRMQR ELAKRAEQEG DDSLLITVVP
161    AKSYRAAANR KDPEDLDREH RNGRVSQEEE KTRHEEECRA LKEAKCLSLV MDDETEAKKE SRFPGLKST FEELERQRQE
241    NRKKQAEAAA RRRLEEERRA FEEARRNMVN EEDESQDTET VFKEYRPGKL RLSFEEIERQ RREEEKRAE EEARRMEEE
321    KKAFAEARRS MVLDDDSPEI YKAVSQESLT PGKLEINFEQ LLRQKMEEER RTTEEERRQK LEMEKQEFEQ LRQEMGKEEE
401    ENBSFGLSRE YEELIKLRRS GSIQAKNLKS KFEKIGQLSE KEVQKKIEE RAKRRRIDLE IKEREAENFH EDDVDVVKPA
481    KKSESPFTHK VNMKARFEQM AKARQEEER RIEEQKLLRM QFEQKEIDAA LQKKREDDEE EEGSIVNGST TEDEEQTRSG
561    APWFKKPLRN TSVVDSEPV RFTVKVTGEPK PEVTWWFEGE LLQDGEDYQY IERGETYCLY LPETFPEDGG EYMCKAVNSK
641    GSAASTCILT IEMDDY

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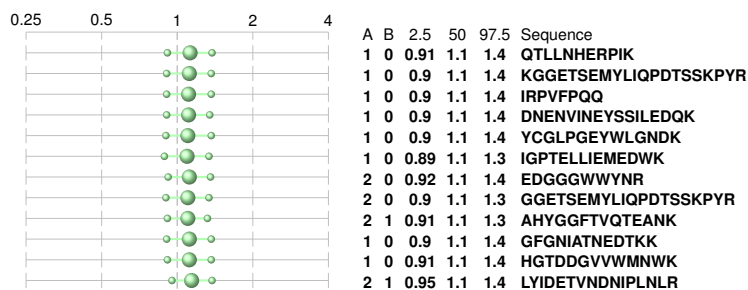
5.275 "PREDICTED: similar to aldo-keto reductase family 1, member C4 [Rattus norvegicus]"

Protein Accession	gi 109505098	
Mean Expression Ratio	0.9	
Median Expression Ratio	0.9	
Credible Interval	(0.772, 1.05)	
Associated Peptides	8	
Associated Spectra	14	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	0.923
Avg..iTRAQ.Ratio....116.114.	0.93	0.693
Avg..iTRAQ.Ratio....117.114.	0.774	1.55



5.276 "fibrinogen, beta polypeptide [Rattus norvegicus]"

Protein Accession	gj 29789106	
Mean Expression Ratio	1.11	
Median Expression Ratio	1.11	
Credible Interval	(0.97, 1.27)	
Associated Peptides	12	
Associated Spectra	18	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	1.31
Avg..iTRAQ.Ratio....116.114.	1.39	0.998
Avg..iTRAQ.Ratio....117.114.	1.06	1.19

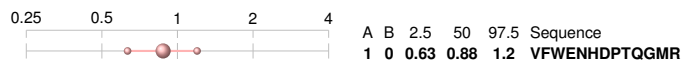


5.277 methionine sulfoxide reductase A [Rattus norvegicus]

Protein Accession	gi 16758004
Mean Expression Ratio	0.9
Median Expression Ratio	0.901
Credible Interval	(0.669, 1.21)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0558
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.782
Avg..iTRAQ.Ratio....116.114.	0.679
Avg..iTRAQ.Ratio....117.114.	0.639

```

1      MLSASRRTLQ LLSSSIPVRM MGDSSSKVIS AEEALPGRTE SIPVAAKHHV SGNRTVEFPF EGTQMAVFGM GCFWGAERKF
81     WLLKGVYSTQ VGFAGGYTRN PTYKEVCSEK TGHAEVVRVV YRPEHVSFEE LLKVPWENHD PTQGMKQGND CGTQYRSAYV
161    PTSAVQMEAA LKSKEEYQKV LSKHGFGPIT TDIREGQVVF YAEDYHQQYL SKNPDGYCGL GGTGVSCPTA IKK
    
```



5.278 apolipoprotein A-II [Rattus norvegicus]

Protein Accession	gi 6978517	
Mean Expression Ratio	1.11	
Median Expression Ratio	1.11	
Credible Interval	(0.889, 1.38)	
Associated Peptides	2	
Associated Spectra	5	
Coverage	0.196	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	1.18
Avg..iTRAQ.Ratio....116.114.	1.53	1.01
Avg..iTRAQ.Ratio....117.114.	1.05	1.11

```

1      MKLLAMVALL VTICSLEGAL VRRQAAETDV QTLFSQYLQS LTDYGKDLME KAQPSEIQNQ AKAYFQNAQE RLTPFVQRTG
81     TNLMDFLSRL MSPEEKPA PA AK
    
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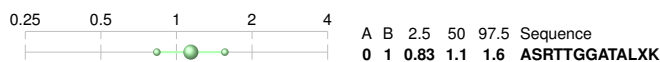




5.279 PREDICTED: interferon-stimulated protein (predicted) [Rattus norvegicus]

Protein Accession	gij109462180
Mean Expression Ratio	1.11
Median Expression Ratio	1.11
Credible Interval	(0.827, 1.49)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0774
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.34
Avg..iTRAQ.Ratio....116.114.	1.41
Avg..iTRAQ.Ratio....117.114.	1.16

1 MVGLGPQGXV ASPAAALXTS TAQSSMTSTS SLRERSRTE PKSAGSRLST WRGPRHLLKP GXRSCSFKA SWWWAMTXSM
 81 TSVPXRRTXE NTPSTTRPQT CCCGTRPSC ATAVCPXGCC ASACTRASR **TTGGATALXK** MGPQWSSTK SLSDSEPSEG
 161 CPAWEHQP

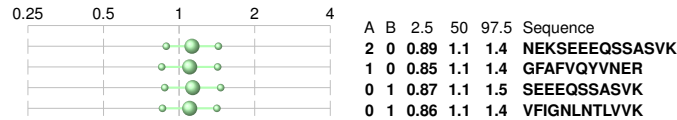


5.280 heterogeneous nuclear ribonucleoprotein C [Rattus norvegicus]

Protein Accession	gij71043810	
Mean Expression Ratio	1.11	
Median Expression Ratio	1.11	
Credible Interval	(0.893, 1.38)	
Associated Peptides	4	
Associated Spectra	5	
Coverage	0.124	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	1.02
Avg..iTRAQ.Ratio....116.114.	1.01	0.884
Avg..iTRAQ.Ratio....117.114.	1.55	1.58

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1      MASNVTKTD PRSMNSRVFI GNLNLTLVVK SDVEAIFSKY GKIVGCSVHK GFAPVQYVNE RNARAAVAGE DGRMIAGQVL
81     DINLAAEPKV NRGKAGVKRS AAEMYGSSFD LDYDFQRDY DRMYSYPARV PFPPIARAV VPSKRQRVSG NTSRRGKSGF
161    NSKSGQRGSS SKSVKDDLQ AIKKELTQIK QKVDSLLES EKIKEQSKQ ADLSFSSPVE MKNEKSEEEQ SSASVKKDET
241    NVKMESEAGA DDSAEEDLL DDDDNEDRGD DQLELKDDEK EPEEGEDDRD SANGEDDS
    
```



5.281 "PREDICTED: similar to LSM3 homolog, U6 small nuclear RNA associated [Rattus norvegicus]"

Protein Accession	gij 27712626	
Mean Expression Ratio	0.905	
Median Expression Ratio	0.902	
Credible Interval	(0.704, 1.16)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	0.826
Avg..iTRAQ.Ratio....116.114.	0.966	0.301
Avg..iTRAQ.Ratio....117.114.	0.924	0.787



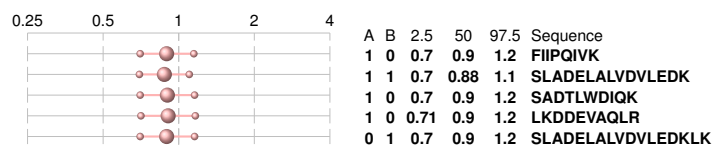
5.282 lactate dehydrogenase B [Rattus norvegicus]

Protein Accession	gij 6981146	
Mean Expression Ratio	0.901	
Median Expression Ratio	0.903	
Credible Interval	(0.736, 1.10)	

Associated Peptides	5	
Associated Spectra	6	
Coverage	0.135	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	0.633
Avg..iTRAQ.Ratio....116.114.	0.844	0.691
Avg..iTRAQ.Ratio....117.114.	0.881	0.805

```

1      MATLKEKLI A FVADDEAVP N NKITVVGVG Q VGMACAISI L GKSLADELA LVDVLEDKLK GEMMDLQHGS LFLQTPKIVA
81     DKDYSVTANS KIVVVTAGVR Q QEGESRLNL VQRNVNVFK F IIPQIVKYSP DCTIIVVSNP VDILTYVTWK LSGLPKHRVI
161    GSGCNLDSAR FRYLMAEKL G IHPSSCHGWI LGEHGDSSVA VWSGVNVAGV SLQELNPEMG TDNDSENWKE VHKMVVDSAY
241    EVIKLKGYN WAIGLSVADL IESMLKNLSR IHPVSTMVKG MYGIENEVFL SLPCILNARG LTSVINQK LK DDEVAQLK K S
321    ADTLWDIQKD LKDL
  
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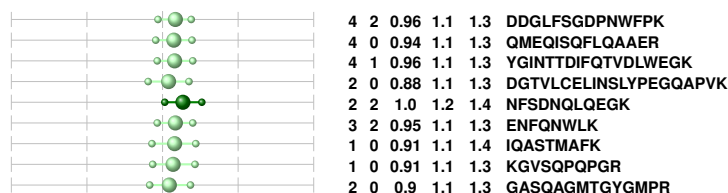
5.283 transgelin 2 [Rattus norvegicus]

Protein Accession	g 61557028	
Mean Expression Ratio	1.11	
Median Expression Ratio	1.11	
Credible Interval	(0.992, 1.24)	
Associated Peptides	10	
Associated Spectra	32	
Coverage	0.653	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.13	1.36
Avg..iTRAQ.Ratio....116.114.	1.07	0.979
Avg..iTRAQ.Ratio....117.114.	1.13	1.61

```

1      MANRGPSYGL SREVQQKIEK QYDPDLEQIL IQWITTQCRK GVSQPQPGRE NFQNWVKDGT VLCELINSLY PEGQAPV K I
81     QASTMAFKQM EQISQFLQAA ERYGINTTDI FQTVDLWEGK NMACVQRTL M NLGGLAVAR D DGLFSGDPN W FPK KSKENP R
161    NFSDNQLQEG KNVIGLQMG T NRGASQAGMT GYGMP R QIL
  
```



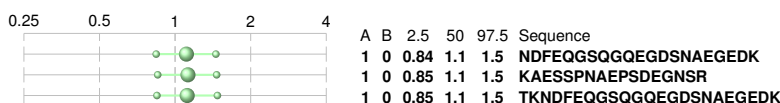


5.284 extracellular matrix protein 2 [Rattus norvegicus]

Protein Accession	gij6978789
Mean Expression Ratio	1.11
Median Expression Ratio	1.11
Credible Interval	(0.87, 1.41)
Associated Peptides	3
Associated Spectra	3
Coverage	0.0631
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	1.90

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1      MKAVLLLLYA  LGIAAAVPTT  FLSDHSNPTS  ATLPTLEDAT  VPTVPAEAAA  DIEKHPNHKA  EKPSALNSEE  EAHEQSTEQD
81     KTYSEVDLK  DEEDGDGDL  VDPTERTLDL  QEGTSEPQQK  RLPENADFFA  TVSTPFVDS  QPANITKGE  SQEQPVSDS
161    QQQDESGKQT  QDSMTEESH  QDPGIPNEEK  EEEEDPEDVG  APSDNQEEK  EPPEEQPTS  WEGNGDQSE  ILQESSQPTQ
241    ISKTKNDFEQ  GSQGGEGDS  AEGEDFAAGS  KEHLPHTEWQ  GQEGRAGLDA  IGNRKDTDE  KAVSTPTDA  AVVPRNHGAS
321    DNGGGDDSKH  GASDDYFIP  QEFLEAERMH  SLSYYLKYGE  ETPDESENRS  EAGDNQGAK  AESSPNAEPS  DEGNSRGHSA
401    DSCMNFQCKR  GHTCKTDQH  KPHVCVDPE  TCPPAKILD  ACGTDNQTYA  SSCHLFATK  MLEGTKKHQ  LQLDYFGACK
481    SIPACTDFEV  AQFPLRMRD  LKNILMQLYE  PNPKHGGYLN  EKQRSKVKKI  YLDEKRLLAG  DHPIELLRD  FKKNYHMYVY
561    PVHWQFNELD  QHPADRILTH  SELAPLRASL  VPMEHCITRF  FEEDPNKDK  HITLKEWGH  FGIKEEDIDE  NLLF
    
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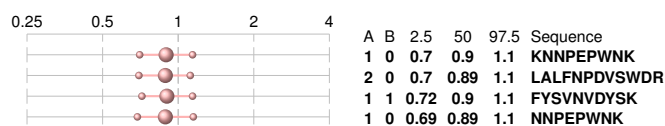


5.285 PREDICTED: similar to NADH-ubiquinone oxidoreductase MLRQ subunit (Complex I-MLRQ) (CI-MLRQ) [Rattus norvegicus]

Protein Accession	gij109473144
Mean Expression Ratio	0.902

Median Expression Ratio	0.903	
Credible Interval	(0.735, 1.11)	
Associated Peptides	4	
Associated Spectra	6	
Coverage	0.397	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.785	0.811
Avg..iTRAQ.Ratio....116.114.	0.92	0.903
Avg..iTRAQ.Ratio....117.114.	0.873	0.968

1 MIYSMDPRKE LIPLFVFIGA GGTGAALYVM RLALFNPDVS WDRKNNPEPW NKLGPNEQYK FYSVNVVDYSK LKKEGPDF



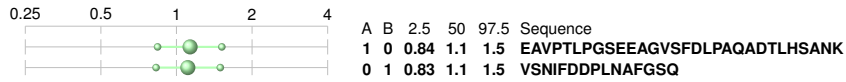
5.286 hypothetical protein LOC297530 [Rattus norvegicus]

Protein Accession	gij40363268	
Mean Expression Ratio	1.11	
Median Expression Ratio	1.11	
Credible Interval	(0.847, 1.44)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	0.0339	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.9	0.793
Avg..iTRAQ.Ratio....116.114.	1.26	1.47
Avg..iTRAQ.Ratio....117.114.	1.58	1.14

NHLBI Zile/Grant, Aged Rat

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1      MNRTSPDSEQ PPASEPVWER PWSVEEIRRS SQNWSLAADA GLLQFLQEFSS QQTISRTHEI KKQVDGLIQE TKATHCRLHN
81     VFNDFLMLSN TQFIENRVYD EEVEDQALKT EAEKAEQEKI REQKEIDLIP KVQEAVNRYGL QVLDSAFEQL DIKAGNSDSE
161    EEDANERVEL ILEPKDLYID RPLPYLIGSK LFMQEDEVGL GELSSEEGSV GSDRGSIVDS EDEKEEESD DFASHSDNEQ
241    NQHITQMSDE EEDDDADLFA DSEKEGDDIE DIEESAKSKR PTFADLAA RIKGDVSNQR KEGHTDGKPK RTVKEKKERR
321    TPADDEEDIL FPPPTLTDED FSPFGSRGGL FSDRQGLFDD DDESDFLKEA PRGQPAQGPV SEESPPSPKP GKkipAGAVS
401    VFLGYTDVSG STSAPSLKEF QKHEQSTPGK SPHLPAPTGL FDDDDNDSDS DDFFMPSSS KPSKTDKVKP TTIIFDDDEG
481    DLFKEKTAL PAASVSQTDE NKARTDKTIT LPSSKNPKLV SETKTQKGLF SDEEDSEDLF SSQSSSKTKS ASVLSQQPPA
561    SVSLFGDEDE EDNLFPSAAA KKQTSLLPQP SQEKAKPSEQ PPKKASALFS SDEEDQWSVA DSQTKLASER KSKGERWDAG
641    TNQGQEAQAV KKTNLFEEED DDGVDLFAIA KDSQKKTQRT SLLFEDDTDS GSSLFSLPPT SVPPAATKKE SIPKVPLLFS
721    DEEDSEVPSG VKPVDLKAEN AAASPEVGS A DVANVAQKEG LLPTSDQEAG GPSDIFSSSS PLDKGAKGRT KTVLSLFDDE
801    EDKVEDDSNT CAPQGGLEKG VKTDRRPKST GVFQDEELF SHKLQKDNDF DVDLFAQTKK TRLSMPSGGS LFGDDDDDDL
881    FSTAKTQPAQ PVPVEKKGTL RKDHKPELPT EGSKEKSTWK AETAQDSSGL TPFKSREPSS RIGKIQANLA INPATLLPSV
961    APQIPGAKPA SCELAFPSSE PARSHIREAV PTLPGSEEAG VSFDLPAQAD TLHSANKGRV KVRGKRRPQT RAARRLAAQE
1041   SSEAEDVTID RGPVTQLSSS PVLPNHGQPL LQPRMASGET SSEKAMAVPW EGGPVLSAVD RSEFFVKSLPQ TGNEAHLFDS
1121   GDIFPKSTGS QSMEGASVKA GETPAHSSAG RKEKSLVFPD LSEASGVDDL FQSAPKRPRTK KRNPFPILLED EEDLFADQKG
1201   KKNQWKS DSH QDVVSKTQDI FEDDIFATEA IKKFPFKRE KERTLEPNLF DDNIDIFADL TVKPKKPKPK KVTAKSMFDD
1281   DTDDIFSSGL QAKASKPKSQ SAEAVSELRS ENK VSNIFDD PLNAFGSQ
    
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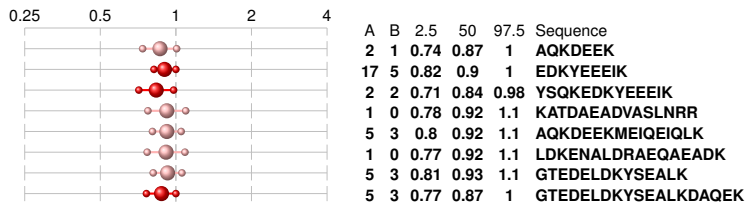


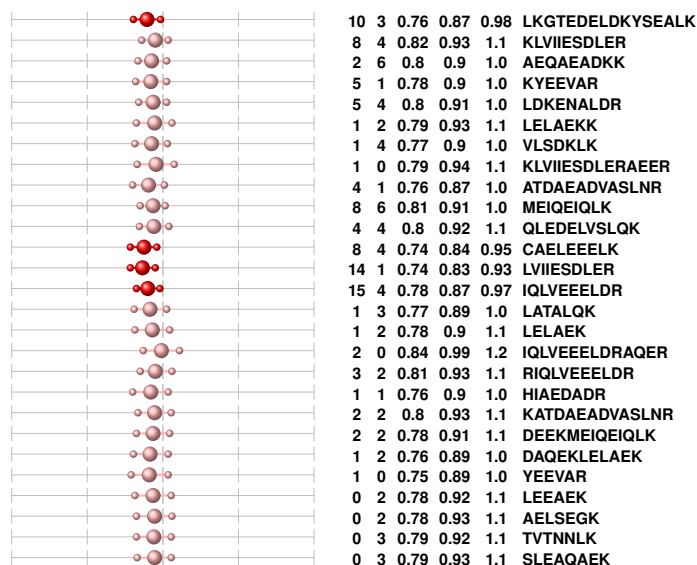
5.287 "tropomyosin 1, alpha isoform a [Rattus norvegicus]"

Protein Accession	gi 78000188	
Mean Expression Ratio	0.903	
Median Expression Ratio	0.904	
Credible Interval	(0.856, 0.952)	
Associated Peptides	35	
Associated Spectra	223	
Coverage	0.68	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.985	0.664
Avg..iTRAQ.Ratio....116.114.	0.88	0.945
Avg..iTRAQ.Ratio....117.114.	0.94	0.779

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1      MDAIKKKMQM LKLDKENALD RAEQAEADKK AAEDRSKQLE DELVSIQK KL KGTEDELDKY SEALKDAQEK LELAEEKATD
81     AEAADVASLNR RIQLVEEELD RAQERLATAL QKLEEAEEKAA DESERGMKVI ESRAQKDEEK MEIQEIQLKE AKHIAEDADR
161    KYEEVARKLV IIESDLERAE ERAELSEGKC AELEELKTV TNNKLSLEAQ AEKYSQKEDK YEEEIKVLSL KLEAETRAE
241    FAERSVTKLE KSIDDLLEDF LCFSPPKTSP SSRMSHLSSEL CICLLSS
    
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5.288 PREDICTED: similar to Protein C6orf115 [Rattus norvegicus]

Protein Accession	gij109460484	
Mean Expression Ratio	0.902	
Median Expression Ratio	0.904	
Credible Interval	(0.688, 1.18)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.160	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.955	0.56
Avg..iTRAQ.Ratio....116.114.	1.05	0.823
Avg..iTRAQ.Ratio....117.114.	1.05	0.366

1 MNVEHEVNLL VEEIHRGSK NADGKLSVKF GVLFDQDDRCA NLFEALVGTLL KAAKRRKIVT YAGELLQGV HDDVDIVLLQ
81 D

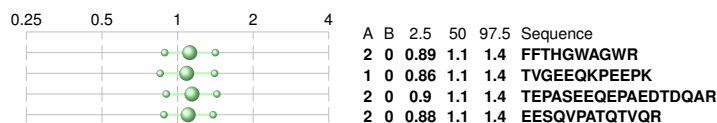


5.289 A kinase anchor protein 12 isoform beta [Rattus norvegicus]

Protein Accession	gi 75905811
Mean Expression Ratio	1.11
Median Expression Ratio	1.11
Credible Interval	(0.91, 1.35)
Associated Peptides	4
Associated Spectra	7
Coverage	0.033
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.22
Avg..iTRAQ.Ratio....116.114.	1.27
Avg..iTRAQ.Ratio....117.114.	1.24

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1      MLGTITITVVG QRESEDEVREK DRVEEMAANS TAVEDITKDG QEETSEIIEQ IPASESNVEE MVQPAESQAN DVGFKKVFKF
81     VGFKFTVKKD KNEKSDTVQL LTVKKDEGEG AEASVGAGDH QEPSVETAVG ESASKESELK QSTEQEGTL KQEQSSTEIP
161    LQAESDQAAE EEAKDEGEEK QEKEPTKSPE SPSSPVSET TSSFKKFFTH GWAGWFKKTS FKKSKEDDL EAEKRKQEA
241    EKVDDEEEKK TEPASEEQEP AEDTDQARLS ADYEKVELPL EDQVGDLEAS SEEKCAPLAT EVFDEKMEAH QEVVAEVHVS
321    TVEKTEEQG GGGEAEGGVV VEGTGESLPP EKLAEPQEVV QEAEPAEELM KSREMCVSGG DHTQLTDLSP EEKTLPKHPE
401    GIVSEVEMLS SQERIKVQGS PLKKLFSSSG LKKLSGKKQK GKRGGGGDEE PGEYQHIHTE SPESADQKG ESSASSPEEP
481    EETTCKLEKGP LEAPQDGEAE EGTTSDGEEK REGITPWASF KKMVTPKKRV RRPSESDKEE ELEKVKSATL SSTDSTVSEM
561    QDEVKTVGEE QKPEEPKRRV DTSVSWREALI CVGSSKKRAR KASSSDDEGG PRTLGGDSHR AEEASKDKEA GTDAVPASTQ
641    EQDQAQGS S PEPAGSPSEG EGVSTWESFK RLVTPRKSK SKLEEKAE DS SVEQLSTEIE PSREESWVSI KKFIPGRRKK
721    RADGKQEQAT VEDSGPVEIN EDDPDVPAVV PLSEYDAVER EKMEAQGNAE LPQLLGAVYV SEELSKTLVH TVSVAVIDGT
801    RAVTSVEERS PSWISASVTE PLEHTAGEAM PPVEEVTEKD IIAEETPVLT QTLPEGKDAH DDMVTSEVDF TSEAVTATET
881    SEALRTEEVT EASGAEETD MVSAVSQLTD SPDTTEEATP VQVEGGVLD TEEERQTQA ILQAVADKVK EESQVPATQT
961    VQVTGSKALE KVEEVEEDSE VLASEKEKDV MPKGPVQEAG AEHLAQGSET GQATPESLEV PEVTADVHV ATCQVIKLOQ
1041   LMEQAVAPES SETLTDSETN GSTPLADSDT ADGTQQDETI DSQDSKATAA VRQSQTVEE AATAQKEEPS TLPNNVPAQE
1121   EHGEPEGRDV LEPTQQLAA AAVPVLAKTE VGQEGEVDWL DGEKVKEEQE VVHSGPN SQ KAADVTDSE VMGAGCQEK
1201   ESTEVQSLSL EEGEMTDVE KEKRETKPEQ VSEEGEQETA APEHEGTYGK PVLTLDM PSS ERGKALGSLG GSPSLPDQDK
1281   AGCIEVQVQS LDTTVTQTAE AVEKVIETVV ISETGESPEC VGAHLLPAEK SSATGGHWTL QHAEDTVPLG PESQAESPI
1361   IVTPAPESTL HPDLQGEISA SQRERSEED KPDAGPDADG KESTAIEKVL KAPEIILELE SKSNKIVLNV IQTAVDQFAR
1441   TETAPETHAY DSQTQVPAMQ ADSQGAQQML DKNESCQDET PSAAAQRGLA SPDRSGGMS ASEMLAALAV ESAGVKV SIE
1521   KLPPQPKDQK EHAADGPPQLQ SLAQAEASAS GNLTKESPD T NGPRLTEEGD APKVEVQEEE MSTKSVRENK AQAEEDLQEP
1601   KGDLAES
    
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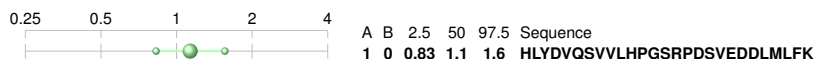
5.290 adipsin [Rattus norvegicus]

Protein Accession	gi 117647198
Mean Expression Ratio	1.11
Median Expression Ratio	1.11
Credible Interval	(0.823, 1.49)

Associated Peptides	1
Associated Spectra	1
Coverage	0.103
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.61
Avg..iTRAQ.Ratio....116.114.	1.36
Avg..iTRAQ.Ratio....117.114.	1.92

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1      MHSSVYLVAL VVLEAAVCVA QPRGRILGGQ EAMAHARPYM ASVQVNGTHV CGGTLVDEQW VLSAAHCMDG VTKDEVVQVL
81     LGAHSLSSPE PYKHLVDVQS VYLHPGSRPD SVEDDLMLFK LSHNASLGPH VRPLPLQRED REVKPGTICD VAGWGVVTHA
161    GRRPDVLQQL TVSIMDRNTC NLRTYHDGAI TKNMMCAESN RRDTCRGDSG GPLVCGDAVE AVVTWGSRVC GNRKPGVFT
241    RVATYVPWIE NVLSGNVSVN VTA
  
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5.291 LIM domain only protein 7 [Rattus norvegicus]

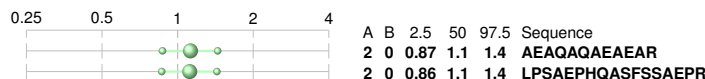
Protein Accession	gi 48040390
Mean Expression Ratio	1.10
Median Expression Ratio	1.10
Credible Interval	(0.875, 1.39)
Associated Peptides	2
Associated Spectra	4
Coverage	0.0168
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.53
Avg..iTRAQ.Ratio....116.114.	1.19
Avg..iTRAQ.Ratio....117.114.	1.24

NHLBI Zile/Grant, Aged Rat

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1      MEGMEDAEAD CSIAFAEAQR WVEAVTEKNF ETRDFRASLE NGVLLCDLIN KLKPGVVRKI NRLSTPIAGL DNINVFLKAC
81     EQIGLKEAQL FHPGDLQDLS NRVTVKQEEET DRRLKKNVLIT LYWLGRKAQN NPYYHGPLYL LKAFETLLGQ ALTKALEDS
161    CLKRRSGRDSG YGDIWCPCDRG DFPAPPGSHR REDSFESLDS LGSRLTSCS SDLTLLRGGRE GCESDNDWDF TFKMQDYKND
241    DMSYRRISAI EPKSALPFNR FLPNKSQPS YVPAPLRKKR PDKNEDNRRS WASPVYTETE GTFSSSTQRRR WGPKMENWHT
321    VQETSTSSWC LEEEEKVTNR LPNVVKKDDLY VVKLSPVMPG PGSSFDQFLP KGWTPEDMNW KKIKREYKPK WYKEFQGLSQ
401    FLLLQALQTY SDDILSSETN VKLDPTSGPR LITRRKNFSP TPGYRAHDLE PQSLDPDLEN DDFVVRKTRA FHANPCVLR
481    FEDFRRFSEP DDAVERDIIL QCREGELVLP DLEKDDMIVR RIPAQKKEVP LSGAPDRYQP VPFPEPWTLP PEIQAKFLSV
561    LERTCPPKDK PSSCRVLPVS HRLKKDDMLT RKIQSWKLT AVVPI SFRPG PCSEADLRKW EAIREASRLR HRKRLMVERL
641    FQKIYGENGS KSLSDVSAED VQSLRQLRYE EMQKIKSCLK EQDQKWQDDL AKWKDRRKS Y TSDLQKKKEE REEIEKQALE
721    KSDRSSKTFR EMLQDRESQS STTTSRRRIY SDDILDGVP LPPTVTLSET SYQSERLEDK ARAHPAEMP K EDSTTFASRE
801    DGIAAEIPLA SHIPEERRQA PWPSAETRQA SSSSAESHQA SLPSTESDQA R LPSAEPHQ A SPSSAEP RQV PLVSAEPHQ
881    SSFSSTEPHQ ASLSSALQRP SSSSSSQSWS STRGESTRIS ASLPRSYQRS DTARLTSVVT ARPFGTSSRG ISSLPRSYTM
961    DDGWIYNGDV EVVKREQHDS GRAAGMKPDS SHFILGSSSE KEVATGEDGA SLSSVFLPSS SLSLSDQAAS SKATFSSSTSG
1041   LDSVSDSGEG RSSSLRLEVSR SPDQFSDMRI SINQTPGTKH DFGFTIKWDV SGISVASVEK GSPAEFSQLQ VDDEILAINN
1121   TKFSYKDTKK WEEAMANAQE TGNLVMVDRR YGKSGSPETK WIDTSTGIYS TEKSSLSVST TDFSESLSQP YSESKEINGI
1201   HEGSNAPFSK ASESISLKNL KRRSQFTEQG SSSSVAPDLP VPTLSAPSRW AWDQEEERRR QERWQKEQDR LLQEKYQREQ
1281   EKLREEWQRA QQEAERENSK YLDEELMVLN SNSISLTSRE SVTASWEP SW SEGSKSLDRE GTRAGDEDRG QLEDDAVYED
1361   QSQKLQERLM LEHEKRRKEQ EAQEEELRQK REAEAQARAE AEAQARAEQ AR AEAQAQAE AEAARKRAEAQ KLQAEERRET
1441   SVKIYQYRRP IDSYDLPKRE EESSGLLPID RSKRSRSTEL NDPLIEKSGS SKYSDRIGTT SFSQRSKSKD QGPSEAELE
1521   QQILQEMRKK TSLHNDNSWI RQRSAVSNKE PICLTGMRRR GESLDNLD SQ RFGSWRQSSW HSQPAGVYAS SSVQDFSRLP
1601   PQLLSTSNRA YMRNPSSAVP PLAGSVKTSF GSPSPRSHP SMSQSGSGLR NRSVSGKRV C SYCNSILGKG AAMIETLGL
1681   CYHLHCFKCV SCERDLGGSS SGAEVRIRNH QLYCNDCYLR FKSGRPTAM

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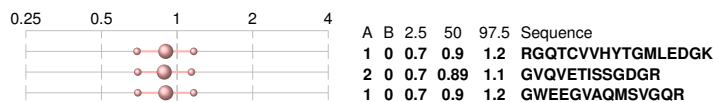
5.292 FK506-binding protein 1a [Rattus norvegicus]

Protein Accession	gi 47271544
Mean Expression Ratio	0.904
Median Expression Ratio	0.906
Credible Interval	(0.723, 1.13)
Associated Peptides	3
Associated Spectra	4
Coverage	0.407
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.888
Avg..iTRAQ.Ratio....116.114.	0.926
Avg..iTRAQ.Ratio....117.114.	0.804

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1      MGVQVETISS GDGRTFPKRG QTCVVHYTGM LEDGKFKDSS RDRNKPFKFT LGKQEVIRGW EEGVAQMSVG QRAKLIISP
81     YAYGATGHPG IIPPHATLVF DVELLKLE

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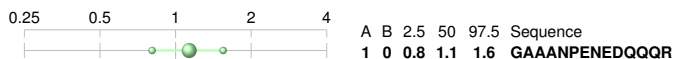


5.293 PREDICTED: similar to talin 2 isoform 2 [Rattus norvegicus]

Protein Accession	gij109484980
Mean Expression Ratio	1.10
Median Expression Ratio	1.10
Credible Interval	(0.815, 1.49)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00551
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.86
Avg..iTRAQ.Ratio....116.114.	1.61
Avg..iTRAQ.Ratio....117.114.	1.75

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1      MVALSLKICV RHCNVVKTMQ FEPSTAVYDA CRVIRERVPE AQTGQASDYG LFLSDEDPRK GIWLEAGRTL DYYMLRNGDI
81     LEYKKKQRPQ KIRMLDGSVK TVMVDDSKTV GELLVITCSR IGITNYEESY LIQETIEEKK EEGTGTLRKD RTLLRDERKM
161    EKLKAKLHTD DDLNWLHDSR TFRQGVNEN ETLLRRKFF YSDQNVDSRD PVQLNLLYVQ ARDDILNGSH PVSFEKACEF
241    GGFQAQIQFG PHVEHKKHPG FLDLKEFLPK EYIKQRGAEK RIFQEHKNGC EMSEIEAKVK YVKLARSIRT YGVSFFLVKE
321    KMGKKNLVP RLLGITKDSV MRVDEKTKEV LQEWPLTVK RWAASPKSFT LDFGGEYQESY YSVQTTEGEQ ISQLIAGYID
401    IILKKKQSKD RFLGEGDEES TMLEESVSPK KSTILQQQFN RTGKAEHGSV ALPAVMRSGS SGPETFNVGS MPSPQQQVMV
481    GQMRGHMPP LTSAQQALMG TINTSMHAVQ QAQDDLSELD SLPLPGQDMA SRVWVQNKVD ESKHEIHSQV DAITAGTASV
561    VNLTAGDPAD TDYTAVGCAI TTISSNLTEM SKGVKLLAAL MDDDVGSGED LLRAARTLAG AVSDLLKAVQ PTSGEPRQTV
641    LTAAGSIGQA SGDLLRQIGE NETDERFQDV LMSLAKAVAN AAAMLVLKAK NVAQVAEDTV LQNRVIAAAT QCALSTSQLV
721    ACAKVVSPFI SSPVCQEQLI EAGKLVDRSV ENCVRACQAA TGDSELLKQV SAAASVVSQA LHDLLQHVRO FASRGEPIGR
801    YDQATDTIMC VTESIFSSMG DAGEMVRQAR VLAQATSDLV NAMRSDAEAE IDMENSCKLL AAKKLLADST ARMVEAAKGA
881    AANPENEDQQ QRLREAAEGL RVATNAAAQN AIKKKIVNRL EVAAKQAAAA ATQTIAASQN AAISNKNPSA QQQLVQSCKT
961    VADHIPQLVQ GVRGSQAQAE DLSAQLALII SSONFLQPGS KMVSSAKAAV PTVSDQAAAM QLSQCAKNLA TSLAELRTAS
1041   QKAHEACGPM EIDSALNTVQ TLKSELQDAK MAAAESQLKP LPGETLEKCA QDLGSTSKGV GSSMAQLLTC AAQGNHEHYTG
1121   VAARETAQAL KTLAQAARGV AASTNDPEAA HAMLDSARDV MEGSAMLIQE AKQAL IAPGD TESQORLAQV AKAVSHSLNN
1201   CVNCLPGQKD VDVALKSIGE SSKKLLVDSL PPSTKPFQEA QSELNQAAD LNQSAGEVVH ATRGQSGELA AASGKFSDDF
1281   DEFLDAGIEM AGQAQTKEDQ MQVIGNLKNI SMASSKLLA AKSLSVDPGA PNAKNLLAAA ARAVTESINQ LIMLCTQQAP
1361   GQKECDNALR ELETVKGMLE NPNEPVS DLS YFDCIESVME NSKVLGESMA GISQNAKTGD LPAFGECVGI ASKALCGLTE
1441   AAAQAAYLVG ISDPNSQAGH QGLVDP IQFA RANQAIQMAC QNLVDPGSSP SQVLSAATIV AKHTSALCNA CRIASSKTAN
1521   PVAKRHFVQS AKEVANSTAN LVKTIKALDG DFSEDNRNKC RIATPLIEA VENLTAFAVN PEFASIPAQI SSEGSQAQEP
1601   ILVSAKTMLE SSSYLIR TAR SLAINPKDPP TWSVLGHSH TVSDSIKSLI TSIRDKAPGQ RECDYSIDGI NRCIRDIEQA
1681   SLAAVSQSLA TRDDISVEAL QEQLTSVVQE IGHLDIP IAT AARGEEAQLG HKVTQLASYF EPLILAAVGV ASKMLDHHQQ
1761   MTVLDQTKTL AESALQMLYA AKEGGGNPKA QHTHDAITEA AQLMKEAVDD IMVTLNEAAS EVGLVGMVD AIAEAMSKLD
1841   EGTPEPEKGT FVDYQTTVVK YSKAIAVTAQ EMMTKSVTNP EELGGLASQM TTDYGHLLAQ GQMAAATAEP EEIGFQIRTR
1921   VQDLGHGCI F LVQKAGALQV CPTDSYTKRE LIECARSVTE KVSLLVLSALQ AGNKG TQACI TAATAVSGII ADLDTTIMFA
2001   TAGTLNAENG ETFADHRENI LKTAKALVED TKLLVSGAAS TPKLAQAAQ SSAATITQLA EVVKLGAASL GSNDPETQVV
2081   LINAIKDVAK ALSDLIGATK GAASKPADDP SMYQLKGAAK VMVTNVTSLL KTVKAVEDEA TRGTRALEAT IEYIKQELTV
2161   FQSKDPEKT SPSEESIRMT KGITMATAKA VAAGNSCRQE DVIATANLSR KAVSDMLIAC KQASFYDVS EEVTRALRY
2241   GTECTLGYLD LLEHLVLIQ KPTPELKHQL AAFSKRVAGA VTELIQAAEA MKGTEWVDPE DPTVIAETEL LGAAASIEAA
2321   AKKLEQLKPR AKPKQADETL DFEEQILEAA KSIAAATSAL VKSASAAQRE LVAQGVGS I PANAADDGQW SQGLISAARM
2401   VAAATSSLCE AANASVQGHA SEEKLISSAK QVAASTAQLL VACKVKADQD SEAMKRLQAA GNAVKKRASDN LVRAAQKAAF
2481   GKADDDVVV KTKFVGGIAQ IIAAQEEMLK KERELEEAR KLAQIRQQY KFLPTELRED EG
    
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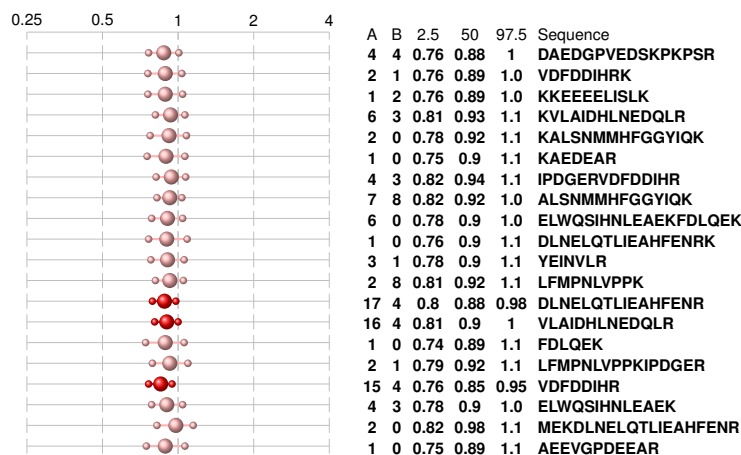


5.294 "troponin T2, cardiac [Rattus norvegicus]"

Protein Accession	gij6981666	
Mean Expression Ratio	0.906	
Median Expression Ratio	0.906	
Credible Interval	(0.847, 0.97)	
Associated Peptides	20	
Associated Spectra	143	
Coverage	0.482	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.97	0.666
Avg..iTRAQ.Ratio....116.114.	0.884	0.939
Avg..iTRAQ.Ratio....117.114.	0.844	1.08

```

1      MSDAEEVVVE YEEEQEEEDW SEEEEDEQEE AVEEEDGEAE PDPEGEAEAE EDKAEVGPDP EEARDAEDGP VEDSKPKPSR
81     LFMFNLVPPK IPDGERVDFD DIHRKRMKED LNELQTLIEA HFENRKKKEE ELISLKDRIE KRAERAEEQQ RIRNEREKER
161    QNRLAEEERAR REEENRRKA EDEARKKKAL SNMMHFGGYI QKAQTERKSG KRQTEREKKK KILAERRKVL AIDHLNEDQL
241    REKAKELWQS IHNLEAEKFD LQEKFKQQKY EINVLRNRIN DNQKRVSKTRG KAKVTGRWK
    
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5.295 PREDICTED: similar to Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like protein) (ABP-280-like p

Protein Accession	gij109502223	
Mean Expression Ratio	0.908	
Median Expression Ratio	0.907	

Credible Interval	(0.678, 1.21)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.349
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	0.524



5.296 PREDICTED: similar to AHNAK nucleoprotein isoform 1 [Rattus norvegicus]

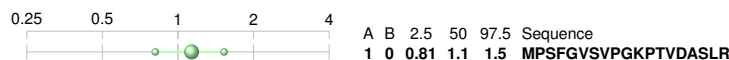
Protein Accession	gij109478783
Mean Expression Ratio	1.10
Median Expression Ratio	1.10
Credible Interval	(0.812, 1.46)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00221
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.27
Avg..iTRAQ.Ratio....116.114.	1.4
Avg..iTRAQ.Ratio....117.114.	1.83

NHLBI Zile/Grant, Aged Rat

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81 AGRGDYTSQL SRQPAPRVAR QRCAPAGFRR ASSVSTPFC GVANSAPPMP VLSSLFRDAT CRGEDAGCTA VGSLLPWS
161 GRRHLPVLPRL SLITSPSCRY RNSGFRVQGS GGPWRDFTNC NLEAFCGTGL RGRGRRPSPG ASAPGPRLDA QGRRRPPAPLA
241 AKMCDCFHV LPTWGAAGS GAPHRLQPA SLGRVGSAGV TGPRMSGRQL QQQPEAEATE DDYSVTEGVP GEVVRPRPQG
321 SSPVVEYTA E GAGFGQGETG QGRHSSSSGR RSNWRRDSGE STAFASMSHP GESTEVTLKT DVESGASGYS VTGGGQDQIF
401 VKQVLKSSA AKFLNLRREG QLLSATIFFD HMKYEDALKI LQYSEPYKVQ FKIKRKL SAN EGEQAVQHP QQQQKGEKQ
481 DIADGCTETP TKSVDGAGDR ERLISKSRDD RRRRPQDRFS WPKFQALRSK RRAGPRRSHS SSEASEHRDT RDLSPSTSDT
561 ELQLTTDRED QSSGAGRQRR RFLNLRIGMT SGQSPVTEQ KDSKPDORRE QAAVLGEGKS KEDERKDTQG AEEQTKDKK
641 QKTGFMTTR QKTRDNYSN LEKEADGKKE FKTERHQKKK KQVKEKKKDE KLVQITKEIP QELQWEDSWE EVQSLIEGIA
721 RLSLKDTEQ HLD AEIQGGD GKQDKDMASK DTFKMPKFP MFSFVSAPG KFTVDTSLV GAKPVEGDMA LPYVQGD LK
801 TDVSIQLPSA NLEKAGKEG VKQPEDQSTD AETPTQAAAG AGLKGHLPKV QMPSLKM PKV DVKGPVHDLM ATKPDVTGVP
881 GEVRSPLDLE V LPGVEVDIQ APAAKVEGDK ALGDKDLATK DSKFKMPKFK MPSFVGSVPG KPTVDASLHV GTPKVEGEVA
961 LPVSEGLDKT PDISIQLPSA HLELRPRQEG VKLAEDQPTD AETSVAQAAG TSLKGHLPKV QMPSLKM PKV DSKGPHVDVK
1041 GPKVDFKMPK FVSKAGKGV RAPDLDVALP KVEGDVLLG AKLEGDVLG DQDVAAKDSR FKMPKFKMPS FSVSASGKPS
1121 VEASLEVGA P KVEGDVALPS VQGD LKTPDV SIQLPSTDL EIRAGQEVNL MKDHPDPVET HARAAAGGGL KGHMFKMHP
1201 SIKMFKVELK GPHVDMKGP LEVKGAEGEV SGEVDIQAPS GVEVDIQAPS VNLEGDVLLA EKDLAAKDTV FKMPKFKMPS
1281 FGVSIPGKPT MEASLEVGA P KVEGDVALPS GKGD LKTPDV SIQLPSAHL L RAGQVGVKL AEDQPTDAET SVQAAAGVSL
1361 KGHLPKVPQMP SLKMPKVDVK GPHVDLKDPK VDVTVGKGEV RSPDLEVTLP GVEVDIQAPA ARVEGDKALG DKDLATKDSK
1441 KMPKFKMPS FRVSAHGKPT VEASLEVGA P KVEGDVLLG AKLEGDVLG SIQLPSAHL L RAGQVGVKL AEDQPTDAET
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1601 DVLLGDQDLA GKDTFKMFP FKMPFSVSA SGKPSVEASL EVGAPKVEGD VALPSVQGD L KTFDVSITQL STDL EIRAGQ
1681 VGVNLMKDQP PDVETHARAA AGGGLKGHMP KVHMPSTKMP KVELKGPVHD MKGPKLEVKG AEGEVSGDEL EVSIPGVEVD
1761 IQAPSVNLEG DVLVLAEKDIA AKDTFKMFP FKMPFSFVSI PGKPTMEASL EVGAPKVEGD VALPSGKGD L KTFDVSITQL
1841 SAHLDLRAGQ VGVKLAEDQP TDAETSVAQA AGVSLKGLHP KVQMPSLKMP KVDVKGPHVD VKGVEVRSDDL
1921 EVTLPGVEVD IQAPAAKVEG DKALGDKDLA TKDSKFKMFP FKMPFSFRVSV PGKPTVEASL RVGAPKVEGE VVLPVQGD L
2001 KTFDVSITQL SADDL RASQ EGKLSLEDL SDAETSQAQA AGASLKGHL KVPMPSLKVP KVDLKGPHVD VKGPKVDVKA
2081 AKDEVRA PDL DVTLLPSVEVD IQAPCAKLEG VILLGDQDVA AKDTFKMFP FKMPFSFVSA PGKPTVEASL EVGAPKVEGD
2161 VALPSVQGD L KTTDASIQLP SAHLDLRPGQ VGVKLSLEDL TDAETSQAQA AGASLKGHL KVPMPSLKMP KVDVKGPHVD
2241 LKVPKVDMTG DKGEVRSPEL EVALPGVEVD IQQPAKVG E DMALGEKEVA TKDSKFKMFP FKMPFSFVSI PGKPTMEASL
2321 RVGAPKVEGE VVLPVQGD L KTFDVSITQL SADDL RASQ EGKLSLEDL RDAETSQAQA AGASLKGHL KVPMPSLKVP
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2721 ETSQAQAAGA SLKGLHPKVP MP SLKMPKVD VKGPHVDLKV PKVDMTGDKG EVRSPLDLEVA LFGVEVDIQAPA PAARVGGDMA
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2961 KVPKVDMTGDK GEVRSPELE VALPGVEVD IQQPAKVG E DMALGEKEVA TKDSKFKMFP FKMPFSFVSI PGKPTMEASL
3041 VGAPKVEGEV VLPVQGD LKTP DVSMQDLKTP ADLELRPRQE GEKLSLEDLPR DAETSQAQA GASLKGHLKVP QMPSLKM PKV
3121 VDLKGPVHDV KGPVVDVDP KVDVKGAKGE VRAPDLDVAL PGVEVDIQAPA CAKLEGDVL L GDQDVAAGD L KTFKMPKFKM
3201 SFSVVSASGK PSVEASLEVGA P KVEGDVALPS VQGD LKTPDV SIQLPSTDL EIRAGQVGV NLMKDQPPDV EIAKRAAAGG
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3521 GEKEVATKDS KFKMFPKFKM PSFVGSVPGK PTVDASLRVG APKVEGEVVL PSVQGD LKTP DVSMQDLKTP THARASQEGQ
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3681 CAKLEGVILL GDQDVAAGD L KTFKMPKFKM PSFVGSAPGK PTVEASLELV VALPGVEVD IQQPAKVG E DMALGEKEVA
3761 DLRFQGVGV LSEDDQPTDAE TSVQAAAGVSL LKGLHPKVP MP SLKMPKEDV KGPYVDLKP KVDVKGDKGE VVLPVQGD L
3841 PGVEVDIQAPA GVKLEGGDVL AEKDLAAKDT KFKMFPKFKM PSFVSTPGK PTVEASLELV VALPGVEVD IQQPAKVG E
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4081 SVQGD LKTPDV VSIQLPSAHL DL RAGQVGLK LAEDQPTDAE TSAQAAGAAS LKGLHPKVP MP SLKMPKVD VKGPHVDLKV
4161 KVDMTGDKGE VRSPDLEVAL PGVEVDIQAPA AARVGGDMA GEKEVATKDS KFKMFPKFKM PSFVGSVPGK PTVEASLELV
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5521 VTGVKGEVRS PELEVALPGV EVDIQPPAAK VEGDMLGK E EVDLKGPHVD VKGPKVDV D PKVDVKGAKG EVRAPDLVDA
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5681 DVSIQLPSTDL EIRAGQVGV KLPDVEVTPAK AAAGVGLKGLH LPEVQMPSLK MPKVELKGP H VDKGPTVEA LKAGVEVSA
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6561 VQAAAGVSLK GQLPKVQMPF LKMPKVDVKG PHVDLKAAPV GMTGVKGEVR SPDLEVTLPG VEVDIQAPAA KVEGDKALGD
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8321 IPASTIQTFS YGFSLLKVKI PEPMPQACVY TVGPDSEQE GGVMPAAAG GHSIPAEVPP DTGEPFEIIS SGTGMPPGPQ
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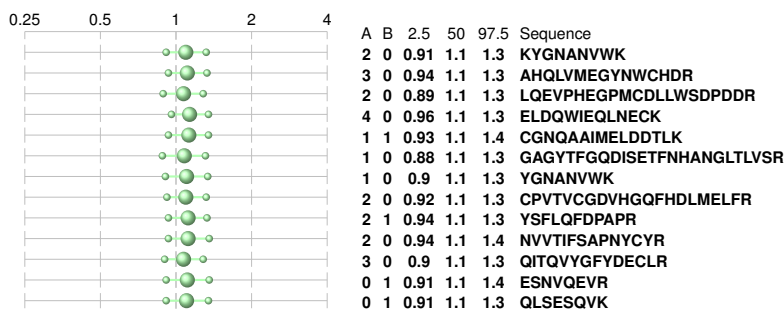


5.297 "protein phosphatase 2a, catalytic subunit, alpha isoform [Rattus norvegicus]"

Protein Accession	gij8394018	
Mean Expression Ratio	1.1	
Median Expression Ratio	1.10	
Credible Interval	(0.984, 1.23)	
Associated Peptides	13	
Associated Spectra	27	
Coverage	0.563	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.10	1.18
Avg..iTRAQ.Ratio....116.114.	1.2	0.992
Avg..iTRAQ.Ratio....117.114.	1.18	1.05

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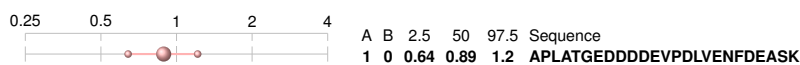
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161 GQIFCLHGGL SPSIDTLDHI RALDR LQEVV HEGPMCDLLW SDPDRGGWG ISPRGAGYTF GODISETFNH ANGLTLVSRRA
241 HQLVMEGYNW CHDRNVVTFP SAFNYCYRCG NQAIMEELDD TLKYSFLQFD PAPERGEPHV TRRTPDYFL
    
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5.298 PREDICTED: similar to basic transcription factor 3 [Rattus norvegicus]

Protein Accession	gi 62656185
Mean Expression Ratio	0.908
Median Expression Ratio	0.908
Credible Interval	(0.676, 1.22)
Associated Peptides	1
Associated Spectra	1
Coverage	0.154
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.807
Avg..iTRAQ.Ratio....116.114.	0.668
Avg..iTRAQ.Ratio....117.114.	0.715

1 MKETIMNQEK LAKLQAQGRM GKGKTARRKE KVPRTATAD DKKLQFSLKK LGVNSISGIE EVNVFTNQGT VIHFNPKVQ
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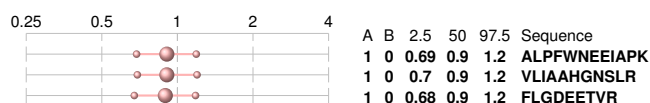


5.299 phosphoglycerate mutase 2 [Rattus norvegicus]

Protein Accession	gi 8393948
Mean Expression Ratio	0.91
Median Expression Ratio	0.908
Credible Interval	(0.715, 1.15)

Associated Peptides	3
Associated Spectra	3
Coverage	0.126
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.975
Avg..iTRAQ.Ratio....116.114.	0.894
Avg..iTRAQ.Ratio....117.114.	0.778

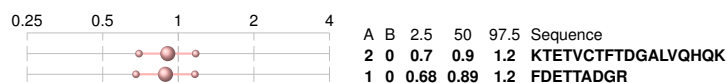
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 241 KAMEAVAAQG KAK



5.300 "fatty acid binding protein 5, epidermal [Rattus norvegicus]"

Protein Accession	gi 22024394
Mean Expression Ratio	0.908
Median Expression Ratio	0.908
Credible Interval	(0.714, 1.16)
Associated Peptides	2
Associated Spectra	3
Coverage	0.2
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.92
Avg..iTRAQ.Ratio....116.114.	0.859
Avg..iTRAQ.Ratio....117.114.	0.894

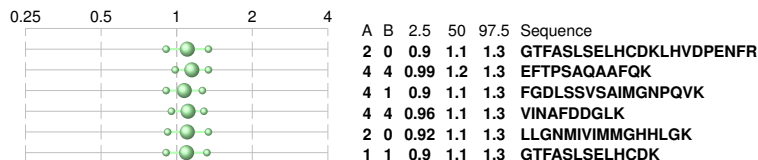
1 MASLKDLEGG WRLVESHGFE DYMKELGVGL ALRKMAMAK PDCIITLDNN NLTVKTESTV KTVFVSCSLG EKFDETTADG
 81 RKTETVCTFT DGALVQHQQW EGKESTITRK LKDGKMVVEC VMNNAICTRV YEKVQ



5.301 beta-glo [Rattus norvegicus]

Protein Accession	gj 40445397	
Mean Expression Ratio	1.10	
Median Expression Ratio	1.1	
Credible Interval	(0.97, 1.25)	
Associated Peptides	6	
Associated Spectra	27	
Coverage	0.524	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.37	1.65
Avg..iTRAQ.Ratio....116.114.	1.29	1.11
Avg..iTRAQ.Ratio....117.114.	0.795	0.597

1 MVHLTDAEKA TVNGLWGKVN PVEIGAESLA SLLIVYPWTQ RYFSKFGDLS SVSAIMGNPQ VKAHGEKVIN AFDDGLKHLDD
 81 NLKGTFFASLS ELHCCKLHVD PENFRLLGNM IVIMMGHHLG KEFTPSAQAA FQKVVAGVAS ALAHKYH



5.302 PREDICTED: similar to Y50C1A.1 [Rattus norvegicus]

Protein Accession	gj 62640413	
Mean Expression Ratio	0.908	
Median Expression Ratio	0.909	
Credible Interval	(0.677, 1.22)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0160	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.716	
Avg..iTRAQ.Ratio....116.114.	0.762	
Avg..iTRAQ.Ratio....117.114.	0.677	

```

1      MVSSLLP NLP SAECWAALLH DPMTLDM DAV L SDFV RSTGA EPGLARDLLE GKNWDLTAAL SDYEQLRQVH TANLPHVFNE
81     GRCAKQPERE LPQPGHKVER PCLQRQDDIA QEKRLSRGIS HASSAIVSLA RSHVANECNN EQFPLEMPIY TFQLPDLSVY
161    SEDFRSFIER DLIEQATMVA LEQAGRLNWW STVCTSCKRL LPLATTGDGN CLLHAASLGM WGFHDDRDLVL RKALYTM MRT
241    GAEREALKRR WRWQQTQNK ESGLVYTEEE WEREWTELLK LASSEPRTHF SKNGSGTGGG VDNSEDPVYE SLEEFHVFVL
321    AHILRRP IVV VADTMLRDSG GEAFAP IFFG GIYLFLEVPV NRCHCSPLVL AYDQAHFSAL VSMEQRDQQR EQAVIPLTDS
401    EHKLLPLHFA VDPGKDW EWG KDDNDNARLA NLILSLEAKL NLLHSYMNVT WIRIPSETRA PLAQPESPTA SAGEDVQSLA
481    ESLDSDRDSV CSNSNSNNGK NGKDKEKEKQ RKDKDKTRAD SVANKLGSFS KTLGIKLKKN MGGGLGGLVHG KMGRANSANG
561    KNGDSTERNK EKKSRSRKG S KEESGASAST SPSEKTPSP TDKAAGASPA DKGSGSRSDA WKYSTDVKLS LNILRAAMQG
641    ERKFIFAGLL LTSHRHQFHE EMIGYLTSA QERFSAEQEQ RRRDAAAAA AANANANATA KRPARRPEAE GAPGERASP
721    GPPAAPPTQL VLKLRKPPSP GTGGSARATR AAGGAASEPGL GGGARRVAPG TGGPTPGRSP PAPTPARQSV IHVQAAARDE
801    ACAPTVGALR PCATYPQQR SLWSQSYSPA RSALR TVNTV ESLAPGGADA PGPAEHKSQT YSNGFGAARD GLEFADADAP
881    AARSNAECGR GPGGPAQRRC QRENCIFYGR AETEHFCSYC YREELRRRRE ARAARP
    
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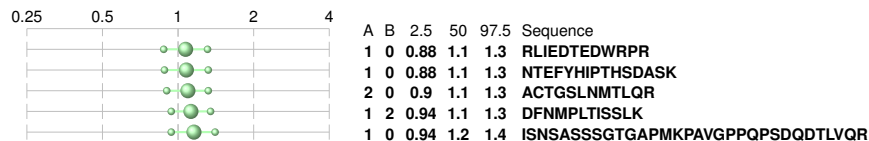


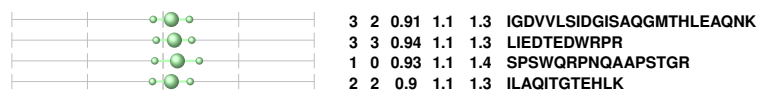
5.303 enigma homolog [Rattus norvegicus]

Protein Accession	gij16758028	
Mean Expression Ratio	1.1	
Median Expression Ratio	1.1	
Credible Interval	(0.968, 1.25)	
Associated Peptides	9	
Associated Spectra	24	
Coverage	0.228	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.29	1.06
Avg..iTRAQ.Ratio....116.114.	0.917	0.909
Avg..iTRAQ.Ratio....117.114.	1.40	0.898

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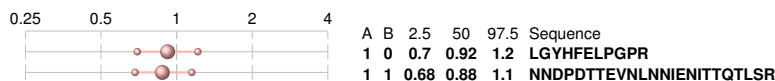
1      MSNYNVSLVG PAPWGFRLQG GKDFNMPLTI SSKLDGGKAS QAHVRIGDVV LSIDGISAQG MTHLEAQNKI KACTGSLNMT
81     LQFASAAAKS EPVAVQKGEP KEVVVKVPIT SPAVSKVTST TNMAYNKVPR PFGSVSSPKV TSIPSPSSAF TPAHAATSSH
161    ASPPFVAAVT PPPLSASGLH ASANPSAAQC SSPNTGKPA VHVPRQPTVT SVCESAQEL AEGQRRGSQG DIKQNGPFR
241    KHIVERNTEF YHIPTHS DAS KRLIEDTED WRPRTGTTQS RSFRLLAQIT GTEHLAESEN DNAKKANSTP EPSQQSASPL
321    SAAESLESPG SNRPV VAGLR SAAAFKPVGS TSVKSPSWQR PNQAAPSTGR ISNSASSSGT GAPMKPAVGP PQPSDQDTLV
401    QRAEHIPAGK RTPMCAHCNQ AIRGPF LVAL GKSWHPEEFN CAHCKNTMAY IGFVEEKGAL YCELCEYKFF APECGRQQRK
481    ILGEVINALK QTWHVSCFVC VACGKPIRNN VFHLEDGEPY CETDYALFG TICRCGEFPI EAGDMFLEAL GSTWHDTCFV
561    CSVCCESLEG QTFFSKKDKP LCKKHAHSV N F
    
```





5.304 PREDICTED: similar to leiomodrin 2 (cardiac) [Rattus norvegicus]

Protein Accession	gi 109473183	
Mean Expression Ratio	0.909	
Median Expression Ratio	0.909	
Credible Interval	(0.71, 1.16)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.21	0.379
Avg..iTRAQ.Ratio....116.114.	0.984	0.373
Avg..iTRAQ.Ratio....117.114.	0.985	1.24

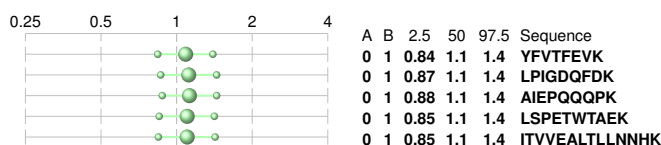


5.305 hormone-regulated proliferation-associated 20 kDa protein [Rattus norvegicus]

Protein Accession	gi 38454320
Mean Expression Ratio	1.1
Median Expression Ratio	1.1
Credible Interval	(0.89, 1.35)
Associated Peptides	5
Associated Spectra	5
Coverage	0.287
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.02
Avg..iTRAQ.Ratio....116.114.	0.949
Avg..iTRAQ.Ratio....117.114.	1.13

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1      MGARMTRAFR NFNVEKRAEQ EISKRRKPSMA PKHPSTRSLL QEHLSEQYPEI EEEVSRKDNK LLSLLRDVYV NSKDPVPSLP
81     VKAIEPQQQP KEFR LPIGDQ FDKNIKDIPK GKITVVEALT LLNNHKLSPE TWTAEKIAQE YHLELEDVNS LLKYFVTFEV
161    KIVPPEDRKA IQSK
    
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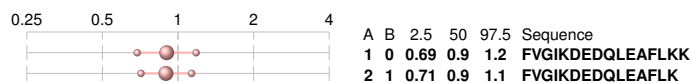


5.306 thioredoxin 2 [Rattus norvegicus]

Protein Accession	gij16758038	
Mean Expression Ratio	0.91	
Median Expression Ratio	0.91	
Credible Interval	(0.722, 1.15)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.0964	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.911	0.566
Avg..iTRAQ.Ratio....116.114.	0.742	1.11
Avg..iTRAQ.Ratio....117.114.	0.807	1.09

```

1      MAQRLLLLRRF LTSVISRKPP QGVWASLTST SLQTPPYNAG GLTGTSPSPAR TFHTTRVCST TFNVDGPDF QDRVVNSETP
81     VVVDFAQWC GPCKILGPRL EKMVARQH GK VVMAKVDIDD HTDLAIEYEV SAVPTVLAIK NGDVVDR FVG IKDEDQLEAF
161    LKKLIG
    
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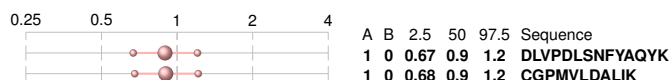


5.307 PREDICTED: similar to succinate dehydrogenase Ip subunit [Rattus norvegicus]

Protein Accession	gij109477603
Mean Expression Ratio	0.91
Median Expression Ratio	0.91
Credible Interval	(0.697, 1.19)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0887
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.89
Avg..iTRAQ.Ratio....116.114.	0.758
Avg..iTRAQ.Ratio....117.114.	0.844

```

1      MAAVVGVS LK  RGFSATALGR  VGLQFQACRE  AQTAAAAAPR  IKTFAIYRWD  PDKAGDKPRM  QTYKVDLNKC  GPMVLDALIK
81     IKNEIDSTLT  FRRSCREGIC  GSCAMNINGG  NTLACTRRID  TDLGKVSKEY  PLPHMYVIK  LVPDLSNFYA  QYSIEPYLK
161    KKDESQEGKQ  QYLQSIEDRE  KLDGLYECIL  CACCSTSCPS  YWWNGDKYLG  PAVLMQAYRW  MIDSRDEFTE  ERLAKLQDPF
241    SLYRCHTIMN  CTQTCPKGLN  PGKAIAEIKK  MMATYKEKRA  LA
  
```



5.308 PREDICTED: similar to eukaryotic translation initiation factor 5A2 [Rattus norvegicus]

Protein Accession	gij27689593
Mean Expression Ratio	0.908
Median Expression Ratio	0.91
Credible Interval	(0.702, 1.17)
Associated Peptides	1
Associated Spectra	4
Coverage	0.0784
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.663
Avg..iTRAQ.Ratio....116.114.	0.873
Avg..iTRAQ.Ratio....117.114.	0.645

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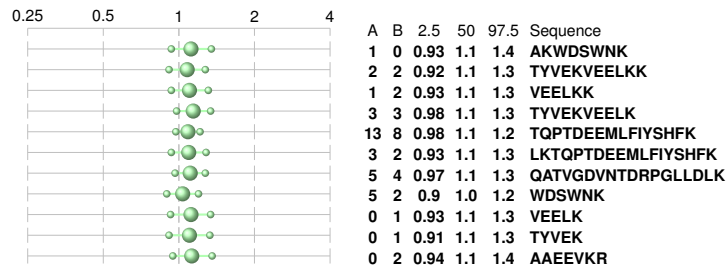
1      MADEIDFTTG  DAGASSTYPM  QCSALRKNF  VVLKGRPCKI  VEMSTSKTCK  HGHAKVHLVG  IDIFTGFKYE  DICPSTHNMD
81     VPNIKRNDYQ  LICIQDGYLS  LLTETGEVRE  DLKLPEGELG  KEIEGKYNAG  EDVQVSVMCA  MSEEYAVAIK  PCK
  
```




5.309 diazepam binding inhibitor [Rattus norvegicus]

Protein Accession	gij13937379	
Mean Expression Ratio	1.10	
Median Expression Ratio	1.10	
Credible Interval	(0.997, 1.21)	
Associated Peptides	11	
Associated Spectra	60	
Coverage	0.713	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.02	1.09
Avg..iTRAQ.Ratio....116.114.	1.05	1.06
Avg..iTRAQ.Ratio....117.114.	1.18	0.976

1 MSQADFDKAA EEVKRLKTQP TDEEMLFYIS HFKQATVGDV NTRPGLLDL K GKAKWDSWN K LKGTSKENA MKTYVEKVEE
81 LK KYGI



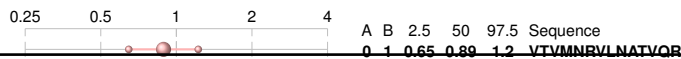
5.310 PREDICTED: similar to hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC)

Protein Accession	gij109497411
Mean Expression Ratio	0.91
Median Expression Ratio	0.91

NHLBI Zile/Grant, Aged Rat

Credible Interval	(0.674, 1.23)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00333
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.566
Avg..iTRAQ.Ratio....116.114.	0.584
Avg..iTRAQ.Ratio....117.114.	0.699

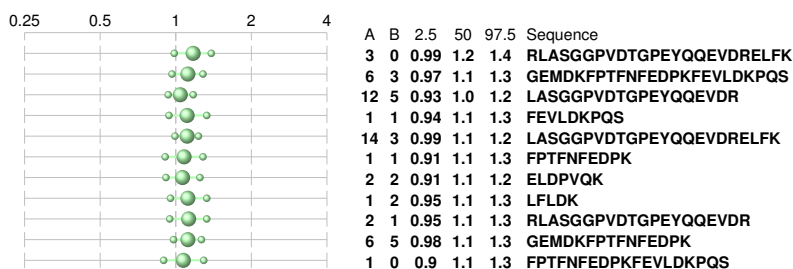
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81	LLTMGSSAAA	AAAAAAAAAD	SAQWLSVKEE	TIFLHDGLIR	VTDLAELPSE	ILGAPEAADT	DLEILTFETK	NPTELAERLR
161	SVCNGQSNAY	ARLLEYRLNA	LRGLWNAQRQ	LALAEQHERE	GSGDEETLAL	LKRQGLLQQP	EQAPFTSRVG	LLLVFPLIQS
241	QSRTPDPSLCN	ITAEVLLNCL	RDCQPLSLTK	EPADCLSGIE	TLLCSWLEET	SDTGRHIPHK	QKENAAAAALV	ALACARGSLK
321	TFVHTVHLQ	RQTELGSLPV	ADVLYRLLLL	EGGPGSPSCL	LGGKHIVSWG	YEDMLFAPDS	NPSSSENKD	ADLGRCLTAD
401	GHYLYTTNSA	GRGLSKLGS	LHGTLRGFVY	CRNEELEPGW	VAYGSGHLLH	RFVSPDNKPH	SLFQVIDQNT	LQVCQTVMPM
481	ASPLPVGSTM	STVHLSSDGT	YFYWIWSPAS	LNEKTPKGRS	VFMDIFELVV	YKEPTLTVA	LTVALTVALT	VALTVALTVA
561	LIVENGVFVA	NPLQERTILM	RKEGESAKSI	NEMLLSRLSR	YRASPSATLA	ALTGSTISNT	LKEDQAVLAS	SLVYNISDQG
641	FASRADLIDA	AGSSLGRGAL	VPGLGACYDT	VNNMLWTCNS	DYIDQWCNPG	NQAFHYVCQR	LGVSHIPEP	KEEAISTNEV
721	INQLLHVGA	MCIHQLNLLA	TNPPLPITSV	LGKQHPPEAR	HLLSSICDIME	KAMVNGDTCI	VRCILVVFQV	LGDSLADVGE
801	RNSGLSQLRD	VILTNLAEQL	QNNRFSGDED	DHYRLNDELL	HYILKIVVRE	SCILITKCCQT	VSKDDDFQKLL	STVPAASSCL
881	RYLMAVQNH	LSNTVLIKPD	DNEDSDSSLQ	GETLKVQVLT	GCDEVLEMLQ	QVTTALINS	MPDREQLKKG	LEQVTKATML
961	GHLPLVLLTS	LMHPNLQTLT	MADALMPQLV	QLVLYTSQCP	VFAEVGCSFC	GTSDDQKCRLF	PDERMLEEKE	EPGFLTGLKI
1041	PAPWAAGKT	ETVHPVRDNY	KFKETVHIPG	ARCLYLRFDT	RCSSQYDYDK	ESSEDEVSGGL	PFLVDLALGL	SVLACSMRLI
1121	LYNGPEITKE	EEACQDLLRS	KLLQRCQWQV	EANGVISPAL	TPSPSPPLPT	IEEDREFTYP	SDVLVPPVGN	YFDLPRIRLP
1201	PGIMIKLREI	SGRARPPQFRP	SIKEVIQPDV	MEEMVVS CVI	KHLNLVDALQ	SLINFQYQEE	HAEEDYDLCK	IMGETFFKLN
1281	AMERQLQSV	ELEQKWQSEA	EDAMQKLEN	NMPFFYDYHF	NEKPSHPLAK	TKTLVKSLMN	RAELLLHVTI	AAQSGLTRSI
1361	SGTFAETPAC	KSASETKVAS	HAVRQPVFLR	SMSAPSDLEM	IGNEDLEFTR	ANQRRRHVTS	HRSSSFLLQ	SLAIEDSRDK
1441	PTYSVLLGQL	FAFIGTNPDQ	AVSSSSFLLA	AQTRRRRGNT	RKQALVHMRE	LTAAVRVGG	VTHLVGPVTM	VLGGGPRIE
1521	LTCGGMVEQV	QEAFFGETM	VVSLCARYPI	ACANSIGLLC	TIPYTRSEEK	CLVRSGLVQL	MDRLCSLSSQ	TESSSSEKQT
1601	KKQKVATMAW	AAFQVLANRC	VEWEKEEGGS	TEAVHSGLAR	QVSSLLTNHL	ARATECCGNQ	AAGNDALQDV	LSSLNDLRS
1681	HIGKAILSQP	ACVSKLLSL	LDQRPSPKLV	LIIQLCRAA	LPLMSVEDCG	NVELPPWSYS	VPSLNSSEQD	PSDPASKIAS
1761	LLLAKLADYV	VPGCQTVLSP	TASEPDTTTL	KTSFKNSLKG	DKDPGEESEA	VDGKLSIFIH	KREDQSSHEV	LQPLLSSSEQ
1841	RFRLGTGAN	MEKVKMDRD	MTKGGCEVPI	TEEASAALRK	ATKWAQSGLI	VSVGPPVESI	NPETVSGLST	GDKKTAQTS
1921	ICRERNSELA	RTDPVRPFIS	GHVANSMAAE	VIALHLSLLM	APESNAAQIW	TTTAERKVLRS	ALMYIPQLGK	YAESILENGS
2001	SSGRKLAKLQ	RIARQAVAA	CALGGFKETI	KIGSEVQALP	LHKLSITEKV	VQAVQSMMLP	QEGSLSIHTS	LPATGDGSP
2081	VMAVVRLLAE	IRTRRVAVEL	CEPEEGSGSY	FLLYKDYSER	LAVVEVQGER	LRMLYRDCAR	PPPPPLQADR	RQPKAITNSP
2161	SRVFPVPRAC	MFSSSLTSTV	FLADPSAGGG	LPRGTFIYAT	SPLPVQAPSF	YWEIEIVSYG	DTDDDDTGP	IVSFGFATEAEK
2241	RDGAWTNPG	TCLFHNNGRA	VHYNGSLLQ	WKSVRLDVTL	CPGLVAGIGW	ERTEGTTPPPP	GQPAKGRVYF	TYCGQRLTYP
2321	LEDDVGGMWP	VVHIQKKNTK	TRANFGSRPF	AYAEQGHRN	AADLCTDLAE	EISANFEALP	FAMASDSDND	AGTSIASDPG
2401	THGPPCRIAA	VATAQQQYDS	DTSCHYKVEL	SYENFITS GP	DPHPPIADD	ESDDDDDDDI	PQEDHYALLV	KAWETKVFPT
2481	IRRRFRNEAE	RKSGLDQIKG	ALQLGMVDIA	RQTFEFLYEE	NGGIPRDLYL	PTIEDIKDEA	NKFTIDKVRK	GLTVVTRSPD
2561	SSNVASSAVG	TALPKFAIRG	MLKTFGLHGV	VLDVDSVNE	VQVETYLRSE	GVLVRYWYPI	DMLERPPAGY	RRTATNGLVT
2641	LDNTNLQIHR	ELLRCEAALA	RLYCRMALLN	IFAPKPLPHL	TRLFHIPAIR	DITLEHLQLL	SNQLLAPPLP	DGTSSSSSIL
2721	LAQSLQHCIH	SQSCSATDLF	YQNSQTLRE	WLSVAITRTL	HQGEDSLLEL	TKQICAFLOT	APQFPSEEF	PVSESKVSM
2801	VNFPGAAPV	VSCKESQSGF	RKDDSSLYKAP	WARVLVYGLG	HKVVRTGQLN	LIEAACYPDR	ASPANTGLAP	PPTADQYPSV
2881	VLSTDKVHIK	LGVSPPPGAV	LVLHSLPLEF	PLAMAFAEQL	LSWKSSESEG	KSEDEPDSIP	TSVLLHVVEL	LGFLWTTDM
2961	AACVKELVFH	LLAELLRTVH	TLEQRKHPAG	LSSSIALQLN	PCLAMLALQ	SELHKLYDEE	TQGWVSSSTC	GGSGAAAVGD
3041	QGRFSTYFHA	LMEGCLAVAE	VTLPNTISVT	ASGVTSTTTP	NLSDSSSSSS	SSPGQTPQSP	SLLSKRRKVK	MKREKASSSN
3121	KRQSSRAFDA	DSTVLSIGGS	KPEDMLWFHR	ALTLIIILRH	LTKKDPQGLG	VTSDAIADAC	QALVGPHTAS	RLLVISGPT
3201	HLEAVVRGA	IRKACNAHGG	VFKDEIYIPL	QDEDPKRPK	KAEGGDSKVE	SEKLLGFPSV	DSLEGSTSSS	LAPAMISAS
3281	ASTSQASVCS	SQCVSQTASD	LSVDPPLPSGL	ELPVPPVLE	PHVSSQESL	DISLCSGTSL	GSLGSLGEPL	DNPETASVSD
3361	VGSMTVTSL	DTQPLTTRPI	KGFVAVEIRS	RAKIEKVRAS	LFNNNDLIGL	SSLDGEEELM	EMSTEEILT	SVVNQSLFDT
3441	QGSFGLEDYF	NDKSIKGEKL	VPGAREVLTE	IFKSCAHSEQ	TLSLTPAKPI	RVSDIYLSKE	QINSQTPGNL	LHLFFTNRVP
3521	PKKVLEDQLT	QILRKYGVPK	PKLDSKSKYSK	AGKEQHPVKV	VSTKRPVTKP	PAKDKAVLSS	LRALTSEKPK	TVKPKSPEKS
3601	KPDEKDPKES	PTKKQEVPEE	KYLTLEGFHK	FVIDRAKQDI	RSVWRAILSC	GVDLHFERCA	CIDVRHAQKA	SRKWALEMDV
3681	ALVQYINRLC	RHLAITPARL	HPHEVYLDPA	DATDPRMACL	SNVPESLRL	RFALLQSLNT	TLETFFLPLV	ELRQTPMYAH
3761	SIAALLKEAK	GLIFYDTK	VT VNNRVLNATV	QR TADHAAP	ITLDPLETVG	GEIRASENSY	FCQAARQLAS	VPSSQLCVKL
3841	ASGGDPTYAF	NIRFTGEEVH	GTSGSFRHFL	WQVCKELQSS	LSLSSLLCPS	SAVNKNKGKY	ILTPSPITYG	EEQLLHLFLGQ
3921	LLGTAIRADV	PPLDPLPSF	WKTTLVGEPLD	PDQDLQEADI	LTNYVKKKFE	SINDESELEA	LCAEIASQHL	ATDPEGPKP
4001	CCRFTYLTMT	GEEVELCSR	RHIPVAWENK	DIYAAAIRSL	RLRELQNMEC	VTAVRAGLGS	IIPLQLLTTL	SPLMELRTEC
4081	GLPYVNLFFL	KAHTMYQVGL	METDQHIELF	WGALETFTQE	ELCKFIKFC	NQERIFFTCP	CKDGGPDTAH	VPPYPMKIAP
4161	PDGTAGPPDS	RYIRVETCMF	MIKLPQYSSL	EIMLEKLRC	IHYREDPLSG			



5.311 "ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit F6 [Rattus norvegicus]"

Protein Accession	gij16758388	
Mean Expression Ratio	1.10	
Median Expression Ratio	1.10	
Credible Interval	(1.00, 1.20)	
Associated Peptides	11	
Associated Spectra	72	
Coverage	0.556	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.998	1.10
Avg..iTRAQ.Ratio....116.114.	0.997	1.05
Avg..iTRAQ.Ratio....117.114.	1.24	1.24

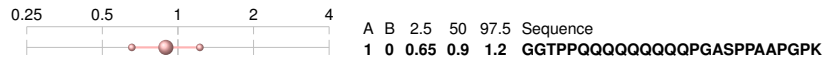
1 MTVQRIFRLS SVLRSVAVSVH LRRNIGVTAV AFNKELDPVQ KLFLDKIREY KAKRLASGGP VDTGPYQQE VDRELFK LKQ
81 MYGKGEMDKF PTFNFEDPKF EVLDPKQS



5.312 glutaminase [Rattus norvegicus]

Protein Accession	gij6980954	
Mean Expression Ratio	0.912	
Median Expression Ratio	0.91	
Credible Interval	(0.676, 1.23)	
Associated Peptides	1	
Associated Spectra	1	

Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	2.22
Avg..iTRAQ.Ratio....116.114.	0.288
Avg..iTRAQ.Ratio....117.114.	0.98



5.313 actin alpha cardiac 1 [Rattus norvegicus]

Protein Accession	gi 77993370
Mean Expression Ratio	0.91
Median Expression Ratio	0.91
Credible Interval	(0.813, 1.01)
Associated Peptides	12
Associated Spectra	46
Coverage	0.507
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	0.814
Avg..iTRAQ.Ratio....117.114.	1.02

```

1   MCDDEETAL VCDNGSGLVK AGFAGDDAPR AVFPSIVGRP RHQGMVGMG QDSYVGDEA QSKRGILTLK YPIEHGIITN
81  WDDMEKIWHH TFYNELRVAP EEHPTLLTEA PLNPKANREK MTQIMFETFN VPAMYVAIQA VLSLYASGR TGI VLDSDGDG
161 VTHNVPIYEG YALPHAIMRL DLAGRDLTDY LMKILTERGY SFVTTAEDEI VRDIKEKLCY VALDFENEMA TAASSSSLEK
241 SYELPDGQVI TIGNERFRCP ETLFQPSFIG MESAGIHETT YNSIMKCDID IRKDLYANNV LSGGTTMYPG IADHMQKEIT
321 ALAPSTMKIK IIAPPERKYS VWIGGSILAS LSTFQQMWIS KQEYDEAGPS IVHRKCF
    
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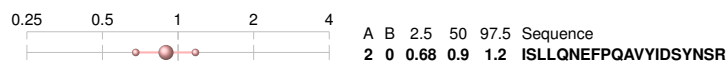


5.314 nuclear protein E3-3 isoform a [Rattus norvegicus]

Protein Accession	gi 9910324
Mean Expression Ratio	0.914
Median Expression Ratio	0.91
Credible Interval	(0.699, 1.19)
Associated Peptides	1
Associated Spectra	2
Coverage	0.108
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.02
Avg..iTRAQ.Ratio....116.114.	0.791
Avg..iTRAQ.Ratio....117.114.	0.783

```

1   M A T A L G F R C L   Y R T R P A T L G R   Y V D R L W R S P S   R G H R L S P A D D   E L Y Q R T R I S L   L Q N E F P Q A V Y   I D S Y N S H G F T   I N G N R V F G P C
81  A L L P Q T V V Q W   N V G S H Q D I T E   E S F S I F W M L E   P R I E I V V V G T   G N K T E R L H S Q   V L Q A M R Q R G I   A V E I Q D T P N A   C A T F N F L C H E
161 G R V T G A A L I P   P P G E T A L A S S   G Q T T E
  
```



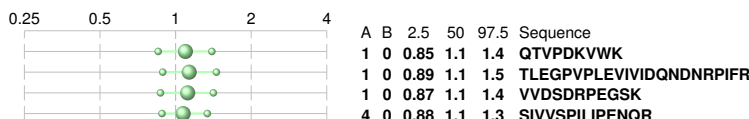
5.315 cadherin 13 [Rattus norvegicus]

Protein Accession	gi 20302073
Mean Expression Ratio	1.10
Median Expression Ratio	1.10
Credible Interval	(0.904, 1.34)
Associated Peptides	4
Associated Spectra	7
Coverage	0.0798
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	1.18
Avg..iTRAQ.Ratio....117.114.	1.24

NHLBI Zile/Grant, Aged Rat

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1      MQPRTPLTLC VLLSQVLLVT SAGDLDCPTG FQQKVLHIHQ PAEFIEDQPV LNLTFSDCKG NKKLHYEVSS PYFKVNSDGT
81     LVAVRNITAV GRTLTVHART PHAEDMAELV IVGGKDIQGS LQDIFKFART SPVPRQKRSI VVSPILIPEN QRQPFPRDVG
161    KVVSDRPEG SKFRLTGKGV DQDPKGTFR I NENTGSVSVT RTLDRETIAT YQLFVETDDA SGRTELEGPVP LEVIVIDQND
241    NRPIFRREGPY IGHVMEGSPT GTVMRMTAF DADDPATDNA LLRYNIRQQT PDKPSPNMFY IDEPEKDIVT VVSPALLDRE
321    TLENPKYELI IEAQDMAGLD VGLTGTATAT IVIDDKNDHS PKFTKKEFQA TVEEGAVGVI VNLTVEDKDD PATGAWRAAY
401    TIINGNPGQS FEIHTNPQTN EGMLS VVKPL DYEISAFHTL LIKVENEDFL VPDVSYGPPS TATVHITVLD VNEGPFVFPD
481    PMMVTKQENI SVGSVLLTVN ATDPDSLQHQ TIRYSVYKDP AGWLSINPIN GTVDTTAVLD RESPPFHNSV YTALFLAIDS
561    GNPPATGTGT LMITLEDVND NAPVIYPTVA EVCDDARNLS VVILGASDKD LHPNTRDPFKF EHKQTVPDK VWKISKINNT
641    HALVSLQLNL NKANYNLPIM VTDSGKPPMT NITDLRVQVC SCKNSKVD CN AAGTLHLSL LLLLFLSLSL LSGL
  
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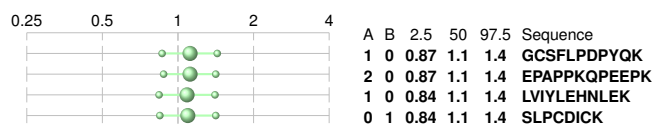


5.316 prosaposin [Rattus norvegicus]

Protein Accession	gij6981424	
Mean Expression Ratio	1.10	
Median Expression Ratio	1.10	
Credible Interval	(0.89, 1.36)	
Associated Peptides	4	
Associated Spectra	5	
Coverage	0.0758	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.18	1.21
Avg..iTRAQ.Ratio....116.114.	1.24	1.11
Avg..iTRAQ.Ratio....117.114.	1.33	0.623

```

1      MYALALLASL LVTALTSPVQ DPKICSGGSA VVCRDVKTAV DCRAVKHCQQ MVWSKPTAKS LPCDICKTVV TEAGNLLKDN
81     ATEEEILHYL EKTCAWIHDS SLSASCKEVV DSYLPVILDM IKGEMSNPGE VCSALNLCQS LQEYLAEQNQ RQLESNKIPE
161    VDLARVVAPF MSNIPLLLYP QDRPRSQQPQ KANEDVCQDC MKLVTDIQT VRTNSSFVQG LVDHVKEDCD RLGPGVSDIC
241    KNYVDQYSEV AVQMMHMGP KEICVMVGF C DEVKRVPMT LVPATEAIKN ILPALELTD YEQDVIQAQN VIFCQVCQLV
321    MRKLSELIIN NATELLIKG LSKACSL LPA PASTKCEVL VTFGPSLLDV LMHEVNPFL CGVISLCSAN PNLVGTLEQP
401    AAIVSALPK EPAPPKQPEE PQQSALRAHV PPQKNGFCE VCCKLVIIYLE HNLEKNSTKE EILAALKEGC SFLPDPYQRQ
481    CDEFVAEYEP LLEILVEVM DPSFVCSKIG VCP SAYS KLLL GTEKCVWGP YWCQNSETA RCNAVDHCKR HVWN
  
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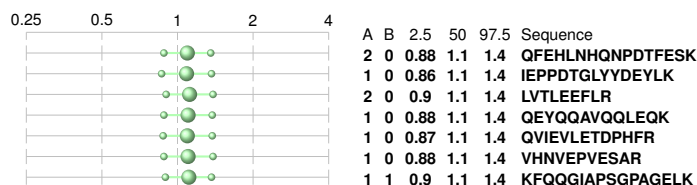


5.317 NEFA precursor [Rattus norvegicus]

Protein Accession	gi 11072106	
Mean Expression Ratio	1.10	
Median Expression Ratio	1.10	
Credible Interval	(0.927, 1.3)	
Associated Peptides	7	
Associated Spectra	10	
Coverage	0.221	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.12	0.868
Avg..iTRAQ.Ratio....116.114.	1.12	1.05
Avg..iTRAQ.Ratio....117.114.	1.27	1.82

```

1      MRWRTIQARY C FLLVPCVLT ALEAVPIDVD KTKVHNVEVPV ESARIEPPDT GLYYDEYLKQ VIEVLETPPH FREKLQKADI
81     EEIRSGRLSQ ELDLVSHKVR TRLDELKRQE VGRRLRLIKA KLDALQDTGM NHHLLKQQFE HLNHQNPDTF ESDLDMLIK
161    AATADLEQYD RTRHEEFKKY EMMKEHERRE YLKTLSSEKR KEEAKFAEM KRKHEDHPKV NHPGSKDQLK EVWEETDGLD
241    PNDFDPKTFE KLHDVNNDGF LDEQELEALF TKELDKVYNP QNAEDDMIEM EEERLRMREH VMNEIDNNKD RLVTLEEFLR
321    ATEKKEFLEP DSWETLDQQQ LFTTEELKEY ESIIAIQESE LKKKADELQK QKEELQRQHD HLEAQKQEVQ QAVQQLEQKK
401    FQQGIAPSGP AGELFFEPHT
  
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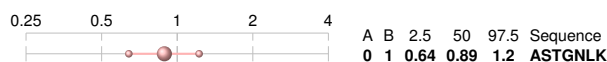
5.318 "tumor necrosis factor (ligand) superfamily, member 10 [Rattus norvegicus]"

Protein Accession	gi 21728412
Mean Expression Ratio	0.909
Median Expression Ratio	0.911
Credible Interval	(0.672, 1.21)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0244
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.616
Avg..iTRAQ.Ratio....116.114.	0.587

Avg..iTRAQ.Ratio....117.114. 0.546

```

1      MASTGNLGP SFSQHFTMTV ICIVLLQVLL QALTVAVTYM YFNNEVKQLQ DNYSKIGLAC FSKEDGDFWD STDEGILNRP
81     CLQVKRQLYQ LIEEVTLRTF EKTISTVPEK QLSTPPLPRG RRPQRVAHI TGITRRSNLA LIPISKDGKT LGQKIETWES
161    SRRGHSFLNH VHLRNGELVI QEEGLYIYS QTYRRFKEAK EASKTVSKDG GRIKQMVQYI YKYTSYPDPI LLMKSARNSC
241    WSREAEYGLY SIYQGGLFEL KENDRIFVSV TNEHMLDLDH EASFFGA
    
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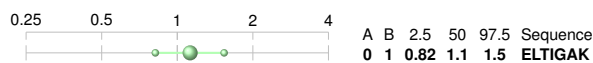


5.319 S100 calcium binding protein A6 (calcylin) [Rattus norvegicus]

Protein Accession	gi 16758986
Mean Expression Ratio	1.10
Median Expression Ratio	1.10
Credible Interval	(0.813, 1.48)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0787
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.19
Avg..iTRAQ.Ratio....116.114.	1.10
Avg..iTRAQ.Ratio....117.114.	1.45

```

1      MACPLDQAIG LLVAIFHKYS GKEGDKHTLS KKEKELIQK ELTIGAKLQD AEIARLMDDL DRNKDQEVNF QEYVAFLGAL
81     ALIYNEALK
    
```



5.320 phospholamban [Rattus norvegicus]

Protein Accession	gi 12083675
Mean Expression Ratio	0.91
Median Expression Ratio	0.911

Credible Interval	(0.735, 1.13)
Associated Peptides	1
Associated Spectra	7
Coverage	0.212
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.815
Avg..iTRAQ.Ratio....116.114.	0.894
Avg..iTRAQ.Ratio....117.114.	0.964

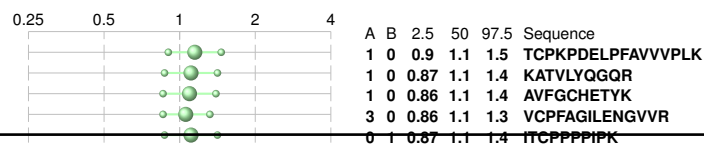
1 MEKVQYLTRS AIRR**ASTIEM** P**QQA**RQNLQN LFINFCLILI CLLLICIVM LL



5.321 apolipoprotein H [Rattus norvegicus]

Protein Accession	gij57528174	
Mean Expression Ratio	1.10	
Median Expression Ratio	1.10	
Credible Interval	(0.905, 1.34)	
Associated Peptides	5	
Associated Spectra	7	
Coverage	0.177	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.18	0.998
Avg..iTRAQ.Ratio....116.114.	1.17	1.22
Avg..iTRAQ.Ratio....117.114.	1.14	1.07

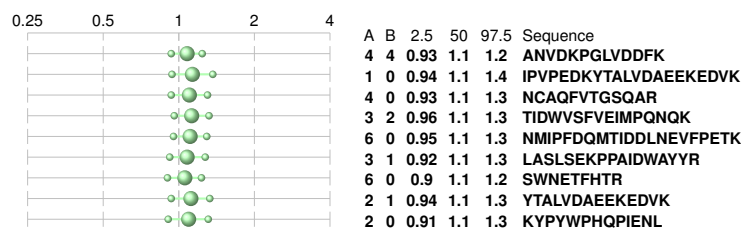
1 MISPALIFFS AFLCHVAIAG R**TC**PK**P**DEL**P** FAVVV**PL**KTF YDPGEQIVYS CKPGYVSRGG MRRFTCP**L**TG MWPINTLKCI
 81 PR**V**CP**F**AGIL EN**G**VVR**Y**TFE EYPNTIGFAC NPGYYLN**G**TS SSKCTEEGKW SPELPVCAR I **T**CP**P**PP**I**PKF AALKEYKTSV
 161 GNSSFYQDTV VFKCLPHFAM FGNDTVTCTA HGNWTQL**P**EC REVKCPF**P**SR PDNGFVN**P**A KPVLSYKDKA V**F**GC**H**ET**Y**KL
 241 DGPEEVE**C**TK TGNWSAL**P**SC KASCKLSV**K** AT**V**LY**Q**Q**R**V KI**Q**D**Q**FK**N**GM MHGDKV**H**FYC KNKEK**K**CS**Y**T EEA**Q**CID**G**TI
 321 EIPK**C**F**K**EH**S** SLAF**W**KT**D**AS D**V**TP**C**



5.322 "ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit d [Rattus norvegicus]"

Protein Accession	gi 9506411	
Mean Expression Ratio	1.10	
Median Expression Ratio	1.10	
Credible Interval	(0.986, 1.22)	
Associated Peptides	9	
Associated Spectra	39	
Coverage	0.758	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.947	1.32
Avg..iTRAQ.Ratio....116.114.	1.14	1.08
Avg..iTRAQ.Ratio....117.114.	1.27	0.99

1 MAGRKLALKT IDWVSFVEIM PQNQKAIGNA LKSWNETFHT RLASLSEKPP AIDWAYYRAN VDKPGLVDDF KNKYNALKLP
 81 VPEDKYTALV DAEKEDVKV CAQFVTGSQA RVREYEQLE KIKNMIPFDQ MTIDDLNEVF PETKLDKRKY PYWPHQPIEN
 161 L

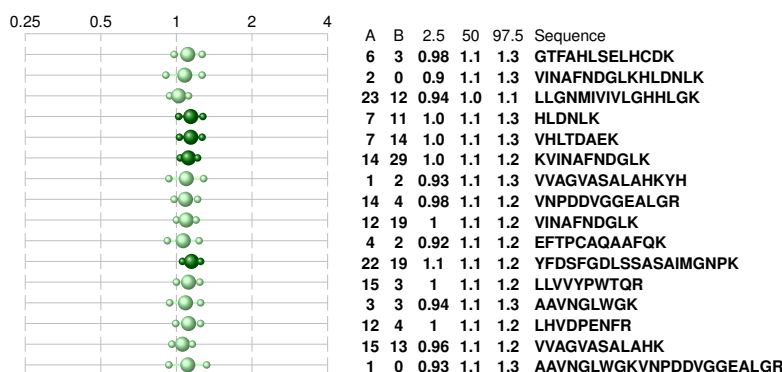


5.323 hemoglobin beta chain complex [Rattus norvegicus]

Protein Accession	gi 17985949	
Mean Expression Ratio	1.10	
Median Expression Ratio	1.10	
Credible Interval	(1.03, 1.16)	
Associated Peptides	16	
Associated Spectra	296	
Coverage	0.952	

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.31	1.75
Avg..iTRAQ.Ratio....116.114.	1.22	1.08
Avg..iTRAQ.Ratio....117.114.	0.814	0.579

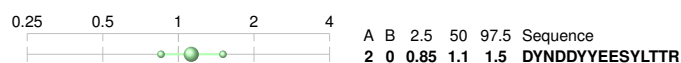
1 MVHLTDAEKA AVNGLWGVN PDDVGGGALG RLLVVPWTQ RYFDSFGDLS SASAIMGNPK VKAHGKKVIN AFNDGLKHL D
 81 NLKGTFAHLS ELHCCKLHVD PENFRLNGM IVIVLGHHLG KEFTPCAQAA PQKVVAGVAS ALAHKYH



5.324 emerlin [Rattus norvegicus]

Protein Accession	gij 6978805
Mean Expression Ratio	1.10
Median Expression Ratio	1.10
Credible Interval	(0.838, 1.44)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0577
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.24
Avg..iTRAQ.Ratio....116.114.	1.42
Avg..iTRAQ.Ratio....117.114.	1.45

1 MDDYAVLSDT ELAAVLRQYN IPHGPI LGST RKLVEKKIFE YETQRRRLSP PSSSSSSFSY RFSDDLDSASV DSDMYDLPKK
 81 EDALLYQSKD YNDYYEESY LTRRTYGEPE SVGMSKSFRR PGTSLVDADD TFHHQVRDDI FSSSEEGKD RERP IYGRDS
 161 AYQSIAEYRP ISNVSRSSLG LSYYPRSSTS SVSSSSSSPS SWLTRRAIRP EKQAPTAALG QDRQVPLWGQ LLLFLAFATF
 241 LLFVYYSIQ A QEGNPFWMDF

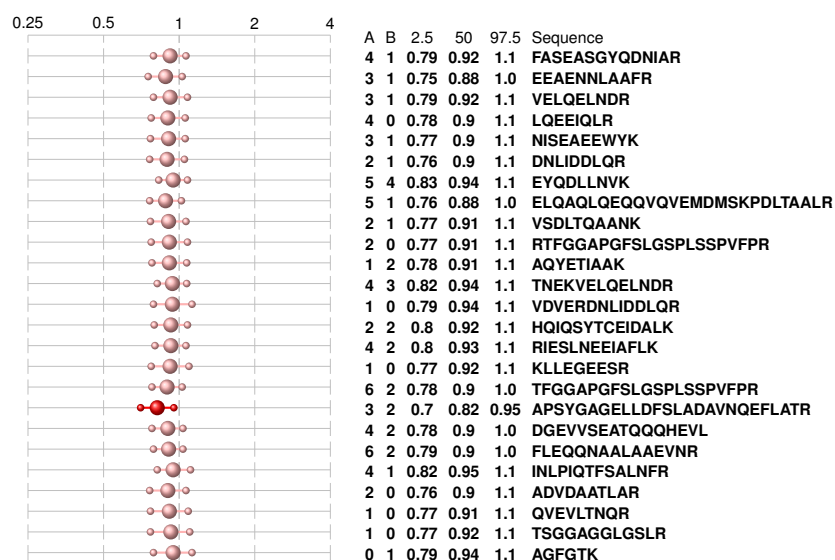


5.325 desmin [Rattus norvegicus]

Protein Accession	gij11968118	
Mean Expression Ratio	0.912	
Median Expression Ratio	0.912	
Credible Interval	(0.85, 0.976)	
Associated Peptides	25	
Associated Spectra	103	
Coverage	0.62	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.897	1.10
Avg..iTRAQ.Ratio....116.114.	0.825	0.788
Avg..iTRAQ.Ratio....117.114.	1.08	0.814

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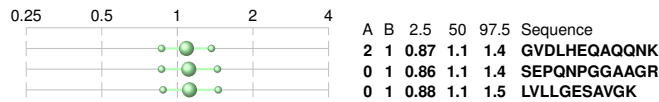
1  MSQAYSSSQR VSSYRRTFGG APGFSLGSPL SSPVFPRAGF GTKGSSSSVT SRVYQVSRTS GGAGGLGSLR ASRLGTTRAP
81  SYGAGELLDL SLADAVNQEF LATRTNEKVE LQELNDFAN YFEKVRFLEQ QNAALAAEVN RLKGREPTRV AELYEEMRE
161 LRRQVEVLTN QRARVDVERD NLIDDLQRLK AKLQEEIQLR EEAENNLAAF RADVDAATLA RIDLERIES LNEEIAFLK
241 VHEEEIRLQ AQLQEQVQV EMDMSKPDLT AALDIRAQY ETIAAKNISE AEEWYKSKVS DLTQAANKNN DALRQAKQEM
321 MEYRHQIQSY TCEIDALKGT NDSLMRQMR LEDRFASEAS GYQDNIALE EEIRHLKDEM ARHLREYQDL LNVFMALDVE
401 IATYRKLLEG EESRINLPQ TFSALNFRET SPEQRGSEVH TKKTVMIKTI ETRDGEVVSE ATQQQHEVL
    
```



5.326 "RAB5B, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gij121583768	
Mean Expression Ratio	1.10	
Median Expression Ratio	1.10	
Credible Interval	(0.888, 1.37)	
Associated Peptides	3	
Associated Spectra	5	
Coverage	0.163	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.10	1.12
Avg..iTRAQ.Ratio....116.114.	1.24	1.06
Avg..iTRAQ.Ratio....117.114.	1.16	1.29

1 MTSRSTARPN GQPQASKICQ FKLVLLGESA VGFSSLVLRV VKGQFHEYQE STIGAFLTQ SVCLDDTTVK FEIWDTAGQE
 81 RYHSLAPMY RGAQAIVVY DITNQETTFAR AKTWVKELQR QASPSIVIAL AGNKADLANK RMVEYEEAQA YADDNSLLFM
 161 ETSAKTAMNV NDLFLAIKAK LPKSEPQNP GGAAGRSRQVD LHEQAQQNFS QCCSN

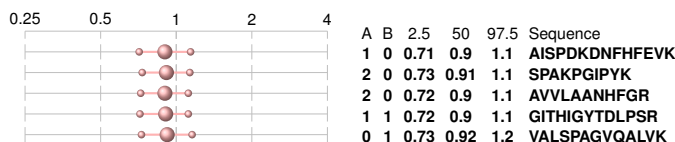


5.327 nicotinamide nucleotide transhydrogenase [Rattus norvegicus]

Protein Accession	gij61557127	
Mean Expression Ratio	0.912	
Median Expression Ratio	0.913	
Credible Interval	(0.755, 1.09)	
Associated Peptides	5	
Associated Spectra	8	
Coverage	0.0562	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.903	0.904
Avg..iTRAQ.Ratio....116.114.	0.895	0.831
Avg..iTRAQ.Ratio....117.114.	0.88	0.805

```

1    MAHLLKTVVT  GCLCPSVSNL  GSCKVLPGKK  DFLRTRFRTHQ  ALWCKSPAKP  GIPYKQLTVG  VPKEIFQNEK  RVALSPAGVQ
81   ALVKQGFNVV  VESGAGEASK  FPDDLYRAAG  AQIQGTKEVL  ASDLVVKVRA  PMVNP TLGAH  EADFLKPSGT  LISFIYPAQN
161  PDLLNKLSEK  KTTVLAMDQV  PRVTIAQGYD  ALSSMANISG  YKAVVLAANH  FGRFFFTGQIT  AAGKVPPAKI  LIVGGGVAGL
241  ASAGAAKSMG  AVVRGFDTRA  AALEQFKSLG  AEPLEVDLKE  SGEQGGYAK  EMSKEFIEAE  MKLFAQQCKE  VDILISTALI
321  PGKKAPVLFK  KEMIESMKEG  SVVVDLAAEA  GGNFETTKPG  ELYVHKGITH  IGYTDLPSRM  ATQASTLYSN  NITKLLKATS
401  PDKDNFHFV  KDDDFDFGMS  HVIRGTVMK  DGNVIFPAPT  PKNIPKEAPA  KQKTVAELEA  EKAGTVSMYT  KTLRTASVYS
481  AGLTGMLGLG  IVAPNLAFSQ  MVTTFGLAGI  IGYHTVWVGT  PALHSPMSV  TNAISGLTAV  GGLALMGGHF  YPSTTSQSLA
561  ALATFISSVN  IAGGFLVTQR  MLDMFKRPTD  PPEYNYLYLL  PGGTFVGGYL  AALYGGYNI  EIMYLGSGLC  CVGALGGLST
641  QGTARLGNAL  GMIGVAGGLA  ATLGGLKPPD  QLLAQMSGAM  AMGGTIGLAI  AKRIQISDLP  QLVAAFHSLV  GLAAVLTOMA
721  EYIVEYPHFA  MDATSNFTKI  VAYIGTYIGG  VTFSGSLVAY  GKLGILKSA  PLLLPGRHAL  NAGLLAASVG  GIIPFMADPS
801  FTTGIMCLGS  VSALSTLMGV  TLTAAGGAD  MPVVITVLS  YSGWALCAEG  FLLNNLLTI  VGALIGSSGA  ILSYIMCVAM
881  NRSLANVILG  GYGTSTAGG  KPMEISGTH  EINLDNAVEM  IREANSIVIT  PGYGLCAAKA  QYP IADLVKM  LTEQGKRVF
961  GIHPVAGRMP  GQLNVLLAEA  GVPYDIVLEM  DEINSDFPDT  DLVLVIGAND  TVNSAAQEDP  NSI IAGMPVL  EVWKSQVIV
1041 MKRSLGVGYA  AVDNPIFYKP  NTAMLLGDAK  KTCDALQAKV  RESYQK
    
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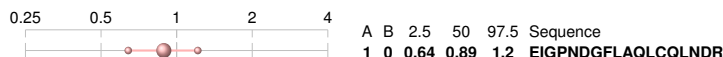


5.328 PREDICTED: similar to Dual specificity protein phosphatase 3 (T-DSP11) [Rattus norvegicus]

Protein Accession	gij 109491956
Mean Expression Ratio	0.91
Median Expression Ratio	0.913
Credible Interval	(0.673, 1.22)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0664
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.924
Avg..iTRAQ.Ratio....116.114.	0.68
Avg..iTRAQ.Ratio....117.114.	0.624

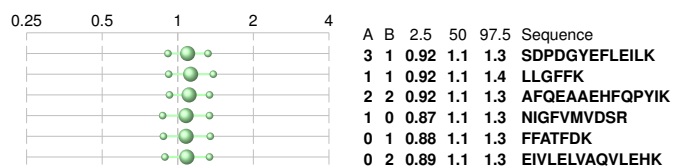
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1    MCGGTTQCLY  ALCYDDPIK  PAPGSCGAWA  GRACPLSCVA  RRQLPSPSP  ASGAGRGGSR  LGSPAPLTRL  LPLARSCPGM
81   QGPAAAMSGS  FELSVQDLN  LLSDGSGCYS  LPSQPCNEVI  PRVYVGNASV  AQDITQLQKL  GITHVLNAEE  GRSEMHVNTS
161  ASFYKDTGIT  YMGIKANDTQ  EFNLSAYFER  AADFIDQALA  HKNGRVLVHC  REGYSRSPTL  VIAYLMLRQK  MDVRSALSTV
241  RQNR EIGPND  GFLAQLCQLN  DLAEEGKVK  L
    
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5.329 calsequestrin 2 [Rattus norvegicus]

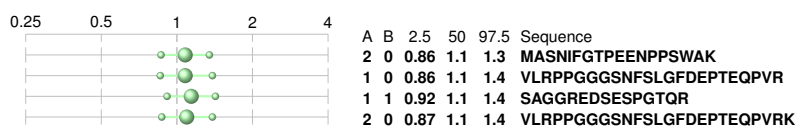
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Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.94, 1.28)	
Associated Peptides	6	
Associated Spectra	14	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	1.04
Avg..iTRAQ.Ratio....116.114.	1.00	1.01
Avg..iTRAQ.Ratio....117.114.	1.23	1.17



5.330 hematological and neurological expressed sequence 1 [Rattus norvegicus]

Protein Accession	gi 54312084	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.906, 1.33)	
Associated Peptides	4	
Associated Spectra	7	
Coverage	0.389	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.38
Avg..iTRAQ.Ratio....116.114.	1.03	1.66
Avg..iTRAQ.Ratio....117.114.	1.48	1.02

1 MTTTTFKGV DPNSRNSSRV LRPPGGGSNF SLGFDEPTEQ PVRI¹NKMASN IFGTPEENPP SWAKSAGGRE DSESPGTQ²RS
 81 NSSEASSGDF LDLKGESDVH ENVDTFQAS LAQVEEKVVP AAPVPSVPAP APAPSRRNPP G GKSSLVLG



5.331 PREDICTED: similar to peptide deformylase-like protein [Rattus norvegicus]

Protein Accession	gij109508083
Mean Expression Ratio	0.914
Median Expression Ratio	0.915
Credible Interval	(0.68, 1.22)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0394
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.821
Avg..iTRAQ.Ratio....116.114.	0.78
Avg..iTRAQ.Ratio....117.114.	0.585

1 MRELRF¹PASL ALAGGRAAAF SCTMALLGRL LLP²AWVTLSR GQSCSSASL EGAARTRSY³W RYLRLRVGA P⁴PPYTRVCO
 81 VGDPVLR⁵TVA APVEPKQLAG PELQR LVEQL VQVMRRGCV GLSAPQLGVP LQVLVLEFPD RLFRAFSPRL RELRQME⁶FPF
 161 LRVLVNPSLR VLDSRLVTFP EGCESVAGFL ACVPRFQAVQ ISGLDPKGE⁷P VVWSASGWTA RIIQHMDHL HGCLFIDKMD
 241 SGTFTNLHWM EVND



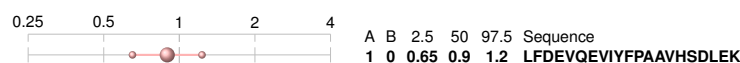
5.332 secernin 3 [Rattus norvegicus]

Protein Accession	gij61557143
Mean Expression Ratio	0.915

Median Expression Ratio	0.915
Credible Interval	(0.678, 1.23)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0691
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.748
Avg..iTRAQ.Ratio....116.114.	0.81
Avg..iTRAQ.Ratio....117.114.	0.786

```

1      MQPYSCDTFV ALPPATVGNR VIFGKNSDR L FDEVQEVYIF PAAVHSDLEK RLKCTYIEVD QVPETYAVVL SRPAWLWGAE
81     MGANEHGVC I GNEAIWGRED ISKEEALLGM DLVRLGLERA DTAEKALNVI VDLLGKYGG GNCAEGEEFS YNSFLIADR
161    NEAWILETSG KFWAAEKVQG VRNISNQFSI TTKIDREHPD MRNYAKQRGW WDGKEEFDA AAYSYTDTAT MMTSPSRVCO
241    GHKLLNKHG NITYETMVEI LRDRPSGINM KGEFLTAS M VSILPQDPSL PCIHLLTGT P HPER
  
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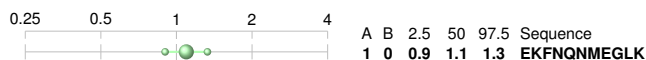


5.333 apolipoprotein A-IV [Rattus norvegicus]

Protein Accession	gi 8392909	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.969, 1.23)	
Associated Peptides	14	
Associated Spectra	24	
Coverage	0.448	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.13	1.02
Avg..iTRAQ.Ratio....116.114.	1.20	0.873
Avg..iTRAQ.Ratio....117.114.	1.17	1.05

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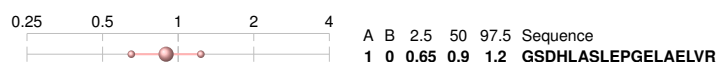
1      MFLKAVVLT V ALVAITGTQA EVTSDQVANV MWDFYFTQLSN NAKEAVEQLQ K DVTQQLNT LPQDKLGNIN TYADDLQNKI
81     VFFRVQLSGH LTKETERVRE EIQKELEDLR ANMMPHANKV SQMPGDNVQK LQEHLRYPAT DLQAQINAQT QDMRQLTPY
161    IQRMQTTIQD NVENLQSSMV PFANELKEKF NQNMEGLK GQ LTPRANELKA TIDQNLLEDLR SR LAPLAEGV QEKLNHQMEG
241    LAFQMKNNAE ELHTK VSTNI DQLQK NLAPL VEDVQSKLKG NTEGLQKSLE DLNKQLDQQV EVFRRAVEPL GDRFNMALVQ
321    QMEKFRQQLG SDSGDVESH L SFLEK NLREK VSSF MSTLQK KGSPDQPLAL PLPEQVQEQV QEQVQPKPLE S
  
```





5.334 PREDICTED: similar to N-acetylneuraminic acid synthase (sialic acid synthase) [Rattus norvegicus]

Protein Accession	gij109474889
Mean Expression Ratio	0.916
Median Expression Ratio	0.916
Credible Interval	(0.685, 1.25)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.846
Avg..iTRAQ.Ratio....116.114.	0.846
Avg..iTRAQ.Ratio....117.114.	0.652



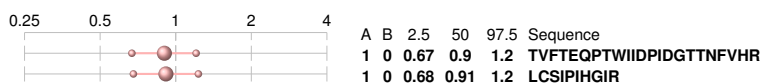
5.335 Inositol (myo)-1(or 4)-monophosphatase 1 [Rattus norvegicus]

Protein Accession	gij14091736
Mean Expression Ratio	0.915
Median Expression Ratio	0.916
Credible Interval	(0.701, 1.19)
Associated Peptides	2

Associated Spectra	2
Coverage	0.119
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	0.795
Avg..iTRAQ.Ratio....117.114.	0.734

```

1      MADPWQECMD YAVILARQAG EMIREALKNK MDVMIKSSPA DLVTVTDQKV EKMLMSSIKE KYPYHSFIGE ESVASGEKTV
81     FTEQPTWIID PIDGTTNFVH RPFVAVSIG FVFNKEMEFV VVYSCVEDKM YTGRKGGKGF CNGQKLRVSQ QEDITKSLLV
161    TELGSSRRKPE TLRIVLSNME RLCSIPIHGI RSVGTAAVNM CLVATGGADA YYEMGIHCWD MAGAGIIVIE AGGVLLDVTG
241    GPFDLMSRRI IAASNIALAE RIAKELEIIP LQRDDDES
    
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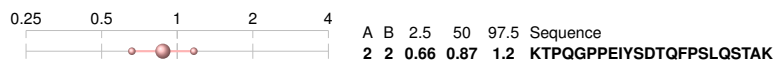


5.336 PREDICTED: similar to carnitine deficiency-associated gene expressed in ventricle 3 isoform CDV3B [

Protein Accession	gij62641098
Mean Expression Ratio	0.917
Median Expression Ratio	0.916
Credible Interval	(0.697, 1.21)
Associated Peptides	1
Associated Spectra	4
Coverage	0.145
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.583
Avg..iTRAQ.Ratio....116.114.	0.94
Avg..iTRAQ.Ratio....117.114.	0.729

```

1      MIEPEKKDPS AHDNQYTKYT EQRKNIKNLQ GSGAEKSSGP WNKTALVQAP PAPVTVTETP EPAMPSGVYR PPGARLTTTR
81     KTPQGPPPEIY SDTQFPSSLQS TAKHVESRNR DKEMEKSEFV VRHKNRVREE VSKNQALKLE LDNQYAVLEN QKYSPTQYS
    
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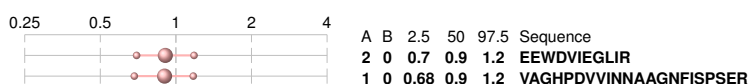


5.337 "2,4-dienoyl CoA reductase 1, mitochondrial [Rattus norvegicus]"

Protein Accession	gij17105350
Mean Expression Ratio	0.916
Median Expression Ratio	0.916
Credible Interval	(0.715, 1.17)
Associated Peptides	2
Associated Spectra	3
Coverage	0.0985
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.985
Avg..iTRAQ.Ratio....116.114.	0.899
Avg..iTRAQ.Ratio....117.114.	0.786

```

1      MALLARAFFA GVSRLPCDPG P QKFFSFGTK TLYQSIDAPQ SKFFPPILKP MLPPNAFQ GK VAFITGGGTG LGKAMTTFRS
81     SLGAQCVIAS RNIDVLKATA EEITSKTGNK VYAIRCDVRD PDMVHNTVLE LIK VAGHPDV VINNAAGNFI SPSERLSPNG
161    WRTITDIVLN GTAYVTIEIG KQLIKAQKGV AFLAITTIYA ESGSGFVMPS SSAKSGVEAM NKSLAAEWGR YGMRFNIIQP
241    GPIKTKGAFS RLDPTGKFEK DMIERIPCGR LGTVEELANL ATFLCSDYAS WINGAVIRFD GGEEVFLSGE FNSLKKVTK E
321    EWDVIEGLIR KTKGS
  
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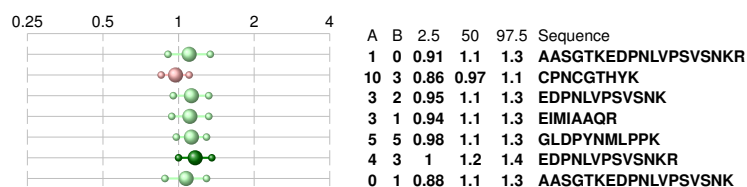


5.338 cytochrome c oxidase subunit Vb [Rattus norvegicus]

Protein Accession	gij16758362	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.978, 1.22)	
Associated Peptides	7	
Associated Spectra	41	
Coverage	0.364	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.23
Avg..iTRAQ.Ratio....116.114.	1.06	1.22
Avg..iTRAQ.Ratio....117.114.	1.08	0.822

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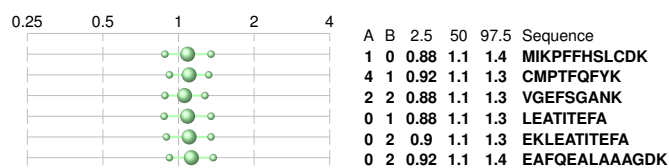
1      MASRLLRGVG ALAAQALRAH GPRGVAATRS MASGGGVPTD EEQATGLER E IMIAAQRGLD PYNMLPPKAA SGTKEDPNLV
81     PSVSNKRIVG CICEEDNCTV IWFWLHQGES QR CPNCGTHY KLVVPQMVH
  
```



5.339 thioredoxin [Rattus norvegicus]

Protein Accession	gij16758644	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.938, 1.27)	
Associated Peptides	6	
Associated Spectra	15	
Coverage	0.514	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.06	1.03
Avg..iTRAQ.Ratio....116.114.	1.11	1.03
Avg..iTRAQ.Ratio....117.114.	1.19	0.942

1 MVKLIESKEA FQEALAAAGD KLVVVDFSAT WCGPCKMIKP FFHSLCDKYS NVVFLEVDVD DCQDVAADCE VKCMPTFQFY
81 KKGQKVGEFS GANKEKLEAT ITEFA



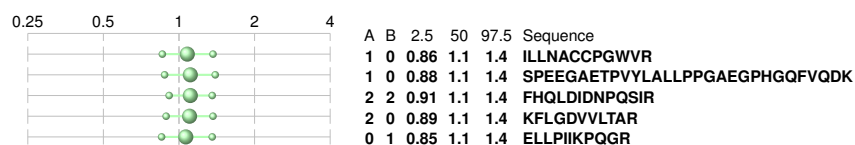
5.340 carbonyl reductase [Rattus norvegicus]

Protein Accession	gij9506467	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.912, 1.3)	

Associated Peptides	5	
Associated Spectra	9	
Coverage	0.278	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.27	1.02
Avg..iTRAQ.Ratio....116.114.	1.36	0.728
Avg..iTRAQ.Ratio....117.114.	0.97	1.40

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1      MSSDRPVALV TGANKGIGFA IVRDLCKFL GDVVLTADE SRGHEAVKQL QTEGLSPRFH QLDIDNPOSI RALRDFLLQE
81     YGGLNVLVNN AGIAFKVVDP TPFHIQAEVT MKNFFFGTQD VCKELLPIIK POGRVVNVSS SVSLRALKSC SPELQQKFRS
161    ETITEEELVG LMNKFIEDAK KGVHAKEGWP NSAYGVTKIG VTVLSRIYAR KLNEERREDK ILLNACCPGW VRTDMAGPKA
241    TKSPEEGAET PVYLLALLPPG AEGPHGQFVQ DRKVEPW
  
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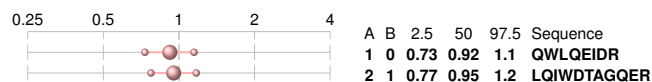


5.341 similar to Ras-related protein Rab-1B [Rattus norvegicus]

Protein Accession	gi 56605816	
Mean Expression Ratio	0.918	
Median Expression Ratio	0.917	
Credible Interval	(0.779, 1.08)	
Associated Peptides	5	
Associated Spectra	13	
Coverage	0.333	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.934	1.11
Avg..iTRAQ.Ratio....116.114.	0.89	0.575
Avg..iTRAQ.Ratio....117.114.	1.01	1.09

```

1      MNPEYDYLK LLLIGDSGVG KSCLLRFAD DTYTESYIST IGVDFKIRTI ELDGKTIKIQ IWDTAGQERF RTITSSYRQ
81     AHGIIVVYDV TDQESYANVK QWLQEIDRYA SENVNKLLVG NKSDLTTKKV VDNTTAKQFA DSLGVPFLET SAKNATNVEQ
161    AFMTMAAEIK KRMPGAASG GERPNLKIDS TPKSASGGC C
  
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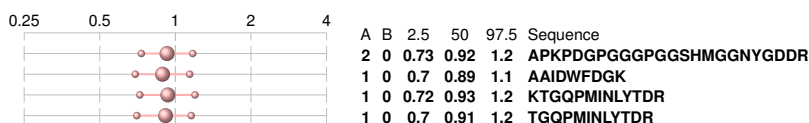


5.342 fusion (involved in t(12;16) in malignant liposarcoma) (predicted) [Rattus norvegicus]

Protein Accession	gij58865844
Mean Expression Ratio	0.917
Median Expression Ratio	0.917
Credible Interval	(0.745, 1.13)
Associated Peptides	4
Associated Spectra	5
Coverage	0.0888
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.894
Avg..iTRAQ.Ratio....116.114.	0.977
Avg..iTRAQ.Ratio....117.114.	0.89

```

1      MASNDYTQQA  TQSYGAYPTQ  PGQGYSQSN  QPYGQSYSY  YGQADTSGY  GQSSYGSSYG  QTQNTGYGTQ  SAPQGYGSTG
81     GYGSSQSSQS  SYGQSSSYPG  YGQQPAPSS  SGSYGGSSQS  SSYGQPQSGG  YGQQSGYGGQ  QQSYGQQQSS  YNPFQGYGQQ
161    NQYNSSSSGGG  GGGGGNYGQ  DQSSMSGGG  GGGYGNQDS  GGGGGYGGG  QQDRGGRGRG  GGGYNRSSG  GYEPGRGGG
241    RGRGGMGGG  DRGGFNKFG  PRDQGRHDS  EQDNSDNNTI  FVQGLGENVT  IESVADYFKQ  IGIKTNKKT  GQPMINLYTD
321    RETGKLKGEA  TVSFDDPPSA  KAAIDWFDGK  EFSGNPIKVS  FATRRADFNR  GGGNGRGGRG  RGGPMGRGGY  GGGSGGGGR
401    GGFPSGGGG  GGQQRAGDWK  CPNPTCENMN  FSWRSECNCQ  KAPKPDGPGG  GPGGSHMGGN  YGDDRGRGRG  YDRGGYRGRG
481    GDRGGFRGGR  GGGDRGGFGP  GKMSRGEHR  QDRRERP Y
    
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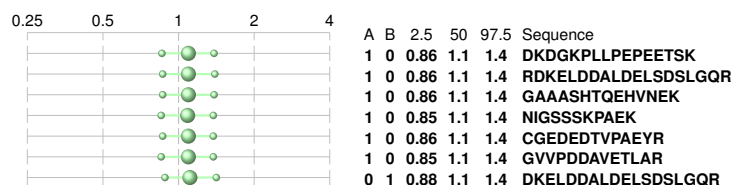
5.343 calpastatin isoform a [Rattus norvegicus]

Protein Accession	gij76159282
Mean Expression Ratio	1.09
Median Expression Ratio	1.09
Credible Interval	(0.901, 1.32)
Associated Peptides	7
Associated Spectra	7

Coverage	0.121	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.20	1.15
Avg..iTRAQ.Ratio....116.114.	1.06	0.839
Avg..iTRAQ.Ratio....117.114.	1.25	2.13

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1      MSRPGPKPAA  SSRPRRGAAA  SHTOEHVNEK  NIGSSSKPAE  KKSDEVTAS  SAATGTSPRM  STGAKAVKI  ESEKSQSSEP
81     FVIHEKKPKG  KPKEGSEPQT  LPKHASDTGS  KHAKKEKALS  RSNEQIVSEK  SSESKTKFQD  APSADGESVA  GGVTVATASD
161    KVVVKKKEKK  SLTPTLPMES  TLNKLSDKSG  VNAALDDLID  TLGCEEDTNK  DDDPPYTGPPV  LDPMDSTYLE  ALGIKEGTIP
241    PEYRKLLEKN  EAITGLPLDS  PKPMGIDHAI  DALSSDFTCS  SPTGKQTEKE  KSTGESSKAQ  SAGVTRSAPV  PQEKRRVEE
321    EVMNDQALQA  LSDSLGTRQP  DPQSHLRQAK  QVKEAKAKEE  RQEKCGEDED  TVPAEYRLKP  AKDKDGKPLL  PEPEETSICL
401    SESELIGELS  ADFVQPTYQE  KPSMPAAKIK  KGVVDDAVE  TLAISLGTRK  EDPDEKSLV  DKVKEKAKEE  DHEKLGEKEE
481    TIPDYRLEI  VKDKDGKPLL  PKEAEEQLPP  LSDDFLLDAL  SQDFSSPANI  LSLGFEDAKL  SAAVSETVSQ  VPAPSNHTAA
561    PPGTERRDK  ELDDALDELS  DSLGQFQDPD  DENKPLDDKV  KEKIKAEHSE  KLGERRDTIP  PEYRHLLDND  GKDKPEKPLT
641    KNTEKPGDQ  DPIDALSEDL  DSCPPTTETS  QNTTKEGK  TSSSKASKNE  ETKDSSKKT  EEVPPKPVDE  DAT
    
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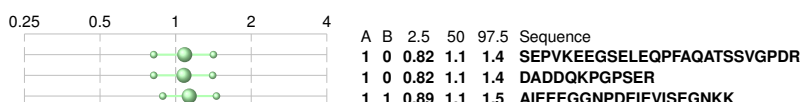
5.344 scaffold attachment factor B [Rattus norvegicus]

Protein Accession	gij11693164	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.862, 1.36)	
Associated Peptides	3	
Associated Spectra	4	
Coverage	0.0675	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.13	1.68
Avg..iTRAQ.Ratio....116.114.	1.02	1.43
Avg..iTRAQ.Ratio....117.114.	1.12	1.82

NHLBI Zile/Grant, Aged Rat

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1   MERLKKAIIE EGGNPDEIEV ISEGNKMKP RPSKGKKPED EGVEDNGLEE NSGDGQEDVE TSLLENLQDMD MMDISVLDEA
81  DIDNGSVADC VEEEEATLP EGLGLLRIGR LQSKGLPEQL QELAIDDKEA INNVDTSSTD FTILQEMEEA SLEPENEKIL
161 DILGETCKSE PVKEEGSELE QPFAQATSSV GPDRKLAEEE DLFESCGHPE EEEEEEEEEE QEEEQEEEGD LALASSSKSE
241 SSTRCQWSE ADALLAVVKR EPAAEPGGGT GMDREPVGLE EPVEQSSTAA QLPETTSQEL VRAPTAAPSP EPRDSKDDVK
321 KFAFDACNDV PAAPKESSAS EGADQKMSSV EDDSDTKRLS REEKGRSSCG RNFVWVSLSS TTRATDLKLNL FSRYGKVVGA
401 KVVTNARSPG ARCYGFVTMS TAEAAATKCN HLHKTELHGK MISVEKAKSE PAGKRVPPDR DGDSKKEKTS TSDRSANLKR
481 EEKGRKDDA KKTDDGSTK SKDADDQKPG PSESRRTKS GSRGTERTV MDKSKGVVPI SVKTSGSKER ASKSQDRKSV
561 SREKRSVVSF DKVKEsrksr DSESRRERER ERSEREQRLQ AQWEREERER LEIARERLAF HRRHLERERM ERERLERERM
641 HVEQERRREQ ERIHREREEL RRQELRYEQ ERFPVRRPY EVDGRRDDAY WPEAKRAALD DRYHSDFSRQ DRFHDFDHRD
721 RGRYPNHSVD RREGSRMMG DREGQHYPER HGGPERHGRD SRDGWGYGSN KRLSEGRGLP LLPRRDWGEH ARLEDDRAW
801 QGTADGGMME RDQQRWQGE RSMGSHSGPG HMMNRGGMSG RGSFAPGGAS RRHVIPRGGM QAGFGGTEPG QQTQ
  
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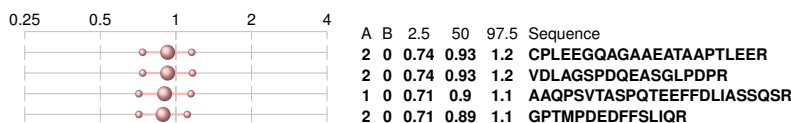


5.345 "G-protein signalling modulator 1 (AGS3-like, *C. elegans*) [*Rattus norvegicus*]"

Protein Accession	gi 21426765
Mean Expression Ratio	0.916
Median Expression Ratio	0.918
Credible Interval	(0.754, 1.11)
Associated Peptides	4
Associated Spectra	7
Coverage	0.123
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.929
Avg..iTRAQ.Ratio....116.114.	0.97
Avg..iTRAQ.Ratio....117.114.	0.916

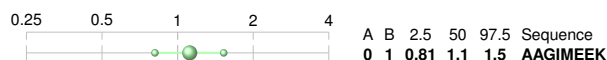
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1   MEASCLELAL EGERLCKAGD FKAGVAFFEA AVQVGTEDLK TLSAIYSQLG NAYFYLKEYA RALQFHKHDL LLARTIGDRM
81  GEAKASGNLG NTLKVLGRFD EAIVCCQRHL DIAEQGDQV GEARALYNIG NVYHAKGKQL SWNAAQDPGH LPPDVRETLH
161 RASEFYERNL SLVKELGDRA AQGRAYGNLG NTHYLLGNFT EATTFHKEERL AIAKEFGDKA AERRAYSNLG NAHIFLGRFD
241 VAAEHYKRTL QLSRQIRDQA VEAQACYSLG NYTYLLQDYE RAAEYHLRHL VIAQELADRV GEGRACWSLG NAYVSMGSPA
321 QALTFAKKHL QISQEIQRN GELTARMNIA HLQLALGRLT SPAAAQKPDV AGYEAQGARV KRTQRLSAET WDLRLRPLDR
401 EQNGETHHTG DWRGPSRDSL PLPMRSRKYQ EGPDAIERRP REGSHSPLDS ADVRVQVPRV GIPRAPSSDE ECFDLSKQ
481 QSSRMDDQRC PLEEGQAGAA EATAAPTLER RAAQPSVTAS PQTEEFFDLI ASSQSRRLDD QRASVGSPLG LRITLNNVGH
561 LRGDGDPQEP GDEFFNMLIK YQSSRIDDRQ CPPFDVLRG PTMPDEDFPS LIQRVQAKRM DEQRVDLAGS PDQEAASGLPD
641 PRQQCPPGAS
  
```



5.346 PREDICTED: similar to acyl-Coenzyme A oxidase-like [Rattus norvegicus]

Protein Accession	gij109470635
Mean Expression Ratio	1.09
Median Expression Ratio	1.09
Credible Interval	(0.805, 1.47)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	1.35



5.347 "solute carrier family 16 (monocarboxylic acid transporters), member 1 [Rattus norvegicus]"

Protein Accession	gij6981542
Mean Expression Ratio	1.09
Median Expression Ratio	1.09
Credible Interval	(0.812, 1.47)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0445
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.26
Avg..iTRAQ.Ratio....116.114.	0.603
Avg..iTRAQ.Ratio....117.114.	3.67

```

1      MPPAIGGPVG YTPPDGGGW AVVVGAFISI GFSYAAPKSI TVFFKEIEII FSATTSEVSW ISSIMLAVMY AGGPISSILV
81     NKYGSRPVMI AGGCLSGCGL IAASFCNTVQ ELYFCIGVIG GLGLAFNLNP ALTMIGKYFY KKRPLANGLA MAGSPVFLST
161    LAPLNQAFFG IFGWRGSFLI LGLLLNCCV AGSLMRPIGP QQGRVEKLS KESLQEAGKS DANTDLIGGS PKGEKLSVFQ
241    TVNKFLDLSL FTHRGFLLYL SGNVVMFFGL FTPLVFLSNY GKSKHFSSEK SAFLLSILAF VDMVARPSMG LAANTRWIRP
321    RVQYFFAASV VANGVCHLLA PLSTTYVGFC IYAGVFGFAF GWLSSVLFET LMDLVGPQRF SSAVGLVTIV ECCPVLLGPP
401    LLGRLNDMYG DYKYTYWACG VILIIAGLYL FIGMGINYRL VAKEQKAEK KRDGKEDETS TDVDEKPKKT MKETQSPAPL
481    QNSSGDPAAE ESPV
    
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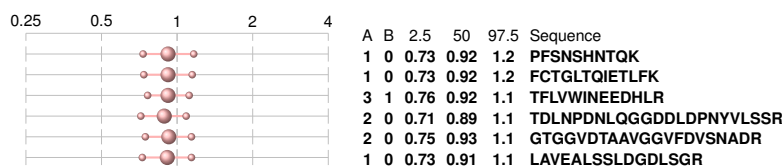


5.348 "creatine kinase, brain [Rattus norvegicus]"

Protein Accession	gj 31542401	
Mean Expression Ratio	0.916	
Median Expression Ratio	0.918	
Credible Interval	(0.777, 1.08)	
Associated Peptides	6	
Associated Spectra	11	
Coverage	0.252	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.978	1.11
Avg..iTRAQ.Ratio....116.114.	0.898	0.922
Avg..iTRAQ.Ratio....117.114.	0.93	0.892

```

1      MPFSNSHNTQ KLRFPAEDEF PDLSSHHNHM AKVLTPELYA ELRAKCTPSG FTLD DAIQTG VDNPGHPYIM TVGAVAGDEE
81     SYDVKDLFD PIIEDRHGGY QPSDEHK TDL NPDNLQGGDD LDPNYVLSSR VRTGRSIRGF CLPPHCSRGE RRAIEKLAVE
161    ALS SLDG DLS GRYYALKSMT EADEQQ LIDD HFLFDKPVSP LLLASGMARD WPDARGIWHN DNK TFLVWIN EEDHLRVISM
241    QKGGNMKEVF TRFCTGLTQI ETLFKSKNYE FMWNP HLG YI LTCPSNLGTG LRAGVHIKLP HLGKHEKFSE VLKRLRLQKR
321    GTGGVD TAAV GGVFDVSNAD RLG FSEVELV QMVVDGVKLL IEMEQRL EQG QFIDDLMPAQ K
    
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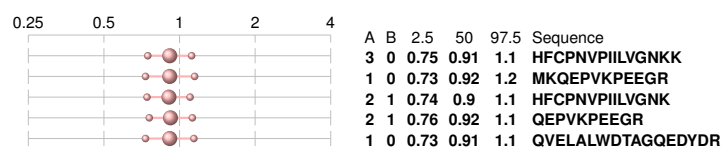


5.349 aplysia ras-related homolog A2 [Rattus norvegicus]

Protein Accession	gj 16923986	
Mean Expression Ratio	0.92	
Median Expression Ratio	0.919	
Credible Interval	(0.777, 1.09)	
Associated Peptides	5	
Associated Spectra	11	
Coverage	0.228	

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.926	1
Avg..iTRAQ.Ratio....116.114.	0.79	0.671
Avg..iTRAQ.Ratio....117.114.	0.946	1.53

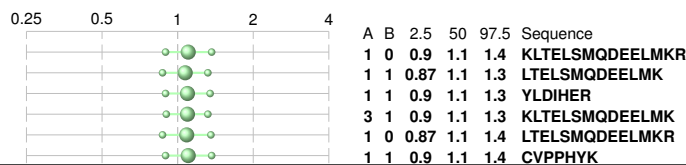
1 MAAIRKKLVI VGDGACGKTC LLIVFSKDQF PEVYVPTVFE NYVADIEVDG KQVELALWDT AGQEDYDRLR PLSYPDTDVI
 81 LMCFSIDSPD SLENIPEKWT PEVKHFCPNV PIILVGNKKD LRNDEHTRRE LAKMKQEPVK PEEGRDMANR IGAFGYMECS
 161 AKTKDGVREV FEMATRAALQ ARRGKKKSGC LIL



5.350 translocase of inner mitochondrial membrane 10 homolog [Rattus norvegicus]

Protein Accession	gij 25742598	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.924, 1.28)	
Associated Peptides	6	
Associated Spectra	12	
Coverage	0.322	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.01	1.13
Avg..iTRAQ.Ratio....116.114.	1.03	1.06
Avg..iTRAQ.Ratio....117.114.	1.19	1.22

1 MDPLRAQQLA AELEVEEMAD MYNRMTSACH RKCVPPHYKE AELSKGESVC LDRCVSKYLD IHERMGKILT ELSMQDEELM
 81 KR VQQSSGPA



5.351 v-crk sarcoma virus CT10 oncogene homolog [Rattus norvegicus]

Protein Accession	gij9506515	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.954, 1.24)	
Associated Peptides	10	
Associated Spectra	19	
Coverage	0.451	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.02	1.37
Avg..iTRAQ.Ratio....116.114.	1.06	1.21
Avg..iTRAQ.Ratio....117.114.	1.07	1.52

1 MAGNFDSEER SSWYWGRLSR QEAVALLQGQ RHGVFLVRDS STSPGDYVLS VSENSRVSHY IINSSGPRPP VPPSPAQPPP
 81 GVSPSRLRIG DQEFDSLPALEF YKIHLYD TTTLIEPVSR SRQSGVILR QEAEYVRAL FDFNGNDEED LPPFKGDILR
 161 IRDKPEEQW NAEDSEGKFG MIPVPYVEKY RPASASVSAL IGGNQEGSHP QPLGGPEPGP YAQPSVNTPL PNLQNGPIYA
 241 RVIQKRV PNA YDKTALALEV GELVKVTKIN VSGQWEGECN GKRGHFFPTH VRLLDQQNPE EDFS



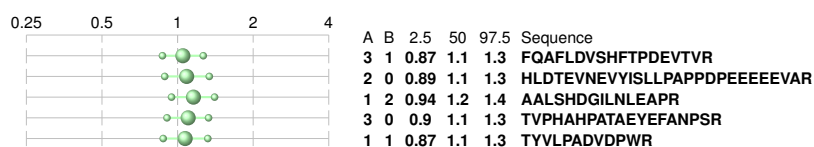
5.352 heat shock 27kD protein 2 [Rattus norvegicus]

Protein Accession	gij18426864	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.932, 1.27)	
Associated Peptides	5	
Associated Spectra	14	
Coverage	0.505	

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	0.954
Avg..iTRAQ.Ratio....116.114.	1.09	0.933
Avg..iTRAQ.Ratio....117.114.	1.20	1.51

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1   MSGRTVPHAH PATAEYEFAN PSRLGEQRFQ EGLLP EEILT PTLYHGYYVR PRAARAGEGG RAGASELRLS EGK FQAFLDV
81  SHFTPDEVTV FTVDNLLEVS ARHPQRLDRH GFVSREFCRT YVLPADVDFW VRAALSHDG ILNLEAPRGG RHLDEVNEV
161 YISLLPAPPD PEEEEVAIV EP
  
```



5.353 PREDICTED: similar to centromere protein F (350/400kD) [Rattus norvegicus]

Protein Accession	gij109499266
Mean Expression Ratio	0.92
Median Expression Ratio	0.92
Credible Interval	(0.682, 1.25)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00355
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.69
Avg..iTRAQ.Ratio....116.114.	1.00
Avg..iTRAQ.Ratio....117.114.	0.575

NHLBI Zile/Grant, Aged Rat

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1      MSWALEEWKE  GLPTRALQKI  QELEGQLDKL  KKEKQQRQFQ  LDSLEAALQK  QKQKVEDGKT  EGADLKRENO  RLMEICENLE
81     KTRQKLSHEL  QVKESQVNFQ  ESQLSSCKKQ  IEKLEQELKR  CKSEFERSQQ  SAEVSLNPCS  TPQKLFSTPL  TPSQYYICST
161    YEDLKEKYNK  EVEDRKRLEA  EVKALHAKKA  SLPVVSQATMN  HRDIARHQAS  SSVFSWQQDK  TPRSLSLSSCSL  RTPLRDVSVA
241    AHFLGEEVTP  NKSSVQIGRG  DCSGLPDDPH  CSQPLHQAKA  QNQLKSKMN  ELELRLRGQE  KEMKDQVNF  QELQLQLEKT
321    KVDLIEKEKI  LNKTRDEVVR  TTAQYEQAAA  KCTALEQKLL  NLTEELSCHR  QNAESAKRSL  EQRVKKEKE  LREELSROHQ
401    SFQALDHEYT  QMKTRLTQEL  QQAKHLSVL  QLELEKVTSV  KQQLERSLEE  IRHKFSRAEQ  ALQASQLTEN  ELRRSSEEMK
481    KENSLIRSQS  EQRTREACRL  EDELGKVKVC  LSQSQSFAEE  MRAKNTSQEI  MLRDLQEKLN  QQENSLTLEK  LKLALADLEG
561    QRDCSQDLLK  KREHHIEQLN  DKLNKIEKEF  ETLLSALELK  KKECEELKEE  KNQISCWKSE  NEKLINQIES  EKEILLGVN
641    HLEASLKTQQ  ISHDYSERVR  TLEMERENLT  VEIRNLHSL  DSKMVEIETQ  KQAYLELQQQ  SESSDQKHQK  EMENMCLKAN
721    KLTGQVESLE  CKLQSLSGEV  ETKDQQYQDL  RMEYETMRDS  LQARGSSLV  DEKNQRSSSA  FEEQPAVSHS  FANLVGKGS
801    IYSERSDSSV  DRGQSPENVA  VLQSRVTLLE  SSLESQNMN  SDLQKQCEEL  LQIKGIEEEN  LIKADQIHQN  FVAETNQRIG
881    KLQEDAAVHQ  NIVAETLATL  ESREKELQLL  KEQLEAQTE  VQKLEKNNCL  LEGALKELQL  LTDTLSEKK  EMNSIISLRK
961    KDIEELTQAN  GALKEVNEAL  RQEKMNLLQQ  HEITRCVAE  GERSIAELSG  QYKQERLLL  QRCCEETTVL  EGLRGDYKAA
1041   QENNAKLEK  LSECTALCEN  KNELEQLKE  TFAKEQQEFL  TKLAFTEEQN  RKLVLLELE  PQTVRSEITN  INKHPVSETD
1121   ALGQESWSK  EEQKEKQKEV  SNLTPEENL  MELTQTEHLY  YHLEVEPVEN  SVKATEEEIR  KSSSQYQMDI  DTKDISLDSY
1201   KAQLVQLEAL  IKVMEVKLDR  SEEEKNSLRQ  ELQTIREELG  TKTSQDTQSQ  ARVGLKCEV  EAEKQYVSVL  QELSTSONEN
1281   VHLQCSLQTA  MNKLNELGKM  CEVLRVEKLO  LESELNDRS  ECITATSQMA  ABEVKLVNEM  KMLNHENALS  HGLMKDTAD
1361   VEFDDKPNHT  SVFLTPLDNS  EQMTSSNKEV  RVHFAEQEK  FSCQSEHKI  LHDQHCEVSS  KMSALRSYVD  TLKAENSVLS
1441   MNLRTLQGD  VKEKEPGAED  GHILPLSFCR  TDSPTLTFNG  ENSFYKDVLE  QTGDTSHLSL  EGNASANPCD  VDEVSYSSLE
1521   EENLTEKEIP  FASLRTVEEL  ELICQVYVLS  IKNLEEKIES  QRIMKNKEIE  ELEQLSSER  KELSCLRKQY  LSEKEQWQK
1601   LTSVTLEMES  KLAEEKQQT  NLSLELEVAR  LQLQELDLS  RSLLTGDTLEG  AVRGPNQDGY  IKESVYISE  TTEKTPKQDT
1681   NQTCNDNDVQ  DICLETSVTE  TETTRLTGDD  CEEQPSKISC  EAPAEDRTQD  YSECISELS  TSPVLVPMVD  LEDGSIQNL
1761   HLQKDTSNEN  LRLLEPEVED  DKKVESLLNE  IKEADSKLSL  QELQLKIKIA  TCIELEKIVK  HLKKEETDLS  EKLESPLCNQ
1841   EVCPRVERSD  LDFNLDMGDD  ELFRETKDD  AANTEDNYKE  KFLDMERELT  RIKSEKANIE  HHIVSVKANL  EVVQAEKICL
1921   ERDTESKQKV  IVDLKGELFT  VISERNRLRE  ELDNVSKESK  ALDQMSKKMK  EKIEELESQ  RESLHHIGAV  ESEVKDKAEL
2001   IQTLFSVDE  LTKDKAHLQE  QLQNLQNSQ  GLSLAIGELE  IQIGQLNKEK  ESLVKESQNF  QVKLSESECE  KQTSKALEV
2081   ALMEKGEFAM  RLSSTQEEVH  QLRQGIKLS  VRIEADKHH  LSAVAKLKE  QRESDSLKDK  VENLERLEEM  SEENQELAIL
2161   DSENKAEVE  TLKAQMDAMA  KSLRVFELD  VNVRSERENL  AKQLQEKQSR  VSELDELCS  LRSLSSEEKQ  ARVQMERDSK
2241   SAMLMLQTL  KELWEEVAAL  YNDQETLKAQ  EQSLDQPEG  VHLKSSIQK  LKVHIDADKK  KQCHILEQLK  ESKHADLFK
2321   DRVENLEQEL  MLSEKNKEHL  IFQAENSKAE  IQTLKTEIQT  MDQNLQDEL  ELTNTTRSEKE  NLMKELKNEQ  EQISKLETIN
2401   SSIERLLKDK  EQEKVQKKE  ARITVEMLQT  QLEKLNTEVV  SLQNDQEA  YK  TKEQNLGSRV  QLELEKAQL  LQDLGEAKNK
2481   YIFQSSVNA  LTQVEAGKQ  KLEKEEEV  RLKEQLKQGE  QLVCKLARVE  GEQQLCQKQK  LELRSLTMEL  EQKVKVLQSE
2561   NDALQTTYEA  LQSSYKSLG  ELGLIKMEKM  ALVERVNTMT  GKEAELQREL  HDVEQKSTQL  KEYSSEKTR  LTEDLEVUME
2641   ELKNTKVSFP  WQSPALLTG  DAYSSVVFVR  SLQCIPPRSH  ERDASLGTMI  SVMKLRTPNH  TGCGRDGLSX  VERGAYFMHL
2721   EMLYFKHNT  VSCFNMFXL  FXILVXNSR  FYMKLTVLV  VAHLKVNHL  EKEFQRAQK  IKLLKSCQK  LEGEKKMLQK
2801   ELSQLEAAQK  QRAGSLVDSN  VDELMTENKE  LKETLEKIK  EADKYLDRYC  SLLISHEELE  KTKEILEIQV  ARLSRQNKQ
2881   DLQSSPLD  SVAGSPSTG  VSERKSTSG  NKTGLKRQRS  SGIGENGT  APSTPETF  KSRKSVNSA  HPADEEETE
2961   FEPEGLPEV  KGFADIP  KTSPYILRRT  TMASTRSPRL  AAQKLLGSS  TLGKENLVE  SKPTAGGSR  SKVQVQESS
3041   MDAHAVFQEL  PAKSLTANM  PGRNSTESPR  EGLRAKRACP  ASSPAAGPDP  MNNENCRVQ

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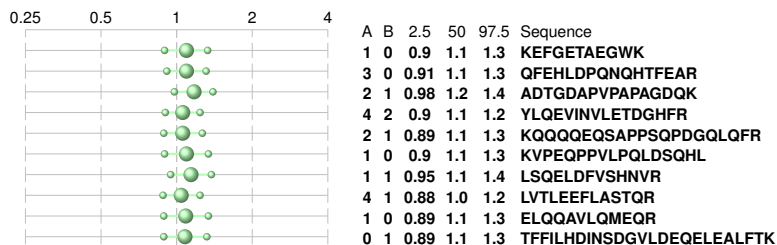


5.354 nucleobindin 1 [Rattus norvegicus]

Protein Accession	gi 16758210	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.964, 1.23)	
Associated Peptides	10	
Associated Spectra	26	
Coverage	0.349	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	1.08
Avg..iTRAQ.Ratio....116.114.	1.07	0.942
Avg..iTRAQ.Ratio....117.114.	1.20	1.30

```

1      MPTSVPRGAP FLLLPLLML SAVLAVPVDR AAPHQEDNQA TETPDTGLYY HRYLQEVINV LETDGHFREK LQAANAEDIK
81     SGKLSQELDF VSHNVRTKLD ELKRQEVSRRL RMLLKAKMDA KQEPNLQVDH MNLLKQFEHL DPQNQHTFEA RDLELLIQT
161    TRDLAQYDAA HHEEFKRYEM LKEHERRRYL ESLGEEQRKE AERKLQEQQR RHREHPKVVV PGSQAQLKEV WEELDGLDPN
241    RFNFKTFIL HDINSDGVLD EQELEALFTK ELEKVYDFKN EEDDMREMEE ERLRMREHVM KNVDTNQDRL VTLEEFLLAST
321    QRKEFGETA E GWKTVEMYP A YTEEELKRFE EELAAREAE L NARAQRLSQE TEALGRSQDR LEAQKR ELQQ AVLQMEQRKQ
401    QQQEQSAPPS QPDGQLQFRA DTGDAPVPAP AGDQKDFPAS EKKVPEQPFV LPQLDSQHL
    
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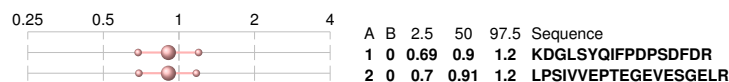


5.355 PREDICTED: similar to limb-bud and heart [Rattus norvegicus]

Protein Accession	gij109479022
Mean Expression Ratio	0.919
Median Expression Ratio	0.92
Credible Interval	(0.712, 1.18)
Associated Peptides	2
Associated Spectra	3
Coverage	0.343
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.863
Avg..iTRAQ.Ratio....116.114.	0.884
Avg..iTRAQ.Ratio....117.114.	0.972

```

1      MSVYFPIHCS DYLRSAEMTE VMMNAPSME E IGLSPR KDGL SYQIFPDPSPD FDR CCKLKDR LPSIVVEPTE GEVESGELRW
81     PPEEFLVQED EQDNCEETTK EKKDQ
    
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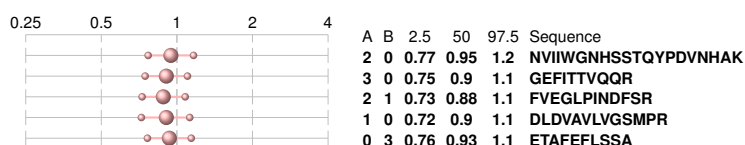


5.356 "malate dehydrogenase 1, NAD (soluble) [Rattus norvegicus]"

Protein Accession	gij15100179	
Mean Expression Ratio	0.918	
Median Expression Ratio	0.92	
Credible Interval	(0.785, 1.08)	
Associated Peptides	5	
Associated Spectra	12	
Coverage	0.195	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.952	0.711
Avg..iTRAQ.Ratio....116.114.	1.07	0.688
Avg..iTRAQ.Ratio....117.114.	0.86	0.938

```

1  MSEPIRVLVT GAAGQIAYS L YSIGNGSVF GKDQPIILVL LDITPMMGVL DGVLMELQDC ALPLLQDVIA TDKEEVAFK D
81  LDVAVLVGSM FREGMERKD LLKANVKIFK SQGAALEKYA KKSVKVIVVG NPANTNCLTA SKSAPSIPKE NFSCLETRLDH
161 NRAKSQIALK LGVTADDVK N V I I W G N H S S T Q Y P D V N H A K V K L Q G K E V G V Y E A L K D D S W L K G E F I T T V Q Q R G A A V I K A R K L
241 SSAMSAAKAI SDHIRDIWFG TPEGEFVSMG VISDGN SYGV PDDL LYSFPV VIKNKTKW F V E G L P I N D F S R E K M D L T A K E L
321 TEEKETAFEF LSSA
    
```



5.357 PREDICTED: similar to Collagen alpha-1(VI) chain precursor [Rattus norvegicus]

Protein Accession	gij109509939	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.824, 1.43)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.0156	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.52	
Avg..iTRAQ.Ratio....116.114.	1.27	
Avg..iTRAQ.Ratio....117.114.	1.37	

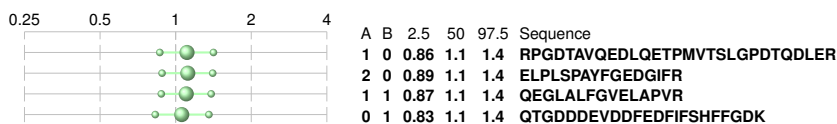
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1   MRLAHTLLPL LLQACWVAAQ DIQGSRAIAF QDCPVDLFFV LDTSESVALR LKPYGALVDK VKSFTKRFID NLRDRYYRCD
81  RNLVWNGAL HYSDEVEIIR GLMRMPSSRD ELKASIDAVK YFGKGTYTDC AIKKGLEELL IGGSHLKENK YLIVVTDGHP
161 LEGYKEPCGG LEDAVNEAKH LGIKVFSVAI TPDHLEPRLS IIATDHTYRR NFTAADWGH S RDAEETISQT IDTIVDMIKN
241 NVEQVCCFE CQAARGPPGP RGDPGYEGER GKPGLPGEKG EAGDFGRPGD LGPVGYQGMK GEKGSRGEKG SRGPKGYKGE
321 KKRGRIDGVD GMKGETGYPG LPGCKGSPGF DGIQGGPPGPK GDAGAFGLKG EKGEAGAEGE AGRPGNSGPP GDEGEFGEFG
401 PPGEKGEAGD EGNAGPDGAP GERGGPGERG PRGTPGVVRF RGDPEAGFPQ GDQGREGPVG IPGDPGESGP IGPKGYRGDE
481 GPPGPELRG APGPVGGPD PGLMGERGED GPPGNGTEGF PGFPGYPGNR GPPGINGTKG YPGLKGDEGE AGDPGEDNND
561 VSPRGVKGAK GYRGEPPQG PPGHVGGPPG DECEILDII KMCSCECTC GPIDILFVLD SSESIGLQNF EIAKDFIIKV
641 IDRLSKDELV KFEPQSHAG VVQYSHNMQ EHVDMRSPNV RNAQDFKEAV KKLQWMAGGT FTGEALQYTR DRLLPPTQNN
721 RIALVITDGR SDTQRDTPPL SVLCGSDIQV VSVGIKDVFG FVAGSDQLNV ISCQGLSQSR PGISLVKENY AELLDDGFLK
801 NITAQICIDK KCPDYTCPIT FSSPTDITIL LDSASVSGSH NFETTKVFAK RLAERFLSAG REDPTQVVRV AVVQYSGGGQ
881 QVQVGRASLQF QQNYTVLASS VDSMDFINDA TDVNALSYV TRFYRENSSG ATKKRVLVLS DGNSQGATAE AIEKAVQEAQ
961 RGGIEIFVMV VGPQVNEPHI RVLVTGKTAE YDVAFGERHL FRVFNQALL RGVLYQTVSR KVALG
  
```



5.358 PREDICTED: similar to pre-B-cell leukemia transcription factor interacting protein 1 [Rattus norvegicus]

Protein Accession	gij109466935	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.892, 1.33)	
Associated Peptides	4	
Associated Spectra	6	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.16	0.982
Avg..iTRAQ.Ratio....116.114.	1.29	1.04
Avg..iTRAQ.Ratio....117.114.	1.46	0.822

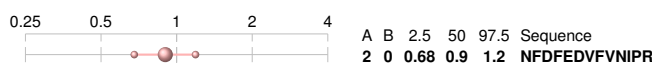


5.359 "PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 [Rattus norvegicus]"

Protein Accession	gij109474252
Mean Expression Ratio	0.92
Median Expression Ratio	0.92
Credible Interval	(0.7, 1.2)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0345
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.875
Avg..iTRAQ.Ratio....116.114.	0.9
Avg..iTRAQ.Ratio....117.114.	0.796

```

1      MAAAVRFQVV RALPMSRPAI SAAATSVFCS SSHRQLHHAV IPHGKGRSS VSGVVATVFG ATGFLGRYVV NHLGRMGSQV
81     IIPYRCDIYD TMLHLRMGDL GQLIFLEWDA RDKDSIRKAV QHSNVVINLI GREWETRNFD FEDVFNIPR AIAQASKEAG
161    VERFIHVSHL NASMKSSAKS LRSKAVGEKE VRTVFPDAII IRPSDMFGRE DRFLNHFANY RWFLAVPLVS LGFKTVKQPV
241    YVADVSKGIA NATKNPDAIG KTFAFTGPNR YLLFHLVKYI FGMTHRTFIP YPLPRFVYSW IGRLFGLSPF EPWTTKDKVE
321    RIHISDVMAT DLPGLEDLGV QPTPLELKSI EVLRRHRTYR WLSSEIEETK PAKTVNY
    
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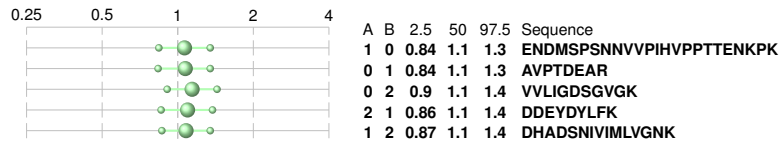


5.360 "RAB11a, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gij13592148	
Mean Expression Ratio	1.09	
Median Expression Ratio	1.09	
Credible Interval	(0.897, 1.31)	
Associated Peptides	5	
Associated Spectra	10	
Coverage	0.31	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	1.07
Avg..iTRAQ.Ratio....116.114.	1.08	0.922
Avg..iTRAQ.Ratio....117.114.	1.09	1.19

NHLBI Zile/Grant, Aged Rat

1 MGTRDDEYDY LFKVVLIGDS GVGKSNLLSR FTRNEFNLES KSTIGVEFAT RSIQVDGKTI KAQIWDTAGQ ERYRAITSAY
 81 YRGAVGALLV YDIAKHLTYE NVERWLKELR DHADSNIVIM LVGNKSDLRH LRAVPTDEAR AFAEKNGLSF IETSALDSTN
 161 VEAFAQTILT EIYRIVSQKQ MSDRRENDMS PSNNVVPIHV PPTTENKPFV QCCQNI



5.361 pyridoxine 5-phosphate oxidase [Rattus norvegicus]

Protein Accession	gi 12018270
Mean Expression Ratio	0.923
Median Expression Ratio	0.92
Credible Interval	(0.68, 1.25)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0421
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.954
Avg..iTRAQ.Ratio....116.114.	0.834
Avg..iTRAQ.Ratio....117.114.	0.683

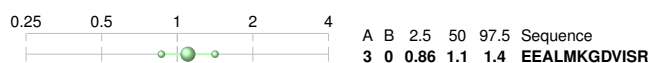
1 MTCGLLSVTV TFRPAKWP GYFRHLCCRGA VMDLGP MRKS YRGDREAFEE AHLTSLDPMK QFASWFEEAV QCPDIGEANA
 81 MCLATCTRDG KPSARM LLLK GFGKDGFRFF TNYESRKGKE LDSNPFASLV FYWEPLNRQV RVEGVPVKLP EKEAENYFHS
 161 RPKSSQIGAV VSRQSSVIP REYLRKNEE LGQLYREQEV PKPEYWGGYI LYPQVMEFWQ GQTNRLHDRI VFRRGLATGD
 241 SPLGPMTHHG EEDWVYERLA P



5.362 PREDICTED: similar to pentatricopeptide repeat domain 2 [Rattus norvegicus]

Protein Accession	gi 109465978
Mean Expression Ratio	1.09
Median Expression Ratio	1.09
Credible Interval	(0.844, 1.40)

Associated Peptides	1
Associated Spectra	3
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.25
Avg..iTRAQ.Ratio....116.114.	1.07
Avg..iTRAQ.Ratio....117.114.	1.38

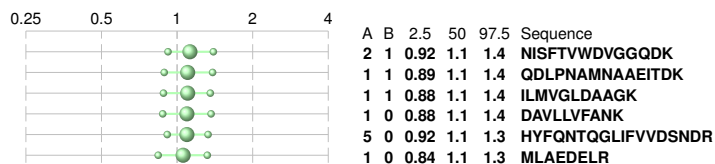


5.363 ADP-ribosylation factor 1 [Rattus norvegicus]

Protein Accession	gi 11968098
Mean Expression Ratio	1.09
Median Expression Ratio	1.09
Credible Interval	(0.92, 1.28)
Associated Peptides	6
Associated Spectra	14
Coverage	0.42
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.23
Avg..iTRAQ.Ratio....116.114.	1.29
Avg..iTRAQ.Ratio....117.114.	0.996

```

1      MGNIFANLFK GLFGKKEMR L MVGLDAAGK TTILYKCLKG EIVTTIPTIG FNVETVEYK N ISFTVWDVGG QDKIRPLWRH
81     YFQNTQGLIF VVDSNDRERV NEAREELMR M LAEDELRAV LLVFANKQDL P NAMNAAEIT D K LGLHSLRH RNWYIQTCA
161    TSGDGLYEGL DWLSNQLRNQ K
    
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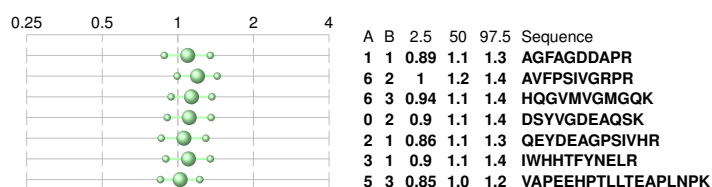


5.364 "actin, alpha 1, skeletal muscle [Rattus norvegicus]"

Protein Accession	gi 9506371
Mean Expression Ratio	1.09
Median Expression Ratio	1.09
Credible Interval	(0.935, 1.26)
Associated Peptides	7
Associated Spectra	36
Coverage	0.225
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.865
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	1.12

```

1      MCDEDETTAL VCDNGSGLVK AGFAGDDAPR AVFPSIVGRP RHQGVVMVGMG QKDSYVGDDEA QSEFRGILTLK YPIEHGIITN
81     WDDMEKIWHH TFYNELRVAP EEHPTLLTEA PLNPKANREK MTQIMFETFN VPAMYVAIQV VLSLYASGRT TGIVLDSGDG
161    VTHNVPIYEG YALPHAIMRL DLAGRDLTDY LMKILTERGY SFVTTAEREI VRDIKEKLCY VALDFENEMA TAASSSSLEK
241    SYELPDGQVI TIGNERFRCP ETLFQPSFIG MESAGIHETT YNSIMKCDID IRKDLYANNV MSGGTTMYPG IADRMQKEIT
321    ALAPSTMKIK IIAPPERKYS VWIGGSILAS LSTFQQMWIT KQEYDEAGPS IVHRKCF
    
```



5.365 vanilloid receptor-like protein 1 [Rattus norvegicus]

Protein Accession	gi 78187981
Mean Expression Ratio	0.923
Median Expression Ratio	0.921
Credible Interval	(0.685, 1.25)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00657
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.824
Avg..iTRAQ.Ratio....116.114.	0.512
Avg..iTRAQ.Ratio....117.114.	0.904

```

1      MTSASSPPAF RLETS DGDEE GNAEVNKGKQ EPPPMESPFO REDRNSSPQI KVNLFNFKRP PKNTSAPSQQ EPDRFDRDRL
81     FSVVSRGVPE ELTG LLEYLR WNSKYLTDSA YTEGSTGKTC LMKAVLNLDQ GVNACIMPLL QIDKDSGNPK PLVNAQCIDE
161    FYQGHSA LHI AIEKRSLQCV KLLVENGADV HLRACGRFFQ KHQGTCFYFG ELPLSLA ACT KQWDVVYLL ENPHQPASLE
241    ATDSLGN TVL HALVMIADNS PENSALVIHM YDGLLQMGAR LCPTVQLEEI SNHQGLTPLK LAAKEGKLEI FRHILQREFS
321    GPYQPLSRKF TEWCYGPVRV SLYDLS SVD S WEKNSVLEII AFHCKSPNRH RMVVLEPLNK LQEKWDRLV SRFFFNFACY
401    LVYMFIFTV V AYHQPSLDQP AIPSSKATFG ESM LLLGHIL ILLGGIYLLL GQLWYFWRRR LFIWISFMSD YFEILFLLQA
481    LLTVLSQVLR FMETEWYLP L LVL S LVLGWL NLLYYTRGFQ HTGIYSVMIQ KVILRDLLRF LLVYL VLF LG FAVALVSLSR
561    EARS PKAPED NNSTVTEQPT VQEEEEPAPY RSILDASLEL KFFTIGMGEL AFQEQLRFRG VVLLLLL LAYV LLTYVLL LNM
641    LIALMSE TVN HVADNSWSIW KLQKAISVLE MENGYWCCR KKHREGRLK VGT RGDGTPD ERWCFRVEEV NWWAVEK TLP
721    TLESDPSGPG ITGNKKNPTS KPGKNSASEE DHLPLQLVLS P
    
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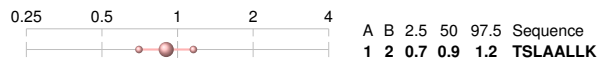


5.366 PREDICTED: similar to CG10632-PA [Rattus norvegicus]

Protein Accession	gij109500365	
Mean Expression Ratio	0.923	
Median Expression Ratio	0.922	
Credible Interval	(0.718, 1.20)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.0104	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.95	0.839
Avg..iTRAQ.Ratio....116.114.	1.05	0.759
Avg..iTRAQ.Ratio....117.114.	0.911	0.51

```

1      MAGELSQEAL LDFLCQAGGR VRNAELLSHF KSFLRDPHPV SGQLQERREL FKGFVNSVAA VRQDPDGTKY VVLKRRYRDL
81     LGE EGLQ RPA PTDQQPRSHR RLDPEPQKPP AGAGTRVDVG DDELVGSSAR KAAGPDPGPG DSPSQRTLGP EAAQARGRCA
161    AVGTRGRCCW ECQNGWGQP TEQPLPEDLG DPAAACEKPE RAAPARDDL G APGWLREGAA AERSPEVTP VWAPAAVEAA
241    GSPTSPPALP PHPAPSREPL ELFTAGFPNH STQQLQQQQQ RTREWVARYP LAPEAGIQGP IRAWSVLPDN FLQLPSETAF
321    GVSETNSALP EPALSFHSL L PGVPDESSES WPGNPLTVF RSIRCQLSLQ DDDDFVDQES HGSESSSGP KESPGTPEEG
401    LQTVLRTSSW GELRDPVEDQ FVSPNEGSPC LIPRGLRNRG NVPSFRKAPT VAKSLGDHPQ ETFFPAPKFRR SVRRSSRTGR
481    TKSPSSSDEE HLEDLLKRS RRPFRSRKPS KAGALPSPRV DVVLIQKLAN ANAVTGQPHS SWVPGRDGSA ALIPHRPSEH
561    RSPLVPLDAR EHEWIVRLAS GSWFHVQMLF WEDPQLALYR DFLTGYTALH WIAKHGDLNA LQDLVSGARK AGVALDVNVR
641    SSCGYTPLHL AAMHGHQGVI KLLVQRLASR VNIRDCSGKK FWQYLN S NVS GETWQLLGAP RGKPIFPVYS LVQSSSPARK
721    VKSREVSRTV TRK TSLAALL K TQHNKWKLA SQYEKFHTPK DREEYS D
    
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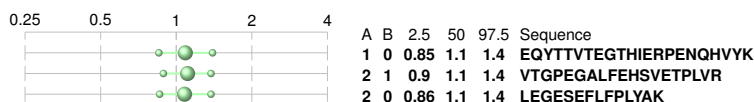
5.367 gamma sarcoglycan [Rattus norvegicus]

Protein Accession	gi 55741776	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(0.888, 1.33)	
Associated Peptides	3	
Associated Spectra	6	
Coverage	0.188	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.14	1.01
Avg..iTRAQ.Ratio....116.114.	1.20	1.18
Avg..iTRAQ.Ratio....117.114.	1.21	1.21

```

1   MVREQYTTVT EGTHIERPEN QHVYKIGIYG WRKRCLYLFV LILLTILVVN LALTIWILRV MWFSPIGMGH LHVTDGLRL
81  EGESEFLFPL YAKEIRSRVD SSLLLQSTQN VTVNARNSEG EVTGRVKVGA QMVEVQSQHL QISSSEDKPL FTAEEQGVVV
161 GTGRLRVTGP EGALFEHSVE TPLVRAEHPF QDLRLESPTR SLSMDAPRGV HIEARAGKME ALSQMDIVLQ SSDGVLVLDA
241 ETVGLAKLKQ GTQGPPGSSN GVYEICACPD GKLYLSMAGE ATTCEEHSHI CL

```



5.368 "tubulin, beta, 2 [Rattus norvegicus]"

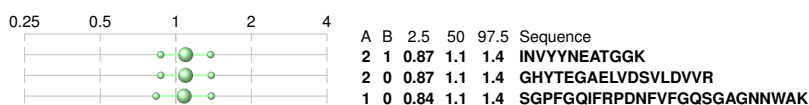
Protein Accession	gi 40018568	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(0.877, 1.33)	
Associated Peptides	3	
Associated Spectra	6	
Coverage	0.126	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.21	1.47
Avg..iTRAQ.Ratio....116.114.	1.11	1.18
Avg..iTRAQ.Ratio....117.114.	1.11	1.05

NHLBI Zile/Grant, Aged Rat

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1   MREIVHLQAG QCGNQIGAKF WEVISDEHGI DPTGTYHGDS DLQLERINYV YNEATGGKYV PRAVLVDLEP GTMDSVRSGP
81  FGQIFRPDNF VFGQSGAGNN WAKGHYTEGA ELVDSVLDVV RKEAESCDCL QGFQLTHSLG GGTGSGMGTL LISKIREEYP
161 DRIMNTFSVV EPSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS ATMSGVTTACL
241 RFPGQLNADL RKLAVNMVFF PRLHFFMPGF APLTSRGSQQ YRALTVPELT QQMFDAKNMM AACDPRHGRY LTVAAVFRGR
321 MSMKEVDEQM LNVQKNSSY FVEWIPNNVK TAVCDIPPRG LKMSATFIGN STAIQELFKR ISEQFTAMFR RKAFLHWYTG
401 EGMDEMEFTE AESNMNDLVS EYQQYQDATA EEEGEFEEEA EEEVA

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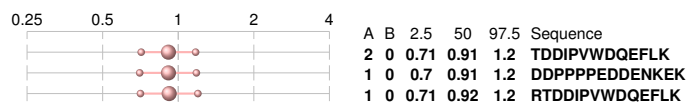
5.369 S-phase kinase-associated protein 1A [Rattus norvegicus]

Protein Accession	gij 56090475
Mean Expression Ratio	0.923
Median Expression Ratio	0.923
Credible Interval	(0.735, 1.15)
Associated Peptides	3
Associated Spectra	4
Coverage	0.172
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.95
Avg..iTRAQ.Ratio....116.114.	0.858
Avg..iTRAQ.Ratio....117.114.	0.925

```

1   MPTIKLQSSD GEIFEVDVEI AKQSVTIKTM LEDLGMDDEG DDDPVPLPNV NAAILKKVIQ WCTHHKDDPP PPEDDENKEK
81  RTDDIPVWDQ EFLKVDQGTL FELILAANYL DIRGLLDVTC KTVANMIKG TPEEIRKTFN IKNDFTEEEE AQVRKENQWC
161 EEK

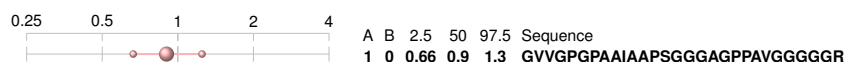
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5.370 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gij 109463606
Mean Expression Ratio	0.924
Median Expression Ratio	0.923

Credible Interval	(0.685, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.985
Avg..iTRAQ.Ratio....116.114.	0.811
Avg..iTRAQ.Ratio....117.114.	0.72



5.371 "ATPase, Na+/K+ transporting, beta 1 polypeptide [Rattus norvegicus]"

Protein Accession	gij6978549
Mean Expression Ratio	0.924
Median Expression Ratio	0.925
Credible Interval	(0.692, 1.25)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.798
Avg..iTRAQ.Ratio....116.114.	0.789
Avg..iTRAQ.Ratio....117.114.	0.663

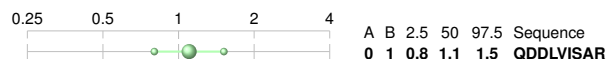


5.372 neural stem cell-derived dendrite regulator [Rattus norvegicus]

Protein Accession	gi 54312094
Mean Expression Ratio	1.08
Median Expression Ratio	1.08
Credible Interval	(0.803, 1.46)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00862
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.27
Avg..iTRAQ.Ratio....116.114.	1.21
Avg..iTRAQ.Ratio....117.114.	1.1

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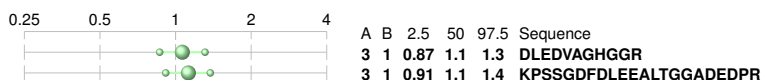
1      MPGIVVFRRR  WSVGSDLLVL  PAIFLFLHHT  TWFVILSVVL  FGLVYNPHEA  CSLNLDVHGR  GYLGILLSCM  IAEMAIWLS
81     MRGGILYTEP  RDSMQYVLYV  RLAILVIEFI  YAIVGIVWLT  QYYTSCNDLT  AKNVTLMGMV  CNWVVILSVC  ITVLCVFDPT
161    GRTFVKLRAT  KRRQRNLRTY  NLRHRLIEEQ  ATSWSRRLKV  FLCCTRTKDS  QSDAYSEIAY  LFAEFFRDL  IVPSDIIAGL
241    VLLRQRQRAK  RNAVLEANN  DILAFLSGMP  VTRNTKYLDL  KNSHEMLRYK  EVCYYMLFAL  AAYGWPMYLM  RKPCTGLCQL
321    ARSCCCLCP  ARPRFAPGVT  IEEDNCCGCN  AIAIRRHFLD  ENMTAVDIVY  TSCHDVAVET  PFYVAVDHDK  KKVVISIRGT
401    LSPKDALTDL  TGDAERLPVE  GHRGTNLGHK  GMVLSAEYIK  KKLEQEMVLS  QAFGRDLGRG  TKHYGLIVVG  HSLGAGTAAI
481    LSFLLRPQYP  TLKCFAYSPP  GGLLSEDAE  YSKEFVTAVV  LGKDLVPRIG  LSQLEGFRRQ  LLDVLRQSTK  PKWRIIVGAT
561    KCI PKSELPE  DQVEVTALAS  TRLWTHPSDL  TIALSASTPL  YPPGRIIHVV  HNHPAEQCCC  CEQEPTFYFA  IWGDNKAFNE
641    VIISPAMLHE  HLPYVMEGL  NKVLENYNKG  KTALLSAAKV  MVSPTVDLT  PELIFQQQPL  PTGPPLPTGL  ALELPATEHR
721    NSSVRSKQS  EMSLEGFSEG  RLLSPVAAAS  AARQDPVELL  LLSTQERLAA  ELQSRRAPLA  TMESLSDTES  LYSFDSRRSS
801    GFRSIRGSPS  LHAVLERDEG  HLFYIDPAIP  EENPSLSSRT  ELLAADSLSK  HSQDTQPLEA  ALGSGGVTP  RPPSAANDEE
881    EAAGGSEGGG  VAPRGELALH  NGRLGDSPPS  QVLEFAEFID  SLFNLDKSS  SFQDLYCMMV  PESPTSDYTE  GPKSPSQQEI
961    LLRAQFEPNL  VPKPRLPFA  SAEPSSGISL  SPSFPLSSSG  ELMDLPTPTGL  SSQECLATDK  IRTSTPTGHG  ASPTKQDDL
1041   ISAR
  
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5.373 PREDICTED: hypothetical protein [Rattus norvegicus]

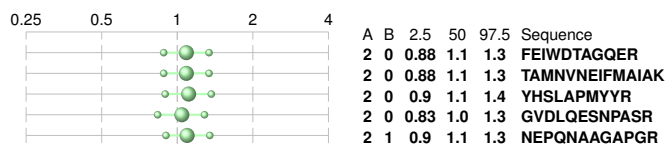
Protein Accession	gi 109510246	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(0.894, 1.31)	
Associated Peptides	2	
Associated Spectra	8	
Coverage	0.2	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.02	1.17
Avg..iTRAQ.Ratio....116.114.	1.06	1.06
Avg..iTRAQ.Ratio....117.114.	1.19	1.44

1 MARAAGITAA ITLALLGVLA LGAGDGDFRL DDALEDTDKK PTPKPPTPKK PSSGDFDLEE ALTGGADED PRRGSRPKPD
 81 PKPPGPPRDS GGISDRDLED VAGHGGRGGG AGDRGTDGAE SEGQFQGLIP GVVAAVLAAL AGAVSSFVAY QKRRLCFREG
 161 GSAFV



5.374 PREDICTED: similar to Ras-related protein Rab-5C [Rattus norvegicus]

Protein Accession	gj 109491867	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(0.916, 1.27)	
Associated Peptides	5	
Associated Spectra	11	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.06	1.31
Avg..iTRAQ.Ratio....116.114.	1.14	1.27
Avg..iTRAQ.Ratio....117.114.	1.23	1.33

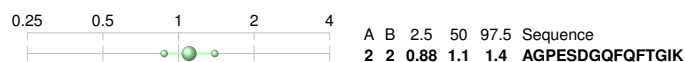


5.375 dapit protein [Rattus norvegicus]

Protein Accession	gj 19424210	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(0.847, 1.38)	

Associated Peptides	1	
Associated Spectra	4	
Coverage	0.259	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.11
Avg..iTRAQ.Ratio....116.114.	1.24	0.996
Avg..iTRAQ.Ratio....117.114.	1.17	1.23

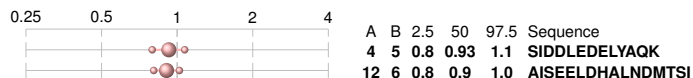
1 MAGPESDGGQF QFTGIKKYFN SYTLTGRMNC VLATYGGIAL LVLYFKLRPK KTPAVKAT



5.376 "tropomyosin 1, alpha isoform i [Rattus norvegicus]"

Protein Accession	gij78000203	
Mean Expression Ratio	0.926	
Median Expression Ratio	0.926	
Credible Interval	(0.799, 1.07)	
Associated Peptides	2	
Associated Spectra	27	
Coverage	0.117	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.98	0.672
Avg..iTRAQ.Ratio....116.114.	0.888	0.936
Avg..iTRAQ.Ratio....117.114.	0.933	0.769

1 MAGSSSLEAV RRKIRSLQEQ ADAAEERAGS LQRELDQERK LRETAEADVA SLNRRIQLVE EELDRAQERL ATALQKLEEA
 81 EKAADSESRG MKVIESRAQK DEEKMEIQEI QLKEAKHIAE DADRKYEEVA RKLVIIESDL ERAEERAELS EGKCAELEEE
 161 LKTVTNNLKS LEAQAEKYSQ KEDKYEEEIK VLSDKLKEAE TRAEFAERSV TKLEKSIDDL EDELYAQKLK YKAISEELDH
 241 ALNDMTSI

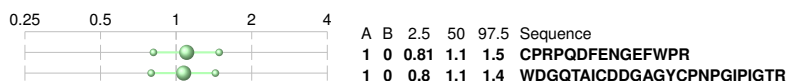


5.377 "B-factor, properdin [Rattus norvegicus]"

Protein Accession	gi 47059181
Mean Expression Ratio	1.08
Median Expression Ratio	1.08
Credible Interval	(0.824, 1.40)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0526
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.48
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.31

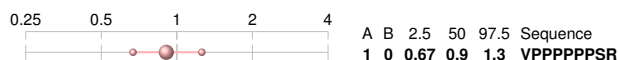
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1      MEGPQLCLVL LVLGLSSGGV SATPVLBARP QVSCSLEGEV IKGGSFQLLQ DGQALEYLCP SGFYYPVQVQ RTCKSTGSWS
81     VLQTRDQKIV KKAECRAIRP PRPQDFENGE FWPRSPYYNL SDQISFQCYD GYTLRGSANR TCQENGRWDG QTAICDDGAG
161    YCPNPGIPIG TRKVGSQYRL EDTVTYHCSR GLVLRGSQQR RCQEGGSWSG TEPSCQDSFM YDSPQEVAAE FLSSLTETIE
241    GADAEDGHSP GEQQKRKIIL DPSGSMNIYM VLDGSDSIGA SNFTGAKRCL ANLIEKVASY GVKPRYGLVT YATVPKVLVR
321    VSEERSSDAD WVTEKLNQIS YEDHKLKSGT NTKKALQAVY SMMSWPGDAP PEGWNRTRHV I IIMTDGLHN MGGDPVTVIE
401    DIRDLLDIGR DRKNPREYDL DYYVFGVGPL VDPVNINALA SKKNNEQHV FVKDMEDLEN VFYKMIDET K SLGLCGMVVE
481    HQKGGDYKQ  FWQAKISVTR PLKGHENCMG AVVSEYFVLT AAHCFTVEDQ KHSIKVNVEG KRRDLEIEEV LFHPNYDING
561    KKAEGISEFY DYDVALIKLK TKLKYSQTLR PICLPCTEGT TRALRLPQTA TCKQHKEELL PMKDVKALFV SEEGKKLTRK
641    EYIKNGEKK ASCERDATKA QGYEKVKVAS EVVTPRFLCT GGVDPYADPN TCKGDSGGPL IVHKRSRFIQ VGVISWGVVD
721    VCKDPRRQQL VPSYARDFHI NLFQVLPWLK EKLKDEDLGF L
  
```



5.378 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gi 109491373
Mean Expression Ratio	0.929
Median Expression Ratio	0.926
Credible Interval	(0.695, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.836
Avg..iTRAQ.Ratio....116.114.	0.789
Avg..iTRAQ.Ratio....117.114.	0.694

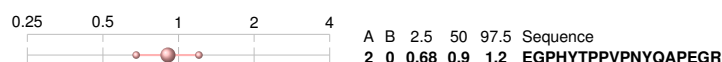


5.379 PREDICTED: similar to mitochondrial ribosomal protein L40 [Rattus norvegicus]

Protein Accession	gij109494702
Mean Expression Ratio	0.926
Median Expression Ratio	0.926
Credible Interval	(0.704, 1.21)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0874
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.25
Avg..iTRAQ.Ratio....116.114.	0.658
Avg..iTRAQ.Ratio....117.114.	0.88

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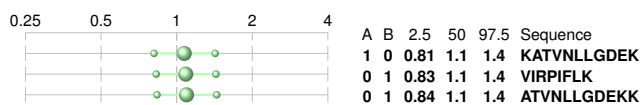
1      MATAAMLCAA RALRPRSWIP GTCQAQVRHT HQRASLLSFW ELIPMRAEPL RKKKKVDPRK DQAAKDRLKK RIRKLERASQ
81     ELVPIEDFIT PVRFLDKSRQ RPQEEHSFEE SERRALLLKR WALYKQQEHE MERDAIRAML EAQQEALEQL KLESTELYAE
161    AIKRDTSLFP FEKEGPHYTF PVPNYQAPEG RYNDITKVYT QVEFKR
    
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5.380 PREDICTED: similar to receptor accessory protein 5 [Rattus norvegicus]

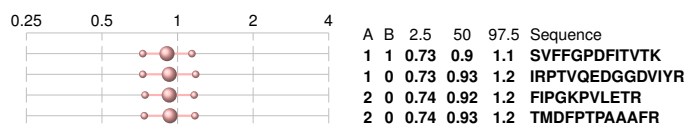
Protein Accession	gij109507117
Mean Expression Ratio	1.08
Median Expression Ratio	1.08
Credible Interval	(0.848, 1.38)
Associated Peptides	3
Associated Spectra	3

Coverage	NA	
	A	B
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.968	0.922
Avg..iTRAQ.Ratio....116.114.	0.998	0.993
Avg..iTRAQ.Ratio....117.114.	1.11	1.41



5.381 PREDICTED: similar to HIRA interacting protein 5 isoform 2 [Rattus norvegicus]

Protein Accession	gij109472303	
Mean Expression Ratio	0.927	
Median Expression Ratio	0.926	
Credible Interval	(0.76, 1.12)	
Associated Peptides	4	
Associated Spectra	7	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.905	0.818
Avg..iTRAQ.Ratio....116.114.	0.999	1.11
Avg..iTRAQ.Ratio....117.114.	0.89	0.58



5.382 "solute carrier family 9, member 2 [Rattus norvegicus]"

Protein Accession	gij 6981560
Mean Expression Ratio	1.08
Median Expression Ratio	1.08
Credible Interval	(0.796, 1.46)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0100
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.83
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	0.788

```

1      MVGLLLGGII FGVDEKSPPA MKTDVFFLYL LPPIVLDAGY FMPTRPFEN LGTIFWYAVV GTLWNSIGIG LSLFGICQIE
81     AFGLSDITLL QNLLFGSLIS AVDPVAVLAV FENIHVNEQL YILVFGESLL NDAVTVVLYN LFKSFCQMKI IQTVDFVAGI
161    ANFFVVGIGG VLIIGILGFI AAFTRRFTHN IRVIEPLVVF LYSYLSYITA EMFHLSGIMA ITACAMTMNK YVEENVSQKS
241    YTTIKYFMKM LSSVSETLIF IFMGVSTVVK NHEWNWAFVC FTLAFCLIWR ALGVFVLTQV INWFRTIPLT FKDQFIIAYG
321    GLRGAICFAL VFLLPATVFP RKKLFITAAI VVIFFTVFIL GITIRPLVEF LDVKRSNKKQ QAVSEEIHR FFDHVKTGIE
401    DVCGHWHGNF WRDKFKKFD KYLRKLLIRE NQPKSSIVSL YKLEIKHAI EMAETGMIST VPSFASLND RREEKIRKLT
481    GEMDEIREIL SRNLYQIRQR TSYNRHNL ADTSEKAKE ILIRRRHSLR ESLRKDNSLN RERRASTSTS RYLSLPKNTK
561    LPEKLQKKNK VSNADGNSD SDMDGTTVLN LQPRARRFLP DQFSKKASPA YKMEWKNEVD VGSARAPPSV TPAPRSKEGG
641    TQTPGVLRQP LLSKDQRFGR GREDSLTEDG PPKPPRLVR RASEPGNRKG RLGNEKP
    
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5.383 PREDICTED: similar to Telethonin (Titin cap protein) [Rattus norvegicus]

Protein Accession	gij 109491807
Mean Expression Ratio	0.928
Median Expression Ratio	0.926
Credible Interval	(0.69, 1.24)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0479
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.899
Avg..iTRAQ.Ratio....116.114.	0.675
Avg..iTRAQ.Ratio....117.114.	0.815

NHLBI Zile/Grant, Aged Rat

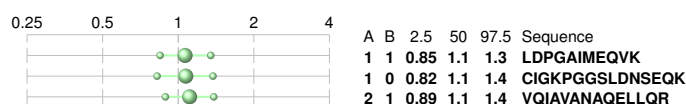
1 MATSELSQV SEENQERR**EA FWA**EWFDLTL STRPEEGCSL HEEDTQRHET YHRQGQCQAV VQRSPWLVMR LGILGRGLQE
 81 YQLPYQRVLP LPIFTPTKVG **ATKEEREETP** IQLRELLALE TALGGQCVER QDVAEITKQL PPVVPVSKPG PLRRTLRSRM
 161 SQEAQRG



5.384 translocase of inner mitochondrial membrane 13 homolog [Rattus norvegicus]

Protein Accession	gj 21955146	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(0.875, 1.32)	
Associated Peptides	3	
Associated Spectra	6	
Coverage	0.421	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.907	1.46
Avg..iTRAQ.Ratio....116.114.	1.05	1.57
Avg..iTRAQ.Ratio....117.114.	1	1.25

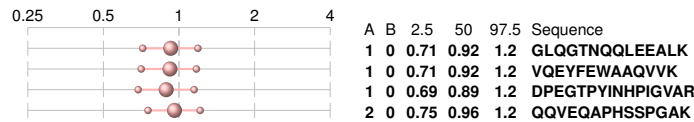
1 MDSGFGSDFG GTGGGK**LDPG AIMEQVKVQI AVANAQELLQ** RMTDKCFRKC **IGKPGGSLDN** SEQKCIAMCM DRYMDAUNT
 81 SRAYNSRLQR ERANM



5.385 PREDICTED: similar to CG11900-PA [Rattus norvegicus]

Protein Accession	gj 109462139
Mean Expression Ratio	0.927
Median Expression Ratio	0.927
Credible Interval	(0.75, 1.15)
Associated Peptides	4

Associated Spectra Coverage	5 NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.928
Avg..iTRAQ.Ratio....116.114.	1.28
Avg..iTRAQ.Ratio....117.114.	0.722



5.386 Arg/Abi-interacting protein ArgBP2 [Rattus norvegicus]

Protein Accession	gij16758606	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(0.94, 1.24)	
Associated Peptides	9	
Associated Spectra	17	
Coverage	0.115	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.16	1.07
Avg..iTRAQ.Ratio....116.114.	0.976	0.75
Avg..iTRAQ.Ratio....117.114.	1.38	0.818

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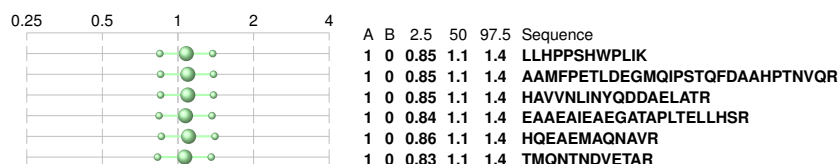
1      MNTDSGGCAR  KRAAMSVTLT  SVKRVQSSPN  LLAAGRESHS  PDSAWRSYNG  RNPETLNGDA  TYSSLAAKGF  RSVRPNLQDK
81     KSPtQSHITI  NGNSGGAVSP  VSYyQRFFSP  SAYSLPASLN  SSIIMPHGRS  LDSABTYSQH  AQSLDGTMGS  SIPLYRSSEE
161    EKRVTVIKAP  HYPGIGPVDE  SGIPTAIRTT  VDRPKDWYKT  MFKQIHMVHK  PDEDTDMYNT  PYTYNAGLYN  SPYSAQSHPA
241    AKTQTYRPLS  KSHSDNGTDA  FKSAPSPVPP  PHVFPRPRDQ  SSTEKHDWDP  PDRKVDTRKF  RSEPRSIFEY  EPGESSILQH
321    ERPVSVYQSS  IDRSLERPSS  SASMAGDFRK  RRKSEPAVGP  PRGLGDHSS  RTSPGRADLP  GSSTFTSF  ISSSPSSPSR
401    AQGGDDSKMC  PPLCSYSGLN  GSPSSELECC  GAYRRHLDVP  QDSQRAITFK  NGWQMARQNA  EIWSSTEEAV  SPKIKSRSCD
481    DLLNDDCGSF  PDPKTKSESM  GSLLCDEGSK  ESDPMTWTSF  YIPEVCGNSR  SRLKHSRSHN  APGFLKMYKK  MHRINRKDLM
561    NSEVICSVKS  RILQYEKEQQ  HRGLLHGWSQ  SSTEEVPRDV  VPTRISEFEK  LIQKSKSMPN  LGDEMLSPVT  LEPPQNGLCP
641    KRRFSIESLL  EETQVRHPS  QGQRSCKSNT  LVPIHIEVTS  DEQPRTHMEF  SDSDQDGVVS  DHSDNVHVER  SSFCSESDFD
721    HFSFTSSESF  YGSSHHHHHH  HHHHGHFISS  CKGRCPASYT  RFTTMLKHER  AKHENIDRPR  RQDMDPGLSK  LAFLVSPVFF
801    RRRKVLTPQK  QTEQAKCKAS  VVEALDSALK  DICDQIKAEK  RRGSLPDNSI  LHRLISELLP  QIPKRNSSLN  ALKRSPMHQP
881    FHPLPQDGAI  HCPLYQNDCG  RMPHSASFPD  VDTTSSYHAQ  DYGSVLSLQD  HESPRSYSST  LTDLGRSVSR  ERRGTPEKEV
961    KLPKAVYDF  KAQTSKELSF  KRGDTVYILR  KIDQNWYEGE  HHGRVGIFFI  SYVEKLTPPE  KAQPARPPPP  VQPGEIGEAI
1041   AKYNFNADTN  VELSLRKGDR  IILLKRVDQN  WYEGKIPGTN  RQGIFPVSYV  EVVKRNTKGS  EDYPDPPLPH  SYSSDRIYSL
1121   SSNKPQRPVF  SHENIQGGGE  PFQALYNYTP  RNEDELELRE  SDVVDVMEKC  DDGWFVGTSR  RTKFFGTFFG  NYVERL

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Credible Interval	(0.885, 1.31)
Associated Peptides	6
Associated Spectra	6
Coverage	0.134
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.36
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.17

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1   MATQADLMEL DMAMEPDRKA AVSHWQQQSY LDSGIHSGAT TTAPSLSGKG NPEEEDVDTS QVLYEWEQGF SQSFTQEQVA
81  DIDGQYAMTR AQRVRAMFPE TLDEGMQIP STOFDAAHPT NVQFLAEP SQ MLKHAVVNLI NYODDAELAT RAIPELTKLL
161 NDEDQVVVVK AAVMVHQLSK KEASRHAIMR SPQMVAIVR TMQNTNDVET ARCTAGTLHN LSHHREGLLA IFKSGGIPAL
241 VKMLGSPVDS VLFYAITTLH NLLHQEGAK MAVRLAGGLQ KMVALLNKTN VKFLAITTDC LQILAYGNQE SKLIILASGG
321 PQALVNIMRT YTYEKLWTT SRVLKVLVSV SSKNPAIVEA GGMQALGPHL TDPSQRLVQN CLWTLRNLSD AATKQEGMEG
401 LLGTLVQLLG SDDINVVVTC AGILSNLTCN NYKNKMMVQC VGGIEALVRT VLRAGDREDI TEPAICALRH LTSRHOEAE
481 AQNAVRLHYG LPVVVLLHFP PSHWPLIKAT VGLIRNLALC PANHAPLREQ GAIPRLVQLL VRAHQDTQRR TSMGGTQQQF
561 VEGVRMEIV EGCTGALHIL ARDVHNRIVI RGLNTIPLFV QLLYSPIENI QRVAAGVLCE LAQDKFAAEA TEARGATAPL
641 TELLHSRNEG VATYAAAVLF RMsEDKPDY KKRLSVELTS SLFRTEPMAW NETADLGLDI GAQGEALGYR QDDPSYRSFH
721 SGGYGQDALG MDPMMEHMGM GHHPGADYPV DGLFPDLGHAQ DLMDGLPPGD SNQLAWFDTD L
    
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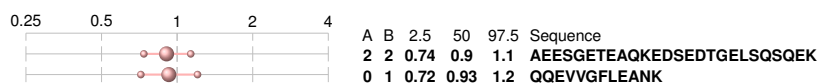
5.389 PREDICTED: similar to SH3 domain-binding glutamic acid-rich protein (SH3BGR protein) [Rattus norvegicus]

Protein Accession	gij109494049	
Mean Expression Ratio	0.928	
Median Expression Ratio	0.927	
Credible Interval	(0.748, 1.15)	
Associated Peptides	2	
Associated Spectra	5	
Coverage	0.186	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.726	0.834
Avg..iTRAQ.Ratio....116.114.	0.584	1.45
Avg..iTRAQ.Ratio....117.114.	0.532	0.907

NHLBI Zile/Grant, Aged Rat

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1      MVIKVFVATS  SGSIAIRKQ  QEVVGFLEAN  KIDFKELDIA  GDEDNRKWMR  ENVPGEKKPQ  NGIPLPPQIF  NEEQYCGDFD
81     SFFSAKEENI  IYSFLGLAPP  PGSKVTKSEE  ASSLPNGDVA  GEAEGAAGET  EKAEESGETE  AQKEDSED TG  ELSQSQEI KE
161    EGEEGEKGE  EGETAETEE  ATEGGAEGER  EEEPEEEGGE  EEDS
  
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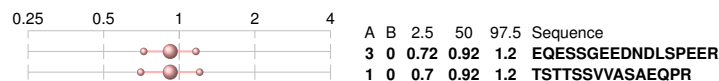


5.390 "protein phosphatase 1, regulatory (inhibitor) subunit 2 [Rattus norvegicus]"

Protein Accession	gij41281691
Mean Expression Ratio	0.927
Median Expression Ratio	0.928
Credible Interval	(0.732, 1.17)
Associated Peptides	2
Associated Spectra	4
Coverage	0.156
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.889
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	0.941

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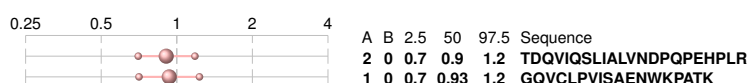
1      MAASTASHRP  IKGILKNKTS  TTSSVVASAE  QPFR TVEEEL  SKKSQKWDEM  NILATYHPAD  KDYGLMKIDE  PDTPYHNMIG
81     DDEDVCS DSE  GNEVMTPEIL  AKKLAAAE GS  EPKFRTRQ E  SSGEEDNDLS  PEEREKRRQF  EMKRKLHYNE  GLNIKLARQL
161    ISKDLHDDDE  DEEMSETADA  DSMNIEESNQ  GSTAGDHLQH  KSQSS
  
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5.391 PREDICTED: similar to Ubiquitin-conjugating enzyme E2 L3 (Ubiquitin-protein ligase L3) (Ubiquitin c

Protein Accession	gij109494773
Mean Expression Ratio	0.928
Median Expression Ratio	0.928
Credible Interval	(0.728, 1.19)

Associated Peptides	2
Associated Spectra	3
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.883
Avg..iTRAQ.Ratio....116.114.	0.93
Avg..iTRAQ.Ratio....117.114.	0.95



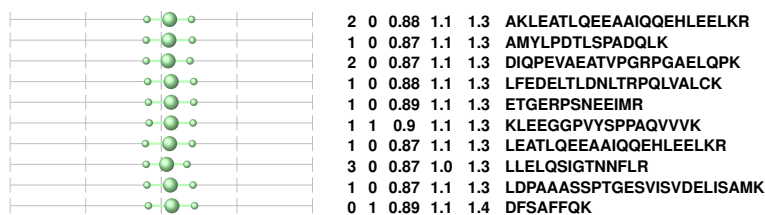
5.392 leucine zipper-EF-hand containing transmembrane protein 1 [Rattus norvegicus]

Protein Accession	gij54400736	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(0.928, 1.25)	
Associated Peptides	10	
Associated Spectra	15	
Coverage	0.215	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.17
Avg..iTRAQ.Ratio....116.114.	1.05	0.896
Avg..iTRAQ.Ratio....117.114.	1.34	1.27

```

1      MASILLRSCR GRGPARLASP RAASPRGSLR DRACLSCTRT VGLTSHESVL SRCCTPANPV YLYFKSEPLS CWTQRPECQG
81     TVARAAWTPA SARLVVTGPQ YLPVRGWHSS SPLGEDSMIE KSLKSLKDKN KLEEGGPVY SPPAQVVVKK SLGQKILDEL
161    KHYHGFRLK WIDTKIAARM LWRILNGHTL TRRERRQFLR ICADLFRLVP FLVVFVVVPM EFLLPVVVKL FPNMLPSTFE
241    TQSIKEERLK KELRVKLELA KFLQDTIEM ALKNKAAKGN ATKDFSAFFQ NIRETGERPS NEEIMF SKL FEDELTLDNL
321    TRPQLVALCK LLELQSIGTN NPLRFQLTMR LRSIKADDKL ISEEGVDSL T VKEQLAACRA RGMRALGVTE DRLKGQLKQW
401    LDLHLYHEIP TSLLLILSR AM YLPDTLSPAD QLESTLQTL P EIVAKEAQQV AAEVEGEQVD NKAKLEATLQ EEAIIQQEHL
481    EELKRAAETA KDIQPEVAEA TYPGRPGAEL QPHMVDVIPP SEILKDTAPV LEGLKGEET KEEIDILSDA CSKLKEQKKS
561    LTRKEEEL LKEDVQDYSE DLQEIKKELS KTGDEKYIEE STASKRLSKR VQQMIGQIDG LITQLETTQQ NGKLDPAAS
641    SPTGESVISV DELISAMQI KHIPEHKLIS LTSALDENKD GNINIDDLVK VIDLVNKEDV QISTTQVAEI VATLEKEEKV
721    EEKEKAKEKA EKEAAEVKN
    
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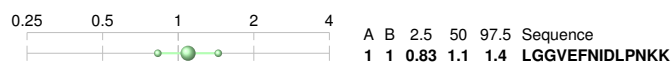




5.393 ATX1 (antioxidant protein 1) homolog 1 [Rattus norvegicus]

Protein Accession	gj 16758088	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(0.828, 1.4)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.206	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	1.17
Avg..iTRAQ.Ratio....116.114.	1.18	1.16
Avg..iTRAQ.Ratio....117.114.	1.24	0.999

1 MPKHEFSVDM TCGGCAEAVS RVLNKLGGVE FNIDLPNKKV CIESEHSSDI LLATLNKTGK AVSYLGPK



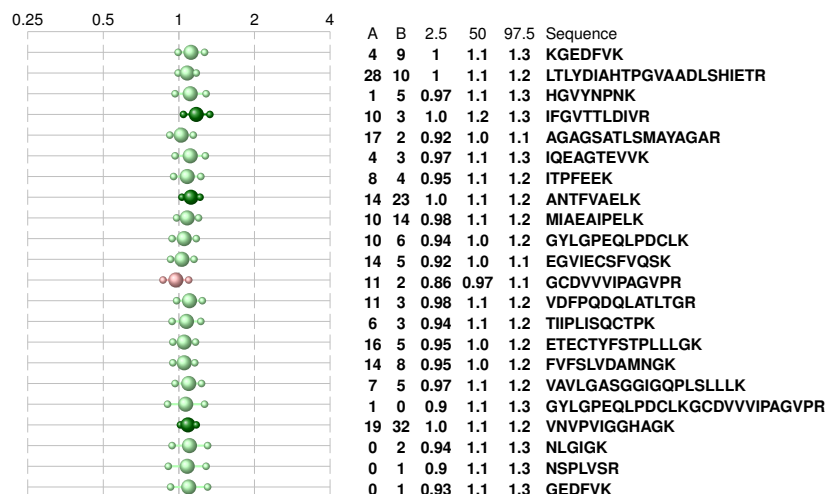
5.394 "malate dehydrogenase, mitochondrial [Rattus norvegicus]"

Protein Accession	gj 42476181	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(1.02, 1.13)	
Associated Peptides	22	
Associated Spectra	351	
Coverage	0.695	

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.09
Avg..iTRAQ.Ratio....116.114.	1.11	1.18
Avg..iTRAQ.Ratio....117.114.	1.01	0.902

```

1      MLSALARPVG AALRRSFSTS AQNNAKVAVL GASGGIGQPL SLLKNSPLV SRLTLYDIAH TPGVAADLSH IETPANVKGY
81     LGPEQLPDCL KGCDVVVIPA GVPRKPGMTR DDLFNTNATI VATLTAACAQ HCPEAMICII SNPVNSTIPI TAEVFKKHGV
161    YNPNKIFGVT TLDIVRANTF VAEKGLDPA RVNVPVIGGH AGKTIIP LIS QCTPKVDFPQ DQLATLTGRI QEAGTEVVKA
241    KAGAGSATLS MAYAGARFVF SLVDAMNGKE GVIECSFVQS KETECTYFST PLLLKGKLE KNLGIGKITP FEEKMIAEAI
321    PELKASIKKG EDFVFNMK
    
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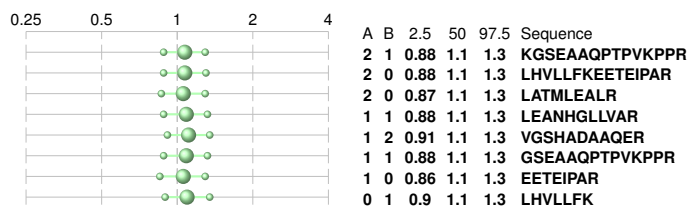


5.395 "protein kinase C, delta binding protein [Rattus norvegicus]"

Protein Accession	gi 19745164	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(0.932, 1.23)	
Associated Peptides	8	
Associated Spectra	16	
Coverage	0.232	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	1.05
Avg..iTRAQ.Ratio....116.114.	0.98	1.20
Avg..iTRAQ.Ratio....117.114.	1.06	1.34

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1      MGESALEPFP VPGAPAGGPV HAVTVVTLE KLATMLEALR ERQGGLAERQ GGLAGSVRRI QSGLGALSRS HDTTSNTLAQ
81     LLAKAERVGS HADAAQERAV HRAAQVQRLE ANHGLLVARG KLHVLLFKEE TEIPAFQAFQK APELLGPEQDQ LVLGPEQPED
161    EVGESSDEEP VESRAQRLRR TGLQKVQSLK RAFSSRKGSE AAQPTPVKPPF LGGPVRNSEG PAEGQPAAQP AMEPVLPSSAL
241    EPEFPQPTKE DPERFVLQIE SAA
    
```



Protein Accession	gij13162357
Mean Expression Ratio	1.08
Median Expression Ratio	1.08
Credible Interval	(0.791, 1.45)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0156
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.46
Avg..iTRAQ.Ratio....116.114.	1.40
Avg..iTRAQ.Ratio....117.114.	1.73

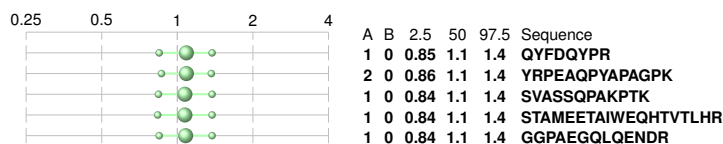
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1      MSNEVETSTT NGQPDQQAAP KAPSKKEKKK GSEKTDEYLL ARFKGDGVKY KAKLIGIDDV PDARGDKMSQ DSMMKLKGMA
81     AAGRSQGQHK QRIWVNISLS GIKIIDEKTG VIEHEHPVNK ISFIARDVTD NRAFGYVCGG EGQHQFFAIK TGQQAEPLVV
161    DLKDLFQVIY NVKKKEEEKK KVEEANKAEE NGSEALMTLD DQANKLKLGV DQMDLFGDMS TFPDLNPNTE SRDILLVDLN
241    SEIDTNQNSL RENPFLTNGV TSCSLPRPKP QASFLPESAF SANLNFFPFP NPDPPRDDPF AQPDQSPSS FHSLSADQK
321    KANPGSLSTP QSKGPLNGDT DYFGQQFDQI SNRTGKQEAQ GGPWPYPSSQ TQQAVRTQNG VSEKEQNGFH IKSSPNPFVQ
401    SPPKGLSVPN GVKQDLESSV QSSAHDSIAI IPPPQSTKPG RGRRTAKSSA NDLLASDIFA SEPPGQMSPT GQPAVPPQANF
481    MDLFKTSAPA PMGSGPLVGL GTVPVTPPQA GPWTPVVFPT STTVVPGAI I SGQPSGFGQP LVFGTTPAVQ VWNQPSFAT
561    AASPPPPAVW CPTTSVAPNT WSSTSP LGNP FQSSNIFPFS TISTQSFPQP MMSSVLVTFP QPPPRNGPLK DTLSDAFTGL
641    DPLGDKEVKE VKEMFKDFQL RQPPLVPSRK GETPSSGTSS AFSSYFNNKV GIPQEHVDHD DFDANQLLNK INEPPKPPAPR
721    QGVLSGTKSA DNSLENPFSSK GFSSTNPSVV SQPASSDAHR SPPFGNFFA
    
```



5.397 PREDICTED: similar to tight junction protein 1 [Rattus norvegicus]

Protein Accession	gij109462106
Mean Expression Ratio	1.08
Median Expression Ratio	1.08
Credible Interval	(0.882, 1.31)
Associated Peptides	5
Associated Spectra	6
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.23
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	1.28



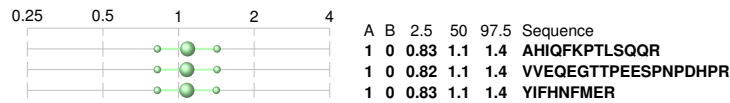
5.398 inter-alpha-inhibitor H4 heavy chain [Rattus norvegicus]

Protein Accession	gij126722991
Mean Expression Ratio	1.08
Median Expression Ratio	1.08
Credible Interval	(0.842, 1.37)
Associated Peptides	3
Associated Spectra	3
Coverage	0.0439
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.37
Avg..iTRAQ.Ratio....116.114.	1.07
Avg..iTRAQ.Ratio....117.114.	1.23

NHLBI Zile/Grant, Aged Rat

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1      MKSPAPAHMW NIVLVLLSL AVLPITTEK NGIDIYSLTV DSRVSSRF AH TVVTSRVVNR ADTVQEATFQ VELPRKAFIT
81     NFSMIIDGVT YPGVVKEKAE AQKQYTAAVG RGE SAGLVKT TGRKTEQFEV SVN VAPGSKT TFE LIYQELL QRR LGM YELL
161    LKVRPEQLVK HLQMDIYIFE PQGISTLETE STFMTQELAN ALTT SQNKTK AHIQFKPTLS QQE KSNQEQD TVLDGDFTVR
241    YDVRSSSTGG TIQIENGYFV HFFAPEDLPT MAKNVLFVID KSGSMAGKKI QQTREALIKI LKDLSTQDQF NII VFSGEAN
321    QWEQLLVQAT EENLNRAVDY ASKIPAQGGT NINKAVLSAV ELLDKSNQAE LLPSKSVSLI ILLTDGEP TV GETNPKI IQK
401    NTQEAINGRY SLFCLGFGFD VNYPFLEKLA LDNGGLARRI YEDSDSALQL QDFYQEVANP LLSSVTFEYP SNAVEDVTRY
481    NFQHHFKGSE M VVAGKLRDQ GPDVLLAKVS GQMH LQNITF QTEASIAQQE KEFQGP KYIF HNFMERLWAL LTIQQQLEQR
561    ISASGAEL EA LEAQVNLNLS KYNFV TPLTH MVVT KPEDQE QFQVAEK PTE V DGGVWSILS AVQRHFKTPT TGSKLLTSRL
641    RGNRFQTL SR LGDGLVGS RQ YMP PPG LPPG PGLP GPPGPP GHPHF ASSID YGRQPSLGRV LDLP SLSQD PAGPSLMLP
721    KVVVEQEGTTP EESPNDHPR APTI ILLP LG SGVDQLCVDI LHSEKPMKLF VDI NQGLEV GKYEKNI GFS WIEVTILKPH
801    LQVHATPERL VVTRGRKNSE YKWKKT LFSV LPGLKMTMDK TGLLQLSGPD KVTISL LSLD DPQRGLMLLL NDTHHFSNDI
881    TGELGQFYQD I IWD DTKQTV RVLGIDYPAT RELKLSYQDG FPGTEISCWT VKI
    
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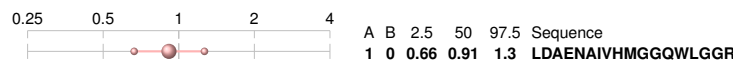


5.399 Tial1 cytotoxic granule-associated RNA binding protein-like 1 [Rattus norvegicus]

Protein Accession	gi 61557246
Mean Expression Ratio	0.93
Median Expression Ratio	0.93
Credible Interval	(0.69, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0459
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.869
Avg..iTRAQ.Ratio....116.114.	0.739
Avg..iTRAQ.Ratio....117.114.	0.786

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1      MMEDDGGPRT LYVGNLSRDV TEVLILQLFS QIGPCKSCKM ITEQPDSRRV NSSVGF SVLQ HTSNDPYCFV EFYEHRDAAA
81     ALAAMNGRKI LGKEVKVNWNA TFPSSQK KDT SNHFHVFVGD LSPEITTE DI KSAFAPFGKI SDARVVKDMA TGKSKGYGFV
161    SFYNK LDAEN AIVHMGGQWL GGRQIRTNWA TRKPPAPKST QETNTKQLRF EDVVNQSSPK NCTVYCGGIA SGLTDQLMRQ
241    TFSFPFGQIME IRVFPEKGY S FVRFS THESA AHAIVSVNGT TIEGHVVVKY WGKESPDMTK NFQQVDYSQW QGWSQVYGNP
321    QQYGQYMANG WQVPPYGVYV QPWNQQGFV DQSPSAAWMG GFQAQPPQGG APPPVIPPPN QAGYGMASFP TQ
    
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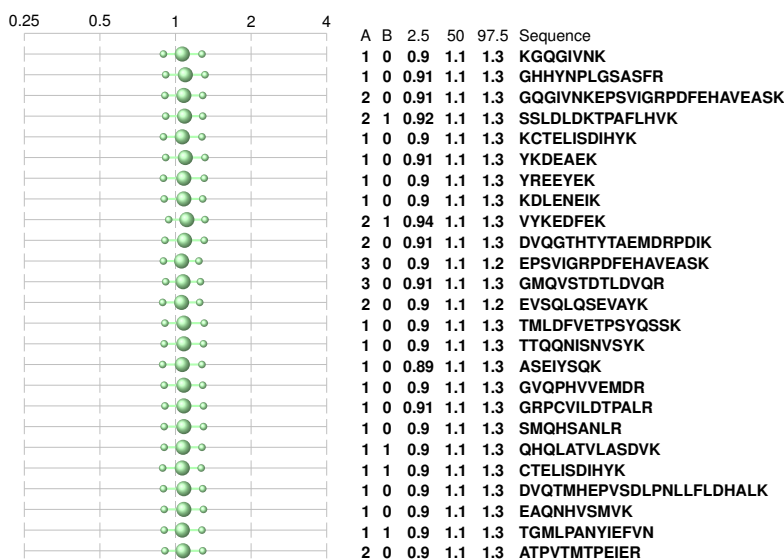
5.400 PREDICTED: similar to Nebulette (Actin-binding Z-disk protein) [Rattus norvegicus]

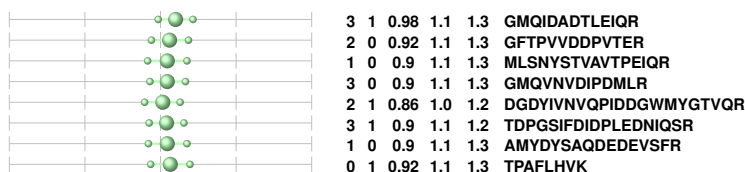
Protein Accession	gij109505234	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.08	
Credible Interval	(0.993, 1.17)	
Associated Peptides	33	
Associated Spectra	59	
Coverage	0.385	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.19	1.08
Avg..iTRAQ.Ratio....116.114.	1.03	1.04
Avg..iTRAQ.Ratio....117.114.	1.18	0.921

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1   MKVPVSGDVK EETEENVEE EEKPEDEVFL KPVVEDLSME LARKCTELIS DIHYKEDYRK SKDKCTSVD TPTLNHVKNI
81  SAFISETKYK GTIKADLSNC LYKDMPATID SVFAREVSQL QSEVAYKQKH EAEKGLSDYA HMKEPPEVRH AMEVNRRHQS
161 ISYRKDVQGT HTYTAEMDRP DIKKATQISK IISNAEYKKG QGIVNKEPSV IGRPDFEHAV EASKLSSQVK YKEKFDNEMK
241 GKGHHYNPLG SASFRQHOLA TVLASDVVKYK KDVQTMHEPV SDLPNLLFLD HALKASRMLS GWEYKKNFEE NKGSYHFDAE
321 APEHLHHRGN ATLQSQVK YR EYEEKNKGKF MLDFVETPSY QSSFEAQKMQ SEKVVKEDFE KEIKGR SSLD LDKTPAFLVH
401 KHISNLMREK EYKKDLENEI FGKGMELSSE VLDIQRAKRA SEMASEKEYK KDLELEIKGK GMQIDADTLE IQRVKRAAKI
481 ASEKDYKRDL ETEIKGKGMQ VSTDTLDVQR AKRASEMASQ KQYRKDLENE IKGKGMQVNV DIPDMLFAKR ASEIYSQFKY
561 KDEAEKMLSN YSTVAVTPEI QEIKTTQQNI SNVSYKEEVR AGTAVRNTPE IERVKNQQHN ISSVKKRKEGI KHATAISDPL
641 ELKRVTEKPE GLQRFQYKEP TYKATPVTMT PEIERVRRNQ EQLSAVKHKG ELKQATSILD LPGLKRVREN QKTISNVYYK
721 GQLGRATALS VTPEMERVKK NQENISSVKY TQDHKQMKGR PCVILDTPAL HVKEAQNHV SMVKYHEDFE KTKGRGFTPV
801 VDDPVTERVR KNTQVVSDAA YKGVQPHVVE MDRRPGIIVD LKVWRTDPGS IFDIDPLEDN IQRSLHMLS EKASQYQSRL
881 SRSHSGSTFG TGLGDDKSEI SELYPSFSCC SEVTRPSDEG APVLPGAYQQ SHSQGYGYMH QTSVSSVRSM QHSANLRTYR
961 AMYDSAQDE DEVSFRDGDY IVNVQPIDDG WMYGTVQRTG RTGMLPANYI EFVN

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5.401 N-acylsphingosine amidohydrolase 1 [Rattus norvegicus]

Protein Accession	gi 40254747
Mean Expression Ratio	0.93
Median Expression Ratio	0.93
Credible Interval	(0.713, 1.21)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0457
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.93
Avg..iTRAQ.Ratio....116.114.	0.909
Avg..iTRAQ.Ratio....117.114.	0.798

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1      MLGRSLLTWV LAAAVTCAQA QQVPPWTEDC RKSTYPPSPG TYRGPVPWYT INLDLPPYKR WHELLAHKAP VLRTLVSNIS
81     NLVNAFVPSG KIMQMVDEKL PGLIGSIPGP FGEEMRGIAD VTGIPLGEEI SFNIFYELFT MCTSIIITEDG KGHLLHGRNM
161    DFGIFLGWNI NNNTWVVTEE LKPLTVNLDF QRNNKTVFKA TSFAGYVGML TGFKPGLLSL TLNERFSLNG GYLGILEWFM
241    GKKNAQWVGF ITRSVLENST SYEEAKNILT KTKITAPAYF ILGGNQSSEG CVITRERKES LDVYELDPKH GRWYVVQTNV
321    DRWKNTLFLD DRRTPAKKCL NHTTQKNLSF ATIYDVLSTK PVLNKLTVFT TLIDVTKDQF ESHLRDCPDP CIGW
    
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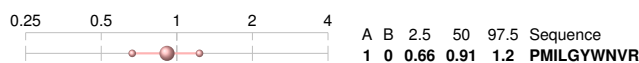


5.402 "glutathione S-transferase, mu 1 [Rattus norvegicus]"

Protein Accession	gi 8393502
Mean Expression Ratio	0.927
Median Expression Ratio	0.93
Credible Interval	(0.69, 1.24)
Associated Peptides	1
Associated Spectra	1

Coverage	0.0459
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.813
Avg..iTRAQ.Ratio....116.114.	0.714
Avg..iTRAQ.Ratio....117.114.	0.839

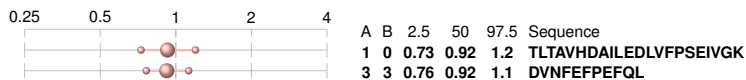
1 MPMLIGYNNV RGLTHPIRL L EYTDSSYEE KRYAMGDAPD YDRSQWLNEK FKLGLDFPNL PYLIDGSRKI TQSNAIMRYL
 81 ARKHHLCGET EEERIRADIV ENQVMDNRMQ LIMLCYNPDF EKQKPEFLKT IPEKMLYSE FLGKRPWFAG DKVTYVDFLA
 161 YDILDQYHIF EPKCLDAFPN LKDFLARFEG LKKISAYMKS SRYLSTPIFS KLAQWSNK



5.403 hypothetical protein LOC497813 [Rattus norvegicus]

Protein Accession	gj 66730357	
Mean Expression Ratio	0.931	
Median Expression Ratio	0.93	
Credible Interval	(0.759, 1.16)	
Associated Peptides	2	
Associated Spectra	7	
Coverage	0.17	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.871	0.457
Avg..iTRAQ.Ratio....116.114.	0.937	1.10
Avg..iTRAQ.Ratio....117.114.	0.916	1.35

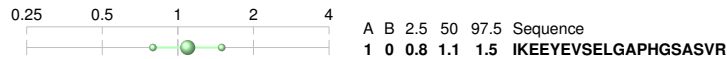
1 MFSSSAKIVK PNGEKPDEF E SGISQALLEL EMNSDLKAQL RELNITAAKE IEVGGGRKAI IIFVVPVQLK SFQKIQVRLV
 81 RELEKKFSGK HVVFIAQRR I LPKPTRKSRT KNKQKRPRSR TLTAVHDAIL EDLVFPSEIV GRIRVRKLDG SRLIKVHLDK
 161 AQQNVEHKV ETFSGVYK L TGKDVNFEFF EFQL



5.404 PREDICTED: similar to Interferon-inducible protein [Rattus norvegicus]

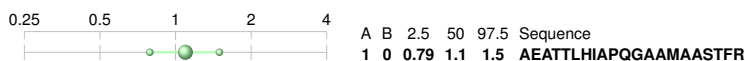
Protein Accession	gi 109463159
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.791, 1.44)
Associated Peptides	1
Associated Spectra	1
Coverage	0.146
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.25
Avg..iTRAQ.Ratio....116.114.	1.56
Avg..iTRAQ.Ratio....117.114.	1.46

1 MNHTSQAFVN AATGGQPPNY ER**IKEEYEVS** ELGAPHGSAS VRTTVINMPR EVSVPDHVVW SLFNTLFMNF CCLGFIAYAY
 81 SVKSRDRKMV GDMTGAQAYA STAKCLNISS LVLSILMVII TIVTVVIAAL NAPRLQT



5.405 PREDICTED: similar to Complement component C8 gamma chain precursor [Rattus norvegicus]

Protein Accession	gi 62644736
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.797, 1.44)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.47
Avg..iTRAQ.Ratio....116.114.	1.28
Avg..iTRAQ.Ratio....117.114.	1.50

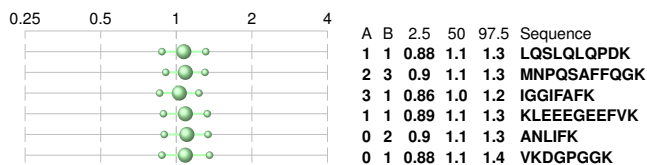


5.406 sterol carrier protein 2 [Rattus norvegicus]

Protein Accession	gij50356003	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.928, 1.24)	
Associated Peptides	6	
Associated Spectra	16	
Coverage	0.0987	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	1.08
Avg..iTRAQ.Ratio....116.114.	0.954	1.17
Avg..iTRAQ.Ratio....117.114.	0.87	1

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1      MPSVALNSPR LPRVFVVGVG MTKFMKPGGE NSRDYDPLAK EAGQKALADR QIPYSAVEQA CVGYVYGEST CGQRAIYHSL
81     GLTGIIPIINV NNNCSTGSTA LFMAQQLVQG GLANCVLALG FEKMEKGS LG TKYSDRSNPL EKHDVLINK YGMSACPFAP
161    QLFGSAGKEH METYGTKVEH FAKIGWKNHK HSVNNPYSQF QDEYSLDEIM KSRPVDFDFT VLQCCPTSDG AAAAIVSSEE
241    FVQKHGLQSK AVEIVAQEMV TDMPTTFEEK SVIKMVG YDM SKEAARKCYE KSGLGPSD VD VIELHDCFST NELLTYEALG
321    LCPFEGGGAL VDRGDNTYGG KWVINPSSGL ISKGHPLGAT GLAQCAELCW QLRGEAGKRQ VPGAKVALQH NLGLGGA AVV
401    TLYRMGFPEA ASSFRTHQIS AAPTSSAGDG FKANLIFKEI EKLEEEGEE FVKLGGIFA FRVKDGGPGGK EATWVVDVKN
481    GKGSVLPDSD KKADCTITMA DSDLLALMTG KMNPQSAFFQ GK LKIAGNMG LAMK LQSLQL QPDKAKL
    
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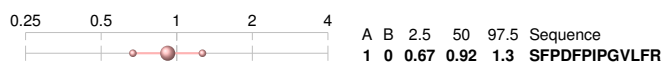


5.407 adenine phosphoribosyl transferase (predicted) [Rattus norvegicus]

Protein Accession	gij61556832	
Mean Expression Ratio	0.934	
Median Expression Ratio	0.93	
Credible Interval	(0.704, 1.25)	
Associated Peptides	1	

Associated Spectra	1
Coverage	0.0722
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.801
Avg..iTRAQ.Ratio....116.114.	0.704
Avg..iTRAQ.Ratio....117.114.	0.85

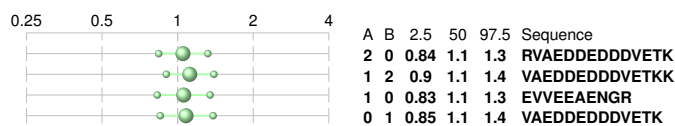
1 M E S E L Q L V A R R I R S F P D F P I P G V L F R D I S P L L K D P D S F R A S I R L L A G H L K S T H G G K I D Y I A G L D S R G F L F G P S L A Q E L G
 81 V G C V L I R K R G K L P G P T V S A S Y S L E Y G K A E L E I Q K D A L E P G Q K V V I V D D L L A T G G T M C A A C E L L S Q L R A E V V E C V S L V E L T
 161 S L K G R E K L G P V P F F S L L Q Y E



5.408 prothymosin alpha [Rattus norvegicus]

Protein Accession	gj 11120684	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.885, 1.3)	
Associated Peptides	4	
Associated Spectra	7	
Coverage	0.223	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.918	1.20
Avg..iTRAQ.Ratio....116.114.	0.92	1.16
Avg..iTRAQ.Ratio....117.114.	1.16	1.42

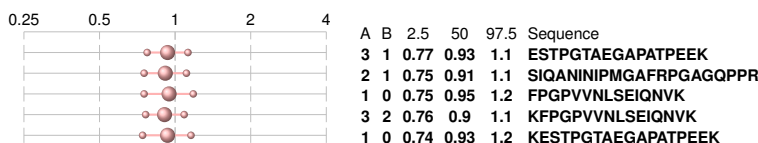
1 M S D A A V D T S S E I T T K D L K E K E V V E E A E N G R D A P A N G N A Q N E E N G E Q E A D N E V D E E E E E G G E E E E E E E G D G E E E D G D E D
 81 E E A E A P T G K R V A E D D E D D V E T K K Q K K T D E D D



5.409 "small muscle protein, X-linked [Rattus norvegicus]"

Protein Accession	gj 16758124	
Mean Expression Ratio	0.93	
Median Expression Ratio	0.931	
Credible Interval	(0.793, 1.09)	
Associated Peptides	5	
Associated Spectra	14	
Coverage	0.659	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.871	1.02
Avg..iTRAQ.Ratio....116.114.	0.924	0.83
Avg..iTRAQ.Ratio....117.114.	1.00	0.646

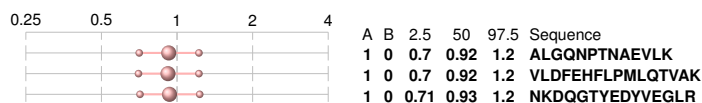
1 MSKQPISNVR SIQANINIPM GAFRPGAGQP PRRKESTPGT AEGAPATPEE KKPVPGMKKF PGPVVNLSEI QNVFSELKYV
 81 PKGEQ



5.410 "PREDICTED: similar to myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Rattus nor]"

Protein Accession	gj 109481431	
Mean Expression Ratio	0.933	
Median Expression Ratio	0.931	
Credible Interval	(0.734, 1.19)	
Associated Peptides	3	
Associated Spectra	3	
Coverage	0.291	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.952	
Avg..iTRAQ.Ratio....116.114.	0.72	
Avg..iTRAQ.Ratio....117.114.	0.886	

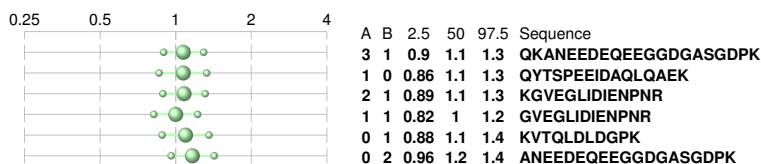
1 MCDFTEDQTA EFKEAFQLFD RTGDGKILYS QCGDVMRALG QNPTNAEVLK VLGPNKSDM NVKVLDFEHF LPMLQTVAKN
 81 KDQGTIEDYV EGLRVFDKEG NGTVMGAEIR HVLVTLGKEM TEEVEMLVA GHEDSNGCIN YEELVRMVLN G



5.411 PDGFA associated protein 1 [Rattus norvegicus]

Protein Accession	gij12018258	
Mean Expression Ratio	1.08	
Median Expression Ratio	1.07	
Credible Interval	(0.92, 1.25)	
Associated Peptides	6	
Associated Spectra	13	
Coverage	0.343	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	0.846
Avg..iTRAQ.Ratio....116.114.	1.05	0.961
Avg..iTRAQ.Ratio....117.114.	1.25	1.33

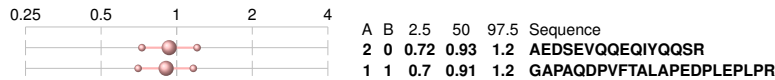
1 MPKGGRRKGGH KGRVRQYTSP EEIDAQLQAE KQKANEEDQ EGGDGASGD PKKEKSLDS DESEDEDDY QQKRKGVEGL
 81 IDIENPNEVA QTTKVTQLD LDGPKELSR EREEIEKQKA KERYMKMHLA GKTEQAKADL ARLAIIRKQR EEAARKKEE
 161 RKAKDDATLS GKRMQSLSLN K



5.412 hypothetical protein LOC299612 [Rattus norvegicus]

Protein Accession	gi 56090409	
Mean Expression Ratio	0.93	
Median Expression Ratio	0.932	
Credible Interval	(0.735, 1.17)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.358	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.917	1.59
Avg..iTRAQ.Ratio....116.114.	0.903	0.312
Avg..iTRAQ.Ratio....117.114.	1.19	0.842

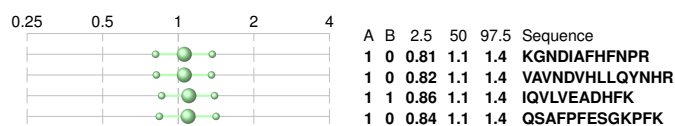
1 MSSKAKKRVV LPTRPAPPTV EQILEDVVRGA PAQDPVFTAL APEDPLEPLP RAEDSEVQQE QIYQQSEYTV AMNERLRQAG
 81 DALRQKFDGL RQAGQRLEQD ISQVTSATS



5.413 galectin 3 [Rattus norvegicus]

Protein Accession	gi 13929190	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.862, 1.34)	
Associated Peptides	4	
Associated Spectra	5	
Coverage	0.191	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	1.12
Avg..iTRAQ.Ratio....116.114.	1.01	1.08
Avg..iTRAQ.Ratio....117.114.	1.24	1.68

1 MADGFSLNDA LAGSGNPNER GWPGAWGNQP GAGGYPGASY PGAYPGQAPP GGYPGQAPPS AYPGPTGPSA YPGPTAPGAY
 81 PGPTAPGAFP GQPGGPGAYP SAPGAYPSAP GAYPATGFFG APTGELTVPY DMPLPGGVMP RMLITIIIGTV KPNANSITLN
 161 FKKGNDIAFH ENPFNENNR RVIVCNTKQD NNWGREERQS AFPPESGKPF KIQVLVEADH FKVAVNDVHL LQYNHRMKNL
 241 REISQLGIIG DITLTSASHA MI

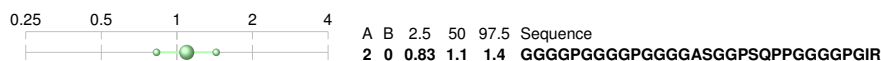


5.414 KH-type splicing regulatory protein [Rattus norvegicus]

Protein Accession	gij 19424312
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.821, 1.39)
Associated Peptides	1
Associated Spectra	2
Coverage	0.043
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	1.22
Avg..iTRAQ.Ratio....117.114.	1.57

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1   MSDYSTGGPP PGPPPPAGGG GGAAGAGGGP PPGPPGAGDR GGGGPGGGGP GGGGASGGPS QPPGGGGPGI RKDAFADAVQ
81  RARQIAAKIG GDAATTVNNN TPDFGFGGQK RQLEDGDQPD SKKLASQGDS IGSQLGPIHP PPRTSMTEEY RVPDGMVGLI
161 IGRGGEQINK IQQDSGCKVQ ISPDSGGLPE RSVSLTGAPF SVQKAKMLD DIVSRGRGGP PGQFHDNANG GQNGTVQEIM
241 IPAGKAGLVI GKGGETIKQL QERAGVKMIL IQDGSQNTNV DKPLRIIGDP YKVQQACEMV MDILRERDQG GFGDRNEYGS
321 RVGGGIDVPV PRHSVGVVIG RSGEMIKKIQ NDAGVRIQFK QDDGTGPEKI AHIMGPPDRC EHAARIINDL LQSLRSPPPG
401 PPGAPGMPFG GRGRGRGQGN WGFPPGEMTF SIPTHKCGLV IGRGGENVKA INQQTGAFVE ISRQLPPNGD PNFKLFVIRG
481 SPQQIDHAKQ LIEEKIEGFL CPVGPFGGGP GPAGPMGPFH PGPFNQGGPP APPHAGGPPP HQYPPQGWGN TPEWQPPAP
561 HDPNKA AAAA TDPNAAWAA YSHYYQQPPG PVPGPAPAPA APPAQGEPPO PPTTGQSDYT KAWEEYYKKI GQQPQQPGAP
641 PQQDYTKAWE EYYKQAQVA TGGGPGAPPG SQPDYSAAWA EYYRQQAAYY GQTPGPGGPQ PPSTQQGQQQ ATEANGYELH
721 L
    
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5.415 "hemoglobin, gamma A [Rattus norvegicus]"

Protein Accession	gij 25742840
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.806, 1.44)
Associated Peptides	1
Associated Spectra	1

Coverage	0.068
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.49
Avg..iTRAQ.Ratio....116.114.	1.54
Avg..iTRAQ.Ratio....117.114.	1.02

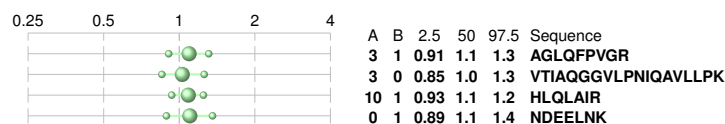
1 MVHFTAEEKA AIISIWEKVD LEKIGGETLG RLLIVYPWQ RFFDKFGNLS SALAIMGNPR IRAHGKKVLT SLGSAVENMD
 81 NLKETFAHLS ELHCDKLHVD PQNFKLLGDM LVIVLSTHFA KEFTPEVQAA WQKLVMGVAN ALSHKYH



5.416 PREDICTED: similar to histone 2a [Rattus norvegicus]

Protein Accession	gj 109504948	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.924, 1.25)	
Associated Peptides	4	
Associated Spectra	19	
Coverage	0.323	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.30	1.11
Avg..iTRAQ.Ratio....116.114.	0.923	1.04
Avg..iTRAQ.Ratio....117.114.	1.14	1.27

1 MSGRGKQGGK ARAKAKTRSS RAGLQFPVGR VHRLLRKGNY SERVGAGAPV YLAAVLEYLT AEILELAGNA ARDNKKTRII
 81 PRHLQLAIRN DEELNKLGR VTIAQGGVLP NIQAVLLPKK TESHKAKGK



5.417 dopamine-responsive protein [Rattus norvegicus]

Protein Accession	gi 19424192
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.822, 1.41)
Associated Peptides	1
Associated Spectra	2
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.06
Avg..iTRAQ.Ratio....116.114.	1.12
Avg..iTRAQ.Ratio....117.114.	1.10

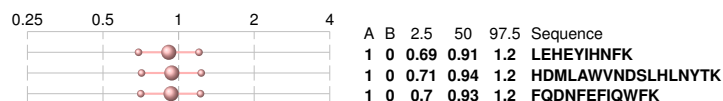


5.418 "microtubule-associated protein, RP/EB family, member 3 [Rattus norvegicus]"

Protein Accession	gi 56090319
Mean Expression Ratio	0.932
Median Expression Ratio	0.932
Credible Interval	(0.73, 1.19)
Associated Peptides	3
Associated Spectra	3
Coverage	0.139
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	0.959

```

1      MAVNVYSTSV TSENLSRHDM LAWVNDLHL NYTKIEQLCS GAAYCQFMDM LFPGCVHLRK VKFQAKLEHE YIHNFKVLQA
81     AFKKMGVDKI IPVEKLVKGG FQDNFEFIQW FRKFFDANYD GKDYNPLLAR QGQDVAPPPN PGDQIFNKS KLIQTAVPQR
161    TSPTGPKNMQ TSGRLSNVAP PCILRKNPPS ARNGGHEADA QILELNQQLL DLKLTVDGLE KERDFYFYSKL RDIELICQEH
241    ESENSPVISG IIGILYATEE GFAPPEDDEI EEHQEDQDE Y
  
```

5.419 PREDICTED: similar to High mobility group protein 2 (HMG-2) [Rattus norvegicus]

Protein Accession	gj 109500754	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.825, 1.40)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.0383	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.31	1.10
Avg..iTRAQ.Ratio....116.114.	0.893	1.10
Avg..iTRAQ.Ratio....117.114.	1.22	1.33

```

1      MGKGDPNKPR GKMSLYAFFV QTCREEHKKK HPDSSVNFAE FSKKCSERWK TMSAKEKSKF EDLAKSDKAR YDREMKNYVP
81     PKGNKKGKKK DPNAPKRPPS AFFLFCSEHR PKIKSEHPGL SIGDTAKKLG EMWSEQSAK DKQPYEQFAAK LKEKYEKDIA
161    AYRAKKGSEV GKKGPGRPTG SKKKNEPEDE EEEEEEDGED EEEEEDEDEE
    
```



5.420 PREDICTED: similar to proline-rich protein [Rattus norvegicus]

Protein Accession	gj 109489144	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.794, 1.45)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.00669	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.57	

Avg..iTRAQ.Ratio....116.114. 0.999
 Avg..iTRAQ.Ratio....117.114. 1.57

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1      MSLQPLIQEL TTFSQSPSWT DHPPNSKETK NYTPGKIY LH FADPPMGLVV EPPDLFFLKT TSKSLVQGNP TQIKKSPKEV
81     AAHTVEYKEA VLPAPLEGQD KSPIPPTMSL QSLDEELITP SHSPGGTHHS PTPIETKRHM SGKIFLNHAE LPMRMVVEPL
161    DLFFLKTTES KPVQEIPIQI TKSPKVVAP SVEYKQWVLP APVDGQDDSP TPPNVSLPL GSKXSPISSP PWKGLSNLQN
241    PKRKVKNSQ KWFSFSIHTL QWEWXLNLXI CSFSKLQNLN LCRSPLLRIL SLQKRLXFKL XNKRKXWFHL XLRVMINTXH
321    PVFHINLXTW NFLNLLALLL RLIIPLLSMR LQFLLOFIKS XVHFCTQNF LXLNNLIQWLN VLLEXRRLLQ RLQRYLWRPX
401    PNLXNIIHQL QFMLILSIQI YQLWKPHNLT SXQLXPLFQR LHILKSOELX LLIQNLHFVK SQQLQFFIQW PHILESQQLX
481    LLLQSLHILK PQGLQLLQN AXQVYLQIRL RDIQAQLQSR FKFVKWNLFX LHILKILIQK MIXVXKKMPT TPTTYVTSAY
561    VKMRHCCVFI PTQYGDSSKC LCQGPAPTMT LLSXISKEM IFLTLTMYG RYTVGLRNXF SVKITXLNCI RIHSKACCP S
641    RFWIYPAIKY AILKEGHLNH YLFXSIXTLG AIYSLNXALE HFRHGMECSF YSSXFSAEIL SLLKPIPTFL NCQHXNIWTW
721    GPHRCNXQL RTSSXRLWSF NIXSYLATWP AASANLKLIL RLSARQSKCI VTLDVXQTPH IVLKKHLXGT QKHSXRCCR
801    PGRGTPALNS LLNQKRTVQT MPMSPLPWRK RXTSVMKRTL XVHXITYCHT SQREIWKTXC PPCYHTLNCC FLNMKMQVIP
881    WGLRRRTQKV LLLQVDLSLV TSLTKINXIN FIFXRICXTO KLMRFKRRKN LGDTRQNLKN XVPNXNEEYL KRGGNLPRQT
961    KTVLQRSRRQ REGSSAXAGP LRGQEA XGRG TSRRXESRAW GASRAPRHLW RTAPRTGSSG AQPQWSCSSS TWSRSPGHXW
1041  EIPSLQSPYS QRIMGRNSLP FXDPPWTRL LLQNRYLSSX TDGKTCCLIPF LCXKVQMLMX REQRVLTQIY NLKRDVETLG
1121  RKNLISSXLQ RGQRQHRQR GAWXIPLHKG SFHLXETXVT QKGPFFQNHIL LQSFLLQKYL KIRQQQIMLK KIFSNQLPLC
1201  LKKLHQKLP LRIPMQLMY LXPVYPTXFP LFSKPVQSXY TSFSGLTHLT TSKNLLTHRQ CHQKNSLNLI XTSSWGRLSP
1281  ITMXESSPT LSGLXRWTVL TPKCNCVPVS SSPQASXSS FSVSSKISSC PGLTGIQTSG KLRPTSTRVE ERKVNGRVWN
1361  QISVQKKGQ LATTAKSSWQ YLXPSXXXFX LSLSVSLRFI PTEQKREMKK SPCGVRKTTD KRRVRKLSG XGGHCGLEIY
1441  XNKTRPRKVG MSYRVIHQW RRRMFRMNHG RSTKKAQWNQ KILKRRRLKH WKTQN
    
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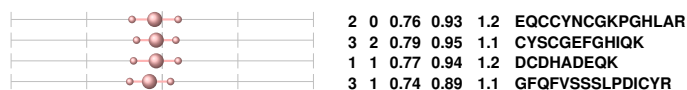
5.421 cellular nucleic acid binding protein 1 [Rattus norvegicus]

Protein Accession	gij12018264	
Mean Expression Ratio	0.933	
Median Expression Ratio	0.932	
Credible Interval	(0.793, 1.1)	
Associated Peptides	4	
Associated Spectra	13	
Coverage	0.288	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.917	0.772
Avg..iTRAQ.Ratio....116.114.	0.998	0.96
Avg..iTRAQ.Ratio....117.114.	0.957	0.733

```

1      MSSNECFKCG RSGHWARECP TGGGRGRGMR SRGRGGFTSD RGFQFVSSSL PDICYFCGES GHAKDCDLQ EDACYNCGRG
81     GHIAKDCKEP KRERQCCYN CGKPGHLARD CDHADEQKCY SCGEFGHIQK DCTKVKCYRC GETGHVAINC SKTSEVNCYR
161    CGESGHLARE CTIEATA
    
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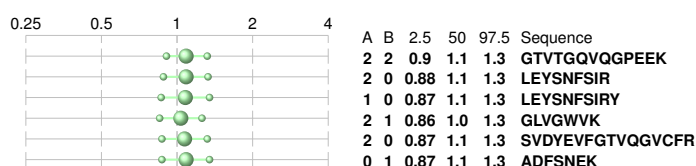




5.422 "PREDICTED: similar to Acylphosphatase, muscle type isozyme (Acylphosphate phosphohydrolase) isoform"

Protein Accession	gj 109501088	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.917, 1.25)	
Associated Peptides	6	
Associated Spectra	13	
Coverage	0.427	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	1.12
Avg..iTRAQ.Ratio....116.114.	1.07	1.16
Avg..iTRAQ.Ratio....117.114.	1.03	1.10

1 MSLRLASVA LSAPHTPLRL LARGLAAMAE PLK^SVDYEVF GTVQGVCFRM YTEGEAKKR^S LVGWV^SNTSK GTVTGQVQGP
81 EELVNSMKS^SW LSKVGS^SPSSR IDR^SADFSNEK TISK^SLEYSNF SIRY



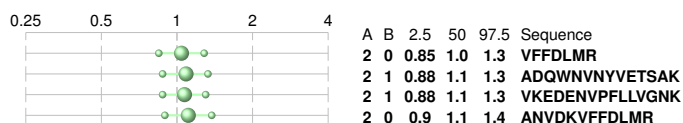
5.423 ras related v-ral simian leukemia viral oncogene homolog A [Rattus norvegicus]

Protein Accession	gj 13592039	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.9, 1.27)	
Associated Peptides	4	

Associated Spectra	10	
Coverage	0.199	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.01	1.07
Avg..iTRAQ.Ratio....116.114.	1.12	0.949
Avg..iTRAQ.Ratio....117.114.	1.21	1.24

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1      MAANKPKGQN SLALHKVIMV GSGGVGKSAL TLQFMYDEFV EDYEPTKADS YRKKVVL DGE EVQIDILDTA GQEDYAAIRD
81     NYFRSSEGFL CVFSITEMES FAATADFREQ ILR VKEDENV FFLVGNKSD LEDKRQVSVE EAKNRADQWN VNYVETSART
161    RANVDKVFED LMREIRARKM EDSKERNGKK KRKSLAKRIR ERCCIL
    
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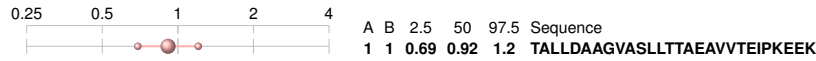


5.424 "PREDICTED: similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin)"

Protein Accession	gij109506917	
Mean Expression Ratio	0.932	
Median Expression Ratio	0.933	
Credible Interval	(0.716, 1.22)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.0325	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.995	1.11
Avg..iTRAQ.Ratio....116.114.	0.886	1.03
Avg..iTRAQ.Ratio....117.114.	1.03	1.09

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1      MGVLDLGLG ENGTAHQRAE KYVVRDNEI QSKFEVFMRR VKQNPYTLFV LVHDNSHVEL TSPSRVLGPS LAADGLPRLV
81     LIRRSPEML RLSTVLRQMR PVSRALAPHL TRAYAKDVKF GADARAFLLQ GVDLLADAVA VTMGPKGRTV IIEQSWGSPK
161    VTKDGVTVAK SIDLKDKYKN IGAKLVQDVA NNTNEEAGDG TTTATVVLARS IAKEGFEEKS KGANTVEIRR AVMLAVDAVI
241    AELKKQSKPV TPPEIAQVA TISANGDKDI GNIISDAMKK VGRKGVITVK DGKTLNDGLE IIEGMKFDRG YISPYFINTS
321    KGQKCEFQDA YVLLSEKKIS SVQSIVPAL EIANHRKPLV IIAEDVDGEA LSTLVNRLK VGLQVAVKA PGFGDNRKNQ
401    LKDMAIATGG AVFGEGLNL NLEDVQAHDL GKVGIVIVTK DDAMLLKGGK DRAHIEKRIQ EITEQLDITT SEYEKEKLN E
481    RLAKLPDQVA VLKVGGSVSDV EVNEEKDRVT AALNATRAAV EEGIVLGGGC ALLRCIPALD SLKPADEDQK IGIEIIRKAL
561    KIPAMTIAKN AGVEGSLIVE KILQSSSEVG YDAMLGDFVN MVERGIIDPT KVVRTALLDA AGVASLLTTA EAVVTEIPKE
641    EKDPGMGAMG GGGEDVGC E KLYFGLNEYS KSLQWGITSP LLRCDETFEK MVSTLLERYP RLHSMVVRVY LLIQQYSEAL
721    MALTTMASLR DHSTPETLSI VDDLITSPGK NKSGRGHMLV IRVPSLQLAM LAKERLQEV RDKLGLQYRFE IILGSPTSEL
801    TVATHFVTRL KVSKEQVNR L FCLPTPGLLD SGITQMIELN KFCTCVTITS LTRFLVDTS F
    
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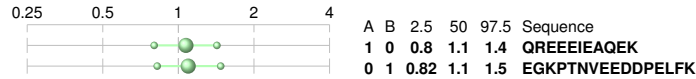


5.425 "DnaJ (Hsp40) homolog, subfamily C, member 8 [Rattus norvegicus]"

Protein Accession	gij61557163	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.828, 1.40)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	0.107	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	1.02
Avg..iTRAQ.Ratio....116.114.	0.917	1.1
Avg..iTRAQ.Ratio....117.114.	1.15	1.73

```

1   MAASGESGAS GGGGSTEAAF MTFYSEVKQI EKRDSVLTSK NQIERLTRPG SSYFNLNPFV VLQIDPEVTD EEIKRFRQL
81  SILVHPDKNQ DDADRAQKAF EAVDKAYKLL LDQEQQKRAL DVIQAGKEYV EHTVKERKKQ LKKGKPTNV EEDDPELQ
161 AVYKQTMKLF AELEIKRKR EAKEMHERKR QREEEIEAQE KAKREREWQK NFEESRDGRV DSWRNFQANT KKKKKKRNRT
241 FLRPPKVKME QRE
    
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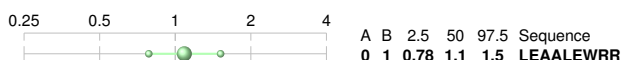
5.426 PREDICTED: hypothetical protein isoform 2 [Rattus norvegicus]

Protein Accession	gij109478697	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.79, 1.44)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0353	
Experiment	B	
Avg..iTRAQ.Ratio....115.114.	0.982	
Avg..iTRAQ.Ratio....116.114.	1.02	

Avg..iTRAQ.Ratio....117.114. 1.76

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1      MGKLRFRWRC LILSQREQCT LLSKIHLYTQ GCHSQQSLGH LLSVAETEMLR DPESQQLLH ALESENARLE AALEWRRCEL
81     VFVQWMDTVL DACSPETPAV TSQPTALPMI SEGGGLGLES VRQELLALQE ELREVAEPRR AAWEASRVGGL GQGEWWSNSR
161    KALREVERE LADLQGSWKL CSTPAQFQRP HRLVRSKDGA PRRQGLQAAE VIRTLSAKED CLKKALHQLO CQCQQLARL
241    AGTLPGLIWW LPPGH
    
```



5.427 "PREDICTED: similar to Spectrin beta chain, brain 4 (Spectrin, non-erythroid beta chain 4) (Beta-V s"

Protein Accession	gij109470679
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.792, 1.45)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00388
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.13
Avg..iTRAQ.Ratio....116.114.	1.32
Avg..iTRAQ.Ratio....117.114.	1.48

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1      MWQDRASDSW QEDHRVCDKE SRAQNSALLS SSLAMDSEYE IGHVRKLOAQ HTHMQEKTFI NWINNIFRLG RVGIRIQNLY
81     TELADGAHLL RLELEISGEA LPAPSPGRRL VHFLENNSHA LAFLRKVPV PFIGPENIVD GDQSLILGLL WVILRFQIS
161    HISLDREDFG ASAALLSAKE ALLVWCQRQT ASYSNVITD FSRWSVDGLA FNALLHAHRP DLLDYGSLSL DRPLYNLSFA
241    FRVAEQQLGI AQLLDAEDVA ARHPDERSIM TYVSQYYHYF SRLQGGQTAR RRLAKVLLQL QETEVLAQAY EQLAADLLCW
321    IEEKQMQLA QDFPDPLPAM RQLLSAFASF RAQEKPPRLQ QQGASETLLF QLQTTLRAQN RRPFLPREGL GPAELAQWA
401    ELERVEASRS QAMQKLLQL ERLDTLARRF QCKASHRESF LNDAEQMLEQ ARASLTDPAT VEAATQRLNM LEAGLLPQEG
481    RFQALGEMAD ILQEEYHSW ADVACRQKEI TGRWRRLLQC LQEERKCLAG TQAVLSLLQE VEAATDQLGE LQGLAGSTAC
561    EPQLAEVVL LQSHDLLEAQ VSAHRTHVNR LVHQTAQLDS SQGTSVQTLQ TKALALDELH HSLVSLVRTR RTTLEQTLQR
641    AQFLHSCEEE EAWLQEHRLQ VEKAAPGRDL TQIANALQKH KALETELHRH QAVCIDLMQR GRNLSVKEPL TQDPPLERAE
721    AVQGIWQLLW TGAARRRTRL QTALLVGQYF SDLAEASWL LQRQKQLESA SYGKDQSDSE ALLQQHLRLE QGLCAFAVDL
801    RELEDQAAA AALVSQMVHT GTREGPRHVP PTPNVRSQPS IGVL SALGLP GEDPRTAPQA EYDFHFDNSA ILQAQADLRQ
881    NYENLRALAK LHRARLEETV TLFSEYSSCR ELQSWLEAQT ALFQTLQPQG DNLEVTQLKY ENVLMTLATG KGHWEAIST
961    AEQLKQRCPG HISKIQQQE ELKHRWQLE ALKEEKLLQL TRAMEVCSLL QESEPTRAQL LSVISRLEAL GTRSSGDSHR
1041   TLQQTQKVL VLEKISYQC KATIELMESG PAEGRLLWEQ VLMLQSLKQ AQGGVAQQVQ VQTKDRVQRG ILQESQKLLL
1121   WAEGIQQLC SKEQLEDVAS AQQLLRKHGA LREETCLWKE RLQQLQAQGG LVAVSGSPQF QEVASALRLL GQHSQQLKAL
1201   WEQRQKQKWA GLELQRFQGE VDSFTATCAS HEASLQLDNL GEDIREAQL LQQHQGLGWL HSSLGSRAT LWARGEKLLL
1281   NHPTAVHRIR ELLHSAQAQW ARVQERSDQR RGQLLASLQL QEWQAQAEGL MLWMEKWRP VADEGPQTGS NILQWHKITK
1361   SELLASHYK EDLQQTGKEL LHSNPYAQED IQDRQLSLNH KWHEELSHKTA EQGDRLFPQTR QQGDLLELLQ DVRGMMHLE
1441   GALQSTETGQ DLCSRRRLQT QHRQLEGKSO ALASKMAALI SQTHNVFTSW TILESQKCO QRFKSLQSKL ATRQQLQAS
1521   VELHKFNLS NLELTWVAEH MPSTSPIYPA QCWHDQSLQ RKHKVLQAEV KGHVGHMHRV LSTGQSLAAS GHPQAQHLE
1601   CQKLEGHWA ELEQACEGRA HCLQQAVIFQ RYLLNVSEME TWVEEKLPLV SSRDYGSENE ATFGLIRKHQ MLRQEIALCW
1681   GSMEDLEQRF QTLAGFEASE RLVVVREKLO ALQKLADRRG QELEGLRLH EFMREAEDLO SWLDSRKQV RGEHGFGEDH
    
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NHLBI Zile/Grant, Aged Rat

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1761  EHVQLCLTEF TKFQHQVETG AQRVETCRQL AESLLELGH5 AAHKSHQRQQ DLQAAWCELW QLTQAQGLLL SDAETTLRVH
1841  RDLELILSQI QEKATNLPND VAQDLHGVEK QLQRHEGLER ELAGMEQQLQ ELLKAGGNVQ KLCPQALATV QOKQAVTQA
1921  WEALQLRMEQ RKAQLEQAYL LVRFHAVTRD YTSWVASVHL ELQMEDDSWE PSSILLRLRA HQWLWALKA REELQEQGTK
2001  MGQALLVAR TPTKVQDGLQ TLQEKRDQVF QAWALKQERL QATLQEQRL RQGDHLVKLL TAQEAFLKAS GLGSSVEEVE
2081  QLIRKLVFQ KVLAIQDKKE SALCEQLKMI P5PKGQNLVY HVQERRAQVK ELAESRGQAL RTSLMIGNFT RTATQVEDWI
2161  QERLQQLRAC SPLGNLKDYL KHLRKHQAFR AEVQAHEQIV TSVAKQEGEL LSQSHFPQARE V5QRLEALWD LWEKLRQAVT
2241  LGGQALEDR5 NFLEFLQSAD LAETWIQEKE RMVDGCDVGL NLEHCLQLCR QVCKLQVRGS VRRVDDTRIR RIKNLSLQLK
2321  NQGPEESEAI CQRQNLNNR WKTFFHGNLLL YKQRL5AAL RHRLSSEL5DN IIEQIREKES LAQALEGTEG LERISWRK5M
2401  LQQEMDLIQT QVESLGG5RV5 RLCEENPEAT GGLRHKQEM MDSW5K5V5WHK ARNRRELLDV GHEVQKLQTM LD5LDQ5WA5Q5
2481  LQAE5MARQAT PCS5P5R5IL5YM LEEHQ5AHK5VE LDV5RT5D5SL5NL V5R5M5G5QR5LLA SGY5PL5AS5G5IR QP5L5AA5VE5Q5EL SGLQ5AS5W5Q5GR
2561  QQQ5L5Q5A5LE5Q Q5L5CL5SS5VE5KV EHW5LD5SE5E5AS LTY5E5V5AD5PL VTVE5ILL5SKH KRRE5Q5GL5KV5Q AEK5I5SA5LE5AT AHS5L5H5Q5G5G5H5
2641  EAHS5V5LD5RC5Q ALL5LR5MD5ALT EQARAR5GR5QL EEL5Q5KL5RK5FL QDS5SE5V5AT5WL REK5NL5VA5LEE GQD5PT5TM5QA Q5L5Q5Q5Q5NL5QA
2721  EL5D5AS5V5H5QR5Q ELQ5ME5G5Q5ELL QG5GH5P5AS5ET5I RGQ5LE5EL5G5GL WAEL5QT5NC5QR KMAR5L5QG5ASK V5L5H5L5Q5R5ML5RE LKN5W5LE5P5MEA
2801  EL5R5AP5VR5S5QD LPR5V5G5ELL5GA QEE5LE5AA5V5DR QAR5Q5V5Q5EL5QG QAQ5AC5F5Q5EG5H RLAK5DV5EE5QA GQ5L5L5Q5R5F5Q5GL WEP5L5Q5ERR5AS
2881  LEA5QR5LL5L5Q5F FRD5V5DE5EM5AW VQEK5LP5S5ATA QD5Y5Q5S5L5GT5V RHL5QE5KH5Q5NL ENE5I5SN5HK5AL SQV5VT5GT5G5HK LVQ5AG5H5FA5E
2961  EVAAR5V5Q5LE VALNH5LE5TEA ARR5GR5ML5Q5QA LEA5Q5QT5L5VEL LEAG5S5W5LA5ER GHIL5D5SE5DL5G QD5TE5AT5Q5ALL RR5LET5TR5DL
3041  EGF5SS5RI5EQ5L QQT5VA5L5LE5SG QG5PG5S5PR5V5LA QLQ5AV5RE5AHA QLL5Q5RA5EG5RG QAL5RE5QL5H5LY QLE5QE5ALL5LD AWL5TT5KL5T5VA
3121  ESQ5DY5G5Q5D5LE GIK5V5LE5DM5FD AFN5RE5V5QS5LG QAR5M5QT5R5REL MAS5LER5G5AP5R FYP5Q5I5QA5Q5KC RVQ5AT5W5ER5LN KAI5K5ART5EN5L
3201  AAAR5D5LR5S5FE QAAS5EL5Q5G5WM QET5TT5L5LE5GE FQV5HD5L5SPA5Q PLL5Q5Q5Q5Q5QR RLQ5RE5VR5VIE NEV5SR5V5Q5TEA QRL5G5HH5PLA
3281  QG5SL5GE5WL5TK VQG5AW5AN5LEA KVQ5E5WS5Q5K5LL QAT5Q5GH5T5FL5G SCRE5LL5V5WA5Q EKQ5EL5LS5SEK QAE5DV5G5AK5Q LLE5Q5HEE5LE5Q
3361  EI5QE5C5CL5QA5Q NAR5QE5G5QR5LL DKG5H5F5MS5LEV AECM5Q5EL5ER5H VQEL5Q5VA5W5AL RGQR5LE5QN5WS LQQL5R5QR5LE5L AEA5WL5TS5CE5C
3441  LLL5D5P5SC5GH5S VLD5V5ER5LL5YR QD5GLE5K5LL5AA HEK5FT5QL5QM MTE5E5AK5GA5HV MEAS5VE5LN5Q5Q PPTE5GR5Q5V5RA NSD5CR5Q5F5HT5Q
3521  QPS5GP5GT5V5AP ARY5QL5LD5QQ5F WDL5G5K5GS5LEP ILR5YE5ES5G5SA KWH5W5GP5V5W5GT QLL5SE5DK5QH5W YH5M5SL5AMP5EM DHD5FI5ARS5RG
3601  KDDNL

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5.428 eukaryotic translation elongation factor 1 gamma [Rattus norvegicus]

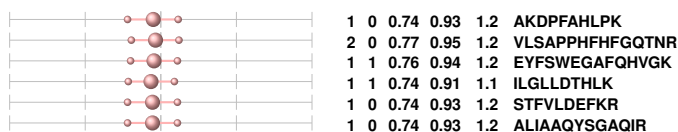
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Mean Expression Ratio	0.934	
Median Expression Ratio	0.933	
Credible Interval	(0.783, 1.12)	
Associated Peptides	6	
Associated Spectra	9	
Coverage	0.165	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.97	0.843
Avg..iTRAQ.Ratio....116.114.	0.89	0.895
Avg..iTRAQ.Ratio....117.114.	0.98	0.755

```

1  MAAGTLYTYP ENWRAFKALI AAQY5SGAQIR VLSAPP5HFHF GQTNRTPEFL RKFPAGKVPA FEGDDGFCVF ESNAIAYV5S
81  NEELRGSTPE AAAQV5VQWV5S FADSDIVPPA STWVFP5TLGI MHNKQATEN AKEEVK5R5ILG LLD5TH5L5TRT FLVGERV5TLA
161  DITV5VCT5LLW LYKQV5LEP5SF RQAF5P5NT5NRW FLTCINQ5P5QF RAIL5GEV5K5LC EKMAQ5F5DAK5K FAESQ5PK5K5DT PRKEK5GS5REE
241  KQK5P5Q5TER5KE EKKA5A5PA5PE EEM5DE5CE5Q5AL AAEP5K5AK5DP5F AHL5PK5ST5F5VL DEF5KN5K5YS5NE DTLS5VAL5PYF WEHF5DK5DG5WS
321  LWY5AEY5RF5PE ELTQ5TF5MSCN LITG5MF5QR5LD KLR5K5NA5F5ASV ILFG5TN5NS5S5S ISG5V5V5F5R5G5Q DLAF5PL5SP5DW QVD5Y5ES5YT5WR
401  KLDPG5SE5ET5Q TLVR5Y5FS5WE GAF5QH5VG5KAV NQ5G5K5IF5V

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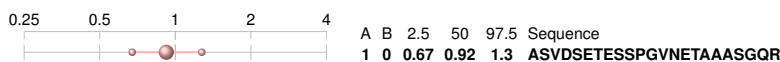


5.429 RNA (guanine-7-) methyltransferase [Rattus norvegicus]

Protein Accession	gj 56605632
Mean Expression Ratio	0.935
Median Expression Ratio	0.933
Credible Interval	(0.697, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0499
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.17
Avg..iTRAQ.Ratio....116.114.	0.714
Avg..iTRAQ.Ratio....117.114.	0.808

```

1      MESSVKASVD SETESSPGVN ETAAASGQRL SEKTRQQADQ PKTQDDLVEQ NSSYVQDSPS KKRKLDVEII LDEKHSDEDDG
81     GASKRSLER GGSSEDEPSP GGLTERKRKL QPQDALETQT RKFQKLEEGH SSAAVAHYNE LQEVGLVKRS QSRIFYLRNF
161    NNWIKSILIG EILEKVRQRK NRDITVLDLG CGKGGDLLKW RKGRISRLVC ADIADISMKQ CQQRVEDMKC RRDNEYIFSA
241    EFITADCSKE LLVEKFHDPE MYFDICSCQF ACHYSFESLE QADMMLRNAC GRLNPGGYFI GTFPNSFELI RRLEASETES
321    FGNEIYTVKF QKKGNYPLFG CKYDFNLEGV VDVPEFLVYF PLLTEMAKKY NMKLIYKKTFF LEFYEEKIKN NENKMLLKRK
401    QALESYPANE NSKLASEKAG DYAHAAEYMK NSQVRLPLGT LSKSEWEATS IYLVFAFEKQ Q
    
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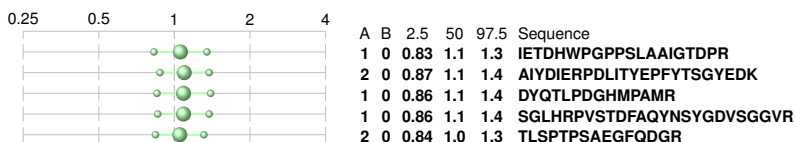
5.430 actin-binding LIM protein 1 [Rattus norvegicus]

Protein Accession	gj 113205045
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.883, 1.29)
Associated Peptides	5
Associated Spectra	7
Coverage	0.230

Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.24
Avg..iTRAQ.Ratio....116.114.	1.14
Avg..iTRAQ.Ratio....117.114.	1.19

```

1      MFTEGEEMYL QGSTVWHPDC KQSTKTEEKL RPTRTSSESI YSRPGSSIPG SPGHITYAKV DNEILDYKDL AAIPKVKAIY
81     DIERPDLITY EPPFYTSGYED YQDRQSLGES PR1LSPTPSA EGFQDGRDRM IHRSTSQGS I NSPVYSRHSY TP1TRSRS1PQH
161    FHRFPDQGINI YRKPPIYKQH AALAAQNKAS EDI1KFSKFP AAQAPDPNEI PK1IETDHWPG PPSLAAIGTD PRRRS1SGREE
241    DEEELRRRQ LQEEQLMKLN SGLGQLILKE EMEKENRERA SLLASRYDSP LHSASHAPSS KTSSLPGYGK SGLHRPVSTD
321    FAQNSYGDV SGGVRDYOTL PDGHMPAMR DRGVSM1PNML EPKIFPYEML MVTNRGRNKI LRDVDRTRLE RHLAPEVFWE
401    IFGMSIQEFD KLPLWRRNDM KKKAKLF
    
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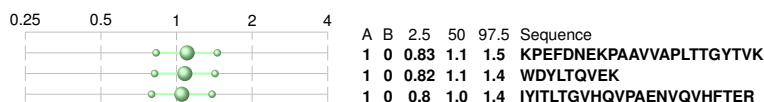


5.431 calcyclin binding protein [Rattus norvegicus]

Protein Accession	gij51948388
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.84, 1.36)
Associated Peptides	3
Associated Spectra	3
Coverage	0.24
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.22
Avg..iTRAQ.Ratio....116.114.	1.12
Avg..iTRAQ.Ratio....117.114.	1.25

```

1      MASALEELQK DLEEVKVLLE KSTRKRLRDT LTNEKSKIET ELRNKMQQKS QK1KPEFDNEK PAAVVAPLTT GYTVKISNYG
81     WDQSDKFVKI YITLTGVHGV PAENYQVHFT ER1SFDLLVKN LNGKNYSMIV NLLKPI1SVE SSSKKV1RTD1 VIILCR1KKAE
161    NTR1WDYLTQV EKECKEKEKP SYDTEADPSE GLMNVLKKIY EDGDDDMKRT INKAWVESRE KQAREDT1EF
    
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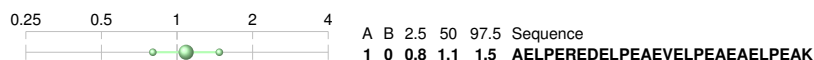


5.432 PREDICTED: similar to protease inhibitor 16 [Rattus norvegicus]

Protein Accession	gij109509865
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.8, 1.43)
Associated Peptides	1
Associated Spectra	1
Coverage	0.058
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.44
Avg..iTRAQ.Ratio....116.114.	1.26
Avg..iTRAQ.Ratio....117.114.	1.76

```

1      MHSSCSPWVM LPQLPLLLLL LLLLLTATGP ATALTEDEKQ TMVELHNHYR AQVSPFASDM LQMRWDELA AFAKAYAQKC
81     VWGHNKERGR RGENLFAITD EGM DVPLAVG NWHEEHEYNN LSTATCDPGQ MCGHYTQVVW SKTERIGCGS HFCETLQGVV
161    EANIHLVCN  YEPPGNVKGR KPYQEGTPCS QCPLGYSCVN SLCEPERKPE KAQDSPPRVT EVPGSRETGI PSLATSESLH
241    FSSVTKVSDS LATEPSPAVE TRAPPSLATE GPSSMATEAQ SFLTEVPSVS ATHIQPSLDE GPNVFLTSTH IPVPKSTDKE
321    ASSKSRAASV SPEKSLYPKM SPTETGESPP QIQEAEAPKA ELPEREDELPEAEVELPEAE AELPEAEAEEL PVSSEALVPV
401    LPAQERGGPK ASLEHSSYPV PTYLPNFPSA SGNATGGRTL ALQSSRTGAE DPEKASWDSK NSAPVWGPPF GLLLPLLLLL
481    GIF
    
```



5.433 zinc finger protein 365 [Rattus norvegicus]

Protein Accession	gij68341937
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.794, 1.45)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0172
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	1.43
Avg..iTRAQ.Ratio....117.114.	2.35

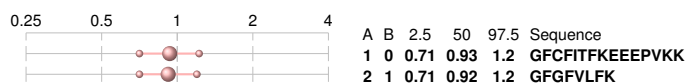
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1      MQQTTFEESR YRWQDSENV AVCLPFRCP R CGDHTRFRSL SSLRAHLEFS HSYEERTLLT KCSLLPSLKD TDLLRSSELP
81     KQGKLLRGHA KVTQKPSYV NLYSISHGHS KDPKPFEMVA ERPVSYVQTY TAVDIRADSL DAPRSSSGLP TQDTKAAFEA
161    HVREKFNRMV EAVDRTIEKR IDKLTKELA Q KTAELELVRA AFVQLTQKKQ EVQRRERALH KQVDVAVEMI AVLKQRLTES
241    EEELLRKEEE VVTFNHFLEA AAEKEVQGKA RLQDFIENLL QRVELAEKQL EYYQSQQASG FSHDTSEHML TDISSSRKSR
321    CLSRGHQHSV CNHPELKAHF HLKGRSYLKK AKDERAGMQP AKAIHEQAES PREFFRPAKK GEHLGLSRKG NFRPKMAKKK
401    PTAIVNII
    
```



5.434 heterogeneous nuclear ribonucleoprotein D isoform d [Rattus norvegicus]

Protein Accession	gij127138754
Mean Expression Ratio	0.935
Median Expression Ratio	0.934
Credible Interval	(0.734, 1.19)
Associated Peptides	2
Associated Spectra	4
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1
Avg..iTRAQ.Ratio....116.114.	0.86
Avg..iTRAQ.Ratio....117.114.	0.861



5.435 PDZ and LIM domain 3 [Rattus norvegicus]

Protein Accession	gij25742666
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.815, 1.39)
Associated Peptides	1

Associated Spectra	2
Coverage	0.0414
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.27
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	1.35

```

1      MPQNVVLPGP ASWGFR LSGG IDFNQPLVIT RITPGSKAEA ANLCPGDMIL AIDGFGTESM THADAQDRIK AASYQLCLKI
81     DRAETRLCPA VSEDGKAHPF KINLEAEPQD VNYFEHKKHNI RPKPFIIPGR TSGCSTPSGI DCGSGRSTPS SVSTVSTICP
161    GDLKVAAKMA PNIPLEMELP GVKIVHAQFN TPMQLYSDDN IMETLQQQVS TALGETPSMS EPTASVPPQS DVYRMLHDNR
241    DEPAAPRQSG SFRVLQELVN DGSDDRPAQT RSVRPVTKVH GGAGGAQRMP LCDKCGSGIV GAVVKARDKY RHPECFCVAD
321    CNLNLKQKGY FFVEGELYCE MHARARARPP EGYDTVTLYP KA
  
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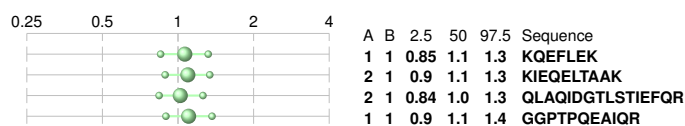


5.436 PREDICTED: similar to Charged multivesicular body protein 4b (Chromatin-modifying protein 4b) (CHMP)

Protein Accession	gij109471140	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.9, 1.27)	
Associated Peptides	4	
Associated Spectra	10	
Coverage	0.167	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.02	0.976
Avg..iTRAQ.Ratio....116.114.	1.06	0.98
Avg..iTRAQ.Ratio....117.114.	1.09	1.27

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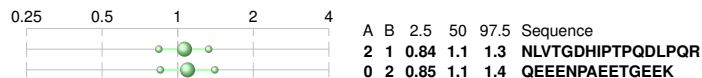
1      MSVFGKLFGA GGGKAGKGGP TPQEAIQRLR DTEEMLSKQ EFLEKKIEQE LTAAN KHGTK NKRAALQALK RKKRYEKQLA
81     QIDGTLSTIE FQREALENAN TNTEVLKNMG YAAKAMKAAH DNMDIDKVDE LMQDIADQQE LAEEISTAIS KPVGFGEEDF
161    EDELMAELEE LEQEELDKNL LEISGPETVP LPNVPSVALP SKPGEYAQSR DTPWRHGKGV ISWSVDFGLG SEPNSMVVIA
241    TMPVLYDFPW FSPEQDFLTS APVT
  
```



5.437 endosulfine alpha isoform 1 [Rattus norvegicus]

Protein Accession	gj 77020283	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.865, 1.33)	
Associated Peptides	2	
Associated Spectra	5	
Coverage	0.265	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.967	1.34
Avg..iTRAQ.Ratio....116.114.	1.14	0.931
Avg..iTRAQ.Ratio....117.114.	0.915	1.19

1 MSQK**QEEENP** **A**EETGEEK**Q**D TQEKEGILPE KAEEAKLKAK YPSLGQKPGG SDFLMKRLQK GQKYFDSDY NMAKAKMKNK
 81 QLPSAGADKN **L**VTGDHIPT**P** **Q**DL**P**Q**R**KSSL VTSKLAG



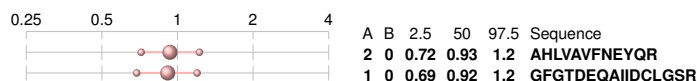
5.438 annexin A11 [Rattus norvegicus]

Protein Accession	gj 58865414	
Mean Expression Ratio	0.933	
Median Expression Ratio	0.934	
Credible Interval	(0.729, 1.19)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	0.0557	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.966	
Avg..iTRAQ.Ratio....116.114.	0.883	
Avg..iTRAQ.Ratio....117.114.	0.848	

NHLBI Zile/Grant, Aged Rat

```

1      MSYPGYPPPA GGYPPGAPGG APWGGASYPP PSMPPIGLDN VANYAGQFNQ DYLSGMAANM SGTFFGGANVP NMYPGAPGGG
81     YPPVPPGGFG QPPPAQQPVP PYGMYPPPGG NPPPGMPSYP AYPGAPVPGQ PMPPPQQQPP GAYPGQPPMT YPGQSPMPPP
161    GQQPVPSYYP YSGSSTITPA VPPAQFGNRG TITDASGFDP LRDAEVLKKA MKGFGTDEQA IIDCLGSRSN KQRQQILLSF
241    KTAYGKDLIK DLKSELSGNF EKTILALMKT PVLFDVYEIK EAIKGAGTDE ACLIEILASR SNEHIRELNR AYKTEFKKTL
321    EEAIRSDTSG HFQRLISLSL QGNRDESTNV DMSLVQRDVQ ELYAAGENRL GTDESKFNAI LCSRSRABLIV AVFNEYQPMT
401    GRDIEKSICR EMSGDLEQGM LAVVKCLKNT PAFFAERLNK AMRGAGTKDR TLIRIMVSR S ELDLDIRAE YKRMYGKSLY
481    HDITGDTSGD YRKILLKICG GND
  
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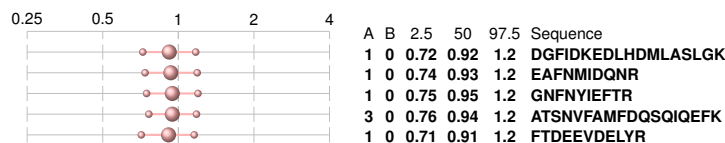


5.439 "myosin light chain, regulatory B [Rattus norvegicus]"

Protein Accession	gij8393781
Mean Expression Ratio	0.934
Median Expression Ratio	0.934
Credible Interval	(0.77, 1.13)
Associated Peptides	5
Associated Spectra	7
Coverage	0.390
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.925
Avg..iTRAQ.Ratio....116.114.	0.804
Avg..iTRAQ.Ratio....117.114.	1.12

```

1      MSSKKAKTKT TKKRPRATS NVFAMFDQSQ IQEFKEAFNM IDQNRDGFID KEDLHDMLAS LGFNPTDAYL DAMMNEAPGR
81     INFMTFLTMF GEKLNQDPE DVIRNAFACF DEEATGTIQE DYLRLLTMM GDRFTDEEVD ELYREAPIDK KGNFNYIEFT
161    RILKHGAKDK DD
  
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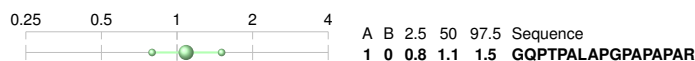
5.440 "DnaJ (Hsp40) homolog, subfamily B, member 6 [Rattus norvegicus]"

Protein Accession	gij61557293
Mean Expression Ratio	1.07

Median Expression Ratio	1.07
Credible Interval	(0.795, 1.45)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0476
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.32
Avg..iTRAQ.Ratio....116.114.	1.40
Avg..iTRAQ.Ratio....117.114.	1.44

```

1      MVDYYEVLGV QRHASPEDIK KAYRKQALKW HPDKNPENKE EAERKFKQVA EAYEVLSDAK KRDIYDKYGK EGLNGGGGGG
81     GSHFDSPFEF GFTFRNPDDV FREFFGGRDP FSDFDFEDPF DDFGNNRRGP RGSRSRGAGS FFSAFSGFPS FSGGFPAFDT
161    GFTPFGLSLGH GGLTSFSSAS FGGSGMGNFK SISTSTKIVN GKKITTKRIV ENGQERVEVE EDGQLKSLTI NGVADENALA
241    EECRRRGGPT PALAPGPAPA PARVPSQARP PTPAPTAPA QTPAPSVSTR PQKPPRPAPT AKLVSKSNWE DEEQDRQRVP
321    GNCDAPMTSA GLKEGGKRKK QKQKEDSKKK KSTKGNH
  
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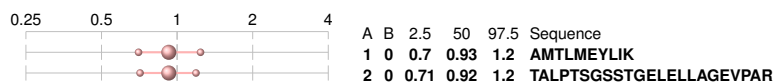


5.441 Epsin 1 [Rattus norvegicus]

Protein Accession	gi 16923990
Mean Expression Ratio	0.935
Median Expression Ratio	0.936
Credible Interval	(0.723, 1.20)
Associated Peptides	2
Associated Spectra	3
Coverage	0.0574
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.925
Avg..iTRAQ.Ratio....116.114.	0.959
Avg..iTRAQ.Ratio....117.114.	0.866

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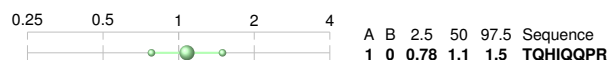
1      MSTSSLRQMQ KNIVHNYSEA EIKVREATSN DPWGPSSSLM SEIADLTYNV VAFSEIMSMI WKRLNDHGKN WRHVYKAMTL
81     MEYLIKTGSE RVSQQCKENM YAVQTLKDFQ YVDRDGDQDQ VNVREKAKQL VALLRDEDRL REERAHALKT KEKLAQTATA
161    SSAAVGSGFP PEAEQAWPQS SGEEELQLQL ALAMSKEEAD QPPSCGPEDD VQLQLALSLS REEHDKEERI RRGDDLRLQM
241    AIEESKRETEG GKEESSLMDL ADVFTTPAPP QASDPWGGPA SVPTAVPVAA AASDPWGAPA VPPAADPWGG AAPTASGDP
321    WRPAAPTGPS VDPWGGTPAP AAGEGPTSDP WGSADGGAPV SGPPSSDPWA PAPA FSDPWG GSPAKPSSNG TAVGGFDTEP
401    DEFSDFDLRL TALPTSGSST GELELLAGEV PAFSPGAFDM SGVGGSLAES VGSPPPAATP TPTPPTRKTP ESFLGPNAAL
481    VDLDSLVSRLP GPTPPGAKAS NPFPLPSGAPA TGP SVTNFFQ PAPPATLTLN QLRLSPVPPV PGAPPTYISP LGGGPGLPFM
561    MPPGPPAPNT NPFLL
  
```



5.442 death-associated protein [Rattus norvegicus]

Protein Accession	gij11968110
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.785, 1.44)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0784
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.31
Avg..iTRAQ.Ratio....116.114.	1.23
Avg..iTRAQ.Ratio....117.114.	1.51

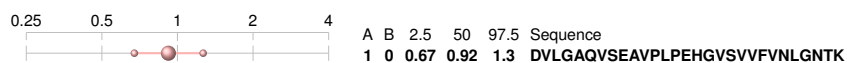
1 MSSPPEGKLE TKAGHPPAVK VAGIRIVQKH PHTGDGKEKK DKDDQEWEST SPPKPTVYIS GVIARGDKDF PPAAAQVAHQ
 81 KPHASMDKHV SPR**TQHIQQP** *K



5.443 "PREDICTED: similar to Methylmalonyl-CoA epimerase, mitochondrial precursor (DL-methylmalonyl-CoA ra"

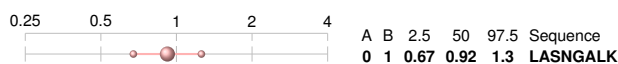
Protein Accession	gij109462104
Mean Expression Ratio	0.935
Median Expression Ratio	0.936
Credible Interval	(0.692, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.936

Avg..iTRAQ.Ratio....116.114.	0.983
Avg..iTRAQ.Ratio....117.114.	0.656



5.444 PREDICTED: similar to apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer of death

Protein Accession	gi 62665965
Mean Expression Ratio	0.934
Median Expression Ratio	0.936
Credible Interval	(0.694, 1.27)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.494
Avg..iTRAQ.Ratio....116.114.	0.811
Avg..iTRAQ.Ratio....117.114.	0.82



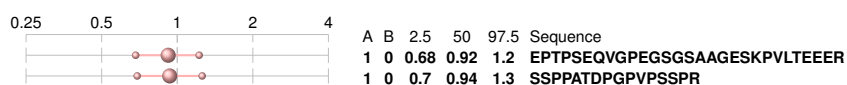
5.445 similar to hypothetical protein MGC6696 [Rattus norvegicus]

Protein Accession	gi 77797839
Mean Expression Ratio	0.935
Median Expression Ratio	0.936
Credible Interval	(0.714, 1.22)
Associated Peptides	2

Associated Spectra	2
Coverage	0.152
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.967
Avg..iTRAQ.Ratio....116.114.	0.872
Avg..iTRAQ.Ratio....117.114.	0.856

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1      MAELTALESL IEMGFPRGRA EKALALTGNQ GIEAAMDWLM EHEDDPDVDE PLETPLSHIL GR EPTPSEQV GPEGSGSAG
81     ESKPVLTEEE FQEQTKRMLE LVAQKQRERE EREEREALER EKQRRRQRQE LSAARQLQE DEIRRAAEER RREKAEELAA
161    RQVRREKIER DKAERAQKYG GTVGSRSPP AIDFGVPVSS PRQEPPTKRE YDQCRIQVRL PDGTSLSLTSF RAREQLAAVR
241    LYVELHRGEE PGQDQDPVQL LSGFPRRAFS EADMERPLQE LGLVPSAVLV VAKKCPS
  
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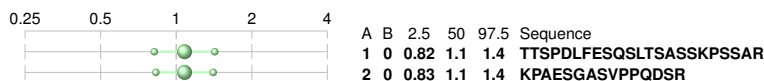


5.446 epsin 2 isoform a [Rattus norvegicus]

Protein Accession	gi 76781454
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.84, 1.37)
Associated Peptides	2
Associated Spectra	3
Coverage	0.0652
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.27
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.25

```

1      MTTSSIRQOM KNIVNNYSEA EIKVREATSN DPWGPSSSLM TEIADLTYNV VAFSEIMSMV WKRLNDHGKN WRHVYKALT
81     LDYLIKTGSE RVAQQCRENI FAIQTLKDFQ YIDRDGKDGQ INVREKSKQL VALLKDEERL KVERVQALKT KERMAQVATG
161    VGSNQITFGR GSSQPNLSTS YSEQYHGKAG GSPASYHGST SPRVSSELEQ ARPQTSGEEE LQLQLALAMS REVAEQEERL
241    RRGDDLRLQM ALEESRRDVT KVPKKKEVKA CCKPGSHSQO TTLLDLMDAL PSSGPVAQKT EPWSTGTPAN QTNPWGQTVA
321    PANISDPWPS FGTKPAASVD PWGVPPTASI QSVPKNSDPW AASQQPASDA GKTADAWGAA KPSPASGSFE LFSNFNGTVK
401    DDFSEFDNLR TSKKPAESCA SVEPPQDSRTE SPDLFESQSL TSAASKPSSA KTPESFLGP NAALVNLDL VTKPNPPAQS
481    LNPFLAPGAA APAPVNPQV NQPQPLTLNQ LRGSPVLGSS ASFGSGPVE TVAPMPSVAP HSALGATGSS LTPLGPTAMN
561    MGVSVGIPPS AAQPAAGTTNP FLL
  
```

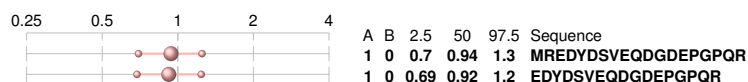


5.447 PREDICTED: similar to RNA-binding protein 8A (RNA-binding motif protein 8A) (Ribonucleoprotein RBM8)

Protein Accession	gij27693451
Mean Expression Ratio	0.936
Median Expression Ratio	0.936
Credible Interval	(0.72, 1.22)
Associated Peptides	2
Associated Spectra	2
Coverage	0.109
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1
Avg..iTRAQ.Ratio....116.114.	0.83
Avg..iTRAQ.Ratio....117.114.	0.959

```

1   MADVLDLHEA GGEDFAMDED GDESIHKLKE KAKRRKGRGF GSEEGSRAR M REDYDSVEQD GDEPGPORSV EGWILFVTGV
81  HEEATEEDIH DKFAEYGEIK NIHLNLDRTT GYLKGYTLVE YETYKEAQAA MEGLNGQDLM GQPISVDWCF VRGPPKGRRR
161 GRRRRSRSPD RRRR
    
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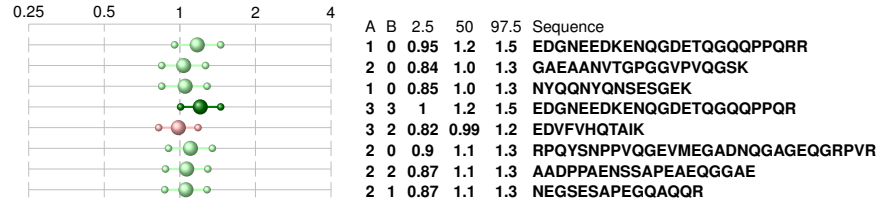


5.448 PREDICTED: similar to Nuclease sensitive element-binding protein 1 (Y-box-binding protein 1) (Y-box)

Protein Accession	gij109490740
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.923, 1.23)
Associated Peptides	8
Associated Spectra	24
Coverage	0.413
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.22
Avg..iTRAQ.Ratio....117.114.	1.20

```

1      MSSEAETQQP PAAPAAALSA ADTKPGSTGS GAGSGGPGGL TSAAPAGGDK KVIATKVLGT VKWFNVRNGY GFINSNDTR E
81     DVFVHQTAIK KNKPRKYLRS VGDGETVEFE VVEGEKGAEA ANVTGPGGVP VQGSYAADR NHYRRYP RRR GPPRNYQQNY
161    QNSESGEKNE GSESAPEGQA QQRFPYRRRR FFPYMR RPY ARRPQYSNPP VQGEVMEGAD NQGAGEQGRP VRQNM YRGYR
241    PRFRRGPPRQ RQPREDGNEE DKENQGD ETQ GQQPPQR YR RNFNYRRRRP ENPKPQDGKE TKAADPPAEN SSAPEAEQGG
321    AE
    
```



5.449 PREDICTED: similar to ubiquitin-conjugating enzyme E2 variant 1 [Rattus norvegicus]

Protein Accession	gij109500281
Mean Expression Ratio	0.936
Median Expression Ratio	0.937
Credible Interval	(0.696, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	0.068
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.945
Avg..iTRAQ.Ratio....116.114.	0.773
Avg..iTRAQ.Ratio....117.114.	0.777

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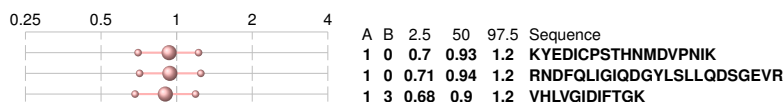
1      MAATTGSGVK VPRNFRLL EEEGQKGVGD GTVSWGLEDD EDMTLTRW TG MIIGPPRTIY ENRIYSLKIE CGPKYPEAPP
81     SVRFVTRVNM SGVSSSNGVV DPRATAVLAK WQNSHSIKVI LQELRRLMMS KENMKLPQPP EGQCYSN
    
```



5.450 eukaryotic translation initiation factor 5A [Rattus norvegicus]

Protein Accession	gi 76096304
Mean Expression Ratio	0.936
Median Expression Ratio	0.937
Credible Interval	(0.735, 1.19)
Associated Peptides	3
Associated Spectra	6
Coverage	0.351
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	0.84
Avg..iTRAQ.Ratio....117.114.	0.891

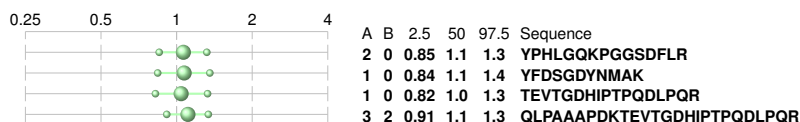
1 MADDLDFETG DAGASATFPM QCSALRKNGF VVLKGRPCKI VEMSTSKT GK HGHAKVHLVG IDIFTGKKYE D ICPSTHNMD
 81 V PNIKRND FQ LIGIQDGYLS LLQDSGEVRE DLRLPEGLG KEIEQKYDCG EEILITVLSA MTEEA AVAIK AMAK



5.451 "cyclic AMP phosphoprotein, 19 kDa [Rattus norvegicus]"

Protein Accession	gi 13928914	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.885, 1.29)	
Associated Peptides	4	
Associated Spectra	9	
Coverage	0.464	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.947	1.41
Avg..iTRAQ.Ratio....116.114.	1.05	1.55
Avg..iTRAQ.Ratio....117.114.	1.08	2.10

1 MSAEVPEAAS AEEQKEMEDK VTSPEKAEEA KLKARYPHLG QKPGGSDFLR KRLQKGQKYF DSGDYNMAKA KMKNKQLPAA
 81 A PDKTEVTGD HIPTPQDL P Q R KPSLVASKL AG

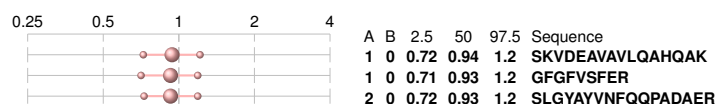


5.452 "poly(A) binding protein, cytoplasmic 1 [Rattus norvegicus]"

Protein Accession	gij19705459
Mean Expression Ratio	0.936
Median Expression Ratio	0.937
Credible Interval	(0.744, 1.17)
Associated Peptides	3
Associated Spectra	4
Coverage	0.066
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.999
Avg..iTRAQ.Ratio....116.114.	0.93
Avg..iTRAQ.Ratio....117.114.	0.944

```

1      MNPSAPSYPM ASLYVGDLP DVTEAMLYEK FSPAGPILSI RVCRCMITRR SLGYAYVNFQ QPADAERALD TMNFDVIK GK
81     PVRIMWSQRD PSLRKSQVGN IFIKNLDKSI DNKALYDTFS AFGNILSCKV VCDENGSKGY GFVHFETQEA AERAIEKMNG
161    MLLNDRKVFV GRFKSRKERE AELGARAKEF TNVYIKNFGE DMDDERLREL FGKFGPALS V KVMTDESGKS KGGFVVSFER
241    HEDAQKAVDE MNGKELNGKQ IYVGRAQKVV ERQTELRKRF EQMKQDRITR YQGVNLYVKN LDDGIDDERL RKEFSPPGTI
321    TSAKVMMEGG RSKGFGFVCF SSPPEATKAV TEMNGRIVAT KPLYVALAQR KEERQAHLTN QYMQRMASVR AVPNPVINPY
401    QPAPPSGYFM AAIPQTQNR AYYPPSQIAQ LRPSPRWTAQ GARPHPFQNM PGAIRPAAAP PPFSTMRPAS SQVPRVMSTQ
481    RVANTSTQTM GPRPAAAATA ATPAVRTVPQ YKYAAGVRNP QQHLNAQPQV TMQQPAVHVQ GQEP LTASML ASAPPQEQKQ
561    MLGERLFLPI QAMHPSLAGK ITGM LLEIDN SELHLMLESP ESLRSKVDEA VAVLQAHQAK EAAQKAVNSA TGVPTV
    
```



5.453 "PREDICTED: similar to poly(A) binding protein, cytoplasmic 4 isoform 1 [Rattus norvegicus]"

Protein Accession	gij109475439
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.798, 1.44)

Associated Peptides	1
Associated Spectra	1
Coverage	0.0229
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.32
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	1.33

```

1      MNAAASSYPM ASLYVGDLSH DVTEAMLYEK FSPAGPVLSI RVCRDMITRR SLGYAYVNFQ QPADAERALD TMNFDVIKGG
81     PIRIMWSQRD PSLRKSQVGN VFIKNLDKSI DNKALYDTFS AFGNILSCKV VCDENGSKGY AFVHFFETQEA ANKAIEKMNG
161    MLLNDRKVFV GRFKSRKERE AELGAKAKEF TNVYIKNFGE EVDDENLREL FSQFGKTLV SVKMRDCSGKS KGFVSVSYEK
241    HEDANKAVEE MNGKEMSGKS IFVGRAQKKV ERQAELEKRF EQLKQERISR YQGVNLYIKN LDDTIDDEKL RKEFSPFGSI
321    TSAKVLEDEG RSKGFGFVCF SSPEEATKAV TEMNGRIVGS KPLYVALAQR KEERKAHLTN QYMQRVAGMR ALPANAILNQ
401    FQPAAGGYFV PAVPQAQGRP PYYTNPQLAQ MRPNPRWQQG GRPQGFQGMF SALRQSGPRP ALRHLAPLGN APASRGLPTT
481    AQRVGSSECPD RLAMDFGGAG AAQQGLTDSQ QSGGVPTAVP NLAPRATVAA AAPRAVAPYK YASNVRSPHP AIQPLQAPQP
561    AVHVQGGQEPF TASMLAAAPP QEQQQLMGER LFPLIQTMHS NLAGKITGML LEIDNSELLH MLESPELRS KVDEAVAVLQ
641    AHHAKKEAAQ KESKAK
  
```



5.454 CD44 antigen [Rattus norvegicus]

Protein Accession	gi 19923703
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.794, 1.43)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0154
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.20
Avg..iTRAQ.Ratio....116.114.	1.28
Avg..iTRAQ.Ratio....117.114.	1.65

```

1      MDKVVWHTAW GLLCLLQLSL AQQQIDLNIT CRYAGVFHVE KNGRYSISRT EAADLCEAFN TTLPTMAQME LALRKGFCET
81     RYGFIEGHVV IPRIHNAIC AANNTGVYIL LASNTSHYDT YCFNASAPLE EDCTSVTDLP NSFDGCVTIT IVNRDGTYS
161    KKGEYRTHQE DIDASNIIDE DVSSGSTIEK STPEGYILHT DLPTSQPTGD RDDAFFIGST LATIASIVYS KSHATAQKQN
241    NWIWSWFGNS QSTTQTQDSP TTTATTALMT TPETPPKRQE AQNWFSWFFQ PSEKSHLHT TTKMPGTESN TNP TGWKPN
321    ENEDETDKYP NFSGSGIDDD EDFISSTIAT TPWVSAHTKQ NQERTQWNPI HSNPEVLLQT TTRMTDIDRN STSAHGENWT
401    QEPQPPFNH EYQDEEETPH ATSTTWADPN STTEEAATQK EKWFENWQQG KNPPPTSEDS HVTEGTTASA HNNHPSQRMT
481    TQSQEDVSWT DFFDPI SHPM GQGHQTESKD TGSSSHSTLQ PTAAPNTHLV EDLNRTGPLS VTFPQSHSQN FSTLPGELEE
561    GEDHPTTSVL PSSTKSGRRR GGS LPRD TTT SLEGYTPQYP DTMENGTLEF VTPAKTEVFG ETEGTVATDS NFNVDGSLPG
641    DGDSSMDPRG GFDVTYHGE IAGHSSGNQD SGVTTTSGPA RRPQIPEWLI ILASLLALAL ILAVCIAVNS RRRCGQKKKL
721    VINSNGTVE DRKPSSELNGE ASKSQEMVHL VNKEPTETPD QFMTADETRN LQSVDMKIGV
  
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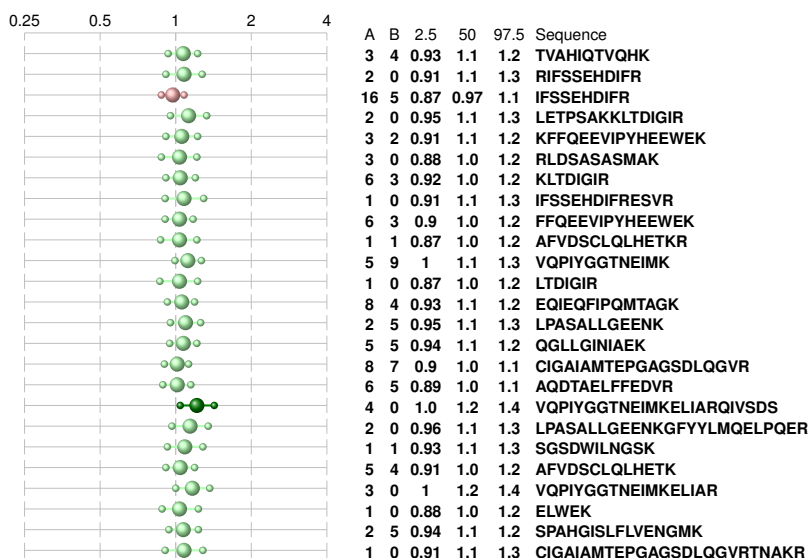


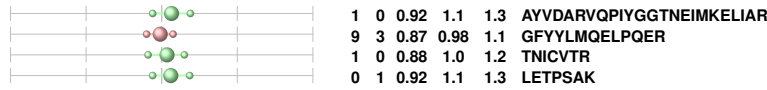
5.455 "acetyl-Coenzyme A dehydrogenase, long-chain [Rattus norvegicus]"

Protein Accession	gi 6978431	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(1.01, 1.13)	
Associated Peptides	29	
Associated Spectra	175	
Coverage	0.553	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	1.05
Avg..iTRAQ.Ratio....116.114.	0.994	1.12
Avg..iTRAQ.Ratio....117.114.	0.87	1.17

```

1   MAARLLLRSL RVLSARSATL PPSARCSSH GAEARLETPS AKKLTDIGIR RIFSSEHDIF RESVRKFFQE EVIPYHEEW
81  KAGEVSRELW EKAGKQLLG INIAEEHGGI GGDLLSTAVT WEEQAYSNCT GPGFSLHSDI VMPYIANYGT KEQIEQFIPQ
161 MTAGKCIGAI AMTEPGAGSD LQGVRTNAKR SGSDWILNGS KVFITNGWLS DLVIVVAVTN REARSPAHGI SLFLVENGMK
241 GFIKGKLHK MGMKAQDTAE LFFEDVRLPA SALLGEENKG FYYLMQELPQ ERLLIADLAI SACEFMFEET RNVVRQRKAF
321 GKPVAHIQTV QHKLAELKFN ICVTRAFVDS CLQLHETKRL DSASASMARY WASELQNTVA YQCVQLHGGW GYMWEYPIAK
401 AYVDARVQPI YGGTNEIMKE LIARQIVSDS
    
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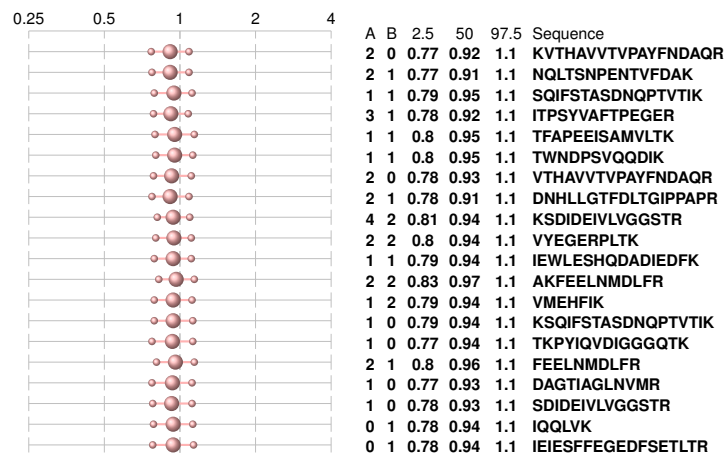


5.456 heat shock 70kD protein 5 [Rattus norvegicus]

Protein Accession	gi 25742763	
Mean Expression Ratio	0.938	
Median Expression Ratio	0.938	
Credible Interval	(0.855, 1.03)	
Associated Peptides	20	
Associated Spectra	48	
Coverage	0.336	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.931	0.807
Avg..iTRAQ.Ratio....116.114.	0.818	0.807
Avg..iTRAQ.Ratio....117.114.	0.96	1.30

```

1      MKFTVVAAL LLLCAVRAE EDKKEDVGTV VGIDLGTTYS CVGVFKNGRV EIIANDQGNR ITPSYVAFTP EGEFLIGDAA
81     KNQLTSNPN TVFDKRLIG RWNDPVSVQQ DIFFLPFKVV EKKTKPYIQV DIGGGQTKTF APEEISAMVL TKMKETAEAY
161    LGKRVTHAVV TVPAYFNDAQ RQATK DAGTI AGLNVMM IIN EPTAAAIAYG LDKREGEKNI LVFDLGGGTF DVSLLTIDNGE
241    VFEVVATNGD THLGGEDFDQ RYMEHFIKLY KKKTKGDVRK DNRAVQKLRK EVEKAKRALS SQHQAR IEIE SFPEGEDFSE
321    TLTRAKFEEL NMDLFRSTMK PVQKVLSDSD LKKSDDIDEIV LVGGSTRIPK IQQLVKEFFN GKPEPSRGINP DEAVAYGAAV
401    QAGVLSGDQD TGDVLVLDVC PLTLGIETVG GVMTKLIPRN TVVPTKKSQI FSTASDNQPT VTIKVYEGER PLTKDNHLLG
481    TFDLTGIPPA PRGVPIEIVT FEIDVNGILR VTAEDKGTGN KNKITITNDQ NRLTPEEIER MVNDAEKFAE EDKCLKERID
561    TRNELESYAY SLKNQIGDKE KLGKLSPEDE KETMEKAVEE KIEWLESHQD ADIEDFKAKK KELEEIVQPI ISKLYGSSGP
641    PPTGEEDTSE KDEL
    
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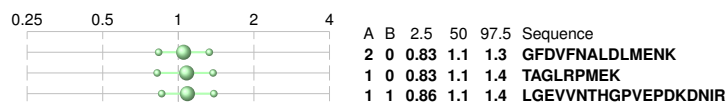


5.457 N-myristoyltransferase 1 [Rattus norvegicus]

Protein Accession	gj 22507314	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.86, 1.31)	
Associated Peptides	3	
Associated Spectra	5	
Coverage	0.0847	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.40
Avg..iTRAQ.Ratio....116.114.	1.08	1.37
Avg..iTRAQ.Ratio....117.114.	1.09	1.32

```

1   MADESETAVK LPAPSLPLMM EGNNGGHEHC SDCENEEDIS HNRGGLSPAN DTGAKKKKKK QKKKKEKGND MDSTQDQPVK
81  MNSLPAERIQ EIQKAIELFS VGQGPACTME EASKRSYQFW DTQPVPKLGE VVNTHGPVEP DKDNIRQEPY TLPQGFTWDA
161 LDLGDRGVLK ELYTLLNENY VEDDDNMFRF DYSPEFLWA LRPPGWLPQW HCGVRVVSRR KLVGFISAIP ANIHIDYTEK
241 KMVEINFLCV HKKLRSKRVA PVLIREITRR VHLEGIFQAV YTAGVVLPKP VGTCRYWHRN LNPRLIEVK FSHLSRNMTM
321 QRTMKLYRLP ETPK TAGLRP MEKKDIPVVH QLLSRYLKQF NLTPVMNQEE VEHWFYPQEN IIDTFVVENA NGEVTDFLSF
401 YTLFSTIMNH PTHKSLKAAAY SFYNVHTQTP LLDLMSDALV LAKMKGFDVF NALDLMENKT FLEKLFKFGIG DGNLQYYLYN
481 WKCPSMGAEK VGLVLQ
  
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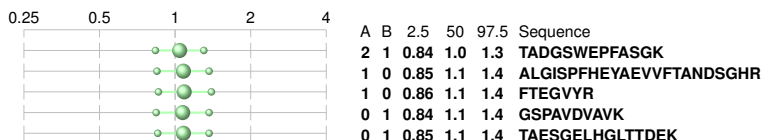


5.458 transthyretin [Rattus norvegicus]

Protein Accession	gj 6981684	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.07	
Credible Interval	(0.88, 1.30)	
Associated Peptides	5	
Associated Spectra	7	
Coverage	0.463	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.23	0.959
Avg..iTRAQ.Ratio....116.114.	1.23	0.873

Avg..iTRAQ.Ratio....117.114. 0.923 1.15

1 MASLRLLFC LAGLIFASEA GPGGAGESKC PLMVKVLDAV RGSPAVDVAV VFKR TADGS WEPFASGKTA ESGELHGLTT
 81 DEKFTGVYR VELDTKSYWK ALGISPFHEY AEVVFTANDS GHRHYTIAAL LSPYSYSTTA VVSNPQN



5.459 secretory carrier membrane protein 2 [Rattus norvegicus]

Protein Accession	gi 55741768
Mean Expression Ratio	0.939
Median Expression Ratio	0.938
Credible Interval	(0.715, 1.22)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0973
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.9
Avg..iTRAQ.Ratio....116.114.	0.83
Avg..iTRAQ.Ratio....117.114.	1

1 MSAFDTNFFA DPVDVNPFD PSVTQLTSAP QSGLAEFNPF SETNAATTVP VTQLPGPSQP AVLQPSVEPA QPSPQAVAAA
 81 AQAGLLRQOE ELDRKAAELE RKERELQNTA ANLHV ENNW PPLPSWCPVK PCFYQDFSTE IPADYQRICK MLYYLWMLHS
 161 VTLFLNLLAC LAWFTSDAAN GTAFGLSILW FLIFTPCAFI CWYRPIYKAF RSDNSFSFFV FFVVFQIG IYFIQLIGLP
 241 NLGTSGWLA LSTVNKGPLA VTIIMMVVAG FFTLCAGLSL FLLQRVHAFY RRTGASFQQA QEEFSQGIFS SRTFRTAASS
 321 AARGTFQGN



5.460 PREDICTED: similar to U2 small nuclear ribonucleoprotein B [Rattus norvegicus]

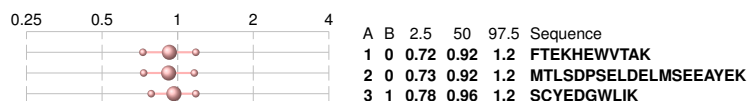
Protein Accession	gij109470907
Mean Expression Ratio	1.07
Median Expression Ratio	1.07
Credible Interval	(0.791, 1.44)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	1.26



5.461 glycine cleavage system protein H (aminomethyl carrier) [Rattus norvegicus]

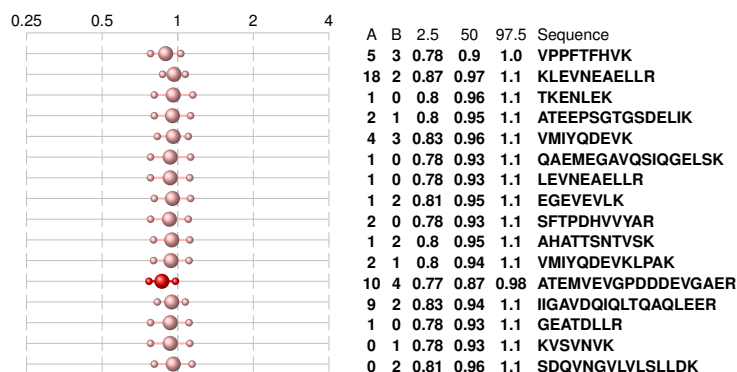
Protein Accession	gij126723054	
Mean Expression Ratio	0.94	
Median Expression Ratio	0.939	
Credible Interval	(0.775, 1.14)	
Associated Peptides	3	
Associated Spectra	7	
Coverage	0.241	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.918	1.03
Avg..iTRAQ.Ratio....116.114.	0.861	0.998
Avg..iTRAQ.Ratio....117.114.	1.01	1.27

1 MSLRVVRSVR AVACSLRIAL ASCPPRPWAP SAAAVRSLRT GSALLSVRK **TEKH**EWVTAK DGIGTVGISN FAQEALGDVV
 81 YCSLPEVGTK LKKQEEFGAL ESVKAASELY SPLSGEVTEV NEALAENPGL VNK**SCY**EDGW LIKMTLSDPS ELDELMSEEA
 161 **YER**YVKSIEE



5.462 PREDICTED: similar to Polymerase I and transcript release factor [Rattus norvegicus]

Protein Accession	gij109491901	
Mean Expression Ratio	0.939	
Median Expression Ratio	0.939	
Credible Interval	(0.862, 1.02)	
Associated Peptides	16	
Associated Spectra	81	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.974	0.85
Avg..iTRAQ.Ratio....116.114.	0.962	0.918
Avg..iTRAQ.Ratio....117.114.	0.953	0.8

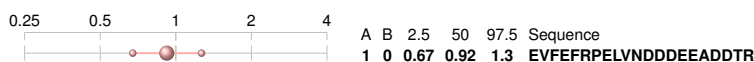


5.463 brain zinc finger protein [Rattus norvegicus]

Protein Accession	gi 58219528
Mean Expression Ratio	0.937
Median Expression Ratio	0.939
Credible Interval	(0.695, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0493
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.961
Avg..iTRAQ.Ratio....116.114.	0.686
Avg..iTRAQ.Ratio....117.114.	0.82

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1      MPPKKQAQAG GSKKAEQKKK EKIIEDKTFG LKNKKGAKQQ KFIKAVTHQV KFGQQNPRQV AQSEAEKKLK KDDKKKELQE
81     LNELFKPVVA AQKISKGADP KSVVCAFFKQ GQCTKGDCK FSHDLTLERK CEKRSVYIDA RDEELEKDTM DNWDEKKLEE
161    VVNKKHGEAE KKKPKTQIVC RHFLEAIENN KYGFWFVCPG GGDNCMYRHA LPPGPFVLKGD KKKKEEKEDEI SLEDLIERER
241    SALGPNVTKI TLESFLAWKK RKRQEKIDKL EQDMERRKAD FKAGKALVIS GREVFEFRPE LVNDDDEEAD DTRYIQGTGG
321    DEVDDSVGVN DIDLSLYVPR DVEETGITVA SLERFSTYAS DKDENKLSEA SGGLAENGER SDLDEDSGGG GQENGSIDAV
401    PVDENLFTGE DLDELEEEELN TLDLEE
  
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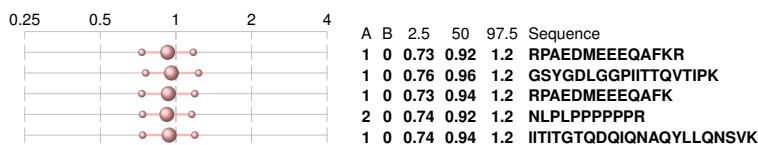


5.464 heterogeneous nuclear ribonucleoprotein K [Rattus norvegicus]

Protein Accession	gi 16923998
Mean Expression Ratio	0.94
Median Expression Ratio	0.939
Credible Interval	(0.775, 1.14)
Associated Peptides	5
Associated Spectra	6
Coverage	0.145
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.04
Avg..iTRAQ.Ratio....116.114.	0.824
Avg..iTRAQ.Ratio....117.114.	1.06

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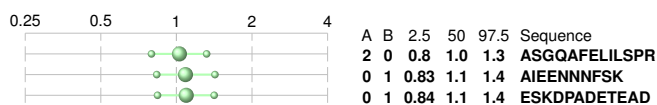
1      METEQPEETF PNTETNGEFG KRPAEDMEEE QAFKRRSRNTD EMVELRILLQ SKNAGAVIGK GGKNIKALRT DYNASVSVPD
81     SSGPERILSI SADIETIGEI LKKIIPTLEE GLQLPSPTAT SQLPLESDAV ECLNYQHYKG SDFDCELRLI IHQSLAGGII
161    GVRGAKIKEL RENTQTTIKL FQECCPHSTD RVVLIGGKPD RVVECIKIL DLISESPIKG RAQPYDPNFY DETYDYGGFT
241    MMFDDRRGRP VGFPMRGRGG FDRMPPGRGG RPMPPSRRDY DDMSPRRGPP PPPPGRGRG GSRARNLLP PPPPRGGDL
321    MAYDRRGRPG DRYDGMVGFS ADETWDSAID TWSPSEWQMA YEPQGGSGYD YSYAGGRGSY GDLGGPIITT QVTIPKDLAG
401    SIIGKGGQRI KQIRHESGAS IKIDEPLEGS EDRIITITGT QDQIQNAQL LQNSVRQYSG KFF
  
```



5.465 stathmin 1 [Rattus norvegicus]

Protein Accession	gi 8393696	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.852, 1.34)	
Associated Peptides	3	
Associated Spectra	4	
Coverage	0.235	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.88	1.20
Avg..iTRAQ.Ratio....116.114.	0.863	1.07
Avg..iTRAQ.Ratio....117.114.	0.923	1.62

1 MASSDIQVKE LEKRASGQAF ELILSPRSKE SVPEFPLSPP KKKDLSLEEI QKKLEAAEER RKSHEAEVLK QLAEKREHEK
81 EVLQKAIEEN NNFSPMAEEK LTHKMEANKE NREAQMAAKL ERLREKDKHV EEVRKNKESK DPADETEAD



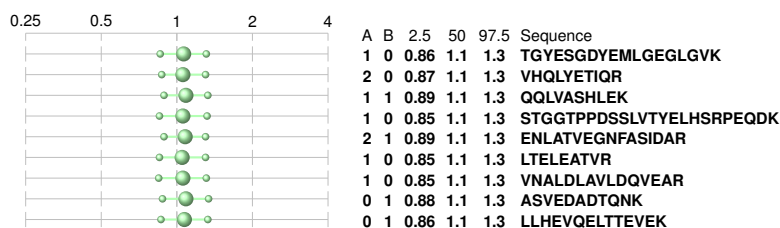
5.466 dynactin 2 [Rattus norvegicus]

Protein Accession	gi 51948450	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.06	
Credible Interval	(0.917, 1.24)	
Associated Peptides	9	
Associated Spectra	13	
Coverage	0.316	

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.963	1.30
Avg..iTRAQ.Ratio....116.114.	1.03	1.30
Avg..iTRAQ.Ratio....117.114.	1.08	1.15

```

1   MADPKYADLP GIARNEPDVY ETSDLPEDDQ AEFDAEELSS TSVEHIIVNP NAAAYDKFKDK RVGTKGLDFS DRIGKTKRQG
81  YESGDYEMLG EGLGVKETPQ QKYQRLLHEV QELTTEVEKI KTTVKESATE EKLTVPVVLAK QLAALKQQLV ASHLEKLLGP
161 DAAINLADPD GALAKRLLLQ LEATKSSKGS SGGKSTGGTP PDSSLVTYEL HSRPEQDKFS QAAKVAELEK RLTELEATVR
241 CDQDAQNPLS AGLQGACLME TVELLQAKVN ALDLAVLDQV EARLQSVLKG VNEIAKHKAS VEDADTQNKV HQLYETIQRW
321 SPVASTLPEL VQRLVTIKQL HEQAMQFGQL LTHLDTTQQM MASSLKDNNTA LLTQVQT TMR ENLATVEGNF ASIDARMKKL
401 GK
    
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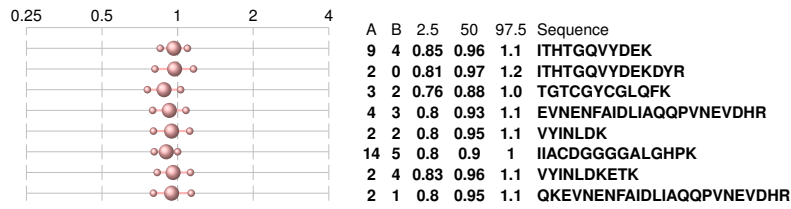


5.467 PREDICTED: NADH dehydrogenase (ubiquinone) Fe-S protein 6 [Rattus norvegicus]

Protein Accession	gij109504524	
Mean Expression Ratio	0.939	
Median Expression Ratio	0.94	
Credible Interval	(0.852, 1.04)	
Associated Peptides	8	
Associated Spectra	59	
Coverage	0.647	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.863	1.00
Avg..iTRAQ.Ratio....116.114.	1.02	0.86
Avg..iTRAQ.Ratio....117.114.	0.94	0.754

```

1   MAAALTFRRL LALPRAARGF GVRVSRSGEK ITHTGQVYDE KDYRIRRFVD RQKEVNFENFA IDLIAQQPVN EVDHRIIACD
81  GGGGALGHPK VYINLDKETK TGTCGYCGLQ FKQQHH
    
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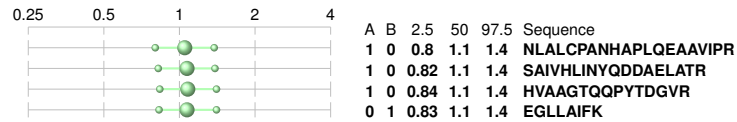



5.468 junction plakoglobin [Rattus norvegicus]

Protein Accession	gj 41529837	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.85, 1.34)	
Associated Peptides	4	
Associated Spectra	4	
Coverage	0.0819	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.19	1.06
Avg..iTRAQ.Ratio....116.114.	1.19	0.967
Avg..iTRAQ.Ratio....117.114.	1.13	1.14

```

1    MEVMNLIEQP IKVTEWQQTY TYDSGIHSGV NTCVPSVSSK GLLDEDDTCG RQYTLKTTT YTQGVPSQSG DLEYQMSTTA
81   RAKRVREAMC PGVSGEDSSL LLATQVEGQT TNLQRLAEPS QLLKSAIVHL INYQDDAELA TRALPELTKL LNDEDPVVVT
161  KAAMIVNQLS KKEASRRALM GSPQLVAADV RTMQNTSDLD TARCTTSILH NLSHHRGGLL AIFKSGGIPA LVRMLSSPVE
241  SVLFYAITTL HNLLEYQEGA KMAVRLADGL QKMVPLLNKN NPKFLAITTD CLQLLAYGNO ESKLIILANG GPQGLVQIMR
321  NYSYEKLLWT TSVRLKVLVS CPSNKPATIVE AGGMQALGKH LTSNSPRLVQ NCLWTLRNLN DVATKQEGLE NVLKILVNQL
401  SVDDVNVLTC ATGTLNLTLC NNSKNKTLVT QNSGVEALIH AILRAGDKDD ITEPAVCALR HLTSRHPPEAE MAQNSVRLNY
481  GIPAIVKLLN QPNQWPLVKA TIGLIRNLAL CPANHAPLQE AAVIPRLVQL LVKAHQDAQR HVAAGTQQPY TDGVRMEEIV
561  EGCCTGALHIL ARDPMNRMEI FRLNTIPLFV QLLYSSVENI QRVAAGVLCE LAQDKEAADA IDAEGASAPL MELLSRNEG
641  TATYAAAVLF RISEDKNPDY RKRVSVELTN SLFKHDPAAW EAAQSMIPIN EPYADDMDAT YRPMYSSDVP LDPLDMHMDM
721  DGDYPMDTYS DGLRPPYPAA DHMLA
    
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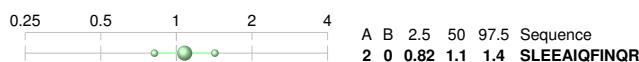
5.469 "aldehyde dehydrogenase family 3, member A1 [Rattus norvegicus]"

Protein Accession	gij14010869
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.808, 1.39)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0265
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.12
Avg..iTRAQ.Ratio....116.114.	1.28
Avg..iTRAQ.Ratio....117.114.	1.27

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1      MSSISDTVKR AREAFNSGKT RSLQFRIQQL EALQRMINE LKSIISGALAS DLGKNEWTSY YEEVAHVLEE LDTTIKELPD
81     WAEDPVAKT RQTQQDDLYI HSEPLGVVLV IGAWNYPFNL TIQPMVGAVA AGNAVILKPS EVSGHMADLL ATLIPQYMDQ
161    NLYLVVKGKV PETTELLKER FDHIMYTGST AVGKIVMAAA AKHLTPVTL LGGKSPCYVD KCDLDVACR RIAWGKFMNS
241    GQTCVAPDYI LCDPSIQNQI VEKLRKSLKD FYGEDAKQSR DYGRINDRH FQRVKGLIDN QKVAHGGTWD QSSRYIAPTI
321    LVDVDPQSPV MQEEIFGPVM PIVCVRSLEE AIQFINQREK PLALYVFSNN EKVKKMIAE TSSGGVTAND VIVHITVPTL
401    PFGGVGNSGM GAYHGKKSFE TFSHRRSCLV KSLNEEAHK ARYPPSPARK PRH

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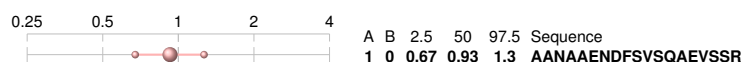


5.470 PREDICTED: similar to ATP-binding cassette sub-family F member 1 (ATP-binding cassette 50) [Rattus]

Protein Accession	gij109509122
Mean Expression Ratio	0.938
Median Expression Ratio	0.94
Credible Interval	(0.694, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0233
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.818
Avg..iTRAQ.Ratio....116.114.	0.835
Avg..iTRAQ.Ratio....117.114.	0.958

```

1      MDKVVKKGGK DKKTKKTFE ELAVEDKQAG EEEKLQKEKE QQQQQQQQKK KRDRTRKGRK KDVDDDDDDG ERVLMERLQK
81     LSVPASDEED EVPVPVPRGR KKAKGGNVFE ALIQDESEEE KEEEEKPVV KPAKPEKNRI NKAVAEPPG LRNKKGKEEK
161    SKGKAKNKPS ATDSEGEDDE DMTKEKEPPR PGKD KDKKGA EQGSEEEKEE KEGEVKANDP YAHLSKKEKK KLKKQMDYER
241    QVESLKAANA AENDFSVSA EVSSQAMLE NASDIKLEKF SISAHGKELF VNADLYIVAG RRYGLVGPNG KGKTLLKHI
321    ANRALSIPPN IDVLLCEQEV VADETPAVQA VLRADTKRLR LLEEKRLQG QLEQGDDTAA EKLEKVEEEL RATGAAAAEA
401    KARRILAGLG FDPENQNRPT QKFSGGWRMR VSLARALFME PTLMLLDEPT NHLDLNAVIW LNNYLQGWK TLLIVSHDQG
481    FLDDVCTDII HLDTQRLHY RGNMYTFKKM YQQKQKELLK QYEKQEKLLK ELKAGGKSTK QAEKQTKEV TRKQKCRK
561    NQDEESQDPP ELLKRPREYT VRFTFPDPPP LSPFVLGLHG VTFGYEGQKP LFKNLDFGID MDSRICIVGP NGVGKSTLLL
641    LLTGKLTPTN GEMRKNHRLK IGFFNQYAE QLHMEETPTE YLQRFNLPY QDARKCLGRF GLESHAHTIQ ICKLSSGGKA
721    RVVFAELACR EPDVLILDEP TNNLDIESID ALGEAINEYK GAVIVVSHDA RLITETNCQL WVVEEQSVSQ IDGDFDDYKR
801    EVLEALGEVM VNRPRD
    
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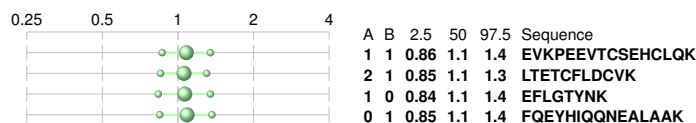


5.471 PREDICTED: similar to Mitochondrial import inner membrane translocase subunit Tim9 [Rattus norvegicus]

Protein Accession	gj 109478321	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.06	
Credible Interval	(0.88, 1.29)	
Associated Peptides	4	
Associated Spectra	7	
Coverage	0.562	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	1.07
Avg..iTRAQ.Ratio....116.114.	1.19	1.05
Avg..iTRAQ.Ratio....117.114.	1.14	0.869

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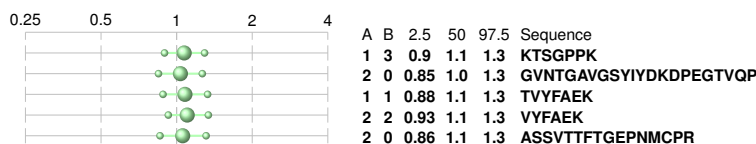
1      MAAQIPESDQ IKQFK EFLGT YNKLTETCF LDCVKDFTRR VKPEEVTCS E HCLQY LKMT QRISMRFQ EY HIQQNEALAA
81     KAGLLGQPR
    
```



5.472 cysteine-rich protein 2 [Rattus norvegicus]

Protein Accession	gij11968068	
Mean Expression Ratio	1.07	
Median Expression Ratio	1.06	
Credible Interval	(0.917, 1.25)	
Associated Peptides	5	
Associated Spectra	14	
Coverage	0.25	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.01	0.975
Avg..iTRAQ.Ratio....116.114.	1.06	1.06
Avg..iTRAQ.Ratio....117.114.	1.16	1.09

1 MASKCPKCDK TVYFAEKVSS LGKDWHKFC L KCERCNKTLT PGGHAEHDGK PFCHKPCYAT LFGPKGVNIG GAGSYIYEKP
 81 PTEAPQVTGP IEVPVVRTEE RKTSGPPKGP SKASSVTFTT GEPNMCPR CN KRVIYFAEKVT SLGKDWHRPC LRCERCSKTL
 161 TPGGHAHEHDG QPYCHKPCYG ILFGPKGVNT GAVGSYIYDK DPEGTVQP



5.473 neural visinin-like Ca²⁺-binding protein type 3 [Rattus norvegicus]

Protein Accession	gij8393864	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.78, 1.44)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0777	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.15	
Avg..iTRAQ.Ratio....116.114.	1.38	
Avg..iTRAQ.Ratio....117.114.	1.73	

1 MGKQNSKLRP EVLQDLREHT EFTDHELQEW YKGF LKDCPT GHLTVDEFKK IYANFFPYGD ASKFAEHVFR TFDTNSDGTI
 81 DFRFIIALS VTSRGKLEQK LKWAFSMYDL DNGYISRSE MLEIVQAIYK MVSSVMKMPE DESTPEKRTD KIFRQMDTNN
 161 DGKLSLEEFI KGAKS DPSIV RLLQCDPSSA SQF

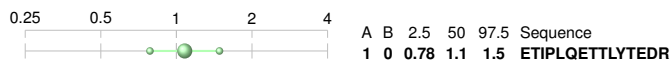


5.474 palmitoyl-protein thioesterase [Rattus norvegicus]

Protein Accession	gi 11968070
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.787, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	0.049
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.44
Avg..iTRAQ.Ratio....116.114.	1.48
Avg..iTRAQ.Ratio....117.114.	1.20

```

1      MASPGRRL  AAALPWCCA  AWALGHLDP  SPPPLVIWH  MGDSCCNPM  MGSIKMVEK  EIPGIYVLS  EIGKNMVED
81     ENSFFLNVL  QVGMACQIL  KDPKLQHG  AIGFSQGG  LRAVAQRCP  PPMMLISVG  GQHQQVFL  RCPGESSHC
161    DFIRKSLN  AYSKVVQER  VQAQYWH  KEEVYRNC  FLADINQER  INESYKENL  ALKKFVMV  FND SIVDP
241    SEWFGFYS  QAKETIPL  TTYTEDRL  LKMKDAG  VFLAKEGD  QISKEWFTA  IIPFLK
    
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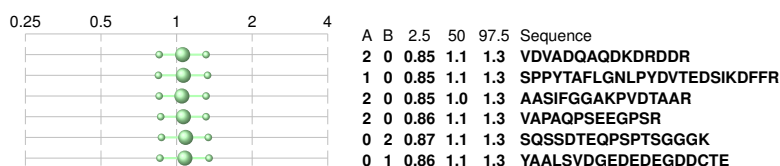


5.475 eukaryotic translation initiation factor 4B [Rattus norvegicus]

Protein Accession	gi 56605726	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.897, 1.26)	
Associated Peptides	6	
Associated Spectra	10	
Coverage	0.172	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.956	0.98
Avg..iTRAQ.Ratio....116.114.	1.06	1.42
Avg..iTRAQ.Ratio....117.114.	1.22	1.10

```

1    MAASAKKKNK KGKTISLTDF LAEDGGTGGG STYVPKPSW ADETDDELDG VSTTWSNDD DVYRAPPIDR SILPTAPRAA
81   REPNIIDRSRL PKSPPYTAFL GNLPYDVTED SIKDFFLGLN ISAVRLPREP SNPDRLKGFY YAEFEDLDSL LSALSLSNEES
161  LGNRRIRVDV ADQAQDKDRD DSFSGRDRNR DSDKTDTDWR ARPATDSFDD YPPRRGDDSF GDKYRDRYES DRYRDGYRDG
241  YRDGPRRDMD RYGGDRDYDD RGSRDYDRGY DSRIGSGRRA FSGYRRDDD YRGGGDRYED RYDRRDRSRW SSRDDYSRDD
321  YRRDDRGFPQ RPKLNLKPRS TPKEDDSSAS TSQSSRAAST FGGAKPVDTA AFEREVEERL QKEQEKLRQK LDEPKLDRRP
401  RERHPSWRSE ETQERERSRT GSESSQTGTS ATSGRNTRRR ESEKSLNET LNKEEDCHSP TSKPPKPDQP LKVMPPPPK
481  ENAWVKRSSN PPARSQSSDT EQSPSTSGGG KVAPAQPSEE GPSKDETKV DGVSTTKGQT GHSSRGPGDG GSRDHWKELD
561  RKDGKKDQDS RSAPEPKKSE ENRASKFSSA SKYAALSVDG EDEDEGDDCT E
    
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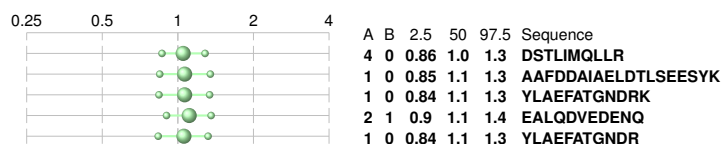


5.476 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein [Rattus norvegicus]

Protein Accession	gi 13928824	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.9, 1.27)	
Associated Peptides	5	
Associated Spectra	10	
Coverage	0.204	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.18	0.987
Avg..iTRAQ.Ratio....116.114.	1.18	0.649
Avg..iTRAQ.Ratio....117.114.	1.16	1.04

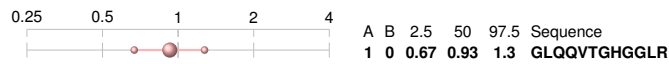
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1    MDDREDLVYQ AKLAEQAERY DEMVESMKKV AGMDVELTVE ERNLLSVAYK NVIGARRASW RIISSIEQKE ENTGGEDKLK
81   MIREYRQMV E TELKLICCDI LDVLDKHLIP AANTGESKVS YYMKGDYHR YLAEFATGND RNEAAENSLV AYKAASDIAM
161  TELPPTHPIR LGLALNFSVF YYEILNSPDR ACRLAKAAFD DAIAELDITLS EESYKDSTLI MQLLRDNLTL WTSDMQGDGE
241  EQNK EALQDV EDENQ
    
```



5.477 PREDICTED: similar to 13kDa differentiation-associated protein [Rattus norvegicus]

Protein Accession	gj 109481873
Mean Expression Ratio	0.94
Median Expression Ratio	0.94
Credible Interval	(0.699, 1.27)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.747
Avg..iTRAQ.Ratio....116.114.	0.795
Avg..iTRAQ.Ratio....117.114.	0.861



5.478 guanylate kinase 1 [Rattus norvegicus]

Protein Accession	gj 61556989
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.78, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0859
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.29
Avg..iTRAQ.Ratio....116.114.	1.27
Avg..iTRAQ.Ratio....117.114.	1.59

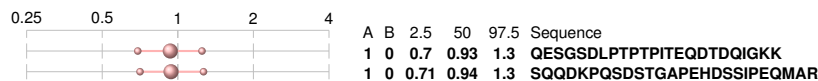
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1   MAGPRPVVLS  GPSGAGKSTL  LKKLFQEHGS  VFGFSVSHTT  RNP RPGEEDG  KDYYFVTREM  MQRDIAAGDF  IEHAEFSGNL
81  YGTSKEAVRA  VQAMNRCIVL  DVDLQGVRSI  KKTDLHPYIY  SVQPPSMDVL  EQRLRQRNTE  TEESLAKRLA  AAQADMESK
161 EPGLFDLVIV  NDNLDEAYVT  LKQALSEEIK  KAEGTEHA
    
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5.479 PREDICTED: hypothetical protein [Rattus norvegicus]

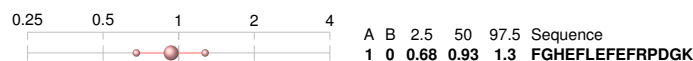
Protein Accession	gij109477815
Mean Expression Ratio	0.941
Median Expression Ratio	0.94
Credible Interval	(0.727, 1.23)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	0.921
Avg..iTRAQ.Ratio....117.114.	0.767



5.480 PREDICTED: similar to Protein mago nashi homolog [Rattus norvegicus]

Protein Accession	gij109476973
Mean Expression Ratio	0.941
Median Expression Ratio	0.941
Credible Interval	(0.697, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	0.103
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.856
Avg..iTRAQ.Ratio....116.114.	1.00
Avg..iTRAQ.Ratio....117.114.	0.811

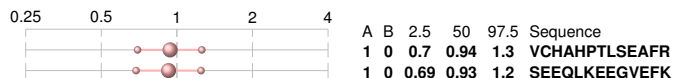
1 MESDFYLRYV VGHKGF**FGHE FLEFFFRPDG** KLRYANNSNY KNDVMIRKEA YVHKSVMEEL KRIIDDSEIT KEDDALWPPP
 81 DRVGRQELEI VIGDEHISFT TSKIGSLIDV NQSKDPEGLR VFYYLVQDLK CLVFSLIGLH FKIKPI



5.481 "dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate com"

Protein Accession	gij 40786469
Mean Expression Ratio	0.94
Median Expression Ratio	0.941
Credible Interval	(0.723, 1.22)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0511
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.975
Avg..iTRAQ.Ratio....116.114.	0.77
Avg..iTRAQ.Ratio....117.114.	0.907

1 MQSWSRVYCS LAKKGHFNRL SHGLQGASSV PLRTYSDQPI DADVTVIGSG PGGYVAAIKA AQLGFKTVCI EKNETLGGTC
 81 LNVGCIPSKA LLNNSHYHHL AHGKDFASRG IEIPEVRLNL EKMMEQKRSA VKALTGGIAH LFKQNKVVHV NGFGKITGKN
 161 QVTATTADGS TQVIGTKNIL IATGSEVTPF PGITIDEDTI VSSTGALS LKVPPEKLVVIG AGVIGVELGS VWQRLGADV
 241 AVEFLGHVGG IGIDMEISKN FQRILQKQGF KFKLNTKVTG ATKKS DGKID VSVEAASGGK AEVITCDVLL VCIGRRPFTQ
 321 NLGLEELGIE LDPKGRIPVN TRFQTKIPNI FAIGDVVAGP MLAHKAEDEG IICVEGMAGG AVHIDYNCVP SVIYTHPEVA
 401 WVGK**SEEQLK EEGVEFKVGK** FFFAANSRAK TNADTDGMVK ILGHKSTDRI LGAHILGPGA GEMVNEAALA LEYGASCEDV
 481 AR**VCHAHPTL SEAF**FEANLA ASFGKPI NF



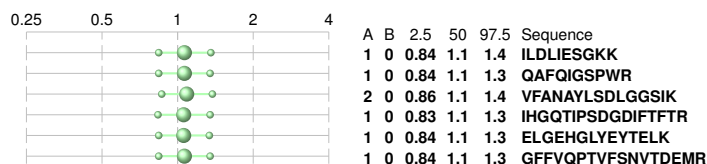
5.482 "aldehyde dehydrogenase family 1, member A1 [Rattus norvegicus]"

Protein Accession	gij 14192935
Mean Expression Ratio	1.06

Median Expression Ratio	1.06
Credible Interval	(0.886, 1.28)
Associated Peptides	6
Associated Spectra	7
Coverage	0.166
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.18
Avg..iTRAQ.Ratio....116.114.	1.07
Avg..iTRAQ.Ratio....117.114.	1.19

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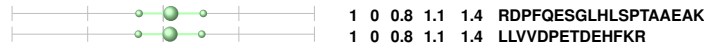
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81     DASERGRLLN KLADLMERDR LLLATIEAIN GGKVFANAYL SDLGGSTAL KYCAGWADK I HGTIPSDGD IFTFTRREPI
161    GVCGQIIPWN FPLLMIWIKI GPALSCGNTV VVKPAEQTPL TALHMASLIK EAGFPFGVNV IVPGYGPTAG AAISSHMDVD
241    KVAFTGSTQV GKLIKEAAGK SNLKRVTLEL GKGSPCIVFA DADLDIAVEF AHHGVEFYHQG QCCVAASRIF VEESVYDEFV
321    RKSVERAKKY VLGNPFLTQGI NQGPPIDKEQ HDKILDLES GKREGAKLEC GGGRWGNKGF FVQPTVFSNV TDEMRIAKEE
401    IFGPVQQIMK FKSIDDVIKR ANNTTYGLAA GVFTKDLDR A ITVSSALQAG VVVVNCYML SAQCPFGGFK MSGNRELGE
481    HGLYEYTELK TVAMKISQKN S
    
```



5.483 solute carrier family 9 isoform 3 regulator 2 [Rattus norvegicus]

Protein Accession	gij 20270217
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.813, 1.38)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.13
Avg..iTRAQ.Ratio....116.114.	1.28
Avg..iTRAQ.Ratio....117.114.	1.24



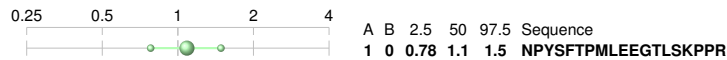


5.484 hypothetical protein LOC309381 [Rattus norvegicus]

Protein Accession	gi 51948490
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.79, 1.44)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0327
Experiment	A
Avg...iTRAQ.Ratio....115.114.	1.32
Avg...iTRAQ.Ratio....116.114.	1.42
Avg...iTRAQ.Ratio....117.114.	1.28

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1   MAASGRGLSR ALHSTPCPAW KRVQSGANGC LKPEYDAVVI GAGHNLVAA AYLQRLGVNT AVFERRHVIG GAAVTEEIIIP
81  GFKFSRASYL LSLLRPQIYT DLELKKHGLK LHLRNPYSFT PMLEEGTLSK PPRSLLLGTD VAENQKQISQ FSRKDAQAFP
161 RYEEFMKRLV LAIDPLDAA PVDIAALQHG SLLQRLRALS TLRPLLKAGR TLGAQLPQYY EVLTAPISKV LDQWFESEPL
241 KATLATDAVI GAMTSPHTPG SGYVLLHHVM GSLEGMQAW SYVQGGMGAL SDAIASSATA HGASIFTEKT VAKVQVNSEG
321 RVQGVVLQGG EEVRSRVVLS CASPQVTFLE LTPQEWLPGA FVKRISQLDT QSPVTRINVA VDRLPNFQAA PNAPGDQPQA
401 HHQCSIHLNC EDTLLLHQAF EDAKGGGPSQ RPMIELCIPS SLDP TLAPT G CHVVS LFTQY TPYTLAGGKV WDEQKKN TYA
481 DKVFD CIEAY APGFKRSVLG RDILTPQDLE RIFGLPGGNI FHGAMSLDQL YFARVPVPQHS DYRCPVQGLY LCGSGAHPGG
561 GVMGAAGRNA AHIVFRDLKN M
    
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5.485 chorionic somatomammotropin hormone 1 variant [Rattus norvegicus]

Protein Accession	gi 15100177
Mean Expression Ratio	0.941
Median Expression Ratio	0.941
Credible Interval	(0.697, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0448

Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.93
Avg..iTRAQ.Ratio....116.114.	0.803
Avg..iTRAQ.Ratio....117.114.	0.754

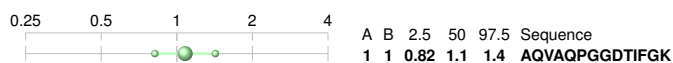
1 MQLTLTSLGS SMQLLLLVS N LLLWENMASK PTVLVSTEDL YHRLVEQSHN TFIKAADVYR EFDINFAKRS WMKDRILPLC
 81 HTASIHVPEN REEVHEIKTE DLLRSIINIS VSWKEPLKHF VSAVTDLPGA SASMRKKA VD MKDKNLIILE GLQKIFNRTQ
 161 TKVEENENFD YPAWSGLKDL QSSDEDTHLF AIYNLCRCFK SDIHKIDTYL KVLRCRVVFK NEC



5.486 PREDICTED: similar to Histidine triad nucleotide-binding protein 1 (Adenosine 5-monophosphoramidase)

Protein Accession	gi 109490737	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.814, 1.38)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.0725	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	1.21
Avg..iTRAQ.Ratio....116.114.	0.97	1.28
Avg..iTRAQ.Ratio....117.114.	0.87	1.48

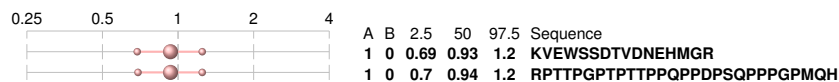
1 MQYILLSPPS PQKEGQTF AK QIQRLRRRRR RQSACAD R PG ASRQSPRALA VPLPTVAAAR EGQRPAAMAD EIAK A QVAQP
 81 G GDTIFGK II RKEIPAKIIF EDDRCLAFHD ISPQAPTHFL VIPKKHISQI SVADDDDES L LGHLMIVGKK CAADLGLKRG
 161 YRMVVNEGAD GGQSVYHIHL HVLGGRQMNW PPG



5.487 "protein phosphatase 1, regulatory (inhibitor) subunit 11 [Rattus norvegicus]"

Protein Accession	gij47087115
Mean Expression Ratio	0.94
Median Expression Ratio	0.942
Credible Interval	(0.716, 1.21)
Associated Peptides	2
Associated Spectra	2
Coverage	0.328
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.898
Avg..iTRAQ.Ratio....116.114.	0.918
Avg..iTRAQ.Ratio....117.114.	1.05

1 MAEAGAGGLS ETVTETTTVV TTEPVRNAGR GANRSLTIKL RKRKPEK**KVE** WSSDTVDNEH MGRSSKCCC IYEKPRAFGE
 81 SSTESDEDEE ECGHTHCVR GHRKGR**RPTT** PGPTPTT**PPQ** PPDPSQ**PPG** PMQH



5.488 hepatoma-derived growth factor [Rattus norvegicus]

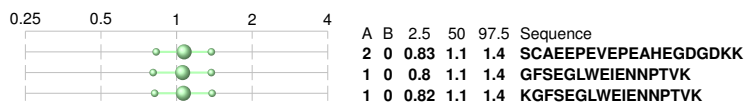
Protein Accession	gij16758528
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.845, 1.32)
Associated Peptides	3
Associated Spectra	4
Coverage	0.156
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	1.48

NHLBI Zile/Grant, Aged Rat

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1      MSRSNRQKEY KCGDLVFAKM KGYPHWPARI DEMPEAAVKS TANKYQVFFF GTHETAFLGP KDLFPYEEESK EKFGKPNKRK
81     GFSEGLWEIE NNPTVKASGY QSSQKKCAE EPEVEPEAHE GDGDKKGNAE GSSDEEGKLV IDEPAKEKNE KGMLKRRAGD
161    MLEDSPKRPK ESGDHEEEK EIAALEGERP LPVEMEKNST PSEPDSSGQGP PEEEEEGEEE AAKEEAQAQG VRDHESL

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5.489 plectin 1 [Rattus norvegicus]

Protein Accession	gj13540714	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.918, 1.22)	
Associated Peptides	13	
Associated Spectra	15	
Coverage	0.0378	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.94	0.864
Avg..iTRAQ.Ratio....116.114.	1.09	1.03
Avg..iTRAQ.Ratio....117.114.	1.43	1.32

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1      MVAGMLMPLD QLRAIYEVLF REGVMVAKKD RRRSLHPHV PGVTNLQVMR AMTSLKARGL VRETFAWCHF YWYLTNEGID
81     HLRQYLHLPP EIVPASLQRV RRPVAMVMPA RRRSPHVQTM QGPLGCPPKR GPLPAEDPAR EERQVYRKE REEGAPETPV
161    VSATIVGTLA RPPPEPTPAT DERDRVQKKT STKVVNKHLI KAQRHISDLY EDLRDGHNLI SLEVLVSGDS LPREKGRMRP
241    HKLQNVQIAL DYLRHRQVKL VNIRNDIAD GNPKLTGLI WTIIHFHFKIS DIQVSGQSED MTAKEKLLW SQRMVEGQQG
321    LRCDNFTTSW RDGRLFNAII HRRHKPLIDM NKVYRQTNLE NLDQAFSVAE RDLGVTRLLD PEDVDVPPQD EKSIITYVSS
401    LYDAMPFVPG AQDGVRADEL QLRWQYREL VLLLLWIRH HTAAFEERKF PSSFEEIEIL WCQFLKFKET ELPKAEADKN
481    RSKGIYQSL EAVQAGQLKI PPGYHPLDVE KEWGKLVHAI LEREKQLRSE FERLECLQRI VSKLQMEAGL CEEQLYQADS
561    LLQSDIRLLA SGKAAQRAGE VERDLDKADG MIRLLFNVDQ TLKDGRRHPQG EQMYRRVYRL HERLVAIRTE YNLRLLKAGVG
641    APVTQVTLQS TQRREPELEDS TLRYLHDLA WVEENQRRID GAEWGVDLPS VEAQLGSHRG MHQSIEEFRA KIERARNDES
721    QLSPATRGAY RDCLGRDLQ YAKLLNSSKA RLSLESLSHG FVAAATKELM WLNEKEEEV GFDWSDRNTN MAARKESYSA
801    LMRELEMKEK KIKEIQNTGD RLLREDHPAR PTVESFQAAL QTQWSWMLQL CCCIEAHLKE NTAYFQFFSD VREABEQLOK
881    LQETLRRKYS CDRSITVTRL EDLLQDAQDE KEQLNEYKGH LSGLAKRAKA IVQLKPRNPA HPVGRGHVPLL AVCDYKQVEV
961    TVHKGDCQL VGPAQPFHWK VLSSSGSEAA VPSVCFVLPV PNQEAQEAVA RLEAQHQALV TLWHQLHVDM KSLLAQWQSLN
1041   RDIQLIRSW S LVTFRTLKPE EQRQALRNLE LHYQAFLRDS QDAGFGPED RLVAEREYGS CSRHYQQLLO SLEQGEQES
1121   RCQRCISELK DIRLQLEACE TRTVHRLRLP LDKDPARECA QRIAEQQKAQ AEVEGLGKGV ARLSAEAEKV LALPEPSPA
1201   PTLRSELELT LGKLEQVRSI SAIYLEKLT ISLVIRSTQG AEEVLKTHEE HLKEAQAVPA TLQLELVTKA SLKKLRAQAE
1281   AQPVFNTLR DELRGAQEVG ERLQQRHGER DVEVERWRER VTQLLRWQA VLAQTDVQR ELEQLGRQLR YYRESADPLS
1361   SWLQDAKSRQ EQIQAVPIAN SQAAEQLRQ EKALLEEIER HGEKVEECQK FAKQYINAIK DYELQLITYK AQLEPVASPA
1441   KKPQVQSGSE SVIQEYVDLR TRYSELTTLT SQYIKFISSET LRRMEEEERL AEQQRAEERE RLAEVEAALE KQRQLAEAHA
1521   QAKAQAELEA RELQRRMQEE VTRREAAVD AQQQRSIQE ELQHLRQSSE AEIQAKAQV EAAERSMRI EEEIRVRLQ
1601   LETTERQGG AEDELQALRA RAEAEAAQR QAQEAERLR RQVQDESQRK RQAEALALR VKAEAEARE KQALQALDE
1681   LKLQAEAEER WLCQAEAEERA RQVQVALETA QRSAAVELQS KRPSFAEKTA QLERTLQEBH VITVTQLFEA ERRAQQQAEA

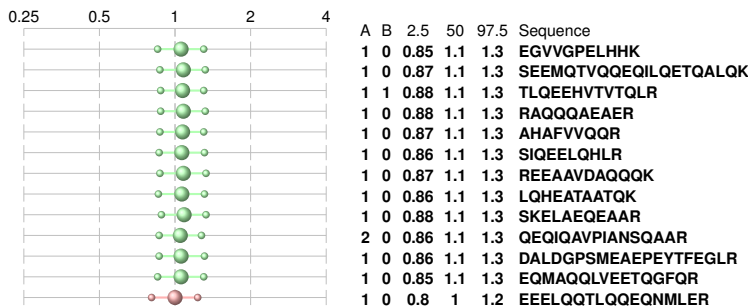
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NHLBI Zile/Grant, Aged Rat

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1761  ERAREEAERE LERWQLKANE ALRLRLQAEV VAQQKSLAQD DAEKQKEEAE REARRRGKAE EQAVRQRELA EQELEKQRQL
1841  TEGTAQQRLA AEQELIRLRA ETEQGEHQRO LLEEELARLQ HEATAATQFR QELEAELAKV RAEMEVLAS KARAEESRS
1921  TSEKSKQRLE AEAGRFRELA EEAARLRALA EEARRHRELA EEDAARQRAE ADGVLTEKLA AISEATRLKT EAEIALKEKE
2001  AENERLRLRA EDEAFQRRRL EEQAAQHKAD IEERLAQLRK ASESELERQK GLVEDTLRQR RQVEEEMAL KASFKAAG
2081  KAELELELGR IRSNAEDTMR SEELASQEAAR QRQLAAEAE QRRREAEERV QRSLAAEAEA ARQKVALEE VERLKAKEVE
2161  ARRLRERAEQ ESARQLQLAQ EAAQKRLQAE EKAHAFVQQE REEELQQTLO QEQNMLERLR SEEAARRAA EEAEEAREQA
2241  EREAAQSRKQ VEEAERLKQS AEEQAQAQAO AQAAAEKLRK EAEQEAARRA QAEQAALKQK QAADAEMEKH KKFAEQTLRQ
2321  KAQVEQELTT LRLQLEETHD QKSILDEELQ RLKAEVTEAA RQRQVVEEL FSVRVQMEEL GKLLKARIEAE NRALLLRDKD
2401  NTQRFLEEEA EKMKQVAEEA ARLSVAAQEA ARLRQLAED LAQQRALAEK MLKMKQAVQ EATRLKAEEA LLQQQKELAQ
2481  EQARRLQADK EQMAQQLVEE TQGFQFTLEA ERQQRLEMSA EAERLKLKRA EMSRAQRAE EDQQRFRKQA EEIGEKLHRT
2561  ELATQEKVTL VQTLEIQRQQ SDQDAERLRE AIAELEREKE KKKQEAQLLQ LKSEEMQTVQ QEQILOETQA LQKSFLEKSD
2641  SLLQRERFIE QEKAKLEQLF QDEVAKAKQL QEEQQRQQQQ MEQEKQELVA SMEEARRRQR EAEEGVRRKQ EELQRLEQQR
2721  QQQEKLLAE NQRLRERLQR LEEEHRAALA HSEEIATSOA AATKALPNGR DALDGPMSMA EPEYTFEGLR QKVAQQQLQ
2801  AGILSMEELR RLTQGHHTVA ELTQREDVRH MHEKLLSAEK AVTGYRDPYS GQSVSLFQAL KKLIPREQG LRLPLTKAAK
2881  DPVNRRLTV NEAVKGVVGV PELHHHLLSA ERAVTGYKDP YTGEQISLFQ AMKKDLIVRD HGIRLLEAQI ATGGIIPVH
2961  SHRVPVDVAY QRGYFDEEMN RVLADPSDDT KGFDPNTHE NLTYLQLLER CVEDPETGLR LLPLTKAAK GGELVYTDTE
3041  ARDVFEKATV SAPFGKFGQK TVTIWEIINS EYPTAEQRDD LLRQFRGTGRI TVEKIKIVI TVVEEHERKQ QLCFEGRLAL
3121  VPAEELLD SG VISHEVYQQ LQRGERSVRE AEADQVQAL RGTSVIAGVW LEEAQQKLSI YEALRRDLLQ PEVAVALLEA
3201  QAGTGHIDP ATSARLTVDE AVRAGLVGPE MHEKLLSAEK AVTGYRDPYS GQSVSLFQAL KKLIPREQG LRLPLTKAAK
3281  GGVDPKSKSH RVPDLDVAYAR GYLDKETNRA LTSRDRDARV YLDPSTREPV TYSQLQRCR SDQLTGLSLL PLSEKAVRAR
3361  QEEVYSELQA RETLEKAKVE VPVGGFKGRA LTVWELISSE YFTEEQRQEL LRQFRGTGVT VEKVIKILIT IVEEVETQRT
3441  ERLSFSGLRA PVPASELLAS KILSRTOFQE LKDGKTSVKD LSEVGSVRTL LQSGSCLAGI YLEDSKEKVT IYEAMRRGLL
3521  RASTATLLE AQAATGFLVD PVRNQRLYVH EAVKAGVVP ELHEKLLSAE KAVTGYKDPY SGSTISLFQA MKKGLVLRDH
3601  AIRLLEAQIA TGGIIDPVHS HRLPVDVAYQ RGYFDEEMN RVLADPSDDT KGFDPNTHE NLTYLQLLER CVEDPETGLR
3681  LPLRGAEKTE VVETQVYTE EETRRAFEET QIDIPGGGSH GGSSMSLWEV MQSDMIPEDQ RARLMDAFQA GRVTKERMII
3761  IIEIEIEKTE IIRQQNLASY DYVRRRLTAE DLYEARII SL ETYNLFREGT KSLREVLME SAWRYLYGTG SVAGVYLPGS
3841  RQPLTIYQAL KKGLLSAEVA RLLLEAQAAT GFLLDPVKGE RLTVDEAVRK GLVGPPELHDR LLSAERAVTG YRDPYTEQPI
3921  SLFQAMKKE IPAEALRLL DAQLATGGIV DPRLGHLPL EVAYQGYLN KDTHDQLSEP SEVRSYVDP TDRLSYTLQ
4001  LKRCRRDDNS QMHLPLSDA RKLTRGLRK QITVEELVRS QVMDEATALQ LQEGLTISIE VTKNLQFLE GTSCIAGVVF
4081  DATKERLSVY QAMKGIIRP GTAFELLEAQ AATGYVDPI KGLKLTVEEA VRMGIVGPEF KDKLLSABRA VTGYKDPYSG
4161  KLISLQAMK KGLLKDHLGI RLLEAQIATG GIIDPEESH RLPVEVAYKRG LFDEEMNEIL TDPSSDDTKG FDPNTEENLT
4241  YLQLMERCIT DPQTGLCLLP LKEKKRERKT SSKSSVRKRR VVIVDPETGK EMSVYEAARK GLIDHQTYLE LSEQECEWEE
4321  ITISSSDGVV KSMIIDRRSG RQYDIGDAIT KNLIDRSALD QYRAGTSLIT EFADMLSGNA GFRSRSSSV GSSSYPISS
4401  AVPRTQLASW SDPTEETGPV AGILDTELE KVSITEAMHR NLVDNITGQR LLEAQAQCTG IIDPSTGERF PVTEAVNKGL
4481  VDKIMVDRIN LAQKAFCGFE DPRTKTKMSA AQALKKGWLY YEAGQRFLV QYLTGGLIEP DTPGRVSLDE ALQGRGTVDR
4561  TAQKLRDVSA YSKYLTCPKT KLIKISYKDAL DRSMVEEGTG LRLLEAAASQ SKGYYSPPYSV SSGSSTAGSR TGSRTGSRAG
4641  SRRGSFDTAG SGFSMTFSSS SYSSSSYGRR YASGPSASLG GPESAVA

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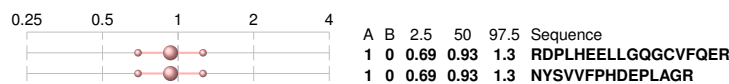
5.490 sarcosine dehydrogenase [Rattus norvegicus]

Protein Accession	gi 25742657
Mean Expression Ratio	0.941
Median Expression Ratio	0.942
Credible Interval	(0.719, 1.22)
Associated Peptides	2
Associated Spectra	2

Coverage	0.0359
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	0.85
Avg..iTRAQ.Ratio....117.114.	0.853

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1   MASLSRVLRV AATCFRGRSA RNLGLQPLAR EARPTTEKSV PYQCTLKEEA QGASVVPQGP SQPLPSTANV VVIGGSLGC
81  QTLYHLAKLG VGGVLLERE RLTSGTWHT AGLLWQLRPS DVEVELLAHT RQVVSHDLEE ETGLHTGWIQ NGGLFIASNQ
161 QRLDEYKRLM SLGKAYGIES HVLSPAETKD LYPLMNVDL YGTLVYPRDG TMDPAGTCTT LTRAAVARGA QVIENCAVTG
241 IRVRTDDFGV RRVTAJETQH GSIQTPCVVN CAGVWASSVG RMAGVKVPLV AMHHAYVVTE RIEGIQNMVN VRDHASVYL
321 RLQGDALSVG GYEANPIFWD EVSDKFAFGL FDLWDVFTQ HIEGAINRVP VLEKTGIKST VCGPESFTPD HKPLMGEAPE
401 LRGFFLGCGF NSAGMMLGGG CGQELAHWIV HGRPEKDMYS YDIRRFHHSI TDHPRWIRER SHESYAKNYS VVFPHDEPLA
481 GKNMRRDPLH EELLGQGCVF QERQGWERPQ WFNPEQTAQV LDYDYGYGAYG HQAHKDYAYS RLLGDEYTFD FPPHHCVIQK
561 ECLACRTAAA VFNMSYFGKF YLLGADARKA PDWLFSDAVN RPPGSTVYTC MLNQRGGTES DLTVSCSLAPG AQA SPLAPAF
641 EGDGYLLAVG GAVAQHNWSH INTVLQDQEF RCQLMDCSED LGMLSIQGPA SRDILQDVLD ADLSNEAFFP STHQLVRAAG
721 HLVRAIRLSF VGELGWELHV PQASCLPVYR AVMAAGAKHG LVNAGYRAID SLSEKGYRH WHADLRSDDS PLEAGLAFTC
801 KLKTSVPFLG REALEKQRAT GLRRRLVCLT VEEVPMFGL EAIWRNGQVV GHVRRADFGF TVNKTIAYGY IRDPSSGGPVS
881 LDFVKNGDYA LERMGVTYAA QVHLKSPFDP DNKRKVGIY
  
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5.491 chromobox homolog 3 [Rattus norvegicus]

Protein Accession	gij56799436	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.824, 1.36)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.0765	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	0.922
Avg..iTRAQ.Ratio....116.114.	1.00	0.946
Avg..iTRAQ.Ratio....117.114.	1.19	1.75

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1   MASNKTLQK MGKKQNGKSK KVEEAEPEEF VVEKVLDRRV VNGKVEYFLK WKGFTDADNT WEPEENLDCP ELIEAFLNSQ
81  KAGKEKDGTK RKSLSDSESD DSKSKKRRDA ADKPRGFARG LDPERIIGAT DSSGELMFLM KWKDSDEADL VLAKEANMKC
161 PQIVIAFYEE RLTWHSCPED EAQ
  
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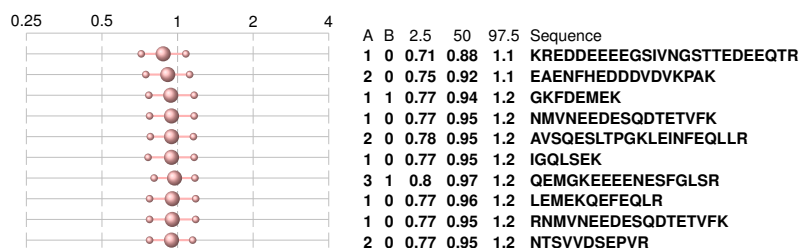
5.492 nexilin isoform b [Rattus norvegicus]

Protein Accession	gi 40538874
Mean Expression Ratio	0.941
Median Expression Ratio	0.943
Credible Interval	(0.817, 1.08)
Associated Peptides	10
Associated Spectra	17
Coverage	0.224
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.931
Avg..iTRAQ.Ratio....116.114.	0.937
Avg..iTRAQ.Ratio....117.114.	1.10

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1      MNDVSQKAEI  KDMLASDEEE  EPSKVEKAYV  PKLTGTVKGK  FDEMEKHRQE  EQRKRTEEER  KRRIEQDLLE  KRKMQRELAK
81     RAEQIEDINN  TGTESASEEG  DDSLLITVVP  AKSYRAAANR  KDPEDLDREH  RNGRVSQEE  KTRHEEECRA  LKEAKCLSLV
161    MDDTEAKKE  SRFPGKLKST  FEELERQRQE  NRKKQAEEEA  RRRLEEEERRA  FFEARRNMVN  EEDESQDTTET  VFEYRPGKL
241    RLSFEEIERQ  RREEEKRKAE  EEARRMEEE  KKAFAEARRS  MVLDDDSPEI  YKAVSQESLT  PGKLEINFEQ  LIRQKMEEER
321    RRTEERRQK  LEMEKQEFEQ  LRQEMGKEE  ENESFGLSRE  YEELIKLKRS  GSIQAKNLKS  KFEKIGQLSE  KEVQKIEEE
401    RAKRRAIDLE  IKEREAENFH  EDDDDVDVKPA  KKSESPFTHK  VNMKARFEQM  AKARQEEEQR  RIEEQKLLRM  QFEQKEIDAA
481    LQKKREDEE  EEGSIVNGST  TEDEEQTRSG  APWFKKPLRN  TSVVDSEPVR  FTVKVTGEPK  PEVTWWFEGE  LLQDGEDYQY
561    IERGETYCLY  LPETFPEDGG  EYMKAVNSK  GSAASTCILT  IEMDDY

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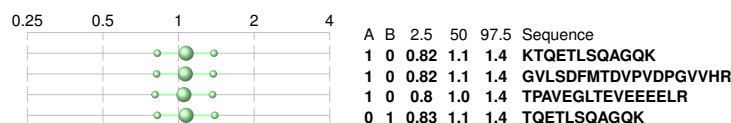
5.493 tumor protein D52-like 2 [Rattus norvegicus]

Protein Accession	gi 38454226
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.852, 1.33)
Associated Peptides	4

Associated Spectra	4	
Coverage	0.214	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	1.05
Avg..iTRAQ.Ratio....116.114.	1.12	1.06
Avg..iTRAQ.Ratio....117.114.	1.14	1.18

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1      MDSASQDINL  NSPNKGVLSL  FMTDVPVDPG  VVHRTPAVEG  LTEVEEEELR  AELAKVEEEI  VTLRQVLAAK  ERHCGELKRR
81     LGLSTLGELE  QNLSRSWHDV  QGSTAYVKTS  EKLGEWNEKV  TQSDLYKKTQ  EQLSQAGQKT  SAALSTMGSA  ISRKLGMDS
161    YSIRHSISMP  VMRNSATFKS  FEDRVGTIKS  KVVGGRENGS  DTLPSSPGSG  DQTLPDHAPF
    
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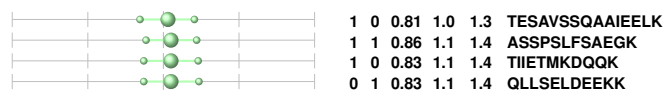
5.494 SH3 domain-containing adapter protein [Rattus norvegicus]

Protein Accession	gi 29789297	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.864, 1.31)	
Associated Peptides	4	
Associated Spectra	5	
Coverage	0.0737	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	1.01
Avg..iTRAQ.Ratio....116.114.	1	1.16
Avg..iTRAQ.Ratio....117.114.	1.04	1.28

```

1      MVEAIVEFDY  QAQHDELTI  SVGEVITNIR  KEDGGWWEQ  INGRRLFPD  NRVREIKDV  KKDLSNKAP  EKPMHDVSSG
81     NSLLSSETIL  RTNKRGERR  RRCQVAFSYL  PQNDDELEL  VGDIEEVVGE  VEEGWEGVL  NGKTGMFPSN  FIKELSGESD
161    ELGISQDEQL  SKSSLRETTG  SESDGGDSSS  TKSEGANGTV  ATAAIQPKKV  KGVGFGDIFK  DKPIKLRPRS  IEVENDFLPV
241    EKTIGKKLPP  ATSTPDPSKT  EMDSRTKTKD  YCKVIFPYEA  QNDDELTIKE  GDIVTLINKD  CIDVGWWEGE  LNRRGVFPD
321    NFVKLLPSDF  DKEGNRPKP  PPSAPVIKQ  GAGTTERKHE  IKKIPPERPE  TLPNRTEEKE  RPEREKLDL  QKPSVPAIPP
401    KKPRPPKTN  LNRPGVLP  RPERPVGPLT  HTRGDSSKID  LAGSTLSGIL  DKDLSDRSND  IDLEGFDSVI  SSTEKLSHPT
481    TSRPKATGRR  PPSQSLTSS  LSSPDIFDSP  SPEEDKEEHI  SLAHRGIDVS  KKTSTRVTIS  QVSDNKASLP  PKPGTMAAAS
561    SGPASLSSVA  SSPMSSSLGT  AGQRASSPSL  FSAEGKAKTE  SAVSSQAAIE  ELKMQVRELR  TIETMKDQQ  KREIKQLLSE
641    LDEEKKIRLR  LQMEVNDIK  ALQSK
    
```





5.495 hypothetical protein LOC308820 [Rattus norvegicus]

Protein Accession	gi 67846044
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.783, 1.43)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0703
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.17
Avg..iTRAQ.Ratio....116.114.	1.45
Avg..iTRAQ.Ratio....117.114.	1.37

```

1      MRNRWIWRF L RPECSGIRWI SSPHGRLSPA LRRGFLTTTT KSDYDRRPVE ITPLEQRKLT FDTHALVQDL ETHGFDKGQA
81     QTIVSVLSTL SNVSLDTPYK EMVTKAQQEETIQQLMAHLDL SIKKDMVILE KSEFANLRAE NEKMKIELDQ VKQQLINETS
161    RIRADNRLDI NLESRVTDM FTDQEKQLME ATNEFTTKDM QTKSIISETS NKIDTEIASL KTMESSKLE TIRYLAASVF
241    TCLAIALGFY RFWKEN
    
```



5.496 PREDICTED: similar to Adrenocorticotrophic hormone receptor (ACTH receptor) (ACTH-R) (Melanocortin r

Protein Accession	gi 109507507
Mean Expression Ratio	0.941
Median Expression Ratio	0.943
Credible Interval	(0.712, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0203
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.878

Avg..iTRAQ.Ratio....116.114. 0.887
 Avg..iTRAQ.Ratio....117.114. 0.785

```

1      MKHIINSYEH TNNTARNNSD CPDVVVEEI FFTISIIGVL ENLIVLLAVI KNKNLQSPVY FFICSLAISD MLGSLYKILE
81     NILIMFRNMG YLKPRGSLES TADDIIDCMF VLSLLGSIFS LSVIAADRYI TIFHALQYHS IVTMRRTVIT LTVIWMFCTG
161    SGITMVIFSH HIPTVLTFTS LFPLMLVFIL CLYIHMFLLA RSHARKISTL PRANMKGAMT LTILLGVFIF CWAPFVLHLV
241    LMTFCPPNPY CVCYMSLFQV NGMLIMCNAV IDPFIYAFRS PELREAFKRM LFCNRY
    
```



5.497 PREDICTED: similar to Lymphocyte-specific protein 1 (Protein pp52) (52 kDa phosphoprotein) (Lymphoc

Protein Accession	gij62641648
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.788, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0483
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.22
Avg..iTRAQ.Ratio....116.114.	1.26
Avg..iTRAQ.Ratio....117.114.	1.40

```

1      MAEAAADPRC QEQEELDAED DKGLTTQWRE EDEEEAAREQ RQRERERQIQ DQDKDEEDED GHFLEQPGQQ ALVSLKSSSL
81     DDEDEFGDWS QKQEPFRQOS WENEGTAEGS EPSSESAAE KQTEDSSHQA KVHLEESNLS HSDPNIEDDV GSGETEEHL
161    ISHQARTPSP LALEDTAELS SPPLSPTVKL ADRTESLNRS IQKSNSVKKS QPTLPISTID ERLQOYTQAT ESAGRTPKLS
241    RQPSIELPSM AVASTKTLWE TGEVQTQSAS KTPSCQDIVA GDMSKKSWE QKGGKISSST IKSTPSGKRY KFBATGHGKY
321    EKVLVDEGSA P
    
```



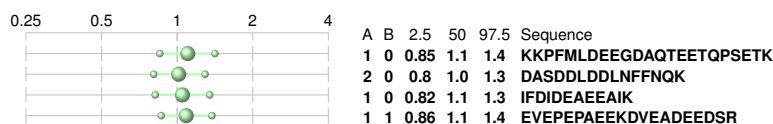
5.498 "eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa [Rattus norvegicus]"

Protein Accession	gij40786451	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.868, 1.30)	
Associated Peptides	4	
Associated Spectra	6	
Coverage	0.210	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	1.1
Avg..iTRAQ.Ratio....116.114.	0.989	1.26
Avg..iTRAQ.Ratio....117.114.	1.42	0.97

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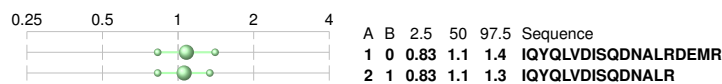
1   MSGDEMIFDP TMSKKKKKK KPFMLDEEGD AQTEETQPS EKEVEPEPAE EKDVEADEED SPKKDASDDL DDLNFFNQK
81  KKKKTKK IFD IDEAEAAIFD VKIESDAQEP AEPEDDLIM LGNKKKKKKN VKFPDEDEIL EKDEALEDED SKKDDGISFS
161 NQTGPAWAGS ERDYTYEELL NRVFNIMREK NPD MVAGEKR KFVMKPPQVV RVGTTKTSFV NPTDICKLLH RQPKHLLAFL
241 LAELGTSGSI DGNNQLVIK RFQKQIENV LRRYIKEYVT CHTCRSPDTI LQKDTRLYFL QCETCHSRCS VASIKTGFQA
321 VTGKRAQLRA KAN

```



5.499 PREDICTED: similar to SH3 domain binding glutamic acid-rich protein-like 3 [Rattus norvegicus]

Protein Accession	gij109477464	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.844, 1.33)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.21	0.557
Avg..iTRAQ.Ratio....116.114.	1.10	1.16
Avg..iTRAQ.Ratio....117.114.	1.37	1.27

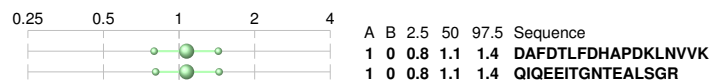


5.500 actopaxin [Rattus norvegicus]

Protein Accession	gij13569846
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.816, 1.39)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0914
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.19
Avg..iTRAQ.Ratio....116.114.	1.12
Avg..iTRAQ.Ratio....117.114.	1.34

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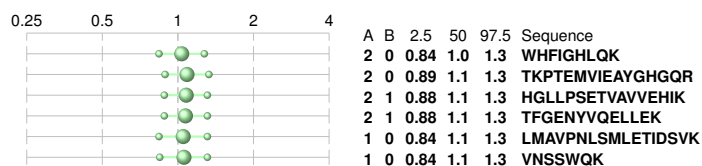
1   MATSPQKSPS VPKSPTPKSP PSRKKDSDFL GKLGGTLARR KKAKEVSEFQ EEGMNAINLP LSPISFELDP EDTMLEENEV
81  RTMVDPNRN DPKLQELMKV LIDWINDVLV GERIIVKDLA EDLYDGQVLQ KLFEKLESEK LNVAEVTQSE IAQKQKLQTV
161 LEKINEALKL PPRSIKWNVD SVHAKNLVAI LHLVLSQY FRAPIRLPDH VSIQVVVVQK REGILQSRQI QEEITGNTREA
241 LSGRHERDAF DTLFDHAPDK LNVVAKTLIT FVNKHLNKLN LEVTELETQF ADGVYLVLLM GLEGEYFVPL HSFFLTPDSF
321 EQRVLNVSFA FELMQDGGLE KPKRPEDIV NCDLKSTLRV LYNLFTKYRN VE
    
```



5.501 PREDICTED: similar to Proline synthetase co-transcribed bacterial homolog protein [Rattus norvegicus]

Protein Accession	gij62662820
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.905, 1.24)
Associated Peptides	6
Associated Spectra	12
Coverage	NA

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.06	1.12
Avg..iTRAQ.Ratio....116.114.	1.20	1.05
Avg..iTRAQ.Ratio....117.114.	1.09	0.968



5.502 PREDICTED: similar to Ribosome-binding protein 1 (Ribosome receptor protein) (mRRp) isoform 4 [Ratt

Protein Accession	gij109470915
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.787, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00711
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.33
Avg..iTRAQ.Ratio....116.114.	1.12
Avg..iTRAQ.Ratio....117.114.	1.93

NHLBI Zile/Grant, Aged Rat

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1      MDIYDTQTIG VVVFGGFMV SAIGIFLVST FSMKETS YEE ALANQRKEMA KTHHQKGEKK KKEKTVEKKG KTKKKEEKP
81     GKIPHEHLD NVTIILKEPM RVPAAVAVPT SVHSSVGRTP VATVPAMPQE KLASPFKDKK KKEKKVAVKE PAVSSIVNSI
161    QVLASKSAIL EASPKEVPMV AVPPVGSKAS APATSSQGKK GQGAQNQAKK GEGAQNQAKK GEGVQNQAKK GEGAQNQAKK
241    GEGAQNQAKK GEGTQNQAKK GEGAQNQGGK GEGAQNQAKK GEGAQNQAKK GEGAQNQAKK GEGAQNQAKK GEGGQNQAKK
321    GEGAQNQAKK GEGAQNQAKK GEGVQNQAKK GVEGAQNQGG KGEANQNQAK KEGEGQNQTK KEGELQNQGG KGEATQKQDK
401    KIEGAQNQGG KPEGTPNQGG KGEGAQNQGG KGEGAQNQGG KGEGAQNQGG KGEGAQNQGG KGEGAQNQGG KGEGAQNQGG
481    KGEGAQNQGG KGEGAQNQGG KEGESPSQNI KAAQNQGKKA EGNQGKKGDD NPNQGKKGEG APNQNRKTD T VANQGTKTEG
561    VSNQKKKAEG APNQGKKEVEG SPNQAKKVDA AAGQGKKSSEM TPAQGKNASM VQSQEPKQGE APAKKSKSKK GEPGPPDCDS
641    PFLFLPYKTLV STVGSVMFSE GEAQRLEIEL SEKTGVIQDT WHKATQKQGD VAVLKRQLEE KEKLLATEQE DAAVAKSKLR
721    ELNKEMASEK AKAAGEAKV KKQLVAREQE IAAVQARMQA SYQDQHVKEVQ QLQGIKIRTLO EQLENGPNTQ LARLQQENSI
801    LRDALNQATS QVESQNTTEL AKLRQELSKV NKELVKSEA SRQEEQQRKA LEAKAATFEK QILQLQASHK ESEALQKRL
881    EEVTRELCRA QTSANLRAD AEKAQEQQQR VAEHLSKLQS SEVEVKSKEE ELSDLHGQLK EARAENSQLT ERIRSI EALL
961    EAGQAQDSQV ILCVSFQASR AEADQQQTRL KELESQVSL EKETSELKEA MEQQKGKNNND LREKNWKAME ALALAERACE
1041   EKLRSLTQAK ESEKQLHLA EAQTKEVLLA LLPELSIPAH QNYADWLQEV KEKGSLLKK PPVSVESLD IVSKLREABE
1121   TQNSLQAECD QYRTILAE TE GMLKDLQKSV EEEERVWKA VGAEEEEELQK SRFTVKHLED LVEKLRGELE SSDQVREHTS
1201   HLEAELEKHM AAASAEQONY AKEVAGLRQL LLDSSQLEE AKSEAQQQSN ELALVRQQLS DMRSHVEDGD VAGSPAVPPA
1281   EQDPVKLKTQ LERTEATLED EQTRRQKLT AEFEEAQSTAC RLQEELEKLR AAGPLESSGI EEVTQLKERL EKEKRLTSDL
1361   GRAATKLQEL LKTTQEQLTK EKDTVKKLQE QLGAEDGSS SKEGTSV

```



5.503 cytoskeleton-associated protein 1 [Rattus norvegicus]

Protein Accession	gi 93277119
Mean Expression Ratio	0.945
Median Expression Ratio	0.945
Credible Interval	(0.698, 1.28)
Associated Peptides	1
Associated Spectra	1
Coverage	0.041
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.02
Avg..iTRAQ.Ratio....116.114.	1.12
Avg..iTRAQ.Ratio....117.114.	0.617

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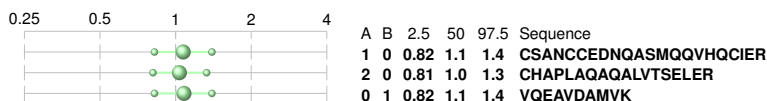
1      MEVSGTSAPT VTVFISSSLN SFRSEKRRYS SLTIAEFKCK LELVVGSPAS CMELELYGAD DQFYSKLDQE DALLGSYPVD
81     DGCRIHVTDH SGVRLGEYED VSKVEKYEIS PEAYERRQNT VRSFMKRSKL GPYNEELRAQ QEAEAAQRLS EEEAQAS AIS
161    VGSRCSEVRAP GQSLRRGTVM YVGLTDFKPG YWVGVRYPDEP LGKNDGVSNG KRYFECQAKY GAFVVKAAVT VGDFPEEDYG
241    LDEM

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5.504 PREDICTED: similar to CG5323-PA [Rattus norvegicus]

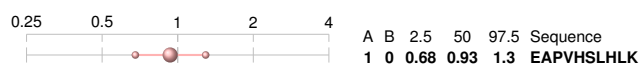
Protein Accession	gij27712200	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.845, 1.33)	
Associated Peptides	3	
Associated Spectra	4	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	1
Avg..iTRAQ.Ratio....116.114.	1.18	1.03
Avg..iTRAQ.Ratio....117.114.	1.07	1.44



5.505 hypothetical protein LOC311428 [Rattus norvegicus]

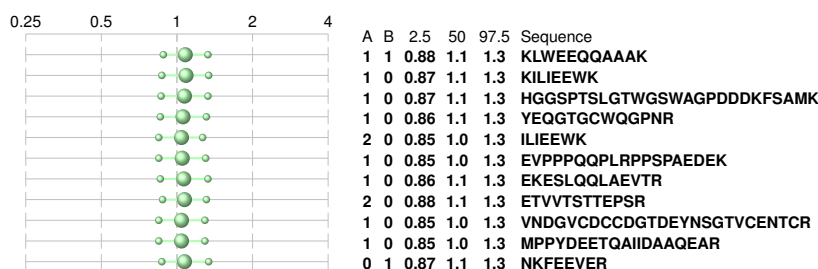
Protein Accession	gij71043764	
Mean Expression Ratio	0.948	
Median Expression Ratio	0.945	
Credible Interval	(0.71, 1.29)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0575	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.852	
Avg..iTRAQ.Ratio....116.114.	0.979	
Avg..iTRAQ.Ratio....117.114.	0.884	

1 MAAANRGSKP RVRSIRFAAG HDAEGSQSHV HFDEKLHDSV VMVTQESDNS FLVKVGF LKI LHRYEITFTL PAVRRLSKDI
81 **REAPVHSLHL** KLLSVTPIPE GYSIKCEYSA HKEGVLKEEM LLACEGDIGT CVHVTVQARV MDRHHGTFML LDGVKCVGAE
161 LEYDSEHSDW HGFD



5.506 "PREDICTED: similar to Glucosidase II beta subunit precursor (Protein kinase C substrate, 60.1 kDa p)"

Protein Accession	gij109483143	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.914, 1.23)	
Associated Peptides	11	
Associated Spectra	14	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	1.21
Avg..iTRAQ.Ratio....116.114.	1.08	1.16
Avg..iTRAQ.Ratio....117.114.	1.14	1.29



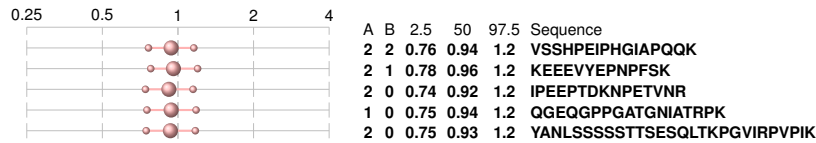
5.507 PREDICTED: similar to Protein C6orf142 homolog [Rattus norvegicus]

Protein Accession	gij109483709
Mean Expression Ratio	0.946
Median Expression Ratio	0.945
Credible Interval	(0.796, 1.13)
Associated Peptides	5
Associated Spectra	12
Coverage	0.194

Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.982
Avg..iTRAQ.Ratio....116.114.	0.986
Avg..iTRAQ.Ratio....117.114.	0.93

```

1      MEFEKHEQGN ALKKNEKLEE RVTVSPGDSE AKPLIFTFVP TLRRLPTHIQ LADTSKFLVK IPEEPTDKNP ETVNRFEYSD
81     HMTFSCESEK ERDQRILDYP SEVSGKNSQR KEFNTKEPQG MQKGDLFKAE YVFI VDS DGE DEATCRQGEQ GPPGATGNIA
161    TRPKSLAISS SLASDVVRPK VRGVDVKVSS HPEIPHGIAP QQKHGQQYKT KSSYKAFAAI PTNTLLLEQK ALDEPARTES
241    NSKASVSDLP VELCFPAQLR QQTEELCATI DKVLQDSLMS HSSDSPSRPS QTMLGSETIK TPTHPRAAG RETKYANLSS
321    SSSTTSESQL TKPGVIRPVP ILSKFLKKE EEVYEPNPFSS KYLEDSGLF SEQDMAIPHK FVSLHPLYQS KLYPPAKSLL
401    RPQTLSHADC LTPGPFSHLS SFSLRDEQEK SPTLLSQDQTY NKTGCFPVAQ RKLKQTRRD TAQ
    
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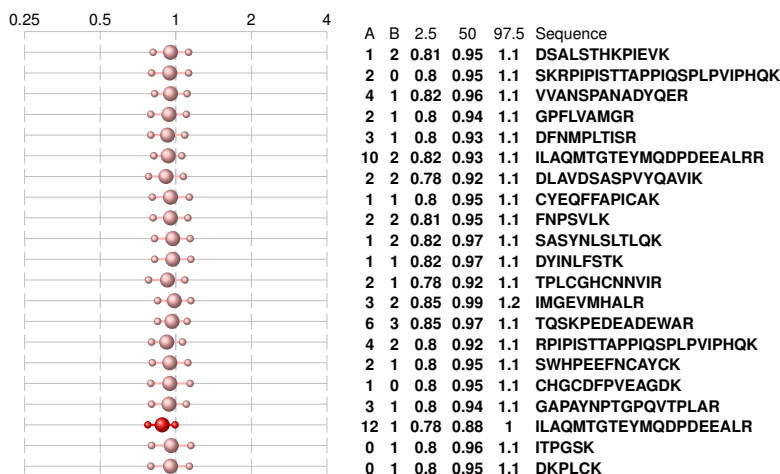


5.508 PREDICTED: similar to LIM domain binding 3 [Rattus norvegicus]

Protein Accession	gij109503718	
Mean Expression Ratio	0.945	
Median Expression Ratio	0.945	
Credible Interval	(0.879, 1.02)	
Associated Peptides	21	
Associated Spectra	90	
Coverage	0.349	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.993	0.888
Avg..iTRAQ.Ratio....116.114.	0.957	0.958
Avg..iTRAQ.Ratio....117.114.	0.965	0.712

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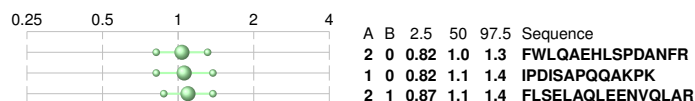
1      MSYSVTLTGP GPWGFRLQGG KDFNMPLTIS RITPGSMAAQ SQLSQGDLVV AIDGVNTDTM THLEAQNKIK SASYNLSLTL
81     QKSKRPPIPI S TTAPPRIQSPL PVIPHQKVVV NSPANADYQE RFNPSVLKDS ALSTHKPIEV KGLGGKATII HAQYNTPI SM
161    YSQDAIMDAI AGQAQAQGSF FSGASPLASL PVKDLAVDSA SPVYQAVIKT QSKPEDEADE WAFRSSLNQS RSFRILAQMT
241    GTEYMQDPDE EALRFSSTPI EHAPVCTSQA TSPLLPASAP SPAAASPIAA SPTLATAAAA HAVAASAAGP ASSPVENPRP
321    QASAYSPAAA TSPAPAAHTS YSEGPAAPAP KPRVVTTASI RPSVYQPVPA SPYSPSPGAN YSPTPYTPSP APAYTPSPAP
401    TYTSPAPTY SPSAPAYTP SPAPNYNPTP SAAYSGGPSE SASRPPWVTD DSFSQKFAPG KSTTSVSKQT LPRGAPAYNP
481    TGPQVTLAR GTFQRAERFP ASSRTPLCGH CNNVIRGFPL VAMGRSWHPE EFNCAYCKTS LADVCFVEEQ NNVCERCYE
561    QFFAPICAKC NTKIMGEVMH ALRQTNHTTC FICAACKKPF GNSLFHMEDG EPYCEKDYIN LPSTKCHGCD FPVEAGDFI
641    EALGHTWHD TCFICAVCHVN LEGQPFYSKK DKPLCKKHAH AINV
    
```



5.509 PREDICTED: similar to myomesin 2 [Rattus norvegicus]

Protein Accession	gj 109504452	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.856, 1.30)	
Associated Peptides	3	
Associated Spectra	6	
Coverage	0.0301	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.15	1.27
Avg..iTRAQ.Ratio....116.114.	0.986	1.05
Avg..iTRAQ.Ratio....117.114.	1.16	1.51

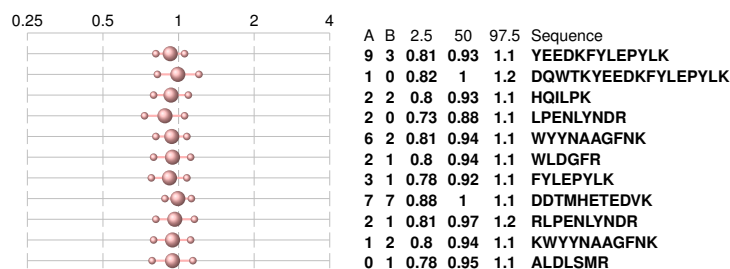
1	MSLVVVVFYQ	KRHKHFDQSY	RNIQTRYLLD	RYASKKQASS	QSSSQRSLTE	RSSSKRASSQ	SSAEGMTCRL	CAKRMSASEE
81	EEVENENRYR	SLAASYGEAK	RQRFLSELIAQ	LEENVQLART	QARNKLDKYF	LEQTVADNLA	LERSSFEDRL	SRAPFILVRL
161	RSHTIWERMS	VRLCFTVQGF	PTPVVQWYKD	GSLICQAGEP	GKYRIESRYG	VHTLEINRAD	FEDTATYSAV	ATNPHGQVST
241	NAAVVVRRYR	GDEEPYHSVG	LP IGLPLSSV	IPYTHFDVQF	LEKFGVTFRR	EGETVTLKCT	LLVTPDLKRV	QPRAEWYRDD
321	VLLKESKWTK	MFFGEGQASL	SFSHLNKDDDE	GLYTLRIVSR	GGVSDHSAFM	FVRDADPLVT	GAPGAPMDLQ	CHDANRDYVI
401	VTWKPPNNTT	ESPVIGYFID	KCEVGTNNWV	QCNDAPVKIC	KYPVTGLFEG	RSYVFRVRAV	NNAGISRPSR	ISDAVAALDP
481	VDLRRLQAIH	LEGEKEIVIV	QDDLEGDVQI	PGPPTNVQAS	EVSRYVVLVLS	WDPPSPRGKE	PLMYFIEKSA	VGSGSWQRVN
561	AQTAVRSPRY	AVFDLAEKGS	YVFRVLSANK	HGLSDPSEIT	PPIQAQDMIV	VPSAPGRVLA	SRNTKTSVVV	QWDRPKHEED
641	LLGYVDCCV	AGTNMWEPEN	HKPIGYNRFV	VHGLTTGEQY	IFRVKAVNAV	GTSSENSQESE	VIKVQAALTV	PSHPYGITLL
721	NCDGHSMTLG	WKVPKFSGGS	AIIGYYLDDR	EVHKNWHEI	NSSPVKERIL	TVEGLTEGSL	YEFKIAATNL	AGIGQPSDPS
801	EHFKCEAWTA	PEPGPAYDLT	FCEVRDTSLV	ILWKAPVYSG	SSPVSGYFVD	FKEEDSGEWEK	TTSEAAATPNR	YLVKCDLHQG
881	KTYVFRVRAV	NASGPGKPSD	TSEPVLVPEAR	PGTKEISAGV	DEEGNIYLG	DCQEMTDASQ	FTWCAYEEI	ADERFEVHT
961	EGDHSKLYFK	NPDKIDIGTY	SVSVDSDTGV	SSSFVLDEEE	LERLMALSNE	IKNPTIPLKS	ELAYEIFDKG	QVR FHLQAEH
1041	LSPDANFFFI	INDREVS DSE	THRIKCDRST	GMIEMVMDFR	TIENEGTYTV	QIQDQKAKNQ	SSLVLIGDAF	RAVLEEAEFQ
1121	RKEFLRKQGP	HFAEYLHWDV	TEECEVRLIC	KVANTKRETV	FKWLKDDVLY	ETETPPPDL	KGICELLIPK	LSKGDHGEYK
1201	ATLKDDRQGD	VSVLEVAGKV	YEDMILAMSR	VCGASASPLK	VLCTPEGIRL	QCQFMKYFTEE	MKVSWSYHKEA	KISSSEHMRI
1281	GGSEEMAWLQ	ICEPTEKDKG	KYTFEIFDQK	DNHQRSRDL	QAFDEAYAE	FQQLKAAAF	EKNRGKVI	IGG LPDVVTIMEG
1361	KTLNLTCTVF	GNPDEPVVWF	KNDKDIELSE	HFSVKVEQSK	YVSLTIKQVT	AEDSGKYSIN	VKNKYGGEKI	DVTVSVKYKHG
1441	EKIPDISAPQ	QAKPFLIPAS	TSAD					



5.510 PREDICTED: similar to ubiquinol-cytochrome c reductase binding protein [Rattus norvegicus]

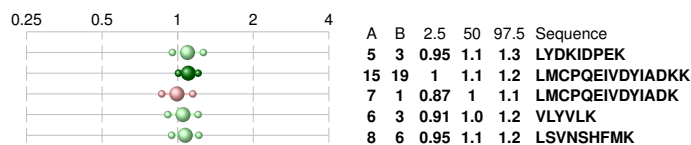
Protein Accession	gij109461775	
Mean Expression Ratio	0.945	
Median Expression Ratio	0.945	
Credible Interval	(0.856, 1.04)	
Associated Peptides	11	
Associated Spectra	55	
Coverage	0.622	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.881	0.946
Avg..iTRAQ.Ratio....116.114.	1.02	0.876
Avg..iTRAQ.Ratio....117.114.	0.93	0.899

1 MAGRPAAVAS SKWLDGFRKW YNNAAGFNKL GLMRDDTMHE TEDVKEAIRR LPENLYNDRM FRIKRALDLS MRHQILPKDQ
81 WTKYEEDKFY LEPYLKEVIR ERKEREWAK K



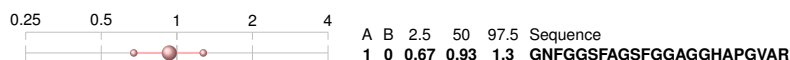
5.511 "PREDICTED: similar to Acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquinone oxidored"

Protein Accession	gj 27679694	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.958, 1.18)	
Associated Peptides	5	
Associated Spectra	73	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.958	1.19
Avg..iTRAQ.Ratio....116.114.	1.13	1.05
Avg..iTRAQ.Ratio....117.114.	0.993	0.982



5.512 heterogeneous nuclear ribonucleoprotein M [Rattus norvegicus]

Protein Accession	gj 56961620	
Mean Expression Ratio	0.946	
Median Expression Ratio	0.945	
Credible Interval	(0.702, 1.28)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	NA	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.887	
Avg..iTRAQ.Ratio....116.114.	0.98	
Avg..iTRAQ.Ratio....117.114.	0.765	

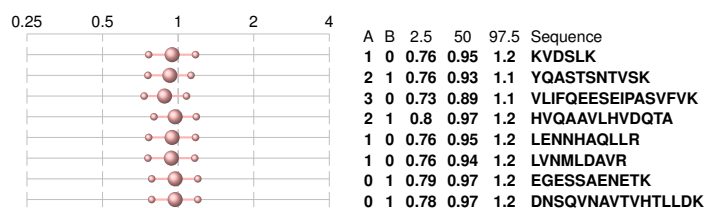


5.513 serum deprivation response protein [Rattus norvegicus]

Protein Accession	gj 56090257	
Mean Expression Ratio	0.946	
Median Expression Ratio	0.945	
Credible Interval	(0.816, 1.1)	
Associated Peptides	8	
Associated Spectra	14	
Coverage	0.223	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.877	1.04
Avg..iTRAQ.Ratio....116.114.	0.936	1.08
Avg..iTRAQ.Ratio....117.114.	0.829	1.16

```

1   MGEDAAQAEK FQHPNTDMLQ EKPSNFPSPMP SSTPSPSLNL GSTEEAIRDN SQVNAVTVHT LLDKLVNMLD AVRENQHNME
81  QRQINLEGSV KGIQNDLTKL SKYQASTSNT VSHLLEKSRK VSAHTRAVRE RLEKQCVQVK RLENNHAQLL RRNHFKVLIF
161 QEESEIPASV FVKEPVPSTA EGKELADENK SLEETLHNVD LSSDDELPGD EEALEDSAE KMEESRAEKI KRSSLKQVDS
241 LKKAFSRQNI EKMMNKLGTK IVSVERREKI KKSILTPNHQK ASSGKSSPFK VSPLSPGRKK IRGESSAEN ETKLEEQVQD
321 DHEEGSFTEG LSEASLPSGL LEGSAEDAER SALRGNNSGV GSNADLTIEE DEEESVALQ QAQQVRYESG YMLNSKEMEE
401 SSEKHVQAAV LHVDQTA
    
```



5.514 PREDICTED: similar to enoyl Coenzyme A hydratase domain containing 2 [Rattus norvegicus]

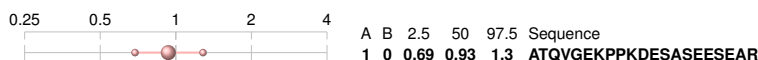
Protein Accession	gj 109475232	
Mean Expression Ratio	0.942	
Median Expression Ratio	0.945	
Credible Interval	(0.698, 1.27)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	NA	

Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.984
Avg..iTRAQ.Ratio....116.114.	0.864
Avg..iTRAQ.Ratio....117.114.	0.69



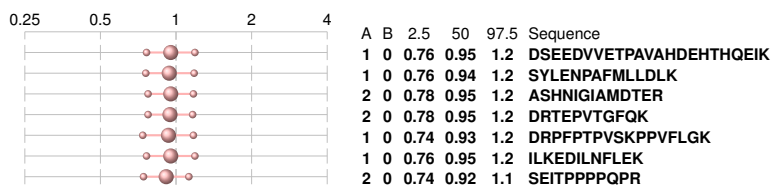
5.515 PREDICTED: similar to Vasodilator-stimulated phosphoprotein (VASP) [Rattus norvegicus]

Protein Accession	gij62639103
Mean Expression Ratio	0.945
Median Expression Ratio	0.946
Credible Interval	(0.705, 1.27)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.815
Avg..iTRAQ.Ratio....116.114.	0.73
Avg..iTRAQ.Ratio....117.114.	1.15



5.516 PREDICTED: similar to Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydro

Protein Accession	gij109467479
Mean Expression Ratio	0.945
Median Expression Ratio	0.946
Credible Interval	(0.8, 1.11)
Associated Peptides	7
Associated Spectra	10
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.975
Avg..iTRAQ.Ratio....116.114.	1.01
Avg..iTRAQ.Ratio....117.114.	0.918



5.517 albumin [Rattus norvegicus]

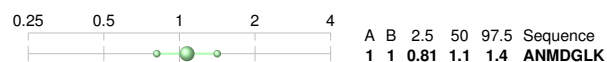
Protein Accession	gij19705431
Mean Expression Ratio	1.05
Median Expression Ratio	1.06
Credible Interval	(0.844, 1.31)
Associated Peptides	3
Associated Spectra	4
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.54
Avg..iTRAQ.Ratio....116.114.	0.778
Avg..iTRAQ.Ratio....117.114.	1.32





5.518 PREDICTED: similar to Signal recognition particle 14 kDa protein (SRP14) [Rattus norvegicus]

Protein Accession	gi 109470613	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.06	
Credible Interval	(0.803, 1.38)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.45	1.8
Avg..iTRAQ.Ratio....116.114.	1.21	1.09
Avg..iTRAQ.Ratio....117.114.	0.647	0.729

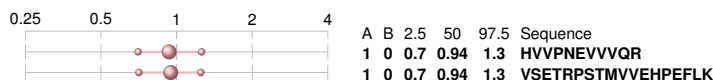


5.519 gelsolin [Rattus norvegicus]

Protein Accession	gi 51854227	
Mean Expression Ratio	0.946	
Median Expression Ratio	0.946	
Credible Interval	(0.73, 1.23)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	0.0372	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.06	
Avg..iTRAQ.Ratio....116.114.	0.727	
Avg..iTRAQ.Ratio....117.114.	0.929	

```

1      MAPYCSSLRs ALLVLALCAL SPSHAATASR GRAQERAPQS RVSETRPSTM VVEHPEFLKA GKEPGLQIWR VEKFDLVPVP
81     PNLYGDFFTg DAYVILKTVQ LRNGNLQYDL HYWLGNECSQ DESGAAAIFT VQLDDYLNGR AVQHREVQGF ESSTFQGYFK
161    SGLKYYKGGV ASGFKHVVPN EVVVQELFQV KGRRVVRATE VPVSWDSFNN GDCFILDLGN NIYQWCGSGS NKFERLKATQ
241    VSKGIRDNER SGRAQVHVSE EGSEPEAMLQ VLGPKPDLPO GTEDTAKEDA ANRRLAKLYK VNSGGGSMV SLVADENPFA
321    QSALRSEDCF ILDHGRDGKI FVWKGKQANM DERKAALKTA SDFISKMQYP RQTQVSVLPE GGETPLFKQF FKNWRDPDQT
401    DGPGLSYLSS HIANVERVPF DAATLHTSTA MAAQHGMDDDD GTGQKQIWR I EGSNKVLVDP ATYQGQFYGGD SYIILYNRHH
481    GGRQQQIIYN WQGAQSTQDE VAASAILTAQ LDEELGGTPV QSRVVQGGKEP AHLMSLFGGK PMIIYKGGTS RDGGQTPPAS
561    TRLFQVRASS SGATRAVEVM PKAGALNSND AFVLKTPSAA YLWVGTGASD AEKTGALELL KVLRAQHVQV EEGSEPDGFW
641    EALGGKTAJR TSPRLKDKKM DAHPPRLFAC SNRIGRFVIE EVPGELMQED LATDDVMLLD TWDQVFWVVG KDSQEEEKTE
721    ALTSAKRYIE TDPANRDRRT PITVVRQGF E PPSFVGVFLG WDDDYWSVDP LDRALAEELAA
    
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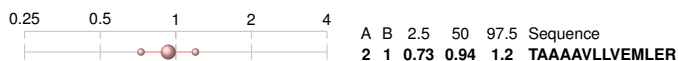


5.520 peptide/histidine transporter PHT2 [Rattus norvegicus]

Protein Accession	gij 21326469	
Mean Expression Ratio	0.948	
Median Expression Ratio	0.947	
Credible Interval	(0.736, 1.22)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.0241	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.89	0.469
Avg..iTRAQ.Ratio....116.114.	1.13	1.09
Avg..iTRAQ.Ratio....117.114.	0.772	0.888

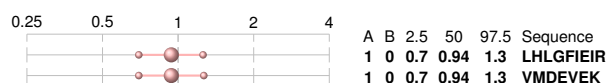
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1      MSALRAEQQP SRSGERQPLV AQRGRWGFRRW RRFAAAVLL VEMLERAAFF GVTSNLVLYL NSLNFNWDGE HASRATLLFL
81     GASYL LAPVG GWLADVYLGR FLAISLSLLL YLAATGLLLT TITDDGRRSF CGEMPELPLK PACPSANCQG SWSSPYCATT
161    LYLVLLLLLAL AASSVRSNLT SFGADQVMDL GRDATRFFFN WFYWSINLGA ILSLLVVAFI EQNISFLQGY SIIVGLVGLA
241    FFIFLIATPV FITKPP TGSQ VSSMLNLAFQ NCCPGWQWWR RPSSRNSEGA HLLPDQRSNQ PGPSPQEDMA NFQVLLKVLV
321    VMVTLVPYWM VYFQMSTYV LQQLHLHIPN IFR TNPNISL PLRSDSSNYR IPEAWLLLAN VAVILILVVP KDHLIDPLLL
401    RCKLLPSALQ KMALGMFFGF TSIIIVAGVLE KERLQYIAAN QTVPQLIGKD LYAAAPLSIW WQIPQYLLIG ISEIFASIPG
481    LEFAYSEAPR SMQGAIMGIF FCLSGVGSLL GSGLVALLSL PGGWMYCPKD FGNINNCRMD LYFFLLAGIQ AVTAVLFLWI
561    AGRYERTRQD PDSQNSTSRV RG
    
```



5.521 PREDICTED: similar to LUC7-like 2 [Rattus norvegicus]

Protein Accession	gij109471928
Mean Expression Ratio	0.946
Median Expression Ratio	0.947
Credible Interval	(0.721, 1.23)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.962
Avg..iTRAQ.Ratio....116.114.	0.995
Avg..iTRAQ.Ratio....117.114.	0.834

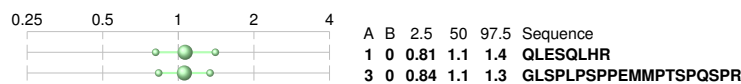


5.522 dystrophin isoform Dp71ab [Rattus norvegicus]

Protein Accession	gij52630316
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.838, 1.33)
Associated Peptides	2
Associated Spectra	4
Coverage	0.045
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.26
Avg..iTRAQ.Ratio....116.114.	1.23
Avg..iTRAQ.Ratio....117.114.	1.12

```

1      MREHLKGHET  QTTCDWHPKM  TELYQSLADL  NNVRFSAYRT  AMKLRRRLQKA  LCIDLLSLSA  ACDALDQHNL  KQNDQPMDIL
81     QIINCLTIY  DRLEQEHNNL  VNVPLCVDMC  LNWLLNVYDT  GRTGRIRVLS  FKTGIISLCK  AHLEDKYRYL  FKQVASSTGF
161    CDQRRRLGLLL  HDSIQIPRQL  GEVASFSGSN  IEPVSRSCFQ  FANNKPEIEA  ALFLDWMRLE  PQSMVWLPVL  HRVAAAETAK
241    HQAKCNICKE  CPIIGFRYRS  LKHFNYDICQ  SCFFSGRVAK  GHKMHPMVE  YCTPTTSGED  VRDFAKVLKN  KFRTRRYFAK
321    HPRMGYLPVQ  TVLEGDNMET  PASSPQLSHD  DTHSRIEHYA  SRLAEMENSN  GSYLNDSISP  NESIDDEHLL  IQHYCQSLNQ
401    DSPLSQPRSP  AQILISLESE  ERGELERILA  DLEENRNLO  AEYDRKQQH  EHKGLSPLPS  PPEMMPTSPQ  SPDAELIAE
481    AKLLRQHKGR  LEARMQILED  HNKOLESQLH  RLRLLEQPQ  AEAKVNGTTV  SSPSTSLQRS  DSSQPMLLRV  VGSQTSESMG
561    EEDLLSPPQD  TSTGLEEVME  QLNNSPFSSR  GHNVGSLFHM  ADDLGRAMES  LVSVMIDEEG  AE
    
```



5.523 "synuclein, beta [Rattus norvegicus]"

Protein Accession	gij77404215
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.787, 1.41)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0672
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.978
Avg..iTRAQ.Ratio....116.114.	0.874
Avg..iTRAQ.Ratio....117.114.	1.42

1 MDVFMKGLSM AKEGVVAAAE KTKQGVTEAA EKTKEGVLYV GSKTKEGVVQ GVASVAEKT EQASHLGGAV FSGAGNIAAA
81 TGLVKKEEFP TDLKPPEVAQ EAAEEPLIEP LMEPEGESYE DSPQEYQEY EPEA

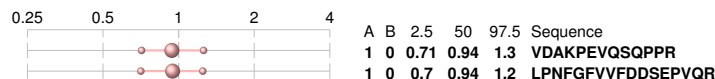


5.524 hypothetical protein LOC305240 [Rattus norvegicus]

Protein Accession	gij62078707
Mean Expression Ratio	0.948
Median Expression Ratio	0.947
Credible Interval	(0.732, 1.24)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0668
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.89
Avg..iTRAQ.Ratio....116.114.	0.926
Avg..iTRAQ.Ratio....117.114.	0.917

```

1      MVMEKPSPLL VGREFVRQYY TLLNKAPEYL HRFYGRNSSY VHGGVDASGK PQEAVYGQND IHHKVLSLNF SECHTKIRHV
81     DAHATLSDGV VVQVMGLLSN SGQPERKFMQ TFVLAPEGSV PNKFYVHNDM FRYEDEVFGD SEPDELDEESE DEVEEEQEDR
161    QPSPEPVQEN ANSAYYEAHP VTNGIEEPLE ESSHEPEPEP ESETKTEELK PQAEKHLLE LEEKSATPPP TEPASLPQEP
241    PKPRVDAKPE VOSOPRVRE QRPRERPFPP PRGPRPGRGD TEQNDSDNRR IIRYPDSHQL FVGNLPHDID ENELKEFFMS
321    FGNVVELRIN TKGVGGKLPN FGFVVFDDSE PVQRILIAKP IMFRGEVRLN VEEKKTRAR ERETRGGGDD RRDIRRNDRG
401    PGGPRGIVGG GMMRDRDGRG PPPRGGMTQK LGSGRGTQM EGRFTGQRR
    
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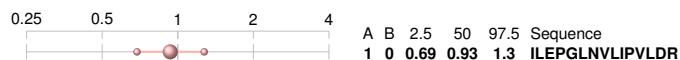


5.525 stomatin (Epb7.2)-like 2 [Rattus norvegicus]

Protein Accession	gi 72255527
Mean Expression Ratio	0.948
Median Expression Ratio	0.947
Credible Interval	(0.706, 1.28)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0425
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.10
Avg..iTRAQ.Ratio....116.114.	0.698
Avg..iTRAQ.Ratio....117.114.	0.904

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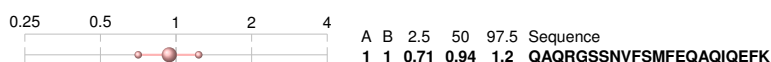
1      MLARAARGTG ALLLRGSVQA SGRIPRRASS GLFRNTVILF VPQQEAWVVE RMGRFHRILE PGLNVLIPVL DRIRYVQSLK
81     EIVINVPEQS AVTLDNVTLQ IDGVLYLRIM DPYKASYGVE DPEYAVTQLA QTTMRSELGK LSLDKVFRER ESLNANIVDA
161    INQAADCWGI RCLRYEIKDI HVPPRVKESM QMQVEAERRK RATVLESEGT RESAINVAEG KKQAQILASE AEKAEQINQA
241    AGEASAVLAK AKAKAEAIRI LAGALTQHNG DAAASLTVAE QYVSASFSLA KDSNTVLLPS NPSDVTSMVA QAMGVYGALT
321    KAPVPGAQNS SEARRDVQTT DTSIEELGRV KLS
    
```



5.526 "PREDICTED: similar to Myosin regulatory light chain 2, atrial isoform (Myosin light chain 2a) (MLC-"

Protein Accession	gi 109500970
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Mean Expression Ratio	0.947	
Median Expression Ratio	0.947	
Credible Interval	(0.723, 1.24)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.20	0.536
Avg..iTRAQ.Ratio....116.114.	0.616	1.04
Avg..iTRAQ.Ratio....117.114.	1.14	0.677



5.527 progesterone receptor membrane component 2 [Rattus norvegicus]

Protein Accession	gi 56605824
Mean Expression Ratio	0.948
Median Expression Ratio	0.947
Credible Interval	(0.701, 1.28)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0369
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.768
Avg..iTRAQ.Ratio....116.114.	0.907
Avg..iTRAQ.Ratio....117.114.	0.98

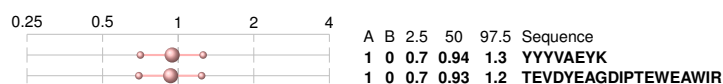
1 MAAGDGDVKL STLGSGGERG GDGSPGGAGA TAARSSWVAA LLATGGEMLL NVALVALVLL GAYRLWVRWG RRGLCSGPGA
 81 GEESPAATLP RMKKR**DFSL**E QLRQYDGART PRILLAVNGK VFDVTKGSKF YGPAGPYGIF AGRDASRGLA TFCLDKDALR
 161 DEYDDLSDLN AVQMESVREW EMQFKEKYDY VGRLLKPGE E PSEYTDEEDT KDHSKQD



5.528 "PREDICTED: similar to Mimitin, mitochondrial precursor (Myc-induced mitochondrial protein) (MMTN) ["

Protein Accession	gij 34854147
Mean Expression Ratio	0.946
Median Expression Ratio	0.947
Credible Interval	(0.725, 1.23)
Associated Peptides	2
Associated Spectra	2
Coverage	0.163
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.86
Avg..iTRAQ.Ratio....116.114.	0.937
Avg..iTRAQ.Ratio....117.114.	0.862

1 MSWWRGVVRS VWSALSREVR EHVGTDLGN **KYYYVAEYKN** WRGQTMREKR IVETANR**TEV DYEAGDIPTE** WEAWIRRRRK
 81 TPPTMEEILK NEKYREEIKI KSQDFYEKDK LGKETSEELL PSPTATQIKG HASAPYFGKE EPSVVPTSTG KTFQPGSWVP
 161 EDRRKQ



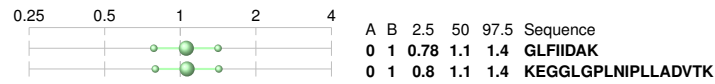
5.529 peroxiredoxin 2 [Rattus norvegicus]

Protein Accession	gij 8394432
Mean Expression Ratio	1.06
Median Expression Ratio	1.06
Credible Interval	(0.806, 1.37)
Associated Peptides	2
Associated Spectra	2
Coverage	0
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	1.07
Avg..iTRAQ.Ratio....117.114.	0.846

NHLBI Zile/Grant, Aged Rat

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1      MKPIRLMSGF FTVGIWTLIS RVMGFVRDVM IAGYLGSGPA AEAFLVAFSL PNMFRFFFAE GAFNMAFVPM FSKKLESGDD
81     PEKFAQDAFV GMAFILTLFT IIGIVAMPGL VLLMASGFAG DERFDLAVEY GRLAFPYILF ISLAALVSGV LNATGRFMAA
161    AAAPVVLNVI FILAVLIGAA LGRDGSEAIG MGIDKALGLQ IGDTLALSVP LAGIAQLALV WWAACKRAGFT LTFGRRPRLT
241    PELKRLAIIA APAALAGGVM QINLLVGRQV ASFYEGAVAW LNYADRLYQL PLGVVGIAGI VVLLPDLSSR LKAGDEQGS
321    TQISRAAEVS LALTIPSAVA LMVIPFTLAT VLFQRGATTT DDAAAIATAV AIYGLGLPAF VLQKILQPLY YAREDTRRPF
401    YFAVVAMVNV VVLAVGLSPV IGWIAPIAT TLAGWAMFAL LAYGARGFGL AAKFDARFHK RIWRIMAAAA VMGGALWIGN
481    LALQPLLAEA WWRGVALVIL TALAAVSYFG TGQLIGAFKL AEFKRALKRS
  
```



5.530 PREDICTED: similar to ferrochelatase isoform 2 [Rattus norvegicus]

Protein Accession	gij109507414
Mean Expression Ratio	1.06
Median Expression Ratio	1.05
Credible Interval	(0.786, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
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Avg..iTRAQ.Ratio....116.114.	0.96
Avg..iTRAQ.Ratio....117.114.	1.34



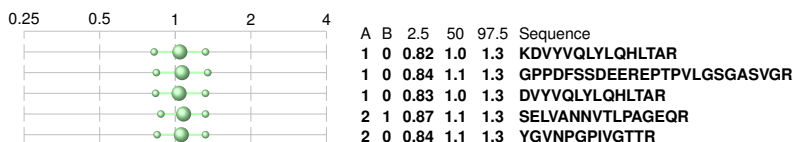
5.531 thymopoietin [Rattus norvegicus]

Protein Accession	gij6981660
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.877, 1.26)
Associated Peptides	5
Associated Spectra	8
Coverage	0.153

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.16	0.915
Avg..iTRAQ.Ratio....116.114.	1.02	1.28
Avg..iTRAQ.Ratio....117.114.	1.13	1.50

```

1      MPEFLEDPSV LTKDKLKSEL VANNVTLFAG EQRKDVYVQL YLQHLTANR PPLAAGANSK GPPDFSSDEE REPTPVLGSG
81     ASVGRGRGAV GRKATKKTDK PRPEDKDDLD VTELSNEELL EQLVRYGVNP GPIVGTRKLYEKKLLKRE QGAESRSTP
161    LPTVSSSAEN TRQNSNDSD RYSDNDEDSK IELKLEKREP LKGRAKTPVT LKQRRIEHNQ SYSEAGVTET EWTSGSSKGG
241    PLQALTREST RGSRRTPRRR VEPSQHFRVD GAVISESTPI AETIKASSND SLVANRLTGN FKHASSILPI TEFSDITRRT
321    PKKPLTRAEV GEKTEERRVE RDILKEMFPY EASTPTGISA SCRREIKGAA GRPLELSDFR MEESFSSKYV PKYVPLADVK
401    SEKTKKGRSV PMWIKMLLFA LVAGFLFLVY QAMETNQGPN FTNFLQDTRK SN
    
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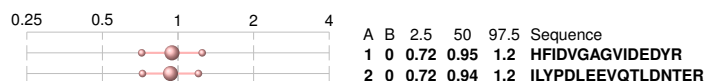


5.532 deoxyuridine triphosphatase isoform 1 [Rattus norvegicus]

Protein Accession	gij16758374
Mean Expression Ratio	0.947
Median Expression Ratio	0.948
Credible Interval	(0.742, 1.21)
Associated Peptides	2
Associated Spectra	3
Coverage	0.156
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.985
Avg..iTRAQ.Ratio....116.114.	0.9
Avg..iTRAQ.Ratio....117.114.	0.994

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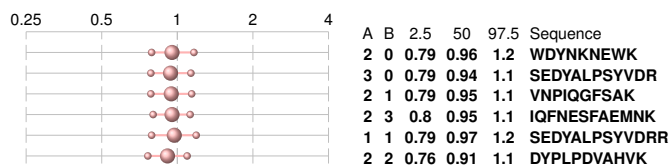
1      MPLLCALLRS RLQPSLLRSL TLTSQAQSLSC GSGRQVVRTWS ARTGPGACAD PAVSVSKRAR AEDDASLRFV RLSEHATAPT
81     RGSARAAGYD LYSAYDYTIP SMEKALVKTD IQIAVPSGCV GRVAPRSGLA VKHFIDVGAG VIDEEDYRGNV GVVLFNFGKE
161    KFEVKKGDRI AQLICERILY PDLEEVQTLN NTERGSGGFG STGKN
    
```



5.533 cytochrome c oxidase subunit IV isoform 1 [Rattus norvegicus]

Protein Accession	gij8393180	
Mean Expression Ratio	0.948	
Median Expression Ratio	0.948	
Credible Interval	(0.826, 1.09)	
Associated Peptides	6	
Associated Spectra	19	
Coverage	0.325	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.929	0.906
Avg..iTRAQ.Ratio....116.114.	1.05	0.695
Avg..iTRAQ.Ratio....117.114.	0.87	1.05

1 MLATRALSLI GKRAISTVC LRAHGSVVK^S EDYALPSYVD RRDYPLPDVA HVKLLSASQK ALKEKEKADW SSSLRDEKVO
 81 LYR^LIQFNESF AEMN^FGTNEW KTVVGLAMFF IGFTALVLIW EKS^VYVYGP^IP HTFDRDWVAM QTKRMLDMKV NPIQGFSAK^W
 161 DYNKNEW^FK



5.534 PREDICTED: similar to mitochondrial ribosomal protein L30 [Rattus norvegicus]

Protein Accession	gij109486989	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.789, 1.42)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	NA	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.60	

Avg..iTRAQ.Ratio....116.114. 1.07
 Avg..iTRAQ.Ratio....117.114. 1.54

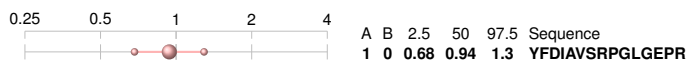


5.535 "RT1 class Ia, locus A1 [Rattus norvegicus]"

Protein Accession	gi 57012424
Mean Expression Ratio	0.947
Median Expression Ratio	0.948
Credible Interval	(0.7, 1.28)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0407
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.796
Avg..iTRAQ.Ratio....116.114.	0.743
Avg..iTRAQ.Ratio....117.114.	1.13

```

1      MGAMAPRTL L LILAAALAPT QTRAGSHSMR YFDIAVSRPG LGEPFIIIVG YVDDTEFVRF DSDAEKPRYE PRAPWMEPEG
81     PEYWEEQTRR AKEGEQTRFV NLRTALHYYN QSEDRSHTIQ RLSGCDVGS D GRLLRGYEQY AYDGRDYIAL NEDLKTWTAA
161    DFAARISRNK WDQAGVAERL RAYLEGECEVE WLRRYLELGK ETLLRSDPPK AHVTLHPRPE GDVTLRCWAL GFYPADITLT
241    WQLNGEDLTQ DMELVETRPA GDGTFQKWAS VVVPLGKEQN YTCRVEHEGL PEPLSQRWEP PPSTDSNMET TVIYVVVLGAV
321    AIIAAVIIGA VVTVVRKRRR NTGGKGVYTP APGTDSSQSS DVSLPDCRA
    
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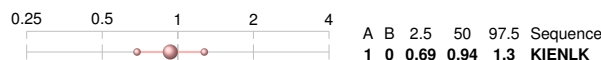
5.536 similar to CTCL tumor antigen se57-1 [Rattus norvegicus]

Protein Accession	gi 117940033
Mean Expression Ratio	0.947
Median Expression Ratio	0.949

Credible Interval	(0.707, 1.26)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0222
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.881
Avg..iTRAQ.Ratio....116.114.	0.956
Avg..iTRAQ.Ratio....117.114.	0.797

```

1      MTTVTVTMEV PSMGKTEDRS IFSGPSSAQI IEETEYVRKI RTTLEKIRNR MFKEEDGRGN ARHKVDAEQS GNVQNGLDST
81     TDPTRLDLLL ESMRRKDQQL LEMNKENEVL QIKLEASREA GAAALRNAAQ RLFDNVQTQS EDLEKHKHDS KHVLRQVNLKLE
161    KEQTLKQRAK NLSQLSEKLG EKHEQIVGLE NRVQRMENME GLKNTLKEQD KKIENLKEKV TVLEAQNEEL KTKVAHWTES
241    PRTSVSKAVS TSELKTEGAS PYLMLIRLRK
  
```



5.537 enabled homolog [Rattus norvegicus]

Protein Accession	gi 58865872
Mean Expression Ratio	1.06
Median Expression Ratio	1.05
Credible Interval	(0.79, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0228
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.13
Avg..iTRAQ.Ratio....116.114.	1.07
Avg..iTRAQ.Ratio....117.114.	1.66

```

1      MDVEFVSYSI PCLRSSQSLR ISEQSICQAR AAVMVDYDAN KKWVPAGGST GFSRVHIYHH TGNNTFRVVG RKIQDHQVVI
81     NCAIPKGLKY NQATQTFHQW RDARQVYGLN FGSKEDANVF ASAMMHAEV LNSQEAGPTL PRQNSQLPAQ VQNGPSQEEM
161    EIQRRLQEQE QRQKELERER MERERLERER LERERLERER LEQEQLERQR QEREHVERLE RERLERLERE RQDRERERER
241    LEQLEREQVE WERERRMSNA GHVLGPPAPP PPPPLPSGPA YASALPPPPG PFFFFFFLPSA GPPPPPPPPP PLPNQVPPPP
321    PPPPAPPLPA SGIFSGSMSE DNRPLTGLAA AIAGAKLRKV SRVEDGSFPS GGNTVSVNLA SSKTDSGRGN GPLPLGGSGL
401    MEEMSALLAR RRRIAEKGST IETEOKEDRS EDAEPVTSKA ASTSTPEPTR KPWERTNTMN GSKSPVISRP KSTPSSQPSA
481    NGVQTEGLDY DRLKQDILDE MRKELAKLKE ELIDAIRQEL SKSNTA
  
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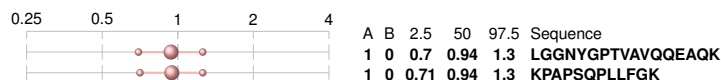


5.538 "branched chain aminotransferase 2, mitochondrial [Rattus norvegicus]"

Protein Accession	gi 11693174
Mean Expression Ratio	0.948
Median Expression Ratio	0.949
Credible Interval	(0.73, 1.24)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0738
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.895
Avg..iTRAQ.Ratio....116.114.	0.846
Avg..iTRAQ.Ratio....117.114.	0.972

```

1      MSAAILGQVW TRKLLPIPWR LCVPGRCVSS NFKAADLQVQ VTREPQKKPA PSQPLLFgkT FTDHMLMVEW NSKTGWGPPR
81     IQPFQNLTLH PACSGLHYSL QLFEGLKAYK GRDKQVRLFR PVLNMDRMLR SARRLCLPDF DKQELLEcir QLIEVDKDwv
161    PDGNGTSLYV RPVLIGNEPS LGVGMVTQAL LFVILCPVGS YFPGDSMPV SLLADPSFVR AWIGGVGDCK LGGNYGPTVA
241    VQQEaqAKGK EQVLWLYGPD HQLTEVGTMN IFVYWTHEDG ELELATPPLD GIILPGVVRQ SLIDLARTWG EFRVAERKVT
321    MKELKRALEE GRVREVFVGS TACQVCPVHQ ILYEGKQLHI PTMENGPELI LRFQKELKAI QYGTSahdwm LRV
  
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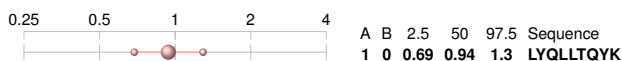


5.539 hypothetical protein LOC500419 [Rattus norvegicus]

Protein Accession	gi 7225551
Mean Expression Ratio	0.95
Median Expression Ratio	0.949
Credible Interval	(0.704, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0290
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.878
Avg..iTRAQ.Ratio....116.114.	0.841
Avg..iTRAQ.Ratio....117.114.	0.79

```

1      MALSSRLWRL LPLLRGAEQS VCQLARSWG S GRCGTWGRF GSEVTGNTRA FKRGLLFSAL SYLGFETYQV ISQAAVHAT
81     AKVEEILEQA DYLYESGETE KLYQLLTQYK ESEDVELLWR LARASRDIAQ LCKTSEEEKK VLLYEALEYA KRALEKKGSS
161    FAAHKWYAIC ISDVGDIYEGI KVKIANAYVI KEHFKAIEL NPKDATSIHL MGIWCYTFAE MPWYQRRIAE VLFANPPSST
241    YEEALKYFHR AEEVDPNFY S KNLLLLGKTY LKLNKKLAA FWLVKAKSYP AHTEEDKQIQ TEAAQLLTGL
    
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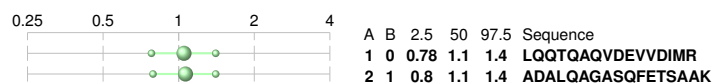


5.540 vesicle-associated membrane protein 2 [Rattus norvegicus]

Protein Accession	gj 6981614	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.802, 1.37)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.284	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.93	1.34
Avg..iTRAQ.Ratio....116.114.	1.01	0.869
Avg..iTRAQ.Ratio....117.114.	1.1	1.37

```

1      MSATAATVPP AAPAGEGGPP APPPNLTSNR RLQQTQAQVD EVDVIMRVNV DKVLERDQKL SELDDRADAL QAGASQFETS
81     AANLKRKYFW KNLKMMIILG VICAILLIII IVYFST
    
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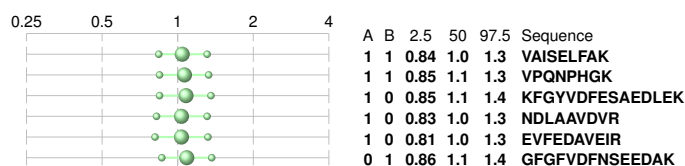
5.541 nucleolin [Rattus norvegicus]

Protein Accession	gj 6981248	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.878, 1.27)	
Associated Peptides	6	

Associated Spectra	8	
Coverage	0.0912	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	1.08
Avg..iTRAQ.Ratio....116.114.	0.936	1.15
Avg..iTRAQ.Ratio....117.114.	1.04	1.19

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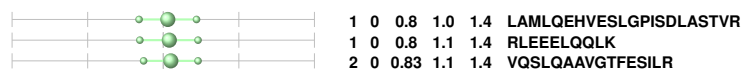
1      MVKLAAGKGT HGESKKMAPP PKEVEEDSED EEMSEDEDD SGEDEVVVPQ KKGKKATTP AKKVVVSQTK KAAVTPPAK
81     AAVTPGKAAA ATPAKKAVTP AKVVPTPGKK GAAQAKALVP TPGKKGAVTP AKGAKNGKNA KKEDSDEDED EDEDDSDSD
161    EDEEDEFEPV VVKGKPKAKA APAAPASEDE DEEDDDDDDD DDDDEEEEEE DDSEEEVMEI TPAKGGKTPA KVVVPKAKSV
241    AEEEEDEDED EDEEDEDDEE DEEDDEDEDE EEEEEPVKAA PGKRKKEMTK QKEAPEAKKQ KIEGSEPTTP FNLFIGNLNP
321    NKSVAELKVA ISELFAKNDL AAVDVL TGTN RKFGYVDFES AEDLEKALEL TGLKVFNEI KLEKPKGRDS KKVRAARTLL
401    AKNLSFNITE DELK EVFEDA VEIRLVSQDG RSKGIAYIEF KSEADAENL EEKQGAIDG RSVSLYYTGE KGQRQERTGK
481    NSTWSGESKT LVLSNLSYSA TEETLQEVFE KATFIK VPON PHGF SKGYAF IEFASFEDAK EALNSCNKME IEGRTIRLEL
561    QGPRGSPNAR SQPSKTLFVK GLSEDTEET LKESFEGSVR ARIVTDRETG SSKGFGFVDF NSEEDAF AAK EAMEDGEIDG
641    NKVTLDWAKP KEGGGFGGGR GGRGGFGGGR GGRGGGGGFG GRGRGGFGGR GGFRRGGGGG GDFKPPQKKK KFE
    
```



5.542 PREDICTED: similar to cytoskeleton-associated protein 4 [Rattus norvegicus]

Protein Accession	gij109481770
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.834, 1.33)
Associated Peptides	3
Associated Spectra	4
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.974
Avg..iTRAQ.Ratio....116.114.	1.14
Avg..iTRAQ.Ratio....117.114.	1.36





5.543 hypothetical protein LOC502782 [Rattus norvegicus]

Protein Accession	gij66730545	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.05	
Credible Interval	(0.805, 1.38)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.143	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.16	1.22
Avg..iTRAQ.Ratio....116.114.	1.08	1.10
Avg..iTRAQ.Ratio....117.114.	1.42	0.835

1 MLTTTCRRLS QALQRPHALS AVAQRCLRAP GARSYADQNE KAEQPRTFHP ALLQFLVCPL SKKPLRYDAS TNELINDELG
81 IAYPIIDGVP NMIPQAARTT RQKEKQEETK QH

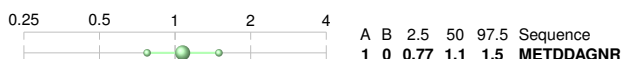


5.544 PREDICTED: similar to Mediator of RNA polymerase II transcription subunit 31 (Mediator complex subu

Protein Accession	gij109491232	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.05	
Credible Interval	(0.786, 1.42)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.072	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.45	

Avg..iTRAQ.Ratio....116.114. 1.05
 Avg..iTRAQ.Ratio....117.114. 1.26

1 METDDAGNRL RFQLELEFVQ CLANPNYLNF LAQRGYFKDK AFVNYLKYLL YWKEPEYAKY LKYPQCLHML ELLQYEHFRK
 81 ELVNAQCAKF IDEQQILHWQ HYSRKRMLQ QALAEQQQN TTAGK



5.545 "3-hydroxybutyrate dehydrogenase (heart, mitochondrial) [Rattus norvegicus]"

Protein Accession	gj 55742813	
Mean Expression Ratio	1.06	
Median Expression Ratio	1.05	
Credible Interval	(0.806, 1.38)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.0349	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	0.968
Avg..iTRAQ.Ratio....116.114.	1.35	1.1
Avg..iTRAQ.Ratio....117.114.	1.06	0.853

1 MMLAARLSRP LSQLPKALS VCDRENGTRH TLLFYPASFS PDTRRTYTSQ ADAASGKAVL VTGCDSGFGF SLAKHLHSGK
 81 FLVFAGCLLK DKGDAGVREL DSLKSDRLRT IQLNVCNSEE VEKAVETVRS GLKDPEKGMW GLVNNAGIST FGEVEFTSME
 161 TYKEVAEVLN WGTVRTTKSF LPLLRRAKGR VVNISSMLGR MANPARSPYC ITKFGVEAFS DCLRYEMHPL GVKVSVVEFG
 241 NFIAATSLYS PERIQAIKK MWDELPEVVR KDYGKKYFDE KIAKMETYCN SGSTDTSSVI NAVTHALTA TPYTRYHPMD
 321 YYWVLRMQVM THFPGAISDK IYIH



5.546 PREDICTED: similar to exonuclease 1 [Rattus norvegicus]

Protein Accession	gij109498236
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.781, 1.41)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.05
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	0.983



5.547 PREDICTED: similar to sarcolemma associated protein [Rattus norvegicus]

Protein Accession	gij109502999
Mean Expression Ratio	1.06
Median Expression Ratio	1.05
Credible Interval	(0.825, 1.35)
Associated Peptides	2
Associated Spectra	3
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	1.43

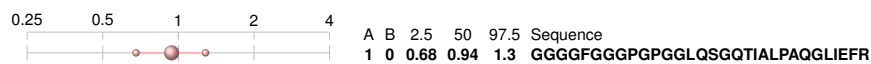


5.548 hypothetical protein LOC498407 [Rattus norvegicus]

Protein Accession	gi 62945366
Mean Expression Ratio	0.95
Median Expression Ratio	0.95
Credible Interval	(0.704, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0984
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.98
Avg..iTRAQ.Ratio....116.114.	0.606
Avg..iTRAQ.Ratio....117.114.	1.18

```

1   MADGDSGSER GGGGPGSFQP APRGGGGPGG EQETQELASK RLDIQNKRFY LDVKQNAKGR FLKIAEVGAG GSKSRLTISM
81  AVAAEFRDSL GDFIEHYAQL GPSSPEQLAA GAEEGGGPRR ALKSEFLVRE NRKYYLDLKE NQRGRFLRIR QTVNRGGGGF
161 GGGGPPGGGQ SGQTIALPAQ GLIEFFDALA KLIDYGGED DELAGGPGGG AGGPPGGGLYG ELPEGTSITV DSKRFFFDVG
241 CNKYGVFLRV SEVKPSYRNA ITVPPKAWGK FGGAFCRYAD EMKEIQERQR DKLYERRGGG SGGGDESEGE EVDED
    
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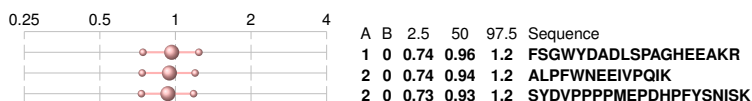


5.549 phosphoglycerate mutase 1 [Rattus norvegicus]

Protein Accession	gi 16757984
Mean Expression Ratio	0.95
Median Expression Ratio	0.95
Credible Interval	(0.766, 1.17)
Associated Peptides	3
Associated Spectra	5
Coverage	0.213
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.952
Avg..iTRAQ.Ratio....116.114.	0.927
Avg..iTRAQ.Ratio....117.114.	1.01

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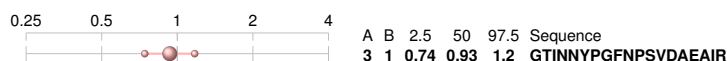
1   MAAYKLVLR HGESAWNLEN R FSGWYDADL SPAGHEEAKR GGQALRDAGY EFDIVFTSVQ KRAIRTLWTV LDAIDQMWLP
81  VVRTWRLNER HYGGLTGLNK AETAAKHGEA QVKIWRRSYD VPPPPMEPDH PFYSNISKDR RYADLTEDQL PSCESLKDTI
161 ARALPFWNEE IVPQIKEGKG VLIPAHGNSY GGIVKHLEGL SEEAIMELNL PTGIPIVYEL DKNLKPDKPM QSLGDEETVR
241 KAMEAVAAQG KVKK
    
```



5.550 Annexin III (Lipocortin III) [Rattus norvegicus]

Protein Accession	gi 6978503	
Mean Expression Ratio	0.949	
Median Expression Ratio	0.95	
Credible Interval	(0.744, 1.21)	
Associated Peptides	1	
Associated Spectra	4	
Coverage	0.0586	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.978	0.784
Avg..iTRAQ.Ratio....116.114.	0.885	0.772
Avg..iTRAQ.Ratio....117.114.	0.893	1.69

1 MAASLWVGPR GTINNYPGFN PSVDAEAIK AIKGIGTDEK TLINILTERS NAQRQLIVKH IQEAYEQALK ADLKGDLSGH
 81 FEHVMVALIT APAVFDAKQL KKS MRGMGTD EDLIEILTT RTSRQMK EIS QAYYTAYKKN LRDDISSETS GDFRKALLTL
 161 ADGGRDESLK VDEHLAKKDA QTLYDAGEKK WGTDEDKFT E ILCLRSFPQL KLTDFEYRNI SQKDIEDSIK GELSGHFEDL
 241 LLAVVRCTR N TPAFLAGRLH QALKGAGTDE FTLNRIMVSR SEIDLLDIRR EFKKHYGCSL YSAIQSDTSG DYRTVLLKIC
 321 GGDD

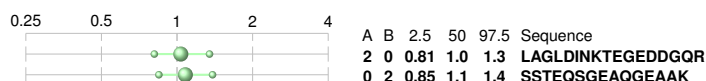


5.551 "protein kinase inhibitor, alpha [Rattus norvegicus]"

Protein Accession	gi 16758610	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.838, 1.33)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.421	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	0.913

Avg..iTRAQ.Ratio....116.114.	0.889	1.1
Avg..iTRAQ.Ratio....117.114.	1.02	1.49

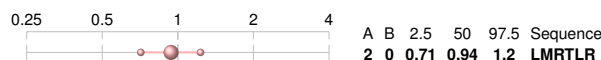
1 MTDVETTYAD FIASGRTGRR NAIHDILVSS ASGNSNELAL **KLAGLDINKT EGEDDGQRSS TEQSGEAQGE AAKSES**



5.552 PREDICTED: similar to SMAD-interacting zinc finger protein 2 isoform 1 [Rattus norvegicus]

Protein Accession	gij109512374
Mean Expression Ratio	0.95
Median Expression Ratio	0.95
Credible Interval	(0.73, 1.24)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0137
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.13
Avg..iTRAQ.Ratio....116.114.	1.23
Avg..iTRAQ.Ratio....117.114.	0.6

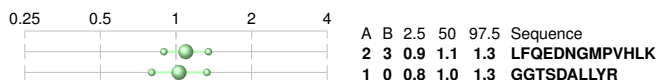
1 MSSAPTQAQG RYCPGTFLWR FLQTRPELLA ESPSILYSDT QLLSGMASLL ARMGNSRRQN AAFMPLAHSM LRALGRSLGP
 81 LIANIAERNI QSFSGRAELA PGEETFENWL SQVHEVLDPW PMSEEDKIKR **LMRTL**RGPARGPAR EAMRLFQADN PNLNVAEFLR
 161 AMKLLFGESE SSITAHGKFL NTLQAQGEKP SLYVIRLEVO LQNAIQAGVL PQSEANRTRL HQLLVGAELS RELRIKLGKGL
 241 LQMHANHEQE SLPDFLELIR MIREEDWDE TFLRNKRPRR SETVMERAAS PVVFQGSPLI VIGSADCNVI EIDDSQDDSD
 321 EDVILVEPED PPLSSPGTSS LRGTVSTQEE MLVIESPDES DEESPSTSSG SGQRNNGPGD VGRTRKRKYP IRCPHCGEEG
 401 HAKETCDNTS NKGQVFENLI VTLQELTHME RPKPPAPY



5.553 "PREDICTED: similar to cytochrome c oxidase, subunit 7a 3 [Rattus norvegicus]"

Protein Accession	gi 109499760	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.855, 1.31)	
Associated Peptides	2	
Associated Spectra	6	
Coverage	0.277	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.808	1.12
Avg..iTRAQ.Ratio....116.114.	0.92	1.06
Avg..iTRAQ.Ratio....117.114.	0.863	1.94

1 MLRNVLALRQ IAQRTISTTS RRHFENKVP E KQKLFQEDNG MPVHLKGGTS DALLYFATML LTVGGTAYAI YMLAMAAPFK
81 KQN



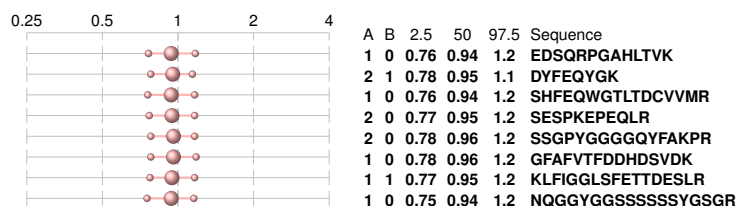
5.554 heterogeneous nuclear ribonucleoprotein A1 [Rattus norvegicus]

Protein Accession	gi 8393547	
Mean Expression Ratio	0.949	
Median Expression Ratio	0.95	
Credible Interval	(0.812, 1.10)	
Associated Peptides	8	
Associated Spectra	13	
Coverage	0.356	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.969	0.923
Avg..iTRAQ.Ratio....116.114.	0.99	1.01
Avg..iTRAQ.Ratio....117.114.	0.833	0.868

NHLBI Zile/Grant, Aged Rat

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1      MSK2ESPKEP EQLRKLFIGG LSFETTDESL RSHFEQWGLT TDCVVMRDPN TKRSRGGFV TYATVEEVDA AMNARPHKVD
81     GRVVEPKRAV SREDSQRPGA HLTVMKIFVG GIKEDTEHH LR2DYFEQY2GK IEVIEIMTDR GSGKKR2GFA2F VTFDDHDSVD
161    KIVIQKYHTV NGHNCEVRKA LCKQEMASAS SSQRGRSGSG NFGGGRGGGF GGNDNFGRGG NFSGRGGFGG SRGGGGYGGG
241    GDGYNGFGND GSNFGGGGSY NDFGNYNQ2S SNFGPMKGGN FGGR2SSGPY2G GGGQYFAKPR NQGGYGGSSS SSSYSGGRF
  
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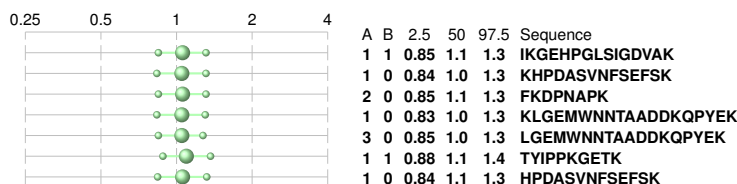


5.555 PREDICTED: similar to High mobility group protein 1 (HMG-1) (High mobility group protein B1) (Ampho)

Protein Accession	gij109495090
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.89, 1.25)
Associated Peptides	7
Associated Spectra	12
Coverage	0.133
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	1.21

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1      MAMDLKVTSQ KRLSEPIPNI SVSSQLGEWE KVQSSMASNP SGFGVREVQN NALCLTKRKK SWRSTGKLEQ NQKKGVQLDA
81     CWWEQPTPLG RVGTLGGSPG EGCLVVGCSN IAVPGPTEAP AFGPQAPEQP PHSRTHPQAR AANLNGSGPE RGAGGGAGLR
161    EPLGPEDA2AV AVAELGPDRA RRGSGVGLAR GRRRHTDIE LRFPRQRRGK R2EPDGHWATL CLAEENQLNM GKGD2PKKPRG
241    KMSSYAFFVQ TCREEHKK2KH PDASVNFSEF2S2 KCSERWKT MSAKEKGF2E DMAKADKARY EREM2KTYIPP2 KGET2KK2F2KD
321    P2NAP2KRP2PSA FFLFCSEYRP K2IKGEHPGLS2 IGDVAKKLG2E MWNNTAADDK2 QPYE2KAAKL KEKYEKL2SLM QLIRRRRESE
401    ASNKHVCLAG SVYCWMRAGP HSPVTF2LQVE GWDFDQGEQP EWSPGRQAQL QAAVPCNCSK RPKGF2LKEGF FHEGVWDEEG
481    STERISCLRS SRKAFN
  
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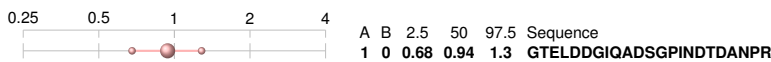


5.556 caspase 7 [Rattus norvegicus]

Protein Accession	gij11560075
Mean Expression Ratio	0.948
Median Expression Ratio	0.95
Credible Interval	(0.703, 1.28)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0759
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.738
Avg..iTRAQ.Ratio....116.114.	0.809
Avg..iTRAQ.Ratio....117.114.	1.32

```

1      MTDDQDCAAE LEMADSSTED GVDAPDRST IISLLWKKK KNASMCVST TRDRVPTYLY RMDFEKMGKC IINNNKFDK
81     ATGMDVRNGT DKDAEALFKC FRSLGFVTV YNDCSCAKMQ DLLRRASEED HSNSACFACV LLSHGEEENLI YGKDGVTPIK
161    DLTAHFRGDR CKTLLEKPKL FFIQACR GTE LDDGIQADSG PINDTDANPR YKIPVEADFL FAYSTVPGYY SWRNPGRKGSW
241    FVQALCSILN EHGKDLEIMQ ILTRVNDRVA RHFESQSDDP RFNEKKQIPC MVSMLTKELY FGR
  
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5.557 TBP-interacting protein Tip120B [Rattus norvegicus]

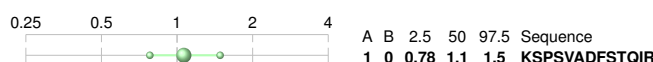
Protein Accession	gij31077144
Mean Expression Ratio	1.06
Median Expression Ratio	1.05
Credible Interval	(0.779, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0105
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.27
Avg..iTRAQ.Ratio....116.114.	1.07
Avg..iTRAQ.Ratio....117.114.	1.43

NHLBI Zile/Grant, Aged Rat

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1   MSTGAFYISS LLEKMTSSDK DFRFMATSDL MSELQKDSIQ LDEDSERKVV RTLRLLEDR SGEVQNLAVK CLGPLVGKVK
81  EYQVENIVDT LKANMRSDKE QLRDIAGIGL KTVLSELPPA ATGSGLAISV CRKITGQLTS AIAQQEDVAV QLEALDILSD
161 MSLRGLGAPLG TFHASLLHCL LFQLSSPRLA VRKRTVVALG HLAACSTDL FVELADHLVD RLPGPRAPAS PAAIRTLIQ
241 LGSVGRQAGH RLG AHLDRML PLVEEFCNLD DDELRESCLQ AFEAFLRKCP KEMDPHPVNV TSLCLQYMKH DPNYNHDSDE
321 EEQMETEDES FSEQESEDEY SDDDDMSWKV RRAAAKMAA LISSRPDLLF DFHCTLAPAL IRCFKEREEN VKADIFGAYI
401 MLLRHTRPPK GWLEAVEEPT QTGRNLNMLR AQVPLVMKAL QRQLKDRNVR TRQGCENLFT ELAGVLPGLC AEHMTVLVSG
481 IVFSLADYSS SSTIRMDALA FLQGLLGTEP AEAFFPHLPT LLPPVMACVA DPFYKVAEEA LLVLQELVRT LWPLDRPRL
561 DPEFYVGEYS TATLARLRAT DLDQEVKERA ISCVGHVGH LGDRLGDDLE PTLTLLLDRL RNEITRLPAV KALTLVAVSP
641 LRRLDLPILA EALPILASF RKNQRALRLA TLAALDALAQ SQGLGLPPPA VRSVLAELPA LVSENDMHVA QLAVDFLTIV
721 TQTQPASLVE VSGPVELELL QLLHSPLLPA GVLAAATEGFL QALVGTTRPPC VEYSELISLL TAPVYNQVGD GGPGLHKQVF
801 HSLARCVAAL SAACPQEAAG TASRLVCDAR SPSSTGVKV LAFSLAEVGV QVAGPGPQRE LKTVLLLEALG SPSEDVRAAA
881 AYALGRVGAG NLPDFLPFLL AQIEAQPRRQ YLLLHALREA LGAAQPDNLK PYVEDVWALL FQRCESPEEG TRCVVAECIG
961 KLVFVNPFPL LPRFRKQLAA GQPYTRSTVI TAVKFLISDQ PHSIDPLLS FIAEFMESLQ DPDLNVRRAT LTFNNSAVHN
1041 KPSLVRDLLD DILPLLYQET KIRRDIREV EMGPFKHTVD DGLDVRKAAF ECMYSLLESC LGQLDICEFL NHVEDGLKDH
1121 YDIRMLTFIM LARLAALCPA PVLQVRDLRI EPLRATCTAK VKAGSVKQEL EKQDELKRSA MRAVAALMTN PEVRKSPSVA
1201 DFSTQIRSNP ELATLFESI QKDTASGFSMD SMELS

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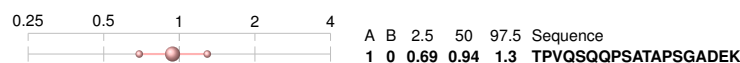
5.558 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 [Rattus norvegicus]"

Protein Accession	gi 72255509
Mean Expression Ratio	0.953
Median Expression Ratio	0.95
Credible Interval	(0.71, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0209
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.912
Avg..iTRAQ.Ratio....116.114.	0.804
Avg..iTRAQ.Ratio....117.114.	1.07

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1   MEEGGRDKTP VQSQQPSATA PSGADEKSSG KERRDAGEKD KEQELSEEDK QLQDELEMLV ERLGEKDTSL YRPALEELRR
81  QIRSSSTTSM SVPKPLKFLR PHYGKLKEIY ENMAPGENKC FAADIISVLA MTMSGERECL KYRLVGSQEE LASWGHEYVR
161 HLAGEVAKEW QELDDAEKAQ REPLLTLVKE IVPYNMAHNA EHEACDLLME IEQVDMLEKD IDENAYSKVC LYLTSCVNYV
241 PEPENSALLR CALGVFRKFS RFPEALRLAL MLNDMELVED IFTSCKDVVV QKQMAFMLGR HGVFLELSED VEEYEDLTEI
321 MSNVQLNSNF LALARELDIM EPKVPDDIYK THLENNRFGG SGSQVDSARM NLAASFVNGF VNAAFGQDKL LTDDGNKWL
401 KNKDHGMLSA AASLGMILLW DVDGGTLQID KYLYSSEDIY KSGALLACGI VNSGVRNECD PALALLSDYV LHNSNTMRLG
481 SIPGLGLAYA GSNREDVTL LPPVMGDSKS SMEVAGVTAL ACGMIAVGC NGDVTSTILQ TIMEKSETEL KDTYARWLPL
561 GLGLNHLGKG EAIEAILAAL EVVSEPPRSF ANTLVDVCAY AGSGNVLVKQV QLLHICSEHF DSKEKEEDKD KKEKKDKDKK
641 EAPADMGAHQ GVAVGLIALI AMGEEIGAEM ALRTFGHLLR YGEPTRLRAV PLALALISVS NPRLNILDITL SKFSHDADPE
721 VSYNSIFAMG MVGSGTNNAR LAAMLRQLAQ YHAKDPNNLF MVRLAQGLTH LGKGTTLTLC YHSDRQLMSQ VAVAGLLTVL
801 VSFLDVRII LGKSHYVLYG LVAAMQPRML VTFDEELRPL PVSVRVGQAV DVVGGQAGKPK TITGFQTHHT PVLLAHGERA
881 ELATEEFLPV TPILEGFVIL RKNPNYNL

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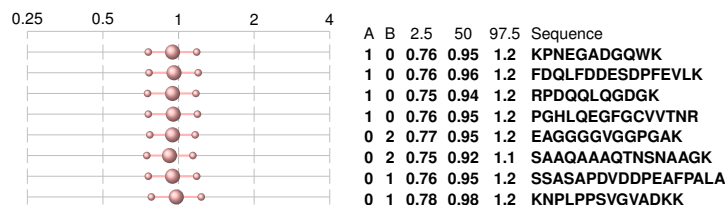


5.559 PAI-1 mRNA-binding protein [Rattus norvegicus]

Protein Accession	gj 57977275	
Mean Expression Ratio	0.95	
Median Expression Ratio	0.95	
Credible Interval	(0.8, 1.12)	
Associated Peptides	8	
Associated Spectra	10	
Coverage	0.291	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.875	0.896
Avg..iTRAQ.Ratio....116.114.	0.927	0.761
Avg..iTRAQ.Ratio....117.114.	1.01	0.91

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1      M P G H L Q E G F G   C V V T N R F D Q L   F D D E S D P F E V   L K A A E N K K K E   A G G G G V G G P G   A K S A A Q A A A Q   T N S N A A G K Q L   R K E S Q K D R K N
81     P L P P S V G V A D   K K E E T Q P P V A   L K K E G I R R V G   R R P D Q Q L Q G D   G K I I D R R P E R   R P P R E R R F E K   P L E E K G E G G E   F S V D R P I I E R
161    P I R G R G G L G R   G R G G R G R G M G   R G D G F D S R G K   R E F D R H S G S D   R S S F S H Y S G L   K H E D K R G G S G   S H N W G T V K D E   L T D L E Q S N V T
241    E E T P E G E E H P   V A D T E N K E N E   V E E V K E E G P K   E M T L D E W K A I   Q N K D R A K V E F   N I R K P N E G A D   G Q W K K G F V L H   K S K S E E A H A E
321    D S V M D H H F R K   P A N D I T S Q L E   I N F G D L G R P G   R G G R G R G R G R   G R G G R P N R G S   R T D K S S A S A P   D V D D P E A F F P A   L A
    
```



5.560 "PREDICTED: similar to pleckstrin homology domain containing, family G, member 3 [Rattus norvegicus]"

Protein Accession	gj 109478374	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.805, 1.37)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.00777	

Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	1.25
Avg..iTRAQ.Ratio....117.114.	1.15

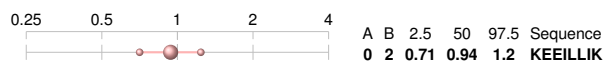
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1      MGSTAFQGGD TRVTIHVRLG ILEFQVARDP HAGPRGLIIS HGGCCLQPET QPARSAAKVP RSPQSRQLLD LSRERSLHPL
81     ETFLVRPSLA CSLLPSSRRS LDLVRPQLPA VCWGTVRIPG VPRSLGARSQ RRLGPRGGQP WAGAAGGYCG FRERLSNSNP
161    LRRATWAAPR AWRVASRRGG HGLNLPVTV PGSDARMPVS TALHQDGSQE RFPPLMSTTS SSGSSRDSHS AMEPTGSEA
241    SAQNGTGSFW GRHIPNSNNN SSSWLNKMGF LSPFNAGRAGT GPAYHKLSYL GRVVREIVET ERMVVDLRS IVEDYLLKII
321    DTPGLLKEPQ VSALFGNIES IYALNSQLLR DLLSCNSDPV AVASCFVERS QEFDIYTQYC NNYPQVMAAL TECMQDKQQA
401    KFFRDRQELL QHSLPLGSYL LKPVQRILKY HLLLQEIAXH FDEEEDGFVEV VEDAIDTMT C VAWYINDMKR RHEHAVRLQE
481    IQSLLINWKG PDLTTYGELV LEATFRVHRV RNERTFFLFD KILLITKKRG DHFVYKSHIP CSSLMLIEST RDSLCTVTTH
561    YKHSKQQYSI QAKTVEEKRS WTHHIKRLIL ENHHATIPQK AKEAILEMDS YPSRYRCS P ERMKKAWSQ DEVS AHVRQG
641    RRQSEPGRTL FSRATLPSRQ QGFEMPGLKG RRKSEPTRHL LRQLSEKARA AGMKHAGSAG ALLDFGQLPH AQDQQPEAEE
721    AAREEEEEEE EIVEEEEQQQ QQTFFVSLD LAGHGGNEKV PGPELPGSEE EEEEEESLAV AEQGKRHGES EGSKSCRFP S
801    DRSPTSVEKR MSFESVSSMP EESSEQVETD PEPRAEQEAF TALEGPSPEE MFSDPPEFPEA LETQLHDPKG LLGVDKPAGE
881    VDFVEPEGSE DLKTLSSEEE EEEEMGATQE PESLLPPSVL DQASVIAERF ASSFSRRSSL AAEDGKCSGL GTPRLISRSS
961    SVLSLEGSEK GLARWSSTGD SLSNPPAPEV IIGTDTVTD T GPSVNGTESL SAGSGCPTEL DRSSCKKKES ALSTRDRQLL
1041   DRIKSYENA EHHDAFSIR RRESLSYIPK GLVRNSVSRF NSLPKPDSEP AAPVGYKRP G SSRPASWTLF DLPGPSRADE
1121   GDPAPITDAE FRPSEIAKI WERMESSERS PRTGGGQQA NGFELQEP LF ILEEHELGAI TEESAVASPE SASPTEHSP S
1201   AHLARELKEL VKELSSGVQG ELVTP LHPRI MQLSHVMDSH VSERVKNKVY QLARQYSLRI KNKAARPP L HWEKATPDGD
1281   EPIPSNSGLP VEAGELSGGK ARKPVLSLL SYEQLVAQEP GTSKSSSAVE TSPRRFSFSP SAVSPRTTSP GSRSSARSPL
1361   SPFDTETFNW PDVRELCSKY TSHDKTAQAE SSWPRSLLVN RSRSLPENII EPPVSGKADY CCSLNTNGRQ GDGEASQPPP
1441   PESPPQSQLN GEALYVTAD LTLENNRRVI IMEKGSHFSS TMGLEEDSGK EPSSSVVLKG QGQGFQESAE HQPKEDSPRD
1521   SADTNKQGRV RNLREKFFAL NSVG
    
```



5.561 "PREDICTED: similar to carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorot"

Protein Accession	gij109478984
Mean Expression Ratio	0.949
Median Expression Ratio	0.95
Credible Interval	(0.72, 1.24)
Associated Peptides	1
Associated Spectra	2
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.904
Avg..iTRAQ.Ratio....116.114.	0.922
Avg..iTRAQ.Ratio....117.114.	0.57

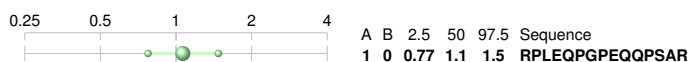


5.562 SH3 domain protein 4 [Rattus norvegicus]

Protein Accession	gi 54114997
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.77, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0205
Experiment	A
Avg...iTRAQ.Ratio....115.114.	1.28
Avg...iTRAQ.Ratio....116.114.	1.15
Avg...iTRAQ.Ratio....117.114.	1.36

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1   MARIPGVGRS STSSLDNKED SESDVALLSP KDPDRVHTKE QLAHPVSSNL DPSMQGLPAG LSLDDFIPGH LRAHIGASSR
81  GTRVPVIRNG GSNTLNFQFH DPAPRTVCNG CPPRRRDGSQ HPDPAWYQTW PGPGSQPSVS PKQPAPQNAQ NWSATWTKDS
161 KRRDKRWVKY EGIGPVDESG MPIAPRSSVD SPRDWYRRMF QQIHRKMPDL QLDWTLEDPP KVVSSRASSA DPRHPGPPQR
241 PASRPGTTGT SSGRNWNHSE ETSRNTLNYN LGPSSRLHAS NQVPRHREKV ENVWTEDSWN QFLHELETGH KPKKSLVDDP
321 VEKPAQPIEV LLERELAKLS AELDKDLRAI ETRLPSPKNS QAPRRPLEQF GPEQQPSAL SSAWRPNSPH APYFGSSRPL
401 SPHRMADGGG SPFLGRRDFV YPSSAREPSA SERGSSPARK EEKKRKAARL KFDFQAQSPK ELTLQKGDIV YIHKEVDKNW
481 LEGEHHGRLG IFPANYVEVL PADEIPKPIK PPTYQVLEYG DAVAQYTFKG DLDVELSFRK GERICLIRKV NEHWYEGRIT
561 GTGRQGIFPA SYVQINREPR LRLCDDSPQL PTSPHLTFTA HLGSHSQPSS IPVDPDWDGG RTSPPRSAFP FPITLQEPRS
641 QPQSLSTFGP TLSHPRGTSH PTNLGSSSLN TTEIHWTPYR AMYQYRPQNE DELELREGDR VDVMQQCDDG WFGVGSRRRTQ
721 KFGTFPGNYV APV
    
```



5.563 PREDICTED: similar to YEATS domain containing 2 [Rattus norvegicus]

Protein Accession	gi 109493555
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.781, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	NA

Experiment	A
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Avg..iTRAQ.Ratio....116.114.	0.85
Avg..iTRAQ.Ratio....117.114.	1.95

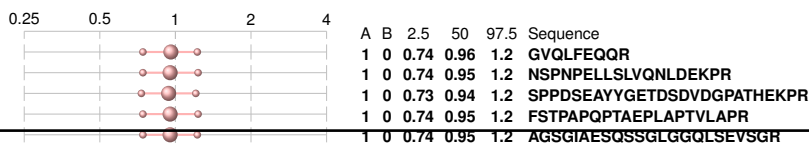


5.564 PREDICTED: similar to synaptopodin 2-like [Rattus norvegicus]

Protein Accession	gij109501180
Mean Expression Ratio	0.952
Median Expression Ratio	0.95
Credible Interval	(0.774, 1.17)
Associated Peptides	5
Associated Spectra	5
Coverage	0.0941
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	0.765
Avg..iTRAQ.Ratio....117.114.	1.10

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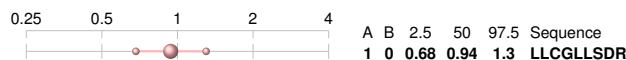
1      MPFNMLGGRG  GSRNLGQEVK  GGVVGPKTDR  RSQMSEIFHI  FQNFMALPA  ERGHCPNSGG  HRPNCAMGAE  EEVQVTLAGG
81     APWGFRLQGG  AEQRKPLQIR  RRSQAGRSGL  RERDQLLSIN  GVSCTDFSHA  SAMTLIDASG  HQLVLTVRRV  AEEGSVRSFS
161    PGELQMLSPL  SPLSPPEPPGA  PVTQAPQPGS  LRSPDSEAY  YGETDSDVDG  PATHEKPRRT  RRRGPPRPSL  PGAPPDEVYL
241    SDSPAEPAPV  KTGSFSQGDS  RVSSPSWEEG  SALQPPPAEA  LLLPHGPLRP  GPHLIPMVGP  VPHPVAEDLT  TTYTQKAKQA
321    KLQRAESLQE  KSVKEAKTKC  RTIASLLTAA  PNPFSKGVLM  FKKRRQRAKK  YTLVSFGAAA  GTGTEEEEDG  IPPTSESELD
401    EEAUSDARSL  TNQSDWDSFY  LDMELARAGS  GIAESQSSGL  GGQLSEVSGR  GVQLFEQQRQ  RVASSSQELA  QVGAAMLNG
481    QSLQSPPRAQ  SAPPEAAVLP  LSPLSAPAAS  PSPFQDGGAP  SPAPSIENRS  ARPFTPGLPG  QRSGETTSVIF  RPVAPKKVNE
561    ALGGTSPAPS  PFAASLQGPT  PLPSFTTVVP  NRTPVSGTSS  STQRSSGPVT  ATSSLYIPAP  SRPVTPGGAP  EPPTPPSAAA
641    MTSTASIFLS  TPLRNSARPE  APGTAPEPEA  SAREQRISVP  AARTGILQEA  RRRGTRKQMF  RPKKEETKNS  PNPELLSLVQ
721    NLDEKPRAGG  AESGPEEDAL  SLGAEACNFM  QPLGGRSYKT  LSQVSPKTFP  PMAKTPPPM  TPKTTPPVAP  KPGRGLPDG
801    LVNGSTSMVG  IPELPRLQGR  GGELFAKRQS  RADRYVVEAT  PGSSLNPLGL  PRSPSPTPSL  PPSWKYSPNI  RAPPPIAYNP
881    LLSPPFPQAA  RTLPNKAQSQ  GPRATPKQGI  KALDFMRHQP  YQLKTAMFCF  DEGPTPAST  SGPPKTARVQ  EIRRSTPAP
961    QPTAEPLAPT  VLAPFAATTL  DEPIWRAELA  SSPVNPNDHL  ESLRSFAATP  TSCGFQVARP  RFSATRTRGLQ  AHVWRPGAGH
1041   H
    
```



5.565 PREDICTED: similar to Macrophage migration inhibitory factor (MIF) (Phenylpyruvate tautomerase) (GI

Protein Accession	gij109461312
Mean Expression Ratio	0.95
Median Expression Ratio	0.95
Credible Interval	(0.702, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0783
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.882
Avg..iTRAQ.Ratio....116.114.	0.863
Avg..iTRAQ.Ratio....117.114.	0.747

1 MPMFIVNTNV PRASVPEGFL SQLTQQLTQA TGKPAQYIAV HVVPDQLMTF SSTNDPCALC SLHSIGKIGG IQNRNYSKLL
 81 CGLLSDR LHI SPDRVYINYY DMNAANVGWN GSTFA

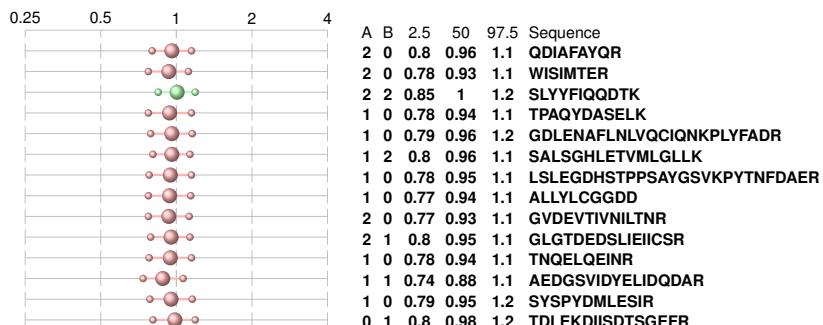


5.566 annexin A2 [Rattus norvegicus]

Protein Accession	gij9845234	
Mean Expression Ratio	0.95	
Median Expression Ratio	0.95	
Credible Interval	(0.844, 1.06)	
Associated Peptides	14	
Associated Spectra	25	
Coverage	0.593	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.867	0.856
Avg..iTRAQ.Ratio....116.114.	1.02	0.567
Avg..iTRAQ.Ratio....117.114.	0.967	1.81

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1   MSTVHEILCK LSLEGDHSTP PSAYGSVKPY TNFDAERDAL NIETAIKTKG VDEVTIVNII TNFSNAQRQD IAFAYQRRTK
81  KELPSAMKSA LSGHLETVM LLLKTPAQYD ASELKASMKG LGTDEDSLIE IICSRTNQEL QEINRVYKEM YKTDLEKDII
161 SDTSGEFPEKL LVALAKGKRA EDGSVIDYEL IDQDARELYD AGVKRKGTDV PKWISIMTER SVCHLQKVFE RYKSYSPYDM
241 LESIRKEVKG DLEN AFLNLV QCIQNKPLYF ADRLYDSMKG KGTRDKVLIR IMVSRSEVDM LKIRSEFKRK YGKSLYYFIQ
321 QDTRGDYQKA LLYLCGGDD
  
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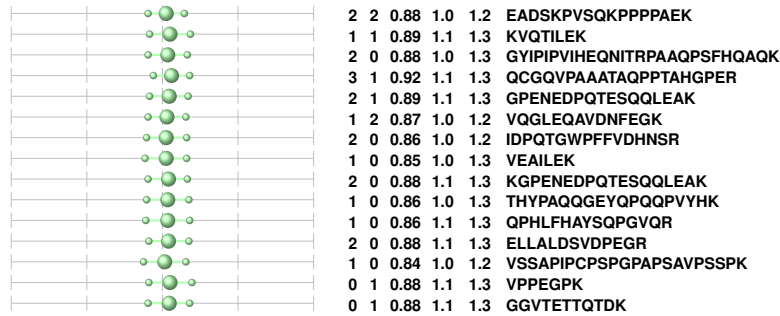
5.567 Bcl2-associated athanogene 3 [Rattus norvegicus]

Protein Accession	gij58865450	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.944, 1.17)	
Associated Peptides	15	
Associated Spectra	30	
Coverage	0.376	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	0.997
Avg..iTRAQ.Ratio....116.114.	1.14	1.12
Avg..iTRAQ.Ratio....117.114.	1.07	0.89

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1   MSAATQSPVM QMASGNASD RDPLPPGWEI KIDPQTGWPF FVDHNSRTTT WNDPRVPPEG PKETASSANG PSRDGSRLLP
81  AREGHPIYPQ LRPGYIPIV HHEGSENROP HLFHAYSQPG VQFRTEAAA AAPQRSQSPL RGGVTETTQT DKQCGQVPAA
161 ATAQPTTAFH PERSQSPAAS DCSSSSSSAS LPSSGRSSLG SHQLPRGYIP IPVIHRONIT RPAAQPSFHO AOKTHYPAQQ
241 GEYQPPQPVY HKIQGDDWEP RPLRATSPFR SPVRGASSRE GSPARSGTPV HCPSPIRVHT VVDRPQPMTH REPPVVTQPE
321 NKPEKPGCLA GPDLPFGHIP IQVIRREADS KPVSQKPPFP AEKVEVKVSS ADIPCPSPGP APSAVPSSPK NVAAPKAAAP
401 SPAPAEASL KSGDAEAPHK HPGVLKVEAI LEKVQGLEQA VDNPEGRKTD KKYLMIEEYL TKELLALDSV DPEGRADVRP
481 ARRDGVRKVQ TILKLEQKA IDVPGQVQVY ELQPSNLEPE QPLQEIMGAV AADKDKKGPE NEDDPQTESQQ LEAF AATPPN
561 PSSTADSAGN PVAP
  
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5.568 PREDICTED: similar to titin isoform N2-B [Rattus norvegicus]

Protein Accession	gij109470142	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.968, 1.14)	
Associated Peptides	36	
Associated Spectra	56	
Coverage	0.0150	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.13	1.10
Avg..iTRAQ.Ratio....116.114.	0.952	0.859
Avg..iTRAQ.Ratio....117.114.	1.26	1.22

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1      MTTQAPTFTQ  FLQSVVVLEG  SAATFEAHIS  GSPVPEVSWF  RDGQVISTST  LPGVQISFSD  GFARLMIPAV  TKANSGRYSL
81     RATNGSGQAT  STAELLVTAE  TAPPNFSQRL  QSMTVRQGSQ  ARLQVRVTGI  PTPVVKFYRD  GAEIQSSLDF  QISQEGDLYS
161    LLIAEAYPED  SGTYSVNATN  SVGRATSTAD  LLVQGEEVVP  AKKTKTIVST  AQISETRQTR  TEKIEAHFD  ARSIATVEMV
241    IDGATGQLPH  KTPPRIPPKP  KSRSPTPPSI  AAKAQLARQQ  SPSPIRHSPS  PVRHVRAPTP  SPVRSVSPAG  RISTSPIRSV
321    KSPLLIRKTQ  TTTVATGPEV  PFPWKQEGYV  ASSTEAEMRE  TTMTSSTQIR  REERWEGRYG  VQEQVTISGA  AGTAASVSAR
401    SSPTAEAVTT  GAKEVKQETD  KSAAVATVVA  AVDMARVREP  VISAVEQTAQ  RTTTTAVHYV  PADKQMRKEA  EKTAVTKVVV
481    AADKAKEQEL  RLRTRREEIIT  KQEQTHIAHE  QIKKETECAF  VPKVVISATK  AKEQETRITG  EITTKQEQKR  ITQETLRQET
561    ETIAASVVVA  TAKSTKLEAA  VGIQEETAIQ  QDQTHLTHGQ  ITKETRKTIV  PKVIVATPKI  KEQDQVRSR  EAITTKRDQV
641    QITQEKKRKE  TETTALSTIA  VATTKAKEQE  TVLRSREAMT  TROEHIQVTH  GRVGVGKKA  AVATVVAAVD  QARVREPREP
721    RHVEESYSQQ  TTLEYGYKEH  ISATKVEEQP  QRPASEPHVV  PKAVKPVVVI  APSETHIKAT  DQVGMHISSQ  VKKTTDISTE
801    RLVHVDKRPR  TASPFFTYSK  ISVVKTEHGY  EASIAGSAIA  TLQKELSTTS  STQKITKSVK  APTVKPGETR  VRAEPTSPK
881    FPPADVPAPD  TYKSQAGIEV  KKEVGSISG  STVREEQFEL  LRGREAKVTE  TARVPAPAEV  PVTPTLVSG  LKNVTVVEGE
961    SVTLECHISG  YSPSPVTWYR  EDYQIESSID  FQITFQSGIA  RLMIREAFAE  DSGRFTCSAV  NEAGTVSTSC  YLAVQVSEEF
1041   DKETTLTEKF  TTEEKRFVES  RDVVMTDTSI  TEEQAGPGEP  AAPFFISKPV  VQKLVEGGSV  VFECQIGGNP  KPHVYWKKS
1121   VPLTTGYRYK  VSYNKQTGEC  RLVISMTFAD  DAGEYTVIR  NKHGETSASA  SLLEEADYEA  LIKSQQETLY  QTQMSSTFIQ
1201   PKVGEIAPGF  AYSEYEKEYE  KEQALIRKMM  AKDTVMVRTF  VEDQEFHISS  FEERLIKEIE  YRIKTTLEE  LLEDGEERM
1281   AVDISESEAV  ESGFDIRIKN  YRILEGMGVT  FHCKMSGYPL  PKIAWYKDGK  RIRRGERYQM  DFLQDGRASL  RIPVVLPEDE
1361   GIYTAFAASN  KGNACISGKL  YVEPAAPFSA  PTYMPTEPAV  SRIRSVSPRS  VSRSPRIRIS  AMSPARMSPA  RMSPARMSPA
1441   RMSPGRRLEE  TDESQLERLY  KPVFVLPKPA  FKCLEGGQTA  FDLKVVGRPM  PETFWFHNGQ  QIVNDYTHKV  VIKEDGTQSL
1521   IIVPALPDS  GEWTVVAQNR  AGKSTISVTL  TVEAVEHQIK  PAFVEKLNK  NIKEGSRLEM  KVRATGNPNP  DIVWLKNSDI
1601   IVPHKYPRIR  IEGTKGEAAL  KIDSTISQDS  AWYTATAINK  AGRDTRCKV  NIEVEFAEPE  PERRLIIPRG  TYRAKEISAP
1681   ELEPLHLRYG  QEQWEEGDLY  DKEKQKQPF  KKKLTSRLK  RFGPAHFECR  LTPIGDPTMV  VEWLHDGKPL  EAANRLRLIN

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1761	EFGYCSLDYE	AAYS RDSGVI	TCRATNKYGT	DHTSATLIVK	DEKSLVEESQ	LPEGKKGKLR	IEELERMAHE	GALTGVTTDQ
1841	KERQKPDIVL	FPEPVRVLEG	ETARFRCRVT	GYPQPKVNWY	LNGQLIRKSK	RFRVRYDGIH	YLDIVDCKSY	DTGEVKVTAE
1921	NPEGVTEHKV	KLEIQQREDF	RSVLRRAPEP	KPEFHVHEPG	KLQFEVQKVD	RFVDTGETKE	VVKLKRARI	THEKVSESE
2001	ELRSKFKRRT	EGEYEAITA	VELKSRKKDE	SVEELLKTK	DELLHWTKE	TEEEKKALAE	EGKVTIPTFK	PERIELSPSM
2081	EAPKIFERRIQ	SQTVGGGSDA	HFRVVRVVGK	DPECEWYKNG	VKIERSDRIY	WYWPEDNVCE	LVIRDVTAED	SASIMVKAIN
2161	IAGETSSHAF	LLVQAKQLIT	FTQELQDVVA	KEKDTMATFE	CETSEPFVVK	KWYKDGIEVH	AGDKYRMHSD	RKVHFLSVLT
2241	IDTSDAEDYS	CVLVEDENIK	TTAKLIVEGA	VVEFVKELQD	IEVPESYSGE	LECIISPENI	EGKWHNDVE	LKSNKYSIT
2321	SRGRQRNLTV	KDVTKEDQGE	YCFVVDGKKT	TCCLKMKFRP	IAILQGLSDQ	KVCEGDIVQL	EVKVSLENVE	GVMWMDGQEV
2401	QHSDRVHIVI	DKQSHMLLIE	DMTKEDAGNY	SFTIPALGLS	TSGNVSVYSV	DVITPLKDVN	VEGTTKAVLE	KCVSVDPVTS
2481	VKWLNDQVI	KPDDRQVQIV	KGTKQRLVIN	RTHASDEGYS	KLMVGRVETS	CNLSVEKIKI	IRGLRDLTCT	ETQNVVFAEQ
2561	LSHSGIDVWV	NFKGQEIKPS	SKYKIEAHGK	IYKLTLDNMM	KDDEGEYAFY	AGENTTSGLK	TVAGGAIKSP	LTDQTVAESQ
2641	EAVFECEVAN	PESEGEWLKD	GKHLTSLNNF	RSESDGHKRR	LVIAAAKDD	IGEYTYKVAT	SKTSAKLKVE	AVKIKKTLRN
2721	LTVTETQDAI	FVSELTHPDV	KGVQWKNGV	VLDSDNKYEI	SVKGTLYSLK	IKNCAMADES	VYGFKLGRGL	ASARLHVETV
2801	KIIRKPKDVT	ALENATVAFE	VSVSHDTPVP	RSSVTLYVNA	PEPPQVLQEL	QPVTVQSGPK	ISPSDAGEYT	AVVQGLCKEA
2881	KLVFETLHIT	KTRMNIIEVPE	TKAASFECVT	SHEFNVTMNL	KNGVEIEMSE	KFKIVVQGLK	HQLIIMNTST	EDSAEYTFVK
2961	GNDQVSTATLT	VTPIIMTSM	KDINAEKEED	ITFEVTVNGE	GISYKWLKNG	VEIKSTDRQC	MRTKKLTSHL	NIRNVHFGDA
3041	ADYTFVAGKA	TSTATLYVEA	RHIEFRKHK	DIKVLKERRA	MFECEVSEPD	ITVQWMDGQ	ELQIVDRIKI	QKEKYVHRL
3121	IPARMSDAG	KYTVVAGGNM	STANLFEVGR	DVIRIRSKKE	VQVIEKQRAV	VEFEVNEDDV	DAHMYKDGIE	INFQVEERHQ
3201	YVVERRIHRM	FISEARHSDA	GEYTFVAGRN	RSSVTLYVNA	PEPPQVLQEL	QPVTVQSGPK	ARFCVIAIAGR	PQPKISWYKE
3281	EQLLSTGFKC	KFLHDGQEY	LLLIEAFPPD	AAVYTCEAKN	DYGVATTSAS	LSVEVEEVVS	PDQEMPVYPP	AIIVPLQDAV
3361	TSEGRPARFQ	QCVSGTDLKV	SWYCRDKKIK	PSRFFRMTQF	EDTYGLEIAE	AFPEDEGTYA	FVANNAVQGV	SSTATLRLEA
3441	PESILHEQIG	QQIEMEMKAA	PVIKRRIEPL	EVVALGHLAKF	TCEIQGAPNV	RFQWFKAGRE	IYESDKCSIR	SSNYISSLEI
3521	LRTQVVDCGE	YTCKASNEYG	SVSCTATLTV	TEAYPPTFLS	RPKSLTTFVG	KAAKFLCTVS	GTPVIETIWQ	KDGTALSPSP
3601	DCRITDADNK	HSLELSNLT	QDRGVYSCKA	SNKFGADICQ	AELTIDDKPH	FIKELEFPVQS	AINKKIHLLEC	QVREDRKEVSI
3681	TWFKDGGKLP	AGKDYKIYFE	DKIASLEIPL	AKLKSDSTYS	CTASNEAGSS	SSSATVAVRE	PPSFVKKVDP	SYMLPAGESA
3761	RLHCCLKGSP	VQIVVFKFNN	KELSESTNVR	MSFANSEAIL	ITDVKVDDSD	GTYSCEATND	AGSDSCSTEV	VIEKPPSFIK
3841	TLEPAHIVRG	ANALLQCEVA	GTGPFVSWF	KDKKQIRSSK	KYRFLTQKTF	VFLEITSFNS	ADIGDYECVU	ANEVGGCCGV
3921	ATHLLKEPPT	FVALLVDDFTA	LQAGTVTLQA	AVRGESEIPV	MWMMKQVEIK	EDGKIRMSFS	SGVAULTISD	VQIGLCKGKY
4001	CLAENEAGSQ	TSVGLIVKE	PAKIIERAEL	IQVTAGSDPT	LEYTVSGTPE	LKPKWYKDR	PLVAASKYRI	SFKNNIAQLK
4081	FYSAELHDSG	QYTFEISNEV	GSSSCTTFT	VALDRDIAPL	TKPLRNVDSV	VGGACRLDCK	IAGSLPMRVS	WFKDGEATA
4161	SDRYQIAFVE	GTASLEISRV	DMNDAGNFTC	RNRNSVGSKD	SRGALIVQEP	PSFVTKPESR	DVLPGSVAACL	KSAFQGSPTA
4241	TIRWFKDGKE	LVSGGSCYIT	KEASESSLEL	YAVKTTDSGT	YTCKVSNVAG	SVECSANLFV	KEPATFTEKL	EPSQLLKKGD
4321	ATQLVCKYTG	TPPIKITWFA	NDRLELRESSK	HKMSFVESTA	VLRLTDVAIE	DSGEYMECAQ	NEAGSDHCTS	IIVIKESPYL
4401	TKEFKSIEVL	KEYDVMLLAE	VAGTPPFEIT	WFKDNTTLRS	GRKYKTFIQD	QLVSLQILKF	VASDAGEYQC	RVTNEVGSST
4481	CSARVTLREP	PSFKKIEETT	SSLRGGTAAF	QATLKGSLPI	TVTWLKNDNE	ITEDDNIRMT	FENNVASLYL	SGIEVHDKGK
4561	YVQKAKNDAG	IQRCSALLSV	KEPATITQEA	VSDIDVTGDP	ATLQYKFSGT	KEISAKWFKD	GOELTLGPKY	KISVTDTVSI
4641	LKIISTEKKD	SGEYTFEVQN	DVGRSSCKAS	INVLDDLIIPP	SFTKLRKMD	SIKGSFIDLE	CIVAGSHPII	IQWFKDDQEI
4721	SASDKYKFSF	HDNTAFLEIS	QLEGTDSGTY	TCSATNKAGH	QCSGHLTVK	EPYFVKEKQP	SQDVNPSSTRV	LKALVJGTA
4801	PMTIKWFKDN	KELHPGAARS	VWKDDTSTIL	ELFSAKAADS	GTIQCQLSND	VGTTSKATI	FVKEPPQFIK	KPSVPLVLRN
4881	GQSTTFECQV	VGTPEIRVSW	YLDGNEITDL	RRYGISFVDG	LATFQISNAR	VENSGTYVCE	ARNDAGTASC	SIELKVKPEPP
4961	IFRELEPVE	VKDSDELVELE	CEVMGTTPFE	VTLNKNKEI	RSKGYTMSSE	RMSVFLYHIT	KCAPSDVGEY	QICITANEKGS
5041	CACTARVALK	EPFISIKKIE	NVTTVLKLSSA	TFQSTVAGSP	PISTITLWDD	QILEENDNVH	ISFDESVATL	QVRSVDNHS
5121	GRYTCQAKNE	SGPERSYAFI	LVQEPAQIIE	KAKSVDVTEP	DKTLECEVVA	GTEPLKVKWL	KDQKQIVPSR	YFRSMFNHV
5201	ASFRIQSVML	QDSGGYTFKV	ENDFGSSSCD	AYLRVLDQDI	PPSFTKKLTK	MDKVLGSSIH	MECKVSGSLP	INAQWFKDQK
5281	EISTSAKYRL	VCHENTVSLK	VSNLEEDTA	NYTCKVSNVA	GDNACSGILT	VKEPPSFLVK	PERQQAIPDS	TVEFKAVLKG
5361	TPPFKIKWLK	DDDELVSQPK	CFIGLEGSTS	FLNLYSVDAS	KTGQYTCQVT	NDVEPPKFVK	KLEASKIVKA	GDSARLECKI
5441	TGSPFIRVVV	YRNEHELTA	DKYQMTFIDS	VAVMOMNSLG	TEDSGDFICE	AQNPAAGSTSC	STKVIVKPEP	VDFSFPVVE
5521	TLKNTVESLE	CELSGTDPPE	VVWYKDKRQL	RSSKKYKIAS	KNFHASIHIL	NVDSITDIGEY	HCKAONEVGS	CTCCIAIKLK
5601	EPKFKISKLN	SLTVVAGEPA	ELQASIEGAP	PISVHWLKEG	EBEVRESENV	RISFVNNVAT	LQFAKAEAPN	AGKYICQVKN
5681	DGQVRENMA	LTVLEPAVIV	EKAGSMVTVT	GETCSLECKV	AGPELSVVEV	YKDGKLLTSS	QKHKFSYFNK	ISSIKLISVE
5761	KEDAGTYTFQ	VQNNVKGSSC	TAVVDVSDRM	VPPSFTRRLL	DIGGVLGTSC	VLECKVAGSS	PISIAWFHEK	TKIVSGAKYQ
5841	TFSDNVCTL	QLNSLDSSDM	GSYTCVAANV	AGSDECRALL	TVQEPSPFVK	EPEPLEILPG	KNITFTSVIR	GTPPFKVGWF
5921	RGARELVKGD	RCNIYFEDTV	AELLEFNIEV	SQSDEYTCVV	SNNAGQASCT	TRLFVKEPAT	FVKLLSDHSV	EPGKSIILEG
6001	TYGTGLPISV	TWKDGVVIT	PSERCNIVTT	EKTCILEILT	STKGDAGHYS	CEIENEAGRD	SCDALVSTLE	PPYFVTELEP
6081	LEASVGDSSV	LQCQVAGTPE	ITVSWFKGDT	KLRSTPEYRT	YFTNNVATLV	FNKVGINDSG	EYTCVAENSI	GTAASKTVFR
6161	IQRQLPSPF	ARQLKDIEQT	VGLPVTLTRC	LNGSAPIHVC	WYRDGVLLRD	DENLQMSFVD	NVATLKILOT	DLSHSGQYSC
6241	SASNPLGTAS	STARLTAREP	KKSPFFDIKP	VSIDVIAGES	ADFECHVTGA	QPMRVTWSKD	NKEIRPGGNY	TITCVGNTPH
6321	LRILKVGKGD	SGQYTCQATN	DVGKDMCSAQ	LSVKPEPKFI	KKLDTSKVAK	QGESIQLECK	ISGSPKIKVV	WFRNDSSELH
6401	SWKYNMSEVN	SVALLTINEA	SVEDTGDYIC	EAHNGVGHAS	CSTALKVKAP	PVFTQKPPPV	GALKGSDVIL	QCEISGTPPF
6481	EVVWVKDRKQ	VRSSKFKFVT	SKNFDTSLHI	FNLEAPDIGE	YHCKATNEVG	SDTCACTVKE	KEPPRFVKKL	SDVSTLIGDP
6561	VELQAVVEGF	QPISVVWLKD	KGEVIRESEN	VRI SFVNDIA	TLQLGSPSEAS	HSGKYVCQIK	NDAGMRECSA	LLTVLEPARI
6641	VEKPEPMTVT	TGNPFTLECV	VAGTPELSAK	WLKDGRELS	GSRHHITFVR	NLASLKIPSA	EMNDKGLYSF	EVENSVGKRS
6721	CTVSVHVSAD	VPPSFIRKL	KDTTATLGAS	VVLECRVGS	APISVGFWD	GNEIISSPKC	QPSFADNVCT	LTLSLLEPSD
6801	TGAYTCVAAN	VAGQDESSAL	LTVQEPSPFE	QTPDSVEVLP	GMSLTFTSVF	RGTTPPFVKV	FKGSRLEESG	EACTISLEDF
6881	VTELELLEVE	PLQSGDYSCL	VTNDAGSASC	THHLFVKEPA	TFVKRLADTS	VETGSPIVLE	ATYSGTPIIA	VSWLKNEVPL
6961	SQSPNCGIIT	TERSISILEIL	ESTIEDYAYQ	ACLIEAGYAE	DICEALVSVL	EPYFIEPLE	HVEAAIGEP	TFLCKVDGTP
7041	EIRISWYKHE	TKRSAPAYK	MOFKNNVASL	VINKVDHSDV	GEYTKAENS	VGAVASSAVL	VIKERKLPPS	FARCKLDVHE
7121	TLGFPVAFEC	KLRSVEPLQV	SWYKDGQLL	DDSNLQMSFV	HHVATLQILQ	TDQSHVGQYN	CSASNPLGTA	SSSAKLILSE
7201	HEVPPFFDLK	PLVVDLALGE	SGSFKCHVTV	TAPIKITWAK	DNREIRPGGN	YKMTLVENTA	TLTVLKVAKG	DAGQYTCYAS
7281	NVAGKDCSCA	QLGVQEPFRF	IKKLDQSRIV	KQDEYTRYEC	KIGGSPEIKV	LWYKDEVEIQ	ESSKFRMSFE	DSVAILEMHN
7361	LSVEDSGDYT	CEARNAAGSA	SSSTSJKVKE	PPVFRKFPFP	VETLKGADVH	LECELQGTTP	FQVSWYKDKR	ELRSKGYKFI
7441	MSENLLTSHI	ILNVDTADIG	EYQCKATNDV	GSPTCVGSVT	LKAPPQFVKK	LSDVSTIIGK	EVQLQTTIEG	AEPISVAWFK
7521	DKGEIVRES	NIWISHSSENV	ATLHFSRAEP	ANAGYTKCQI	KNDAGVQECY	ATLSVLEPAT	IVEKPPESIKV	TTGDTCTLEC
7601	MVSGTEPELST	KWFKDQKELT	GDSKYKISFP	NKVSGLKIIIS	VAPGDSGVYS	FEVQNPVQGD	SVTSVIQVSD	RIIPPSFTRK
7681	LKSTNPLSGS	SVVMECKVFG	SPPIISVWLH	DGNAISSGRK	YQTLTDNCTC	ALTVNMLEDA	DAGDYTCIAT	NVAGSDECSA
7761	PLTVREPPSF	VQKPPDMDVL	TGSNVFTTSI	VKGTPTPTVS	WFKGSSSELVP	GARCNVSLQD	SVAELELFDV	DTSGSGDYTC
7841	IVSNEAGRAS	CTTQLFVKAP	AIFVKRLNDY	SIEKGLPLIL	EGTFSGTPII	SVTWKKNGVN	VTASQRNCTI	TTEKSAILEI

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7921	LSSTVEDSGQ	YNCYIENASG	KDSCSAQILI	LEPPYFVKQL	EPLKVTVGDS	ASLQCQLAGT	PEIGVSWYKG	DTKLRPTTTC
8001	KMHFKNNVAT	LVFTQVDSND	SGEYICRAEN	SVGEVSSSTF	LTVQEQKLFPP	SFSRQLRDVQ	ETVGLPVVFE	CAVSGSEPI S
8081	VSWKYKDGKPL	KDSPNVQTSF	LDNIAITLNF	KTRDSLQAGQY	SCTVTNPIGS	ASSSAKLILT	EKGNPPFFDI	PLAPVDVAVG
8161	ESADLECHVT	GTQPIKVTWA	KDNREIRSSG	NYQISYLENS	AHLTIVKVDK	GDSGQYTCYA	INEVGKDSCT	AQLNIKERLT
8241	PPSFTKKLSE	TIEETEGNSF	KLEGRVAGSQ	PITIAWYKNN	VEIHPTSNCE	ITFKNNALLL	QVKKASMADA	GLYTCKAATND
8321	AGSALCTSSI	VIREPKKPPV	FDQHLTPVTA	SEGDFLQJLSC	HVQGGSEPIRI	QWLRAGREIK	PSDRCSFSFA	SGTAVLELKD
8401	TAKADSDGYV	CKASNVAGSD	TSKCKVTIKE	KPAAAPAAKK	AAVDGKLFV	SEPQSIIRVVE	KTTATFFIAKV	GGDP IPNVKW
8481	TGKQWRQLNQ	GGRILIHQKQ	DESKLEIRDT	TKTDSGLYRC	VAFNKHGIEI	SNVNLQVDER	KKQEKIEGDL	RAMLKKTAL
8561	KKSGSEEEI	DIMELLKNVD	PKEYEKYARM	YGITDFRGLL	QAFELLLKQSQ	EEETHRLEIE	ELEKSERDEK	EFEELVFSIQ
8641	QRLTQTEPVT	LIKDIENQTV	LKDNDAIIFEI	DIKINYPEIK	LSWYKGTTEL	EPSNKYEITI	NGDRHTLRVR	CKQLKQDQNG
8721	RLVCGPHIAS	AKLTVIEPWA	ERHLQDVTLK	EGTCTMTQC	FVSPNVKSEW	FRNGRVLKQP	GRVKTEVEHK	NHKLITADNR
8801	AEDQGRYTC	HEDLETSDEL	RIEAEPIQFT	KRIQNIUVSE	HQSATFECEV	SFDDAIVTWY	KGPTELTSQ	KYNFRNDGRC
8881	HYMTIHNVT	DDEGVYSVIA	RLEPRGEARS	TAEPLYLTKE	IKLEMKPPDI	PDSRVP IPTM	PIRAVPPPEE	PIVAVAPSIP
8961	LLPLPEEKVP	PAKRIVETTK	GVKKTTKVV	PPAVPEIPKK	KVPEEKRPVP	RKEEVPPPKA	PSEI IDVSSK	AAEVPKITE
9041	RKKEIHKEKE	AVYERKEAVY	EKKVLI EPWE	EPYEELETFP	YTEPYEPEY	EEPDEDEYEE	KVEAKKTRR	EWEEDYEEG
9121	EYEREEEGYD	EVEEWEIEY	HEREIIQVQK	EHVEDLHEKK	IPAKVPEKKV	PPPKVVKKPV	VEKIEKTRH	MEEEKVQVTK
9201	VPEVSKKIVP	QKPSRTPVQE	EIEVKVPVAV	HTKKMVISSE	KMFFASHTEE	EVSVTVPEVQ	KKTVTEEKI	H VAVSKKIEPP
9281	PKVPEPPKPP	VPEEVPVPI	PKKVEPPAVK	VPAPKPPVP	EKKKPVPIPK	KEPAAPPKVP	EAPKPPAPEE	KTAVPVAKK
9361	EAPPKVTVEV	QKVVVTEEKI	TIIPQREESP	PPAVPEIPKK	KVPEEKRPVP	RKEEVPPPKA	LTVRNVSNVP	APPKPVPEE
9441	VVPVPIPKKA	PPRAEVSKTT	VVEEKFAFAE	ERLSMAVQOR	VELMRHEEEE	WTYSEEEEQV	SVSVYREER	DEEEAIEFEY
9521	EVLPEPEYV	VEEKLIHVISK	RVEVEPAKVP	EKHEKKIIPR	PKVPAKIEEP	PPTKVPEPPK	KMVPEKKVPA	PPPKKVPEAK
9601	APEEPKPPVP	ERRVPAEVEV	IEEPPPTKVT	EKHMKIQTQE	KVLVAVTKKE	EPPRARVPEE	PKKVVPPEEK	PKLKPRREE
9681	PPAKVTEVRK	RAVKEEKVSI	EVPKREPRPT	KEVTVTEEEK	WSYTREEETV	LEHREEEYED	YEDYEEYKEY	EYEPTEEYD
9761	QYDEYAEREL	EHYEAEKEQE	EYVVPPEPKK	ITRKPQEPV	PAKPKAPPPK	VPKKAIPPEEK	APLLIQVKKL	PLPKKAPPEE
9841	KKVVEEKIQI	SITKREKQVQ	TEPVAKVPMK	PKRVVPEAKI	PAPVAAPVRR	TSLCFYSVNV	GKPIFCYTVL	LKCLNFIEEL
9921	QSSQLKDGIF	KVPGVPPKRE	PEEVVIFKWE	VEAHEEYIV	VEAHEEYIV	EYVHEEYI	EYVHEEYI	HEEYVHEEYI
10001	EEVIAEEEVK	PVAPVKVPV	PKKPVPEEKK	PVPVPPKKEA	PPAKVPEIPK	KPEEKVSVVP	PKKEKAPPA	VPEVPKPPVP
10081	EEKAPVPVPL	KVEPPPAKVP	EVPKPPVPEK	KVPAPTPKKV	EAPPAKPPVE	PKKPIPEEKK	PTPLKPKMEA	PPPKVPPKRE
10161	VVPVVPVAPR	EVEEAEPEE	EVTVPEEIEI	PEEVEVPEEE	EVLPEEEVLE	PEEEVVPPEE	EEALPEIKPK	VPKPAPVEI
10241	KKVVPPEKVV	VPKKEEAPPT	KVPEVPKRVK	EKKVPEEKEE	EVPVPAKVYEE	AEETPPEETP	EEPPSIEBEE	IVEEVEEIEEV
10321	PPPRAPVVKV	KAVPAAPAPV	PKKAAPPTPK	VPKKPIPEEKV	PVPVQKKEAP	PARVPEVPAK	VPEKKKPIEK	KVPVPPKKEA
10401	PPAKGKAVFE	EKISVAYQQE	ERVQERIELE	LVEAQVEEAF	EEEQFHEVQE	YFEEEFHEV	EEFIRVEERR	FQEHKVEEV
10481	HRVIEFLAE	EVEVEKPKI	PPKKGPEVSE	LVPKPKPPT	KVLPKKEPPA	KAPEVTKKMM	VEEKVRVPEE	PKVPAPKEVV
10561	PEKKVSMVPP	KRPEAPPKAV	PEAPKEVVPE	KKVSVAPKKK	PEAPAVKVPE	VPKAAVPQKK	IPEAVPPKPE	SPPEVPEPPP
10641	KEVVPPEKVS	MVPPKRPEAP	PAKVPEASKE	VVPPEKVSVA	PKKKPEAPAV	KVPEVPKAAV	PQKKIPEAVP	PKPESPPPEV
10721	YEEPAEEIVP	EPEPEEVEVE	PEPAPPPKVT	VPPKPPVPEK	KAPPAVVKPP	EPPPAKAPVE	PKEAPEKPKV	PSVPPPEKPA
10801	PPAKVPEVPP	EVPPEKVVAV	PKKPEVPPAK	VPEVPPKPPV	EKKPVIEEKP	AIPVAEKVES	PPTEVEEPEE	EVAQEEPEFA
10881	PVVEEVEYEA	PPPPAVPEE	PKKVVPEKKY	PVIKKPEPPP	PKEPEPEKPV	IEKPKLKP RP	PIRAPSPPEK	DVKEIPELQK
10961	AVSKKKVPEK	PEVVKEVPEP	PLKVP TAEKK	VRKLLPEPPK	QPKKEVV LKS	VLRKRP EEEE	PKVEPKKVEK	VKKPEEPEPE
11041	PKAVEVEAPP	EPPKPKKVP	EPTKVPKIEK	AIDLPGPEPK	PKPEPEVKTM	KAPPPEPAPT	PIAAPVTAPE	VGKKAEPKPK
11121	DEAAKPKGPI	KGVAKKTPSP	IEAERKRLRP	GSGGKPEPDE	APFTYQLKAV	PLKFFVKEIKD	IVLTEAESVG	SSAIFECIUS
11201	PSATAITWKM	CGDNSIRESPK	HRFIADGDKR	KLHIIDVQLS	DAGEYTCVLR	LGNKKEKSTA	KLIVEELPVR	FVCTLEEEVT
11281	VVKGQPLYLS	DELNKRDDVV	WRKDGKIVVE	KPGRIIVGVI	KLMLRALTIND	ADDDTAGYTT	VTVENANNLE	CSSCVKVEI
11361	IREWLKPIR	DQHVKPKGTA	VFTCHIAKDT	PNIKWFKGYD	EIPLEPNDKT	EILKEGNHLI	LKVKNAMPED	IDEYAVEIEG
11441	KRYPAKLTG	ERDVELLKI	EDVTIYEEKS	ASFD AEI SEE	DIPGEWKLG	ELLRPSPTCE	IKAEGGKRF	LTKHVKLDQA
11521	GEVLYQACNA	VTTAILTVKE	IELDFAVPLK	DVTVPEKRRQ	RFECVLTREA	NVIWSKGPDI	IKASDKFDI	ADGKKHILVI
11601	NDQFDDDEGV	YTAEEVGGKT	SAQLFVLTGIR	LKFI SPLLEDQ	TVKGEQTATF	VCELSHEKHM	VVWFKNVDKL	HTTRTVLMS
11681	EGTKYKLEIR	ETTLDDISQI	KAQVKNLSTG	ANLKVLEADP	YFTVKLHDKT	GVEKDEIILK	CEVSKDVPVK	WFKDKVEIVP
11761	SPKHSVKTG	DLRLIKKIKKA	ELKDKGEYTC	DCGTDTTFAN	VTVEARLIKV	EKPLYGVEVF	VGETARFIE	LESEPDVHGQV
11841	KLKGEPLTAS	PDCEI IEDGK	KHVLLVLYNQC	LDMTGEVFSQ	AAANAKSAANL	KVKEPLIFIF	TPLSDDVKEF	KDEAKFECEW
11921	SREPKTFRWL	KGTOEIA GDD	RFELIKDGT R	HSLVIKSAAF	EDEAKYMFEA	EDKRTSGKLI	IEGIRLKF LT	PLKDVTAKER
12001	ENAVFTVELS	HDNIPVSWFK	NDQRLHSTKR	VSMHDEGKTH	SITPKDLSID	DTSQIRVEAM	GISSEAKLVT	LEGDPYFTGK
12081	LQDYTGVEKD	EVPVQCEISK	ADAPVVKFKD	GKEIKPKSKNA	VIKADGKKRM	LILKALKKSD	IGQYTCDCGT	DTSGSKLDIE
12161	DREIKLVRPL	YSVEVME TET	ARFETEISED	DIHANWKLKG	EALLQTPECE	IKEEGKHLVL	ILHNCLDQT	GGVDFQAANV
12241	KSSAHLVRPK	RVIGLLRPLK	DVTVTAGETA	TDFCELSYED	IPVWEYLKKG	KLEPNDKVVT	RSEGRVHTLT	LRVDKLEPAG
12321	EVQLTAKDFK	TQANLFLVKA	HVEFLRPLTD	LQVKEKETAR	FECEISKENV	KVQWFKDGAE	IKKGGKYDII	SKGAVRILVI
12401	NKCLLNDEAE	YSCEVRTART	SGMLTVLEEE	AVFTKNLANL	EVSEGDTIKL	VCEVSKPGAE	VTWYKGDVEV	IETGRFEILT
12481	DGRKRILIIQ	NAQLEDAGSY	NCRLPSSRTD	GKVKVHELAA	FITISKPNLE	ILEGEKAEFV	CTISKESEFV	QWRKDDQTL
12561	SGDKYDI IAD	GKKRVLVVKD	ATLQDMGT YV	VMVGAARAAA	HLTVIEKLR I	VVPLKDTKVK	EQQEA VFNCE	VNTEGAKAKW
12641	FRNDEAIFDS	SKYIILQKDL	VYTLRIRDAR	LDDQANFSVS	LTNHRGENVK	SAANLIVEEE	DLRIIEPLKD	IETMEKKSVT
12721	FWCKVNRILNV	TLKWTKN GEE	VAFDNRISYR	IDKYKHS LII	KDCGFPDEGE	YIVTAGQDKS	VAELLLIEAP	TEFVEHLEDQ
12801	TVTEFDDAVF	SCQLSREKAN	VKWYRNGREI	KEGKKYKFEK	DGSIHRLIK	DCRLEDECEY	ACGVEDRKS	ARL FVEEIPV
12881	EIIRPPQDIL	EAPGADVIFL	AELNKDKVEV	QWLRNMIIV	QGDKKHMMSE	GKIHRQLICD	IKPRDQGEYR	FIARDKEARA
12961	KLELAAPPKI	KTSQDQLVVD	AGQPLTMVVP	YDAYPKAEAE	WFKENEPLST	KTVDTTAEQT	SFRILEAKKE	DKGRYKIVLQ
13041	NKHGKAEGFI	NLQVIDVPGP	VRNLEV TETF	DGEVSLAWEE	PLTDGGSKII	GYVVERRDIK	RKTWVLTDR	ADSCGEFTVTG
13121	LQKGGVEXLF	RVSARRN VGT	GEPPVETDSPV	EAPSKYDVPG	PPLNVTITDV	NRFVGSILTWE	PPPYDGGAAE	TNYVIELRDK
13201	TSIRWDTAMT	VRAEDLSATV	TDVVEGQEYS	FRVRAQNRIG	VGKPSAATPF	VKVADPIREY	SPPVNL SASE	QTOSSVQLTW
13281	EPLLKDDGSP	ILGYI IERQE	EGKDNWIRCN	MKPVPPELTK	VTGLQKGNKY	LYRVAENAA	GVSDPSEILG	PLTADDAVSE
13361	PTMDLSAFKD	GLEVI VPPNI	KILVPSPTGYP	RPAATWTFGD	QVLEAGDRVK	IKTISAYAEI	IISPSERPDK	GIEYTLTLENP
13441	VKSI SGEIDV	NVIARPSAPK	ELKFSVDTKD	SVHLTWEFPD	DDGGSPLTGY	VVEKRDMSRK	TWTKVMDFVT	DLEFTVPDLV
13521	QKGEYLFKVC	ARNKCGPGEF	AYTDEPVNMS	APATVPPDPE	NVKWRDR TAN	SIFLWTDWPP	NDGGSRIKGY	IVEKCPGSD
13601	KWVACGEPV	DTKMEV TGLE	EGKWYAYRVK	ALNRQASGSK	SKPTEIEIQAV	DTQEAPEIFL	DVKLLAGLTV	KAGTKIELPA
13681	TVTGGPEPKI	TWTKADTLR	PDQRI TIENV	PKKSTVITTD	SKRSDTGT YI	IEAVNVCGRA	TAVVEVNVLD	KPGPPA AFDI
13761	TDVTNESCLL	TWNP RRDDGG	SKITNVYVVR	KATSDVVVHK	LSSTVKDTNF	KATKLT P NKE	YIFRVAENM	YGVGEPVQAT
13841	PIIAKYQFDP	PNPPTRLRPS	DITKDAVTLT	WCEPDDDDGS	PITGYWVERL	DPDPTDKWVR	NKMPVKD TTY	RVGLTNKTKK
13921	YRFRVLAENL	AGPGKPSRST	EPILIKDPI D	PPWPPGKPTV	KDIGKTSVLV	NWTKPEHDGG	AKIESVYIEM	LKTGTDDNVR
14001	VAEGVPTTEH	LLTGMEGQGE	YSFRVRAV NK	AGESEPSEPS	DPVLCREKLY	PPSPRRWLEV	INITKNATDL	KWTVPEKEDG

NHLBI Zile/Grant, Aged Rat

14081	SPITNYIVEK	RDVRRKGGQT	VDTTVKDTKC	TVTPLTEGSL	YVFRVAEANA	IGQSDYTEIG	DSVLAKDTFT	TPGGPYALT
14161	VDVTKRHVDL	KWEPKNDGG	RPIQRYIEK	KEKLGTRWVK	AGKTSQPCDN	FRVTDVIEGT	EVQFQVRAEN	EAGVGHSPSEP
14241	TEILSIEDPV	GPPSPPLDLH	VTDAGRKHIA	IANKPPEKNG	GSPIIGYHVE	MCPVGTAKWM	RVNSRPIKDL	KFKVEEGVDP
14321	DKEYVLRVRA	VNAVGVSDPS	EISENVVAKD	PDCKPTIDLE	THDIVVIEGE	KLSIPVPFRA	VPVPTVSHHK	DGKEVKASDR
14401	LTMKNDHISA	HLEVPKSVHA	DAGVYITILE	NKLGSAFASI	NVKKVIGLPGP	CKDIKASDIT	KSSCKLTWEP	BEFDDGSSPIL
14481	HYVLEERREAG	RRTYIPVMSG	ENKLSWTVKD	LIPNGEYFFR	VKAVNKIGGG	EYIELKNPVI	AQDPKQPPDP	PVDVEVHNPT
14561	AKAMTITWKP	PLYDGGSKIM	GYIEKLAAG	EDRWKRCNEH	LVPVLTYTAK	GLEEGKEYQF	RVRAENAAGI	GEPSTRATPPT
14641	KAVDPIDAPK	VILRTSLEVK	RGDEIALDAT	ISGSPYPTIT	WIKDENVIYP	EIKKKRVAPP	VRRKKGEAEE	EEPTLPLTE
14721	RLSINNSKQ	ESQLRVRDSL	RPDHGQYMIK	VENDHGVAKA	PCTVSVLDTF	GPPINVFVFD	IRKDSVLCKW	EPPLDDGGSE
14801	IINYTLEKVD	KTKPDPSEWIV	ITSTLRNCKY	SVTKLIEGKE	YLFVRVAENR	FGGPPPCVSK	PLLAQDFEAP	PDAPDKPIVD
14881	DVTSNSMVVX	WNEPKDNGSP	ILGYWLEKRE	VNSTHWSVRN	KALLSSLKTK	VDGLLEGLTY	VFRVCAENAA	PGDPFSPSD
14961	PKTARDPISP	PGPPVPRVAD	TSSTTTLELEW	EPPAFNGGGE	IMGYFVDKQL	VGTNEWSRCT	EKMVKVRQFT	VKEIREGADY
15041	KLRVSAVNA	GEGPPGETEP	VTVAEPQEPF	TVELDVSVKG	GIQIMAGKTL	RIPAVVTGRP	VPKVVWVIEE	GELDKERVVI
15121	ENVTGKSEL	LIPNQYEFYR	RYVITATNSC	DECKSDRVVI	GSKFAAARVE	IGDYPVGPVLD	LKPVVTRKRM	CLLNWSDPAD
15201	IERKDKAMHT	VRQIETERS	KCDITGLIEG	QYKFRVIAK	NKFGCGPPVE	IGPILAVDPL	GPPSPERLPT	YTERTKSTIT
15281	LDWKEPRSDG	GSPIQGYIIE	KRRHDKPDEF	RVNKRLCPTT	SFLVDNLDEH	QMYEFRVKAV	NDIGESEPSL	PLNVVIQDDE
15361	VPPTIKLRLA	VRGDTIKVKA	GEPVNIADV	TGLPMPKIEW	SKNEKVIEKP	TDALNITKEE	VSRSEAKTEL	SIPKAVREDK
15441	GTXTITASN	LGSVFRNVHV	EYVDRPSPR	NLAVTDIAKE	SCYLTWDAPL	DNGGSEITHY	IDDKRDRASK	KSEWEVNTG
15521	AVERRYGWIK	LIPNGQYEFYR	VRVAVNYGTS	DECKSDRVVI	QDPYRLPGFP	GKPKVLERCT	GSMNVSDTTP	LDNGGSPITG
15601	YWLEKREEGG	AYWSRVSRAP	ITKVGKLGVE	FVSPRLIEGV	KYQFRAMAIN	AAGIGPPSEP	SDPAVAGDPI	YPPGPPSCPE
15681	VKDKTKSSIS	LAWKPPAKDG	GSPIKGYIIE	MQEERTDQWK	KVNEPDKLLT	ACCECVPNLK	ELRKYRFRVK	AVNAGESESE
15761	SDTTGEIPAT	DIQEVPEVFI	DIGAQCCLIC	KAGSQIRIPA	VIKGRPTPKS	SWEFDGKAKK	AMKDGHIHDP	EDAQLETAEN
15841	SSVIVIEPCT	RHSGKGSYIT	AKNKAGQKTA	NCRVKVMDAP	GPPKDLKVS	ITRSGCRLSW	KMPDDDDGDR	IKGYVIEKKT
15921	IDEGKAWTKV	PNCSSTAFV	PDLISEQQYF	FRVRAENRFG	IGPPAETIQR	TTARDPIYPP	DLPIKLLIGL	ITKNTVHLSW
16001	KPKKNDGGSP	VTHYIVECLA	WDPTGKKKEA	WRQCNRRDVE	ELEFTVEDLV	EGGEYEFVRK	AVNEAGVSKP	SATVGPVTVG
16081	DQTCPPSLEI	KHFMEVEEET	DVNIVAKIKK	VFPPTLWVFK	APPKPKDSKE	PVVYDTHVNK	QVDDDTCTLV	IQPSRRSDTG
16161	LCSYITAVNLL	GATSKEMRLN	VLGRPGPPVG	PIKFEESAD	QMLTSLWLPK	DDGGSKITNY	VIEKREANRK	TWVRVSSSEK
16241	EYMTTIPKRL	EGHEVYFRIM	AQNKYGTGEP	LDSEEPFARN	LFTVSGPADK	PTVSSVTRNS	MTVNWEEPEY	DGGSVTSYVW
16321	LEMKDTTSKR	WKRVRNDPIK	AMTLGVSIVK	TGLIEGSDYQ	FRVYAINAAG	VGPASLPSDP	VTARDPVAPP	GGPPFKVTDW
16401	TKSSVDLEVS	PPLQDGGSKI	TGYIVYKKE	GKEEWEKGD	KEVRGTKLVV	TGLKEGAFYK	FRVRAVNIAG	VGEPGEVTDI
16481	IEMKDRIVVSP	DLQLDASVRD	RIVVHAGGVI	RIIAYVSGKP	PPTVHTLVNK	RALPQEAETI	TTAISSSMVI	KNCQKSHQV
16561	YSLAKNEGG	ERKKTIVD	LDVPGVGP	FLSDNLTNDS	CKLTFWSPED	DGGSPITNYV	IQKREADRRR	WTPVYTVTR
16641	QMATVQGLIQ	GKSYFFRIA	ENSIMGPFV	EFTNALVIRD	PITVPERPED	LEVKEVTKNT	VTLTWNPKY	DGGSSEIINYV
16721	LESRLIGTEK	FHKVTNDNLL	SRKYTVKGLK	EGDTYEVRS	AVNIVGQGKP	SFCTKPICTK	DELAPPTLDL	DFRDKLTVRV
16801	GEAFALTGRY	SGKPKPKVDW	FKDEADVLED	DRTHIKTPTT	TLALEKTKAK	RSDSGRYCVV	VENSTGSRKG	FCQVNVDRP
16881	GPVPGPVVFD	EVTKLEYMVIS	WKPLDDGGS	EITNYIIEKK	ELGKDIWMPV	TSASAKTTK	VPKLEGGYK	IFRHNANVLD
16961	GISDPLVSDS	MKARDRFRVP	DAPEQPVVTE	VTKDSALVTW	NKPNDDGGKPI	TNYILEKRET	MSKRWRVGTG	EPIHPIYTYR
17041	VPDLLEGQCY	EFKRSVAENEI	GIGDPSPPSK	PVFARDIAK	PSPINPEAI	DTTCSVDLPT	WQPPRHVGS	KILGYIVTYR
17121	KVGDDEWRRR	NHTPESCPET	KYKVTGLRDL	QTYKFRVLAV	NEAGESDPAH	VPEPVLVKDR	LEPPELILDA	NMAREQHIKV
17201	GDTLRLSAII	KGVPPFKVTV	KKEDREAPT	AQIDVTPVGS	KLEIRNAAHE	DGGIYSLTVE	NPAGSKTVSV	KVLVLDKQGP
17281	PRDLEVSER	KDSCYLTWRE	PLDDGGSVVT	NIYVVERKDV	TAQVSPSLTT	SKKSHMAKH	LNENQYLFR	VAAENQYGRG
17361	PFVETPKPIK	ALNDLHPPGF	PKDLHHVDDV	KTEVSLVWNK	PPDRDGGSPIT	GYLVEYQEEG	AKDWIKFPTV	KNLCECVTGL
17441	QQGKTYFRV	KADENIIGLGL	PDDTPIECQ	ELKEPPSVEL	DKLIEGLLVV	KAGTTRVFRVA	IIRGVVPVFTA	KWADGTBITV
17521	TDDHYTVETD	SFSSVLTIKN	CLRKDTGEYQ	LTVSNAAGTK	TVAVHLTVLD	VPGPPTGPI	ILDVTPPEYMT	ISWQPKDDG
17601	GSPVINIYVE	KQDTRKGTWG	VVSAGSSKLR	LKVPHLQKGC	EYVFRVKAEN	KMGVGPPLDS	IPTVAKHKFS	PPSPGKPVV
17681	TDITENAAVT	SWTLPKSDGG	SPITGYVVER	REITGKWVRV	NKTPADLKF	RVTGLYEGNT	YEFRVFAENL	AGLSNPPSSS
17761	DPKACAPRIK	PPGPIINPKL	KDKTKESADL	VWTKPLSDGG	SPILGYVVEC	QKPGTQWDR	INKDELIRQC	AFRVPLGLEE
17841	NEVRFRRARA	NIVGEGEPRE	LAESVIAKDI	LHPPEVELDV	TCRDVITVRV	GQTIRILARV	KGRPEPDIW	SKEGKVLKVD
17921	KRVDLIHDL	RVELQIKEAV	RADHGKYIIS	AKNSSGHAQG	SAIVNVLDRL	GPCQNLKVS	VTKENCITSW	ENPDLNNGSE
18001	ITNFIVEYRK	PNQKGSIVA	SDVTKRLIKA	NMLANNNEYF	RVCAENKGVV	GPTIETKPTI	LAINPIDRPF	ENPDLNADK
18081	GKTFVYLKWR	RPDYDGGSPN	LSYHVERRLK	GSADWERVHK	GSIKETHYMV	DKCVENQIYE	FRVQTKNEGG	ESDWVRTEEV
18161	VVKEDLQKPV	LDLKLISGLT	VKAGDTIRLE	AGVRGKPFPE	VAMTKDKDAT	DLTRSPRVKI	DTSAESSKFS	LTKAKRSDGG
18241	KYVVTATNPA	GSFVAYATVN	VLDKPGPVRN	LKIADVSSDR	CTIRWDPPED	DGGCEIQNYI	LEKCESKRMV	WSTYSANVLT
18321	PGATVTRLIE	GNEYIFRVR	ENKIGTGPP	ESKPVIAKTK	YDRPGRPDP	EVTKVSKEEM	TVVWNAPEYD	GKGSITGYL
18401	EKKEKHAVRV	VPVNKSALPE	RRLKVQNLPL	GHEYQFRVKA	ENEVGIGEPS	LPSRPVVAKD	PIEPPGPPPT	FKVVDTTKNS
18481	ITLAWGKPVY	DGGAPPIGYV	VEMRPKIADA	SPDEGWKRCN	AAAQLVRMEF	TVTSLDENQE	YEFRVCAQNO	VGIGRPAELK
18561	EAIRPKLELE	PPEIDLDAEM	RKLVVVRAGC	PIRLFAIVRG	RPAPKVTWRK	VGIDNVVRKG	QVDLVDYMAF	LVIENSTRDD
18641	SGKYSLTLVN	PAGEKAVFVN	VKVLDTPGPV	SDLKVSVDTK	TSCHVSWAPP	ENDGGSPVTH	YIVEKREAR	KTWSTVTPVE
18721	KKTSFNVNLT	VPNGEYFFRV	TAVNEYGGPV	PTDVPKPVLA	SDPLSEPPDP	RKVEVTEMTK	NSATLAWLPP	LRDGGAKIDG
18801	YIISYREEDQ	PADRWTYSV	VKDLSLITG	LKEGKKYKFR	VAARNAVGVS	MPREAEGVYE	AKEQALLPPIK	LMPEQITIKA
18881	GKCLRVEAHV	YGKPNPICKW	KKGEDDVVTS	SHLAHKADS	SSVLIKIDVT	RKDSGYYSLT	AENSSGTDQ	KIKVTVMADP
18961	GPPQPPFDIS	EIDADACSL	WHIPLDGG	NITNYIIVEK	DVSRGDWVTA	LASVTKTSCR	VGKLIPGQY	IFRVAENRFR
19041	GISEPLTSPK	MLAKFPFDDV	SEPKNARVTK	VNKDCIPVAV	DRPDSDDGSP	ITGYLIERKE	RNSLLWVKAN	DTIVRSTEYP
19121	CAGLVEGLE	SFRYIALNKA	GSSPPSKPTE	YVTRAMPVDP	PGKPEVVDVT	KNSASLIWAR	PKHDGSSKII	GYFVEACKLP
19201	GDKWRVRCNT	PHQIPLEEY	ATGLENAQY	QFRAIAKTAV	NISQSEPSD	PVTILAENVP	PRIELSVEMK	SLLTVKAGTN
19281	VCLDATVFGK	EMPTVSWKED	STPIKQTEGV	KMAKRNLC	LELFSVNRKD	SGDYTTAEN	SSGSKSATIK	LKVLKDKGPP
19361	ASVKINKMYA	DRAMLSWEP	LEDGGSEITV	IYVDKRETSR	PNWAQVSAIV	PITSCITVEKL	IEGHVYQFRI	CAENKYGVGD
19441	PIFTEPVIAK	NPYDPPGRCD	PPVISNITKD	HMTVSWKAPA	DDGGSPITGY	LVEKRETQAV	NWTKVNRKPV	IERTLKAATGL
19521	QEGTEYEFRV	TAINKAGPGK	PSDASKAVYA	QDPLYPGPP	AFPKVYDTTR	SSVLSWVGK	AFDGGSPIG	YLVEVTKRADS
19601	DHWRCNLPE	KLQKTRFEV	GLMENTEYQF	RVYAVNKIGY	SDPSDVPDKH	CPKDLILIPPE	GELDAELRKL	LILRAGVTRM
19681	LYVVPKGRPP	PKITWSPKPV	NLRERIGLDI	KSTDFDFTLR	CENVNKYDAG	KYILTLENSC	GKKEYTIVVK	VLDTPGPPVN
19761	VTYKESKDS	AYITWDDPII	DGGSPINNY	VERKDAERKS	WSTVTECPK	KYFRVSNLE	GKSYFFRVFA	ENEXYGDGPG
19841	ETRDAVAKSE	TPGPVVDLKV	LAVTKSSCTI	GWKKPRSDGG	SRITGYVVDV	LTEENKQWRV	MKSLSLQYST	KDLREGKYEY
19921	FRVSAENENG	EGTPSEIMV	AKDDVVAPDL	DLKDLPLDLY	LAKENSFNRL	KIPIKQKPP	SVSWKKGEDP	LATDTRVSV
20001	STAVNTLVV	YDCQKSDAGK	YITLKNVAG	TKEGTLSIKV	VKPGIPTGP	IKFDEVTAEA	MTLKWGPPKD	DGGSSEIINYV
20081	LEKRSVNNK	WVTCASAVQK	TFRVTRLHE	GIEYTFRVSA	ENKYGVGEG	KSEPIVAKHP	FVDPDAPPPP	NIVDVRHDSV
20161	SLTWTDPKKT	GGSPITGYHI	EFKERNLLW	KRANKTPIRM	KDFKVTGLTE	GLEYEFRVMA	INLAGVGKPS	LPSEPVVVALD

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20241	PIDPPGKPEV	ISVTRNSVTL	IWTEPKYDGG	HKLTGYIVEK	RDLPSKSWMK	ANHVNVPDCA	FTVTDLVEGG	KYEFRIRAKN
20321	TAGAISAPSE	STGTIICKDE	YEAPTIVLDP	TIKDGLTVKA	GDSIVLSAIS	ILGKPLPKSS	WSKAGKDIRP	SDIAQITSTP
20401	TSSMLTVMYA	TRKDAAGEYTI	TATNPFPGTKE	EHVKVSVLDV	PGPPGPIEIS	NVSAEKATLT	WTPPLEDGGG	PIKAYVLEKR
20481	ETSRLLTWTV	SEDIQACRHW	VTKLIQGNEY	LFRVSAVNHY	GKGEVQVSEP	VKMVDRFGPP	GPPGKPEISN	VTKNTATVSW
20561	KRPIDDDGSE	ITGYHVERRE	KKGLRNVRRAT	KTPVSDLRCK	VTGLQEGNTY	EFRVSAENRA	GIGPPSDASN	PVLMKMDVAYP
20641	PGPPSNAHVT	DTTKKSASLA	WGKPHYDGG	EITGYVVEHQ	KVGDDAWIKD	TTGTALRITQ	FVVPDLQTK	KYNFRISAVN
20721	DAGVGEPAVI	PNVEIVEKET	APDFELDAEL	RRTLUVVRAGL	SIRIFVPIKG	RPAPEVTWTK	DNINLKHRAN	IENTESFTLL
20801	IIPECNRYDT	GKFVMTIENP	AGKKSGFVNV	RVLDTPGPVL	NLRPTDITKD	SVTLHWDLPL	IDGGSRTITNY	IVEKREARTRK
20881	SYSTVTTKCH	KCTYKVTGLT	EGCEYFFRVM	AENEYIGIGEP	TETTEPVRAS	EAPLPPDSL	IMDITKNTVS	LAWPKPRHDG
20961	GSKITGVYIE	AQRKGSQDWT	HISTVKGLEK	VVRLNTEGEE	YTFQVMAVNS	AGRSAPRESR	PVIVKEQTKM	PELDLGRDIYQ
21041	KLVIARAGDN	IKQVEIPDLGR	PKPTVTWKKG	DQILKQTVR	NVENTATSTI	LNINECVRS	SGAYPLTAKN	TVGEVGDVNT
21121	IQVHDIPGPP	TGPIKFDEVS	SDFVTFSWEP	PENDGGVPI	NYVVEMRQTD	STTWELATT	VIRTTYKATR	LTTGVEYQFR
21201	VKAQNRVGVG	PGITSASVVA	NYPFKVPGPP	GTPQVATVTK	DSMTISWHEP	LSDDGGSPILG	YHIERKERNG	ILWQTVSKAL
21281	VPGNVSGLTEG	LTDGDAYEFR	VIAENMAGKS	KPSKPSSEPT	ALDPIDPPGK	PVPLNITRHT	VALKWAKPEY	TGGFITGMYV
21361	VEKRDLPNGR	WLKANFSNLI	ENEFTVSGLT	EDAAEYFRVI	AKNAAGAI	PSEPSDAITC	RDDLEAPRIM	PPGTFVFLA
21441	LKAGEAFKLE	ADVSGRPPPT	MEWAKDGLK	EGTGKLEIKI	ADFSTHLINK	DSSRTDSAGY	ILLATNPPGGF	KHHFNVKVL
21521	DRPGPPEGFL	AVSDVTSEK	VLSWLPPLDD	GGAKIDHYIV	QKRETSRLAW	TNVATEVQVT	KLKVTLLKKG	NEYIFRVMVA
21601	NKXGVGPELE	SEPVLAVDY	GPPDPKPNPE	VTTITKDSMV	VCGHPPSDG	GSEIINYIVE	RDKKAGQRW	KCNKALDLD
21681	RFKVSGLTEG	HEPFRIMAE	NAAGVSAPSA	TSPFYKACDS	VFKPGPPGNP	RVLDTSRSSI	SIWANNKIYD	GGSEITGMYV
21761	EIALPEEDED	QVVTPPAGLK	ATSYTTNLI	ENQEKIRIY	AMNSEGLGEP	ALVPGTPKAE	ERMLPPEIEL	DADLRKVVTI
21841	RACCTLRFLV	PIKGRPAPEV	KWAREHGESL	DKASIESTSS	YTLTLVGVN	RFDGSKYILT	VENSSGSKSA	FVNVRVLPDT
21921	GPPQNLKIKE	VTKTSVTLTW	EPPLLDGGSK	IKNYIVEKRE	STRKAYSTVA	TNCHKTSWKI	DQLQEGCSY	FRVLAENEY
22001	IGLPAETAES	VKASERPLPP	GKITLMDVTR	NSVLSWEKP	EHDGGSRLG	YIVEMQSKGS	DKWATCATVK	VTEATITGLI
22081	QGEYSFRVS	AQNEKGISDP	RQLSVPIAK	DLVIPPFAFKL	LFNFTVLAG	EDLKDVPFI	GRPTPTVWGH	KDDVPLKQAT
22161	RVNAESTENN	SLLTKEACR	EDVGHYTVKL	TNSAGEATET	LNVIPLDKPG	PPTGPKMDE	VADSVTLWS	EPKPYDGGSS
22241	INNYIVEKRD	TSTTAQIVS	ATVARTYTKA	SRLKTCGEY	FRIAAENRYG	KSTYLNSEPV	IAQYFPKVP	PPGTFVFLA
22321	SKDSMEVQWH	EPVSDGGSRV	IGYHLERKER	NSLWVXKLNK	TPIPQTKFT	TGLEEGIEYE	FRVSAENIVG	IGKPSKPE
22401	YAAHDCDPP	GRPEAIIVTR	NSVTLQWKKP	TYDGGSKITG	VYVEKKEP	GRWMKASFTN	IIDTQFEVTV	LIEDHRYEVE
22481	VIARNAAGVF	SEPSESTGAI	TARDEVEPPR	ISMDPKYKDT	VVVQAGESFK	IDADIYKPI	PTTQVKGQD	ELSTARLEI
22561	KTDFATSLR	VWTLVRDVS	NYILKAKNA	GEKSVTVNVK	VLDPRGPEEG	PVAISGVTA	KCMLWAKPPL	QDGGSDITNY
22641	IVERRETSRL	VWTLVVDANV	TLSCVKTKLL	EGNEIYFRIM	AVNKYGVGEP	LESEPLIAKN	PVVVDPADPA	PEVSAITDYS
22721	MIVVWERPAS	DGGSEILGYV	LEKRDKEGIR	WTRCHKRLIG	ELRLRVTGLL	ENHNYEFRVS	AENAAGLSEP	SPPSAYQKAC
22801	DPYIKPGPPN	NPKVMDVTRS	SVFLSWTKPI	YDGGCEIQGY	IVFKCDVSVG	EWTMCTPPTG	INKNTLVEK	LLEKNSVPL
22881	ICAINKAGVG	EHADVPGPVM	VEEKLEAPDI	DLLELRKVI	NIRAGGSLRL	FVPIKGRPTP	EVKWKGVGDE	IRDAAIIDVT
22961	SSFTSLVDN	VNRYDCKGKY	LTLENSSGT	SAPVTVRVL	TPSPVNLKV	TEITKDSVSI	TWEPPLLDGG	SKIKNYIVEK
23041	REATRKYAA	VNNTCHKNSW	KIDQLGEGCS	YFRVYTAENE	YFGLPARTA	DFIKVAEVPQ	PPGKITVDDV	TRNSVSLWST
23121	KPEHDGGSKI	IQYIVEMQAK	NWTKWSECAR	WKSLEAVITS	LTQGEELFR	VIADVNEKGRS	DPRLAVPIT	AKDLVIEPVD
23201	RPAFASVSVQ	VQDILKIEVP	ISGRPKPSIS	WTKDGAPLK	TRINVIDSL	DLTTLISIKET	HNFDEVSAS	ITLWSVPLPY
23281	TGGCQITNYI	VQKRDTTTTV	WDVVSATVAR	TLKVTTLKLT	GTEYQFRIFA	ENRYGQSAL	ESEPIVAQYP	YKPEGPPGTP
23361	FVTAVSKDSM	VVQWHEPINN	GGSPVIGYHL	ERKERNISIL	TKVNKTIIDH	TQFKALNLEE	GIEYEFVRYA	ENIVGVGKAS
23441	KNSECVYARD	PPPTNGPTPE	IIVKRNEITL	QWTKPVYDGG	SMITGYIVEK	RDLPEGRWMK	ASFTNVEBTO	TVTSGLTEDQ
23521	RYEFRVIAKN	AAGATSKPSD	STGGITAKDE	VELPRIEMDP	KFRDITVUNA	GETFRLPADV	HGKPLPTIEW	LRGDKIEIES
23601	ARCEIKNTDF	KALLIVKDAI	RIDGGQYILR	ASNVAGSKFS	PVNVKVLDRP	GPPEGVPQVT	GVTECKTCLA	WSPFLDGGGS
23681	DISHYVVEKR	ETSRLAWTVV	ASEVVTNSLK	VTKLLENGEY	IFRIMAVNKY	GVGEPLESAP	VLKMNPFVLP	GPPKSLEVTN
23761	IAKDSMTVCW	NRPDSDDGSE	IIGYIVEKRD	RSGIRWIKCN	KRRITDLRLR	VTGLTEDHEY	EFRVSAENAA	GVGEPSPATV
23841	YYKACDPVFK	PGPPNTHVIV	DTTKNSITLA	WGKPIYDGG	DLIGYVVEIC	KADEEEWQIV	TPQTGLRVTR	FEISKLEIHQ
23921	EYKIRVICALN	KVGLGEAASV	PGTVKPEDKL	EAPLELDLSE	LRKGIIVVRAG	GSARHIPPK	GRPTPETIWS	KEEGEFTDKV
24001	QIEKGINFTP	LSINDCRND	AGKYILKLEN	SSGSKSAFVT	VKVLDTPPGP	QNLAVKEVRK	DSVLLWNEP	IDGGAKVKN
24081	YVYDKRESTR	KAYANVSSKC	SKTSFKVENL	TEGAIYFRV	MAENEFVGV	PAETSDAVKA	SEPPSPPKG	TLTDVVSQSA
24161	SLMWEKPEHD	GGSRILGYVV	EMQPKGTEKW	SVVAESKVCV	AVVSLSSGQ	EYQFRVKAYN	EKGKSDPRVL	GVPYIAKDLT
24241	IQPSFKLPFN	TYSVQAGEDL	KIEIPVIGRP	RPKISWVKDG	EPLRQTRRVN	VEETATSTIL	HIKESSKDDF	GKYSVTATNN
24321	AGTATENLSV	IVLEKPGPPP	GPVKFDEVSA	DFVVISWEP	AYTGGCQISN	YIVEKRDTTT	TNWQMSVATP	ARTTIKVSKL
24401	KTGTEYQFRI	FAENRYGKST	PLDSKPVVVQ	YFKEKPGPPG	TPFVTSVSKD	QMLVQWHEPV	NDGGSKVIGY	HLEQKKNISI
24481	LWVKLNKIP	QDTKFKTTGL	DEGLEYEFRV	SAENIVGIGK	PSKVSECVVA	RDPDPPGGRP	EAIITIRNSV	TLKWKKPYD
24561	GGSKITGYIV	EKKDLDPDGR	MKASFTNVVE	TEFTVTGLVE	DQRYEFRVIA	RNAADNFSEP	SESSGAI	DEIDAPNASL
24641	DPKYRVDIV	RAGETFFVLEA	DIRGKPIPI	VWSKDGNELE	ETAARMEIKS	TLQKTLTVK	DCIRTDGGQY	TLKLSNVGGT
24721	KTIPITVKVL	DRPGPPEGFL	KVTGVTAEKC	YLAWNPLQD	GGASISHYII	EKRETSRLSW	TQVSTEVQAL	NYKVTKLLPG
24801	NEYIFRVMVA	NGYGVGEPLE	SEPVIACNPI	KLPGPPSTPE	ASAITKDSMV	LTWTRPVDDG	GAEIEGYILE	KRDKEGIRWT
24881	KCNKKTLDL	RFRVTGLTEG	HSYEFVAAE	NAAGVGEFSE	PSVYRACDA	LYPPGPPSNP	KVTDTSRSSV	SLAWNKP
24961	GGAPVRYGVI	ELKEAAADEW	TCTPPSGLQ	GKQFTVTKLK	ENTEYNFRIC	AFNTEGVGEP	ATIPGVSVAQ	ERMAEPIEL
25041	DADLRKVVTL	RASATLRLFV	TIKGRPEPEV	KWEKAEGLLT	ERAQIEVTS	YTMLVIDNVT	RFDSGRYNLT	LENNSGSKTA
25121	FVNVRVLDSP	SAPVNLTVRE	VKKDSVTLSS	EPPLIDGGAK	VTVNIVEKRE	TRKAYATIT	NNCTKTTFKI	ENLQEGCSY
25201	FRVLASNEYG	IGLPAETTEP	VKVSEPLPFP	GRVTLVDVTR	NTATIKWEKP	ESDGGSKITG	YVEMQTKG	EKWSCTQVK
25281	TLEATISGLT	AGEEYVFRVA	AVNEKGRSDP	RQLGVPVAVK	DIEIKPSVEL	PFNTFNVKAN	DQLKIDIPFK	GRQATVAWK
25361	KDQQLRETT	RNVNSSKIV	TLSIKEASR	EDVGTIELCV	SNTAGSITVP	ITVIVLDRP	PPGPIRIDEV	SCDNVSIWST
25441	PPEYDGGCQI	SNYIVEKRET	TSTTQVQVSI	AVARTSIKIV	RLLTGSEYQF	RVCAENRYGK	SSYSESAVV	AEYFSPGPP
25521	PGTPKVVHAT	KSTMVVSQV	PVNDGGSQVI	GYHLEYKERS	SILWSKANVK	LADTQMKVS	GLDEGLIY	RYEYENIATG
25601	GKCSKACEPV	PARDPDPG	QPEVNTITRK	SVSLKWSKPR	YDGGAKITGY	IVERRELPDG	RWLKCNFTNV	QYTYFEVTEL
25681	TEDQRYAKTR	FARNAAVS	EPSESTGPTI	VKDDVEAPRI	MMDVKFRDVI	VVKAGEVLKI	NADIAGRPLP	VISWAKDQVE
25761	IEERAKTEIV	SDSNTTLTV	KDCVRRDTGQ	YVLTLLKNV	TRTMVNCVK	LDKPGPPAGP	LEINLTAEK	CSSLWGRGPE
25841	DGADIDYI	VEKRETSRLA	WTICEAELRT	TSCKVTLLK	GNEYIFRVTV	VNKYGVGEP	ESVAVKALD	FTTSPPTSL
25921	EITSVTKDSM	TLCWRSRPE	GGSDISGYII	ERREKNSLRW	MVNVNKKPYD	LRVKSTGLRE	GCEYEVVFA	ENAGLSLPS
26001	DTSPLVRAED	PVFLPSPPSK	PKIVDSGKTE	ITIGWVXPLF	DGGAPITGYT	VEYKKSSEET	WKVAIQSFRG	TEYMTSGLTT
26081	GAEYVFRVRS	LNVKGASDPS	DITDPQVAK	REEEPADFVD	SEMRKTLTVK	AGSSFTMTVP	FRGRPIPNVS	WSPDMDLRT
26161	RAYIDSRTSR	TSLTENANR	NDSGRTLLTI	QNVLSAASMT	FVVKVLDSFG	PPANITVREV	TKETAVLSDW	VPENDGGAPV
26241	KNYHIEKREA	SKGAWVSVTN	NCSRLSYKVT	NLQEGAVYF	RVSGENEFGV	GVPATKEGV	KITEKPSPE	KLGVTSVSKD
26321	SVLSLWLPKE	HGGSRILHY	VVEALEKQK	NWVKCAVYKT	THVVSGLRE	GHEYFRVFA	ENQAGLSDPR	ELLPLVLIKD

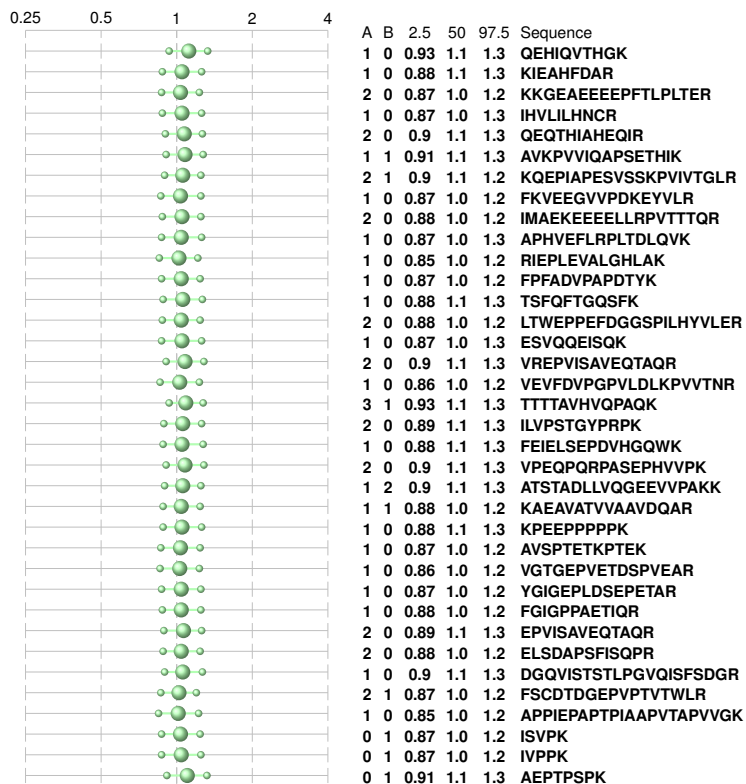
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26401	HLEPPEIDMK	NFPSHTVYVR	AGSNLKVDP	ISGKPLPKVT	LSRDGVPLKA	TMRFNTEITA	ENLTINLKES	VTADAGKYEI
26481	TAANSSGTTK	TFINIIVLDR	PGPPTGPVAI	SDITEESVTL	KWEPFKYDGG	SHVTNYIVLK	RETSTAVWTE	VSATVARTMI
26561	KVMKLTGTEE	YQFRIKAENR	FGISDHIDSA	CVVVKLPYTT	PGPPSTPWVS	NVTRESITVG	WHEPVSNGGS	AVIGYHLEMK
26641	DRNSILWQKA	NKMIIRTTTH	KVTTISAGLI	YEFRVYAENA	AGIGKPSHSS	EPVLAIDACE	PPRNVRTDI	SKNSVNLWQ
26721	QPAPDGGSKI	TGYIVERRDL	PDGRWTKASF	TNVIETQFTV	SGLTQNSQYE	FRVVFARNAVG	SVSNPSEVVG	PITCIDSYGG
26801	PVIDLPLEYT	EVVKYRAGTS	VKLRAGISGK	PEPTIEWYKD	DKELQTNALV	CVENSTDLAS	ILIKDANRLN	SGSYELKLRN
26881	AMGSASATIR	VQILDKPGFP	GGPIEFKTVT	AERITLLWRP	PADDGGAKIT	HYIVEKRETS	RVVWSMVAEN	LEECIITTTK
26961	IIRGNEYIFR	VRAVNKYIGI	EPLESEPVVA	KNSFVTPGPP	SIPEVTKITK	NSMTVVWNRP	TVDDGSEING	YFLEKRDKKS
27041	LAWLKVLDKT	IRDTRQKVTG	LTENS DYQYR	VCAVNAAGMG	PFSEPSDFYK	AADPIDPPGP	PAKIRIADST	KSSITLWNSK
27121	PVYDGGSDVT	GYYVEMRQGE	EEEWTVSTK	GEARTTVEYV	SNLKPGVNYF	FQVSAVNCAG	QGEPIMTPEP	GKADLIEEP
27201	EIDLDVALRT	SIVVAPAGEV	QLLIPFKGPR	PBPTTWRRKE	KNLGS DARYS	IQNTDSSSLL	VIPQVTRNDT	VQYILTIENG
27281	VGQPKSSTVS	VKVLDTAAGC	QKLQVKHVS	GTVTLWDWPP	LIDGGSPIIN	YVIEKRDATK	RTWSIVSHKC	SGTSFKVMDL
27361	SEKTPFFFRV	LAENIGIGIE	PCETTEPVKA	AEVPAPIRTL	SMKDSKTSTV	VLSWTKPDPD	GGSIITDYLV	ERKKGGEQAW
27441	SHAGISKTCE	EIGRGLKEQS	VLEFRVSARN	VLEFRVSARN	GPLTVKELVI	TPEVDLSEIP	GAISIRLFI	WHLPQKTIH
27521	KPKFSISWKL	DGLPIKKESE	VRFSKTENKI	TLSJNAGVKE	NGGKYTVILD	NAVCRNSFP	TIITLGPSPK	PKGPIRFDEI
27601	KADSAIMSWD	IPEDDGGGEI	TCYSIEKREA	SQTNNWMCVS	SVARTTFKVS	NLVKDSSEYQ	RVRAENRYG	SEPLVSNVAT
27681	AKHQFRIPGP	PGKPIYINVT	SDGMSLTWDA	PVYDGGSEVT	GFHVEKKERN	SILWQRVNTS	PISGREYRAT	GLIEGLDYQF
27761	RVYAENSAGL	SSPSPDSKFT	LAVSPVDDPP	TPDYIDVTRT	TITLKNWPP	RDGGSKIVAY	SIEKRQSDR	WVRNCFNTPV
27841	ECQYTVSGLS	PGDRYEFRII	ARNAVGTISP	PSQSSGLIMT	RDENVPPTVE	FGPEYFDGLV	IKSGDSRLIK	ALVQGRPVP
27921	VTWFKDGVVEI	ERRMMEITD	VLGSTSLFVR	DATRDHCRGV	TVEAKNVSGS	TKAEITVKVQ	DTPGKVVGPI	RFTNITGKEM
28001	TLWWEAPLND	GCAPVTHYII	EKRETSRLAW	ALIEDHCEAQ	SYTAIKLITG	NEYQFRVSAV	NKFGVGRPLE	SDPVVAQIQY
28081	TIPDAPGPE	PSNVGNSIT	LWTTRPESDG	GNEIQHYILE	RREKSTRWV	KVISKRPISE	TRFKVTGLVE	GNEYEFHYMA
28161	ENAAGVGPAS	GISRLIKCRE	PVNPPSAPAV	VKVTDTSKT	VSLEWARPVF	DGGMEIGYI	IEMCKADLGD	WHKVNTPECV
28241	KTRYTVTDLQ	AGEEYKFRVS	AINGAGKGS	CEVTGTIKAV	DRLSAPELDI	DANFKQTHIV	RAGASIRLFI	AYQGRPTTA
28321	VWSKPDNSLS	IRADIHHTDS	FSTLTVENCN	RNDAGKTYLT	VENNSGRKSI	TFTVTVLDS	PPGPIITFKD	VTGCSATLWM
28401	DAPLLDGGAR	IHHYVIEKRE	ASRRS WQVVS	EKCTRQLLKV	SDLTEGVPPY	FRVSAENEYQ	VGEPYEMPEP	IVATEQQPAP
28481	RRLDVVDTSK	SSAVLAWLKP	EHDGGSRLTS	YLLEMRQKGS	DFWVEAGHTK	QLTFTVERLV	ENTEYEFVRK	AKNDAGYSEP
28561	REAFSSVVIK	EPQIEPTADL	TGITNQLITI	KAGSTFTIDV	PISGRPAPKV	TWKLEEMRLK	ETDRMSTTTT	KDRTTLTVKD
28641	SMRGDSGRFY	LTLENTAGVK	TFTITVVVIG	RFGPVTPGPIE	VSSVSAESCV	LSWSEPKDDG	GTEITNYIVE	KRESGTTAVD
28721	LINSVVKRQT	IKVTHLTKYK	EYCFRVSSEN	RFGVSKPLVS	PVIVAEHPFV	PPSAPTRPEV	YVVSANAMSI	RWEPPIYHDGG
28801	SKLVGVWVEK	KERNLILWVK	ENKPVCLECN	YKVTGLVEGL	EYQFRTYALN	AAGVSKASEA	SRPIMAQNPV	DDEGRPEVDT
28881	VTRSTVSLVR	SAPMYDGGSK	VVGYI IERKP	VSEVGDGRWL	KCNVYIVSDN	FFTVTALSEG	DYEFYFRVLAK	NAAGIISKGS
28961	ESTGPEVTRD	EYAPPKAELD	ARLQGDVLTI	AGSDDLVLDA	AWLKGKPEPKI	IWTKGDKELD	LCEKVSILQYT	GKRATAVIKY
29041	CDRSDSGKYT	LTVKNASGTK	SVSVMVKVLD	SPGPGCKLTV	SRVTEKCTL	AWSLPQEDGG	AEITHYIVER	RETSRLNWVI
29121	VEAECLTISY	VVTRLIKNE	YTFRVRAVKN	YGLGVPTESE	PIVARNSTFI	PSQPGIPEGV	GAGKEHIIQ	YTPESDGGN
29201	EISNYLVDKR	EKKSIRWTRV	NKDYVVYDTR	LKVTSLMEGC	DYQFRVTAVN	SAGNSEPSEA	SNFISCREPS	WTKPPSAPR
29281	VVDTKKSSIS	LAWTKPMYDG	GTDIIGYVLE	MQEKDTPQWC	RVHTNTTIRN	NEFTVPDLKM	GQKYSFRVAA	VNAKGMDSYS
29361	ETFAEIEPVE	RLEIPDLELA	DDLKKTVIIR	AGASLRMLVS	VSGRPSPVIT	WSKKGDIDLAN	RAIIDNTEYS	SLLIYDKNYR
29441	YDAGKYTEIA	ENQSGKKSAT	VLVKKVYDTPG	PCPSVNVKVE	SRDSVTITWE	IPTIDGGAPV	NNYIIEKREA	AMRAFKTVTT
29521	KCSKTYLRIS	GLVEGTMYYF	RVLPENIYGI	GEPCESTDAV	LVSEVPLVPT	KLEVVDVTKS	TVTLAWEKPL	YDGGSRLLTG
29601	VLEACKAGTE	KWMKVVTLKP	TVLDHTVISL	NEGEQYLFVR	RAQNEKGVSE	PREIVTPVTV	QDLRVLPTID	LSTMPQKTIH
29681	VPAGRPIELV	IPITGRPPPT	ASWFFAGSKL	RESERVYVET	HTKVAKLTR	ETTIRDTGVEY	MLELKNVTGT	TSETIKVVIL
29761	DKPGFPIGPI	KIDEVATSIV	TISWEPPELD	GGAPLSGVVW	EQRDAHRPGW	LPVSESVTRP	TFKFTRLTGE	NEYVFRVAVD
29841	NRFGIGSYLQ	SEVIECRSSI	SIPGPPETLQ	IFDISRDGMT	LWTWPPEDDG	GSQVGTGIIIE	RKEVRADRWW	RVNKVPVMTM
29921	RYRSTGLIEG	LEYEHRVTAI	NARGTGKPSR	PSKPTVAMPD	IAPPGKQPMP	RVDTRTTSV	SLAWSPEDE	GGKYVTGYLI
30001	EMQKVDQREW	TKCNTTPTKI	REYTLTHLPQ	GAEYRFRVLA	CNAGGPGPEPA	EVPGTVKQVTE	MLEYPPDYEL	ERYQGEVFRV
30081	QGGVIRLTIP	IKGKFPFICK	WTKEGQDVSK	RAMIATSETH	TELVIKEADR	NDSGTYDLVL	ENKCKGKTVY	IKVVSIGSPN
30161	TPREGLEYDD	IQTSRVVRSW	RPPADDGGAR	ILGYILERRP	VPKAAWYITD	SRVRGTSLVV	KGLENVEYDH	FRVSAENQFV
30241	ISKPLKSEEP	VFPKTPLNPP	EPSPNPEVLE	DVTKSSVFLS	WSPRKDDGGS	RVTGYI IERK	ETSTDKVVH	NKTIQITTTYI
30321	TVTGLVDPDAE	YQFRIIAQND	VGLSETSPAS	EPVWCKDPFD	KRSPQGELEI	LSISKDSVIL	QWEKPECGRR	KEILGYWQEP
30401	RQSGDSAWKK	SNKERIKDRQ	FTIGGLLEAT	EYEFRVFAEN	ETGLSRPRRT	AMSVKTKLTS	GEAPGVRKEM	ADVTTKLGEA
30481	AQLSCQIVGR	PLPDIKWYRF	GKELVQSRKY	KMSDDGRTHT	LVTMTTEEQED	EGVYTCVATN	EVGEVETSSK	LLQQAAPQFH
30561	PGYPLKKEYY	GAVGSTLRLH	VMIYIGRPVPA	MTWYHGQKLL	QNSSEITIEI	TEHYTHLVKM	NVQRKTHAGK	YKVPQLSNVFG
30641	TVDAILDVEI	QDKPDKPTGP	IVIEALLKNS	VVISWKAAPAD	DGGSWITNYV	VEKCEAKEGA	EWQLVSSAIS	VYTCRIVNLT
30721	ENAGYYFRVS	AQNTFGISEP	LEVASVVIK	SPEFKPSVPG	KPTITAVTKD	SCVVAWKPPA	SDGGAKIRNY	ILLEKREKQN
30801	KWIAVTTTEEI	RETVFSVQNL	IEGLEYEFRV	KENLGGESE	WSETSEPVTP	KSDVPIQAPH	FKEELRNLNV	RYQSNATLVC
30881	KVTGHPKPIV	KWYRQGKEII	ADGLKYRVQE	FKGGYHQLII	ASVTDDDATV	YQVRATNQQG	SVSGTASLEV	EVPAKIHLPK
30961	TLEGMAVHA	LRGEVVSIIKI	PFSGKPPDVI	TWQKGQDLID	NNGHYQVIVT	RSFTSLVFPN	GVERKDAGFY	VVCAKNRFGI
31041	DQKTVELDVA	DVPDPGRGVK	VSDVSRDSVN	LWTEPASDG	GSKVTNYIVE	KCATTAERWL	RVGQARETRY	TVVNLFGKTS
31121	YQFRVIAENK	FGLSKPSEPS	EPTVTKEDKT	RAMNYDEEVD	ETREVTMTKA	SHSKTKELYE	KYMIADLGR	GEFGIVHRCV
31201	ETS SKKTFMA	KFVKVKGTDQ	VLVKKESISL	NIARHRNLY	LHESFESMEE	LVMIFEFISG	LDIFERINTS	AFELNREEVV
31281	SYVRQVCEAL	EFLHSQNIH	FDIRPENIY	QTRKNSI IKI	IEFGQARQLK	PGDNFRLLFT	APYYAPEVH	QHDVNSSATD
31361	MWSLQTLVYV	LLSGINPFLA	ETNQMIENI	MNAEYTFDEE	AFQEISLEAM	DFIDRLLVKE	RKSRMTASEA	LKHPWLQGRM
31441	DRVSTKVIRT	LRHRRYHYTL	IKKDLNMVVS	AARISCGGAI	RSQRGVSVAK	VKVASIEIGP	VSQIMHAIG	EEGGYVKVYC
31521	KIENYDQSTQ	VTWYFVVRQL	ENSEKEYEITY	EDGVAITMYK	DITKFDGDTY	RCKVVNDYGE	DSSYAEFLVK	GREVVYDYVC
31601	RRTKVKVRRD	DAMRLLERPP	EFTLPLYNKT	AYVGENVRFG	VTIIVHPEPR	VTWYKSGQKI	KPGDDDKKTY	FESDKGLYQL
31681	TINSVTTDDD	AEYAVVARNK	HGEDSCKALK	TVT LHPPTDE	TTLRPMFKRL	LANAECHGQ	SVCFEIRVSG	IPAPTLWLEK
31761	DGQPLSLGPH	IEIHEGLDY	YALHIRDTLP	EDTGYRYVTA	TNTAGSTSCQ	AHLQVDRRLY	VKQEFQTKEE	RRHVQKQID
31841	KTLRMAEILS	GTETVPLTPV	AQEALREAAI	LYKPAVSTKT	VKGEYRLETE	EKKEERKLRM	PYEVPEPRRF	KQATVEEDQR
31921	IKQFVPMMSD	KWYKIRIQDY	EMPGKLDREV	QKRPKRIRLS	RWEQFVYVML	PRITDQYRDM	WRIPKLTQDD	LEMVRRPARR
32001	TPSPDYDLYY	YRRRRSLGDD	ISDEELLLPL	DDYLAMKRTI	EERLRLEEL	ELGFSASPPS	RSPPRFELSS	LRYSPPAHV
32081	KVEDRRRDFR	YRTHIPTRE	ETSTS YAE LR	ERHAQASYRQ	PKLRQRIMAE	KEEBELLRPV	TTQRRLSEYK	SELDYMSKE
32161	KSKKSKRQR	QVTEITEIEE	EYEISRAQR	ESSSSVSRLL	RRRRSLSPTY	IELMRPVSEL	IRSRPQPAEE	YEDTTRSP
32241	TPERTRRSP	SPVSSERSLS	RFERSARFDI	FSRYESMKAA	LKRTQKTSERK	YEVLSQQPFT	LDHAPRITLR	MRSRHRVPCGQ
32321	NTRFILNVQS	KPTAEVKKYH	NGVELQESSK	IHYTNTSGVL	TLEILDQCTE	DSGT YRAVCT	NYKGEASDVA	LDVVTGGHYT
32401	TYASQRDEE	VPKSVFPELT	KTEAYAISSF	KRTSEMAEAS	SVREVKSQMT	ETRESLSSYE	HVVSAMKMSA	ASEKKSLEEK
32481	ATVRKIKTTL	AARILTKPRS	ITVHEGESAR	FSCDDTDEGPV	PTVFWLRRGGQ	VVTSARHQV	TTAKYKSTFE	ISSVQASDEG

NHLBI Zile/Grant, Aged Rat

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32561 NYSVVVETD GKQEAQFTLT VQKAKAVEKA VTSPPRVKSP EPRVKSPETV KSPKRVKSPE LVASHPKAVS PTETKPTKGG
32641 QQLPVPAPPK ITQSLKAEAS RDI AKLTC AV ESSALCAKEV AWYKDGKKLK ENGHFQFHYS ADGTIELKIH NLSESDCGEY
32721 VCEVSGEGGT SKTSFQFTGQ SFKSIHEQVS STTETKKSQV KTAESAEAKK QEPIAPESVS SKPVIVTGLR DTTVSSDSVA
32801 KFVIKVTGEP QPTVTWTKDG KAIAQSSKYK LSNDKEEFIL EILKTETSDG GLYSC TVANS AGSVSSSCKL TIKAVKDTEA
32881 QKVSTQKTSE VTAKKESVQ QEISQAVLTS EEIKMSEVKS HETLAIKEEA SKVLIAEEVK KSAASLEKS IVHEEVRTS
32961 QASEEVKTHA EIKALSTQMN ITSGQRVTLK ANIAGATDVK WVLNGTELSN SEEYRYGVSG SDQTLTIKQA SHRDEGILTC
33041 IGRTSQGVVK CQFDLTLSEK LSDAPSFISQ PRSQNINEGQ NVLFSCEISG EPSPEIEWFK NNLPISSN ISVSRSRNMY
33121 TLEIRNASVS DSGKYTVKAK NFRGQCSATA SLTVLPLVEE PPREVVLTKS GDMSLQGSFS SQSVQMSASK QEASFSFS
33201 GSASMTEMKF ASMSAQSMS VQESFVEMSS SSFMGKSMT QLESSTRML KAGGRGIPP I EALPSDISI AEGKVLTVAC
33281 AFTGEPTPEI TWSCGGRIQ SQEQQGRFHI ENTDDLTLI IMDVQKQDGG LYTLISLGNEF GSDSATVNIN IRSM
  
```



5.569 heterogeneous nuclear ribonucleoprotein H2 [Rattus norvegicus]

Protein Accession	gij 62078769
Mean Expression Ratio	0.952
Median Expression Ratio	0.952
Credible Interval	(0.728, 1.24)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0379

Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.996
Avg..iTRAQ.Ratio....116.114.	0.856
Avg..iTRAQ.Ratio....117.114.	0.94

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1      MMLSTEGREG FVVKVRGLPW SCSAEVVMRF FSDCKIQNGT SGVRFIYTRE GRPSGEAFVE LESEDEVKLA LKKDRETMGH
81     RYVEVFKSNS VEMDWVLKHT GPNSPDTAND GFVLRGLPF GCSKEEIVQF FSGLEIVPNG MTLPVDFQGR STGEAFVQFA
161    SQEIAEKALK KHKERIGHRY IEIFKSSRAE VRTHYDPPRK LMTMQRPGPY DRPGAGRGYN SIGRGAGFER MRRGAYGGGY
241    GGYDDYGGYN DGYGFGSDRF GRDLNYCFSG MSDHRYGDGG SSFQSTTGHC VHMRLPYR A TENDIYNFFS PLNPMRVHIE
321    IGPDGRVTGE ADVEFATHED AVAAMAKDKA NMQHRYVELF LNSTAGTSGG AYDHSYVELF LNSTAGASGG AYGSQMMGGM
401    GLSNQSSYGG PASQQLSAGY GGGYGGQSSM SGYDQVLQEN SSDYQSNLA
  
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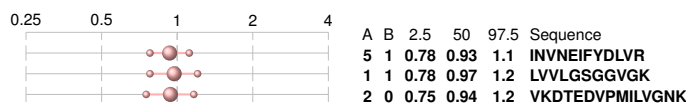


5.570 Ras-related protein RAP-1A [Rattus norvegicus]

Protein Accession	gi 54114993	
Mean Expression Ratio	0.952	
Median Expression Ratio	0.952	
Credible Interval	(0.797, 1.13)	
Associated Peptides	3	
Associated Spectra	10	
Coverage	0.207	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.886	1.24
Avg..iTRAQ.Ratio....116.114.	0.847	1.28
Avg..iTRAQ.Ratio....117.114.	0.819	1.65

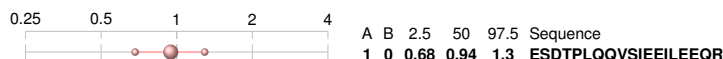
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1      MREYKLVVLG SGGVGKSALT VQFVQGIFVE KYDPTIEDSY RKQVEVDCQQ CMLEILD TAG TEQFTAMRDL YMKNGQGFAL
81     VYSITAQSTF NDLQDLREQI LRVKDTEVDP MILVGNKCDL EDERVVGKEQ GQNLARQWCN CAFLESSAKS KINVNEIFYD
161    LVRQINR RTP VEKKRPKKKS CLLL
  
```



5.571 PREDICTED: similar to U6 snRNA-associated Sm-like protein LSm1 (Small nuclear ribonuclear CaSm) (Ca)

Protein Accession	gij 109503508
Mean Expression Ratio	0.952
Median Expression Ratio	0.952
Credible Interval	(0.703, 1.28)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	0.896
Avg..iTRAQ.Ratio....117.114.	0.833

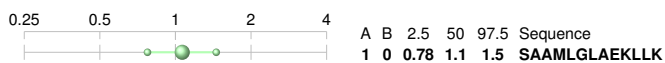


5.572 PREDICTED: similar to D14Ert209e protein [Rattus norvegicus]

Protein Accession	gij 109501553
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.78, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0282
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	1.67
Avg..iTRAQ.Ratio....117.114.	1.17

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1   MATARASRFL LLFCRCSRSL RGPQSRFAAA LVPGVSQVDN RSDFLGKKPH RKHPGILHLP HVHLPQALTD AAQLLLLERP
81  KRSVEKQVQA LTNYLWSRHL PVEPEELQRR AAYLEKKFLE KQDSTQTEEK LREAVLHALR KTYHWQELS YNEELSLIYM
161 AARLDGGFAA VFRAFHEIQA RIPEFQPQTL MDFSGTGSV AWAHSTWGQ SLREYVCVDR SAAMLGLAEK LLKGGSESGK
241 PCIPGVFFRQ FLPVSPKVQF DVVVSFAFALS ELPSRADRTE VLQNLWRKTS HFLVLVNGT KAGHRLMDA RNLIIGDKEK
321 SPLDLRPSFV FAPCPHELPC PQLNAAKSLA CSFSQAYQPI PFHWNKKPKE ETFSMVILAR GSPKEANRWP RITQPVLKRP
401 RHVHCHLCCP DGHMQHAVVT ARRHGRDLYR CARVSSWGDL LPVISPSEFP PPSPAEPEPE S
    
```



5.573 PREDICTED: similar to vacuolar protein sorting 37C [Rattus norvegicus]

Protein Accession	gij109463604
Mean Expression Ratio	0.953
Median Expression Ratio	0.952
Credible Interval	(0.705, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.91
Avg..iTRAQ.Ratio....116.114.	0.839
Avg..iTRAQ.Ratio....117.114.	0.86



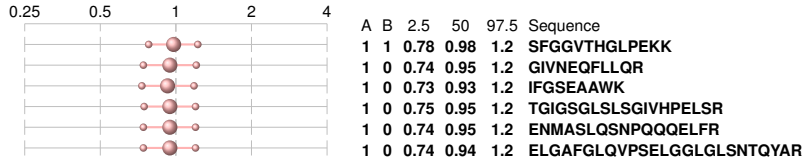
5.574 "acyl-Coenzyme A dehydrogenase, very long chain [Rattus norvegicus]"

Protein Accession	gij6978435	
Mean Expression Ratio	0.951	
Median Expression Ratio	0.952	
Credible Interval	(0.79, 1.14)	
Associated Peptides	6	
Associated Spectra	7	
Coverage	0.144	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.19	0.978
Avg..iTRAQ.Ratio....116.114.	0.974	1.01
Avg..iTRAQ.Ratio....117.114.	0.753	1.21

NHLBI Zile/Grant, Aged Rat

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1      MQSARMTPSV GRQLRLRGAR SSRSAAALQGG PRPTSAQRLY ASEATQAVLE KPETLSSDAS TREKPARAES KSFVGMFKG
81     QLTDDQVFPY PSVLNEGQTQ FLKELVGPVA RFFEEVNDPA KNDSLEKVEE DTLQGLKELG AFGLQVPSEL GGLGLSNTQY
161    ARLAEIVGMH DLGVSVTLGA HQSIGFKGIL LYGTAKQKEK YLPRVASGQA LAAFCLTEPS SGSDVASIRS SAVSPCGKY
241    YTLNGSKIWI SNGGLADIFT VFAKTPIKDA ATGAVKEKIT AFVVERSFGG VTHGLPEKKM GIKASNTSEV YFDGVKVPAE
321    NVLGEVGDGF KVAVNILNNG RFGMAATLAG TMKAIIAKAV DHATNRTQFG DKIHNFQVIQ EKLARMAILQ YVTESMAYML
401    SANMDQGFKD FQIEAAISKI FGSEAAWKVT DECIQIMGGM GFMKEPQVER VLRDIRIFRI FEQTNDILRL FVALQGCMDK
481    GKELTGLGNA LKNPLGNVGL LIGEASKQLR RRFGIGSGLS LSGIVHPELS KSGELAVQAL EQFATVVEAK LMKHKKGIVN
561    EQPFLQRLAD GAIDLYAMVV VLSRASRSLS EGYPTAQHEK MLCDSWCIEA ATRIRENMAS LQSNPQQQEL FRNFRSISKA
641    MVENGGLVTS NPLRV
  
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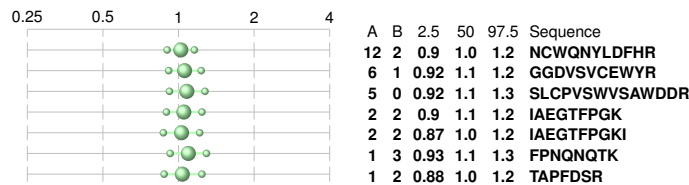


5.575 "PREDICTED: similar to cytochrome c oxidase, subunit VIb polypeptide 1 [Rattus norvegicus]"

Protein Accession	gij109465447	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.942, 1.17)	
Associated Peptides	7	
Associated Spectra	41	
Coverage	0.71	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.974	1.21
Avg..iTRAQ.Ratio....116.114.	1.39	0.994
Avg..iTRAQ.Ratio....117.114.	1.04	0.579

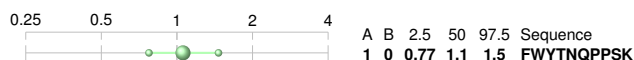
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1      MAEDIKTKIK NYKTAPFDSR FPNQNQTKNC WQNYLDFHRC EKAMTAKGGD VSVCEWYRRV YKSLCPVSWV SAWDDRIAEG
81     TFPGKI
  
```



5.576 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gij109486009
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.774, 1.41)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.21
Avg..iTRAQ.Ratio....117.114.	1.36

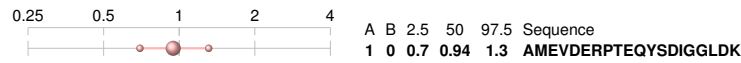


5.577 "proteasome (prosome, macropain) 26S subunit, ATPase 3 [Rattus norvegicus]"

Protein Accession	gij13928808
Mean Expression Ratio	0.955
Median Expression Ratio	0.953
Credible Interval	(0.711, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0452
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.77
Avg..iTRAQ.Ratio....116.114.	0.811
Avg..iTRAQ.Ratio....117.114.	0.935

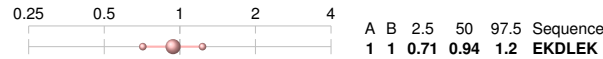
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1      MQEMNLLPTP  ESPVTRQEKM  ATVWDEAEQD  GIGEEVLKMS  TEEIVQRTL  LDSEIKIMKS  EVLRVTHELQ  AMKDKIKENS
81     EKIKVNTLP  YLVSNVIELL  DVDPNDQEED  GANIDLDSQR  KGKCAVIRTS  TRQTYFLPVI  GLVDAEKLKP  GDLVGVNKDS
161    YLILETLPT  YDSRVKAMEV  DERPTEQYSD  IGGLDKQIQE  LVEAIVLPMN  HKEKFENLGI  QPPKGVLMYG  PPGTGKTLA
241    RACAAQTAT  FLKLAGPQLV  QMFIGDGAKL  VRDAFALAKE  KAPSIIFIDE  LDAIGTKRFD  SEKAGDREVQ  RTMLELLNQM
321    DGFQPTQVK  VIAATNRVDI  LDPALLRSGR  LDRKIEFPMP  NEEARARIMQ  IHSRKMNVSP  DVNYEELARC  TDDFNGAQCK
401    AVCVEAGMIA  LRRGATELTH  EDYMEGILEV  QAKKANLQY  YA
    
```



5.578 "PREDICTED: similar to DnaJ (Hsp40) homolog, subfamily C, member 11 [Rattus norvegicus]"

Protein Accession	gij 109477739	
Mean Expression Ratio	0.952	
Median Expression Ratio	0.953	
Credible Interval	(0.725, 1.25)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.819	0.8
Avg..iTRAQ.Ratio....116.114.	0.665	0.9
Avg..iTRAQ.Ratio....117.114.	0.631	1.29

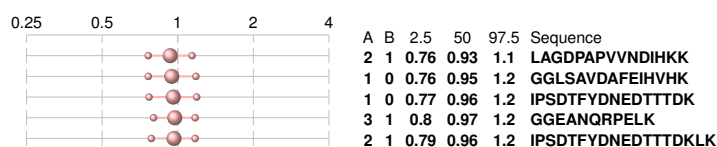


5.579 PREDICTED: similar to Dystroglycan precursor (Dystrophin-associated glycoprotein 1) [Rattus norvegi

Protein Accession	gij 34865933	
Mean Expression Ratio	0.954	
Median Expression Ratio	0.953	
Credible Interval	(0.813, 1.12)	
Associated Peptides	5	
Associated Spectra	12	
Coverage	0.0661	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.02	0.725
Avg..iTRAQ.Ratio....116.114.	0.941	0.777
Avg..iTRAQ.Ratio....117.114.	1.08	0.857

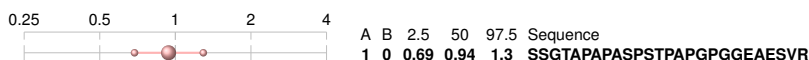
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1      MSVDNWLHLP LWGQTFLLLL SVAVAQAHWP SEPSEAVRDW KNQLEASMHS VLSDFQEAVP TVVGPIDGTA VVGRSFRVSI
81     PTDLIASSGE IIKVSAAGKE ALPSWLHWDV HSHILEGLPL DTDKGVHYIS VSAARLGANG SHVPQTASVF SIEVYPEDHS
161    EPQSVRAASS DPGEVVSSAC AADEPVTVLV VILDADLTKM TPKQRIDLLN RMQSFSEVEL NNMKLVVNVN NRFLDMSAFM
241    AGPGNAKKVV ENGALLSWKL GCSLNQNSVP DIRGVETPAR EGTMSAHLGY PVVGVHIANK KPTLPKRIRR QIHATPTPVT
321    AIGPPTTAIQ EPPSRIVPTP TSPAIAAPTE TMAPPVVRDV PGKPTVTIRT RGAI IQTPTL GPIPPTRVSE AGTTPVGGIR
401    PTLTIPGYVE FTAVVTPTT TTKKPRVSTP KPATPSTDSS TTTTRRPTKK PRTPRPVPRV TTKAPITRLE TASPPTIRI
481    TTSAVPRGGE ANQRPELKNH IDRVDWVGT YFEVKIPSDT FYDNEDTTD KLKLTCLKRE QQLVGEKSWV QFNNSQLMY
561    GLPDSHVVGK HEYFMHATDK GGLSAVDAFE IHVHKRPQGD KAPARFKAKL AGDPPAPVVND IHKKIALVKK LAFAFGDRNC
641    SSITLQNIIR GSIVVEWTNN TLPLEPCPKE QIVGLSRRIA DENGKPRPAF SNALEPDFKA LSVAVAGSGS CRHLQFIPVA
721    PPSFGTSAAP ATEVPDRDPE KSSEDDVYLH TVIPAVVVAA ILLIAGIAM ICYRKKRKGK LTLEDQATFI KKGVPFIIFAD
801    ELDDSKPPPS SSMPILQEE KAPLPPPEYP NQSVPETPL NQDTVGEYTP LRDEDPNAPP YQPPPPFTAP MEGKGSRPKN
881    MTPYRSPPPY VPP
    
```



5.580 PREDICTED: similar to spastin isoform 2 [Rattus norvegicus]

Protein Accession	gij109477951
Mean Expression Ratio	0.953
Median Expression Ratio	0.953
Credible Interval	(0.711, 1.27)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.902
Avg..iTRAQ.Ratio....116.114.	0.893
Avg..iTRAQ.Ratio....117.114.	0.859



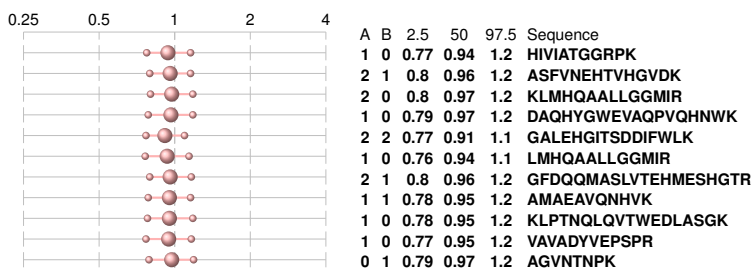
5.581 thioredoxin reductase 2 [Rattus norvegicus]

Protein Accession	gij12018236	
Mean Expression Ratio	0.953	
Median Expression Ratio	0.953	
Credible Interval	(0.835, 1.08)	
Associated Peptides	11	
Associated Spectra	20	
Coverage	0.27	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.965	1.01
Avg..iTRAQ.Ratio....116.114.	1.13	0.92
Avg..iTRAQ.Ratio....117.114.	0.855	0.697

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1   MAAIVAALRG SSGRFRPQTR VLTRGTRGAA GAASAAGGQQ NFDLLVIGGG SGGLACAKEA AQLGRK VAVA DYVEPSPRGT
81  KWGLGGTCVN VGCIPK KLMH QAALLGGMIR DAQHYGWEVA QPVQHNWKAM AEAVQNHVKS LNWGHRVQLQ DRKVYFNIK
161 ASFVNEHTVH GVDK AGKVTQ LSAKHIVIAI GGRPKYPTQV KGALEHGITS DDIFWLKESP GRTLTVVGASY VALECAGFLT
241 GIGLDTTVM RSVPLRGFDQ QMASLVTEHM ESHGTRFLKG CVPSLIRKLP TNQLQVTWED LASGKEDVGT FDTVLWAIGR
321 VPETRNLE KAGVNTNPK QKIIVDAQEA TSVPHIYAIG DVAEGRPELT PTAIKAGKLL AQLRFGKSST LMNYSNVPTT
401 VFTPLEYGCV GLSEEEAVAL HGQEHIEVYH AYYKPLEFTV ADDRASQCYI KMVCMREPPQ LVLGLHFLGP NAGEVTQGFA
481 LGIQCGASYA QVMQTVGIHP TCSEEVVKLH ISKRSGLDPT VTGCUG

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5.582 adipocyte complement related protein of 30 kDa [Rattus norvegicus]

Protein Accession	gij21426809	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.813, 1.35)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.0615	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.17	0.914
Avg..iTRAQ.Ratio....116.114.	1.26	0.997

Avg..iTRAQ.Ratio....117.114. 0.997 1.26

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1      MLLLQALLFL LILPSHEGIT ATEGPGALVP PPKETCAGWM AGIPGYPGHN GIPGRDGRDG TPGEKGEKGD AGVLGPKGDP
81     GDAGMTGAEG PRGFPPTGR KGEPEAAAYM YHSAFVSGLE TRVTVPNVPI RFTKIFYNQO NHYDGSTGKF HCNIPGLYYF
161    SYHITVYMKD VKVSLFKKDK AVLFTYDQYQ EKNVDQASGS MLLHLEVGDQ VWLQVYEGED NNGLYADNVN DSTFTGFLLY
241    HDTN
    
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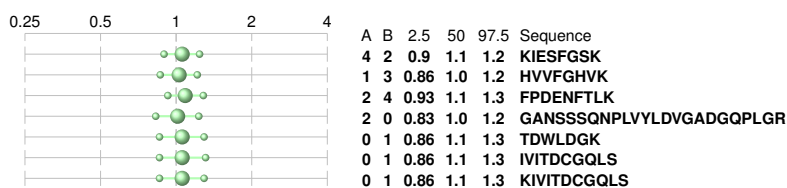


5.583 peptidylprolyl isomerase F (cyclophilin F) [Rattus norvegicus]

Protein Accession	gi 26892289	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.914, 1.20)	
Associated Peptides	7	
Associated Spectra	21	
Coverage	0.325	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.962	1.09
Avg..iTRAQ.Ratio....116.114.	1.03	1.04
Avg..iTRAQ.Ratio....117.114.	0.96	1

```

1      MLALRCGPRL LGLLSGPRSA PLLLSTTRTC SDGGARGANS SSQNPLVYLD VGADGQPIGR VVLELKADV VPKTAENFRAL
81     CTGEKGFYK GSTFHRVIPA FMCQAGDFTN HNGTGGKSIY GSRFPDENFT LKHVGPVLS MANAGPNTNG SQFFICTIKT
161    DWLDGKHVVF GHVLEGMDVV KRIESFGSKS GKTSKKIVIT DCGQLS
    
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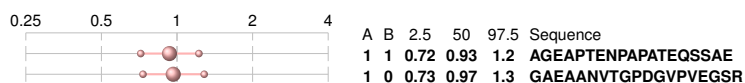


5.584 muscle Y-box protein YB2 [Rattus norvegicus]

Protein Accession	gi 82524639	
Mean Expression Ratio	0.956	
Median Expression Ratio	0.954	
Credible Interval	(0.747, 1.23)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	0.105	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.934	0.844
Avg..iTRAQ.Ratio....116.114.	0.899	0.907
Avg..iTRAQ.Ratio....117.114.	0.97	1.11

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1      MSEAGEATTG GTTLPQAAAD APAAAPPDPA PKSPAASGAP QAPAPAALLA GSPGGDAAPG PAPASSAPAG GEDAEEKVLA
81     TKVLGTVKWF NVRNGYGFIN RNDTKEDVVF HQTAIKKNP RKYLRSVGDG ETVEFDVVEG EKGAEEANVT GPDGVPVEGS
161    RYAADRRRYR RGYYGRRRGP PRNYAGEEEE EGSSESSEGE PPAADGQFSG ARNQLRRPQY RPPYRQRRFP PYHVQOTFDR
241    RSRVFPHPNR MQAGEIGEMK DGVPEGTQLQ AHRNPTYRPR FRRGPARPRP APAIGEAEDEK ENQQAANGPN QPSARRGFRR
321    PYNRRRSRP LNAVSQDGKE TKAGEAPTEN PAPATEQSSA E
    
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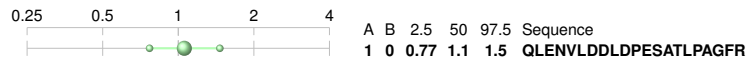


5.585 tropomodulin 2 [Rattus norvegicus]

Protein Accession	gi 13928838	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.776, 1.42)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0598	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.23	
Avg..iTRAQ.Ratio....116.114.	1.25	
Avg..iTRAQ.Ratio....117.114.	1.55	

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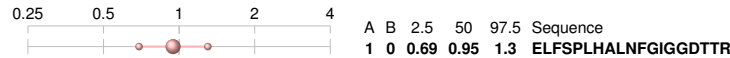
1      MALFFQKGLE KYKNIDEDEL LGKLSEEBELK OLENVLDDLD PESATLPAGE FQKDQTQKAA TGFFDREHLL MYLEKEALEQ
81     KDREDFVFFT GEKKGKRVFIP KEKPVETRKE EKVTLDPELE EALASASDTE LYDLAAVLGV HNLNNPKFD EETTNGQGRK
161    GPVRNVVKGK KAKPVFEPPP NPTNVEASLQ QMKANDPSLQ EVNLNNIKNI PIPTLKEFAK ALETNTHVRK FSLAATRSND
241    PVALAFAEML KVNKTLKSLN VESNFITGAG ILALVEALRE NDTLTEIKID NQRQQLGTA VEMEIAQMLEE NSRILKFGYQ
321    FTRQGPRTV AAATKNNDL VRKKRVEGDR R
    
```



5.586 platelet-activating factor acetylhydrolase alpha 2 subunit [Rattus norvegicus]

Protein Accession	gi 11693154
Mean Expression Ratio	0.955
Median Expression Ratio	0.954
Credible Interval	(0.708, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	0.083
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.903
Avg..iTRAQ.Ratio....116.114.	0.911
Avg..iTRAQ.Ratio....117.114.	0.767

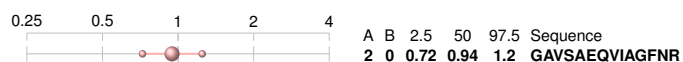
1 MSQGDSNPAA IPHAAEDIQG DDRWMSQHNR FVLDCCKDEP DVLFVGDMSV QLMQQYEIWR **ELFSPLHALN FGIGGDTRH**
 81 VLWRLKNGEL ENIKPKVIVV WVGTTNNHENT AEEVAGGIEA IVQLINTRQP QAKIIVLGLL PRGEKPNPLR QKNAKVNQLL
 161 KVS LPKLANV QLLDIDGGFV HSDGAISCHD MFDLHLTGG GYAKICKPLH ELIMQLEET PEEKQTIA



5.587 PREDICTED: similar to Prefoldin subunit 2 isoform 2 [Rattus norvegicus]

Protein Accession	gi 109498170
Mean Expression Ratio	0.955
Median Expression Ratio	0.954
Credible Interval	(0.733, 1.24)
Associated Peptides	1
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.927
Avg..iTRAQ.Ratio....116.114.	1.05

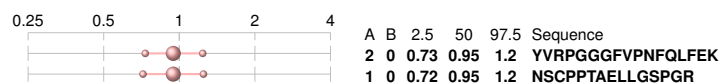
Avg..iTRAQ.Ratio....117.114. 0.827



5.588 glutathione peroxidase 3 [Rattus norvegicus]

Protein Accession	gij41053837
Mean Expression Ratio	0.954
Median Expression Ratio	0.954
Credible Interval	(0.75, 1.21)
Associated Peptides	2
Associated Spectra	3
Coverage	0.142
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.986
Avg..iTRAQ.Ratio....116.114.	0.824
Avg..iTRAQ.Ratio....117.114.	1.03

1 MARILRASCL LSLLLAGFVP PGRGQEKSKT DCHGGMSGTI YEYGALTIDG EEYIPFKQYA GKYILFVNVA SYUGLTDQYL
 81 ELNALQEELG PFGLVILGFP CNQFGKQEPG ENSEILPSLK **YVRPGGGFVP** **NFQLFEK**GDV NGEKEQKFYT FLK**NSCPPTA**
 161 **ELLGSPG**FLF WEPMKIHDIR WNF EKFLVGP DGIPIMRWYH RTTVSNVKMD ILSYMRQAALGARGK



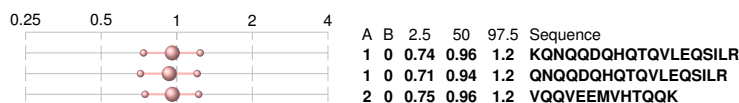
5.589 palmdelphin [Rattus norvegicus]

Protein Accession	gij71043606
Mean Expression Ratio	0.955
Median Expression Ratio	0.954
Credible Interval	(0.762, 1.19)

Associated Peptides	3
Associated Spectra	4
Coverage	0.0581
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.914
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	0.98

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1 MEEAELVKGR LQAITDKRKI QEEISQKRLK IEEKCLKHQH LKKKALREKW LLDGIGSGKE HDEMKKONOO DOHOTQVLEO
81 SILLLEKEIQ DLEKAELOIS ANEEVILKKL KSIERTTEDI IRSVKVEKEE IPEESIEDIY ANIPDLPSSY IPSRLRKERN
161 EESDDEQNRK ALYAMEIKVE KDLKTGESV LSSIPLPSDD FKSTGIKVEE DRQKSVYAVS SNQNTAYNGT DGLAPVEVED
241 LLRQASERNK KSPTHEYHEPV YANPFCRPMY PQRERVISPG PNSQERMVMM KANGLDHHEE ESVHGMTDGL SERRSNGLAH
321 TSPTRPTFPQ RSKVQQVEEM VHTQQIRMPK PWEESSIRQN EYEVSPRTEL SPSRASPGKS GPQCSSPICQ EADVRYNIV
401 HSLFPDVEDT EPVTMIFMGY QQADENEEEK KLLTGVDGVI HAELVVIDDE AEDDEGQAEK PSYHPVAPCS QVYQPAKPTP
481 LPRKRSEVSP HENTNHKSPH KNSISLKEQE ERLGSPARHS PLGVFAGDGD TEDPSLTALR IRMAKLGKKV I
    
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5.590 hypoxia up-regulated 1 [Rattus norvegicus]

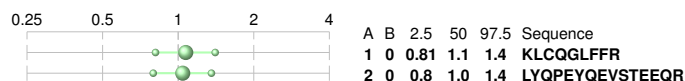
Protein Accession	gi 77404380
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.817, 1.34)
Associated Peptides	2
Associated Spectra	3
Coverage	0.0240
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.17
Avg..iTRAQ.Ratio....116.114.	1.08
Avg..iTRAQ.Ratio....117.114.	1.19

NHLBI Zile/Grant, Aged Rat

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1    MAATVRRQRP RRLLCWALVA VLLADLLALS DTLAVMSVDL GSESMKVAIV KPGVPM EIVL NKESRRKTPV TVTLKENERF
81   LGDSAAGMAI KNPKATLRYF QHLLGKQADN PHVALYRSRF PEHELNVDPQ RQTVRFQISP QLQFSPEEVL GMVLNYSRSL
161  AEDFAEQPIK DAVITVPAFF NQAERRAVLQ AARMAGLKVL QLINDNTATA LSYGVFRRKD INSTAQNIMF YDMGSGSTVC
241  TIVTYQTVKT KEAGTQPQLQ IRGVGFDRTL GGLEMELRLR EHLAKLFNEQ RKGQKAKDVR ENPRAMAKLL REANRLKTVL
321  SANADHMAQI EGLMDDVDFK AKVTRVEFEE LCADLFDRVP GPVQQALQSA EMSLDQIEQV ILVGGATRVV KVQEVLLKAV
401  GKEELGKNIN ADEAAAAMGAV YQAAAALS KAF KVKPFVVRDA VIYPILVEFT REVEEPEGLR SLKHNKRVLV SRMGPPYQPK
481  VITFNRYSHD FNFHINYGDL GFLGPEDLRV FGSQNLTVK LKGVGESFKK YPDYESKGIK AHFNLDESGV LSLDRVESVF
561  ETLVEDSPEE ESTLTKLGNT ISSLFGGGS SDAKENGTDA VQEEEEPAE GSKDEPAEQG ELKEEAEAPM EDTSQPPPSE
641  PKGDAAREGE TPDEKESGDK SEAQKPNEKG QAGPEGVPPA PEEKKQKPA RKQKMVEEIG VELAVLDLDP LPEDELAHSV
721  QKLEDLTLRD LEKQEREKAA NSLEAFIFET QDKLYQPEYQ EVSTEEQNEE ISGKLSATST WLEDEGFGAT TVMLKDKLAE
801  LRKLCQGLFF RVEERRKWPE RLSALDNLN HSSIIFLKGAR LIPEMDQIFT DVEMTTLEKV INDTWTWKNA TLAEQAKLPA
881  TEKPVLLSKD IEAKMMALDR EVQYLLNKAK FTKPRRPKPD KNGTRTEPPL NASAGDQEEK VIPPTGQTTEE AKPILEPDK
961  TGTEPADSEP LELGGPGAES EQAEQTAGQK RPLKNDEL

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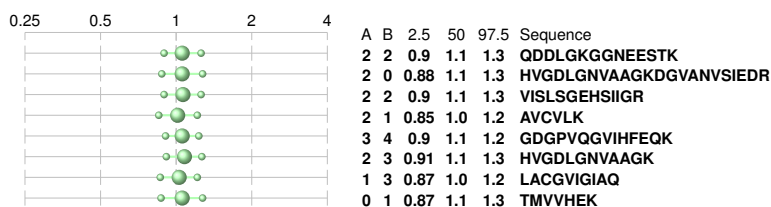
5.591 superoxide dismutase 1 [Rattus norvegicus]

Protein Accession	gij8394328	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.933, 1.17)	
Associated Peptides	8	
Associated Spectra	30	
Coverage	0	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.952	0.998
Avg..iTRAQ.Ratio....116.114.	0.924	1.02
Avg..iTRAQ.Ratio....117.114.	1.12	1.03

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1    MIRQLAPFVL TLWAAPLAH PHVFIDTQLS LVADAQQQLT HVRVTWEYDA LYSLLVTEDM GLD TDGDGAL TETELATLNG
81   FDMQWVDGFN GDLVLSAEAS NIALSGPTEI ATQFDNGQIT TMHTRALETA VPAGTAITIK PYDATYTYTAY DITTAIDTRR
161  APTCRARVAM PDVATMEAL QQQLAQLDAQ TDPSPDAGLPD IGAQMPTVN VTCAAP

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5.592 "NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa [Rattus norvegicus]"

Protein Accession	gij53850628
Mean Expression Ratio	0.954
Median Expression Ratio	0.955
Credible Interval	(0.708, 1.28)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0261
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.883
Avg..iTRAQ.Ratio....116.114.	0.922
Avg..iTRAQ.Ratio....117.114.	0.815

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1      MLRIPVKRAL IGLSKSPKGY VRSTGTAASN LIEVFVDGQS VMVEPGTTVL QACEKVGMI PRFCYHERLS VAGNCRMCLV
81     EIEKAPKVA ACAMPVMKGW NILTNSEKSK KAREGVMEFL LANHPLDCPI CDQGGECDLQ DQSMFMGSDR SRFLLEGKRAV
161    EDKNIGPLVK TIMTRCIQCT RCIRFASEIA GVDDLGTGTR GNDMQVGTYI EKMFMSSELSG NIIDICPVGA LTSKPYAFTA
241    RPWETRKTES IDVMDAVGSN IVVSTRTGEV MRILPRMHED INEEWISDKT RFAYDGLKRQ RLTEPMVRNE KGLLYTSWE
321    DALSRVAGML QSFEGKAVAA IAGGLVDAEA LVALKDLLNK VSDTLCTEE IFPNEGAGTD LRSNYLLNTT IAGVEEADV
401    LLVGTNPRFE APLFNARIK SWLHNDLKVA LIGSPVDLTY RYDHLGDSFK ILQDIASGNH EFSKVLNAAK KPMVVLGSSA
481    LQRDDGAAIL AAVSSIAQKI RVASGAAAEW KVMNHLHRIA SQVAALDLGY KPGVEAIRKN PPKLLFLLGA DGGCITRQDL
561    PKDCFIVYQG HHGVDGAPIA DVILPGAAYT EKSATYVNTE GRAQQTKVAV TFPGLAREDW KIIRALSEIA GITLPHYDTLD
641    QVFNRLGEVS PNLVRYDDVE EANYFQQASE LAKLVDQEFL ADPLVPPQLT IKDFYMTDSI SRASQTMACV VKAVTEGAQA
721    VEEPSIC
    
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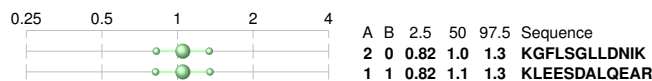


5.593 translocase of inner mitochondrial membrane 44 homolog [Rattus norvegicus]

Protein Accession	gij8394449	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.05	
Credible Interval	(0.83, 1.31)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	0.956
Avg..iTRAQ.Ratio....116.114.	1.05	0.958

Avg..iTRAQ.Ratio....117.114. 1.15 1.05

1 MTETSELLANY RKMQFQLMLM QLFFG



5.594 insulin-like growth factor binding protein 7 [Rattus norvegicus]

Protein Accession	gi 61556795
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.779, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0569
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.24
Avg..iTRAQ.Ratio....116.114.	1.00
Avg..iTRAQ.Ratio....117.114.	1.76

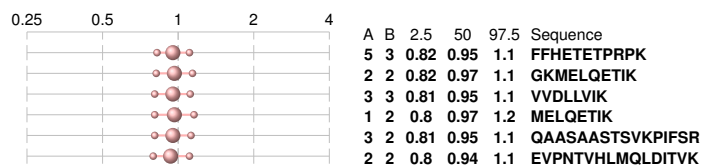
1 MERSPRALLL GAAGLLLLLL PLSSSSSSDA CGPCVPASCP ALPPFGCPLG ETRDAGCCP VCARGEPEPC GGAAGGGHC
 81 APGMECVKSR KRRRGKAGAA AGGPATLAVC VCKSRYPVCG SDGVTYPSGC QLRAASLRAE SRGEKAITQV SKGTCEQGFS
 161 IVTPPKDIWN ITGAKVYLSC EVIGIPTPVL IWNKVKRDHS GVQRTELLPG DRENLAIQTR GGPEKHEVTG WVLVSPLSKE
 241 DTGEYECHAS NSQGQASASA KITVVDIHE IPVKKGEQAQ L



5.595 "PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14) [Rattus norvegicu"

Protein Accession	gj 27663138	
Mean Expression Ratio	0.956	
Median Expression Ratio	0.955	
Credible Interval	(0.847, 1.08)	
Associated Peptides	6	
Associated Spectra	30	
Coverage	0.469	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.838	0.852
Avg..iTRAQ.Ratio....116.114.	1.10	0.856
Avg..iTRAQ.Ratio....117.114.	0.907	0.946

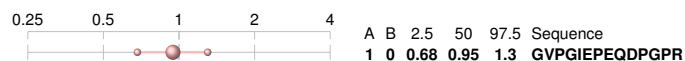
1 MAAAASGLRQ AASAASTSVK PIFSRDLKEA KRRVRELYRA WYREVPNTVH LMQLDITVKQ GRDKVREMFM KNAHVTDPRV
 81 VDLLVIKGM ELQETIKVWK QRTHIMRFFH ETETPRPRDF LSKFYIGHDP



5.596 PREDICTED: similar to reduced pigmentation protein [Rattus norvegicus]

Protein Accession	gj 109458315	
Mean Expression Ratio	0.955	
Median Expression Ratio	0.955	
Credible Interval	(0.709, 1.28)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0718	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.87	
Avg..iTRAQ.Ratio....116.114.	0.995	
Avg..iTRAQ.Ratio....117.114.	0.898	

1 MASSQGRRRR PGTVPGEAA ETDSELSASS SEELYLGPS GPTRGRPTGL RVAGEAAETD SEPEPEPRVA PGDLPLVVQ
 81 RDAVEAWGTE ETPVLAPARS LLQLRLAESQ TRLDHDVAAA VSGVYRRAGR DVAALAGRLA AAQAIGLAAA HSVRLARGDL
 161 CALAERLDIV AGCRLLPDIR GVPGIEPEQD PGPRRA



5.597 "PREDICTED: similar to ATPase inhibitor, mitochondrial precursor [Rattus norvegicus]"

Protein Accession	gij109479491
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.822, 1.35)
Associated Peptides	2
Associated Spectra	7
Coverage	0.119
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	1.32
Avg..iTRAQ.Ratio....117.114.	1.18

1 MGTGAGSIQE AGGPFKGEK AEDRYFREK AR**EQLAALKK** HREEEIDHHS KEIERLQKQT EWQIEED

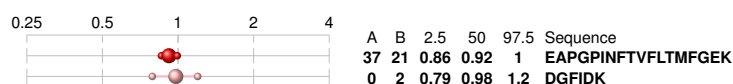


5.598 "PREDICTED: similar to myosin light chain 2, precursor lymphocyte-specific [Rattus norvegicus]"

Protein Accession	gij109495555
Mean Expression Ratio	0.955
Median Expression Ratio	0.955
Credible Interval	(0.821, 1.11)
Associated Peptides	2
Associated Spectra	60
Coverage	0.105

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.02	0.716
Avg..iTRAQ.Ratio....116.114.	0.796	1.18
Avg..iTRAQ.Ratio....117.114.	0.919	0.915

1 MGHQHSWLYI VRCHVQK GAL NNPPVFTQRN VSGMVPGLEE HYLKSHPKLS PDLQQHSHKAR QTMAPRRARK RVEGTASSNV
 81 FSMFDQSQIQ EFKEAFTIMD QNRDGFIDKE DLRDTFAALG RINVKNEELE AMVKEAPGPI NFTVFLTMFG EKLKGTDPPE
 161 TILHAFKVFV SRAKLTYIQC IKEKLMTQAD RFSEEEVKQM FAAFPPDVCG NLDYRNLQCYV ITHGEEKD



5.599 "calpain, small subunit 1 [Rattus norvegicus]"

Protein Accession	gi 67514516
Mean Expression Ratio	1.04
Median Expression Ratio	1.05
Credible Interval	(0.769, 1.4)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0259
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.43
Avg..iTRAQ.Ratio....116.114.	1.18
Avg..iTRAQ.Ratio....117.114.	1.29

1 MFLVNSFLKG GGGGGGGGL GGGLGNVLGG LISGAAGGGG GGGGGGMGL GGGGGGGTA MRILGGVISA ISEAAAQYNP
 81 EPPPPRSHYS NIEANESEEE RQFRKLFVQL AGDDMEVSAT ELMNILNKVV TRHPDLKTDG FGIDTCRSMV AVMDSDTTGK
 161 LGFEFKYLW NNIK KWGGIY RFDTDRSGT IGSNELPGAF EAAGFHLNQH IYSMIIRYS DETGNMDFDN FISCLVRLDA
 241 MFRAFRLDK NGTGQIQVNI QEWLQLTMYS

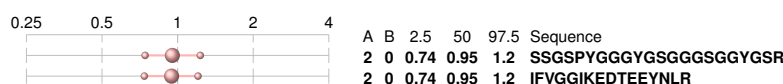


5.600 heterogeneous nuclear ribonucleoprotein A3 [Rattus norvegicus]

Protein Accession	gi 37693507
Mean Expression Ratio	0.954
Median Expression Ratio	0.955
Credible Interval	(0.761, 1.20)
Associated Peptides	2
Associated Spectra	4
Coverage	0.100
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.92
Avg..iTRAQ.Ratio....116.114.	0.879
Avg..iTRAQ.Ratio....117.114.	0.871

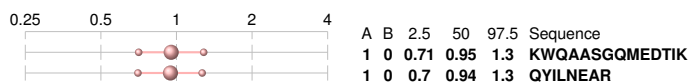
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1      MEVKPPPGRP QPDSGRRRRR RGEEGHDPKE PEQLRKLFIG GLSFETDSDS LREHFEKWT LTDCVVMRDP QTKRSRGFGF
81     VTYSCEVEVD AAMCARPHKV DGRVVEPKRA VSREDSVKPG AHLTVKKIFV GGIKEDTEEY NLFDYFEKYG KIETIEVMED
161    RQSGKKRGFA FVTFDDHDTV DKIVVQKYHT INGHNCEVKK ALSKQEMQSA GSQRGRGGGS GNFMGRGGNF GGGGGNFRG
241    GNFGRRGGYG GGGGSRGSY GGDGGYNGF GGDGGNYGGG PGYSSRGGYG GGGPGYGNQG GGYGGGGGGY DGYNEGGNFG
321    GGNYGGGGNY NDFGNYSQQQ QSNYGPMMKG SFGGRSSGSP YGGGYGSGGG SGGYGSRRF
    
```



5.601 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gi 109459288
Mean Expression Ratio	0.954
Median Expression Ratio	0.956
Credible Interval	(0.727, 1.25)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.968
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	0.797

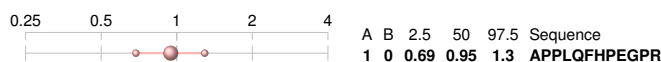


5.602 "amine oxidase, copper containing 3 [Rattus norvegicus]"

Protein Accession	gi 71896590
Mean Expression Ratio	0.956
Median Expression Ratio	0.956
Credible Interval	(0.712, 1.27)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0157
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.978
Avg..iTRAQ.Ratio....116.114.	0.83
Avg..iTRAQ.Ratio....117.114.	0.748

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1      MTQKTTLVLL ALAVITIFAL VCVLLAGRSQ DGGRLSQPLH CPSVLPSVQP QTHPGQSQPF ADLSPEELTA VMSFLIKHLG
81     PGLVDAAQAR PSDNCVFSVE LQLPAKAAAL AHLDRGGPPP VREALAIIFF GGQPKPNVSE LVVGPLPHPS YMRDVTVERH
161    GGPLPYRRP VLTREYQDIQ EMIFHRELPO ASGLLHCCF YKROGHNLK MTTAPRGLQS GDRATWFGIY YNLSGAGFYF
241    HPIGLELLVD HKALDPALWT IQKVFYQGRY YESLTQLEDM FEAGLVNVVL VPDNGTGGSW SLKSSVPPGR APPLQFHPEG
321    PRFSVQGSQV RSSLWAFSFG LGAFSGPRIF DIRFQGERVA YEISVQEAIA LYGGNSPASM STCYMDGSFG IGKYSTPLTR
401    GVDPCYLATY VDWHFLESQ TPKTLRDAFC VFEQNQGLPL RRHHSDFYSH YFGGVVETVL VVRSVATLLN YDYVWDMVFH
481    SNGAIEVKFH ATGYITSAFF FGAGEKFGNR VAEHTLGTVH THNAHFKVDL DVAGLKNWAW AEDLAFVPMN VPWQPEFQMQ
561    RLQVTRKLE TEEEAAPPLG NATPRYLILA SNHSNKWGRH RGYRIQILSF AGKPLPQESP IEKAFTWGRY HLAVTQRKEE
641    EPSSSIYNQ NDPWTPTVDF TDFISNETIA GEDLVAWVTA GFLHIPHAED IPNTVTVGNG VGFFLRPYNF FDEDPSFYSP
721    DSIYFRKQD VTDCEVNSLA CLSQTANCVP DLPAFSHGGF TYK
    
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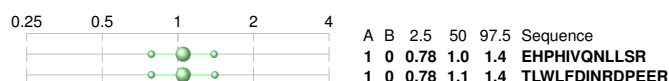
5.603 arylsulfatase B [Rattus norvegicus]

Protein Accession	gi 77993374
Mean Expression Ratio	1.04
Median Expression Ratio	1.05
Credible Interval	(0.803, 1.36)
Associated Peptides	2
Associated Spectra	2

Coverage	0.0492
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.15
Avg..iTRAQ.Ratio....116.114.	1.16
Avg..iTRAQ.Ratio....117.114.	1.26

```

1      MGELSGCTGG SRAGGPGPRL PLLLLLLLWP ARASDAAPP HVVFLVADDL GWNDLGFHGS VIRTPLDAL AAGGVVLDNY
81     YVQPLCTPSR SLLLTGRYQI HMGLQHYLIM TCQPNCVPLD EKLLPQLLKD AGYATHMVGK WHLGMRYRKEC LPTRRGFDY
161    FGILLGSEDY YTHEACAPIE CLNGTRCALD LRDGEEPAKE YTDIYSTNIF TKRATTLIAN HPPEKPLFLY LAFQSVHDPL
241    QVPEEYMEPY DFIQDKHRI YAGMVSLLDE AVGNVTRALK SRGLWNNTVL IFSTDNGGQT RSGGNNWPLR GRKGTWEGG
321    IRGAGFVASP LLKQKGVKSR ELMHITDWLP TLVNLGGST HGTRKPLDGFV VWETISEGSP SPRVELLLNI DPDFDGLPC
401    PGKNTTPEKN DSFPLEHSFA NTSIHAGIRY KNWKLTYGYP GCGYWFPPPS QSNISEVPSV DSPTKTLWLF DINRDPEERH
481    DVSREHPHIV QNLLSRLQYY HEHSVPSYFP PLDFRCDEPKG TGVWSPWM
  
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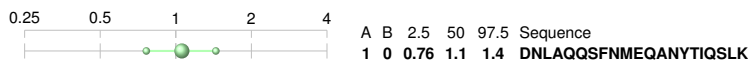


5.604 chromatin modifying protein 5 [Rattus norvegicus]

Protein Accession	gi 70912368
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.772, 1.40)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0959
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.33
Avg..iTRAQ.Ratio....116.114.	1.20
Avg..iTRAQ.Ratio....117.114.	1.37

```

1      MNRFFGKAKP KAPPPSLTDC IGTVDRAES IDKKISRLDA ELVKYKDQIK KMREGPAKMN VKQKALRVLK QKRMYEQQRD
81     NLAQQSFNME QANYTIQSLK DTKTVDAMK LGVKEMKKAY KEVKIDQIED LQDQLEDMME DANEIQEALG RSYGTPELDE
161    DDLEAELDAL GDELLADEDS SYLDEAASAP AIPEGVPTDT KNKDGVLVDE FGLPQIPAS
  
```



5.605 "tropomyosin 3, gamma isoform 2 [Rattus norvegicus]"

Protein Accession	gij29336093
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.77, 1.41)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0605
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.02
Avg..iTRAQ.Ratio....116.114.	0.9
Avg..iTRAQ.Ratio....117.114.	0.916

```

1   MAGSTTIEAV KRKIQVLQQQ ADDAEPRAER LQREVEGERR AREQAEAEVA SLNRRIQLVE EELDRAQERL ATALQKLEEA
81  EKVADESERG MKVIENRALK DEEKMELQEI QLKEAKHIAE EADRKYEEVA RKLVIIEGDL ERTEERAELA ESRCREMDEQ
161 IRLMDQNLKC LSAAEEKYSQ KEDKYEEEIK ILTDKLEAE TRAEFAERSV AKLEKTIDDL EDKLEKCTKEE HLC TQRMLDQ
241 TLLDLNEM
    
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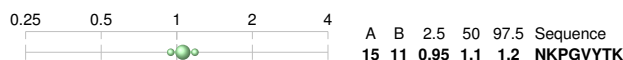
5.606 "PREDICTED: similar to Transmembrane protease, serine 13 (Mosaic serine protease) (Membrane-type mos"

Protein Accession	gij109483420	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.877, 1.25)	
Associated Peptides	1	
Associated Spectra	26	
Coverage	0.0149	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.976	0.991
Avg..iTRAQ.Ratio....116.114.	0.958	0.98
Avg..iTRAQ.Ratio....117.114.	1.23	1.06

NHLBI Zile/Grant, Aged Rat

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1      MDRGSHRNAS PARPSPQASP ARASPQASPA RTPPPQASPA RASPPQASPA RASPARASPV RASPARAPPS RSSSGRSSSA
81     RSASTTSSPT RVYLVRAIPV GTVIRASPAR SAPATRATRE SPGLSFPKFS WQETQRQLPL IGCVLLLIISL VISLILLFYF
161    WRGHTGKIKYK EPLESCPKHA VRCDGVVDCK MKSDELGCVR FDWDKSLKLV YSGSSGEWLP VCSSSSWNTD SERTCQQLGF
241    DSAYRTTEVA HRDVTSSFL SEYNSTIQES LTRSECPSTR YVSLQCAHCG LRAMTGRIVG GALTSESKWP WQVSLHFGTT
321    HICGGTLIDA QWVLTAAHCF FVTREKILEG WKVYAGTNSL HQLPEAASIS QIIINGNYTD EQDDYDIALV RLSPLTLISA
401    HIHPACLPLH GQTFGLNETC WITGFGKTKE TDEKTSFPLR EVQVNLIDFK KCNDYLVDYS YLTPRMMCAG DLRGGDRDSCQ
481    GDSGGPLVCE QNNRWYLAGV TSWGTCGCGQK NKPQVYTKVT EVLPWIYRKM ESEVPRSQ
  
```



5.607 PREDICTED: similar to RAB11 family interacting protein 5 (class I) isoform 1 [Rattus norvegicus]

Protein Accession	gij109473811
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.789, 1.41)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00987
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.24
Avg..iTRAQ.Ratio....116.114.	1.07
Avg..iTRAQ.Ratio....117.114.	1.43

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1      MALVRDDEPA AGSSRWLPTH VQVTVLRASG LRGKSSGAGS TSDAYTVIQV GREKYSTSVV EKTQGCPEWC EECSEFELPPG
81     ALDGLLRAQE TDAGPAPWAS GPNAACELV L TTMHRS LIGV DKFLGRATVA LDEVFRAGRA QHTQWYKLHS KPGKKEKERG
161    EIQVTIQFTR NNLSASMF DL SMKDKPRSPF SKLKDKVKGK KKYDLESASA ILPSSALEDP ELGSLGKMGK AKGFFLRNKL
241    RKSSLTQSN T SLGSDSTLSS TSGSLVYQGP GAELLTRSPS HSSWLATEAG RDSIQSPKLL THKRTYSDEA SQLRAAPPRA
321    LLELQGHLDG ASRSSLCVNG SHVYNEEPQP PLRHRSSI SG PFPSSSLHSV PPRSSEEGSR SSDDSWVRGS HGTSLSLEAVP
401    QGEELSKQTK VLAPGASCSA EEEGTRPPEG KPQVATPMV ASSEAIAAEK ERKPRMGLFH HHHHQGLSRN EVGRRGSVGE
481    KGSPSLGASP HHSSTGEEKA KSSWFLGRES KEPTQKPSLD VSPQVESDPA APHPCFPQAL VPPPAPAAAP MLSTNLFAAA
561    SPATATATAA AANIVLEATP SGFLGVTNPF LTSLQSNPFF EDLKADIALN SPSPAPSLPS ASRASLAPLA SPGKALPEWD
641    DNFNIFAAGR LQSEAGSGIL APAGMGLEED GLQDPPGRTL AVKATEPQGE PGGGRGSSST WLEPKAPVDS VLDQPSTSMS
721    DPGPLGSSGT GPSSRAAQLH LQASASTPDR ELPASEGGAG QSPADSGASL FSSPEVLSVW ERFPGSDDTT GGLEEEAAQD
801    GSQLFQELNT VEDSNPVDVI TISPTAEAA S PVMKGESKGV LSSQVQPEYP DTVPPMGSEG LPSLQLEPEP EQGLEDEGPWL
881    GPPPKPPRL FTPTNSQVEE DKEEENATG GPSSRGPVGE DSTPSALVIG PPESKEE GVN SELEELHRLP SGTLIGEPPEL
961    EDVVGETSSP GSRDCLPRPT SCPEGP IPRS HNSASSTLLS QKDWGTSETD ESFETQSQEL AKEGFGALSV PSQQADLVVK
1041   KEEEEEEKEA EEEEEEEASN PFSCQESQDP LSLPSTSPFG SRGSSTHSGP EELPTPEPEP FPPPLPPWA SHRHGVPPFP
1121   CPPLP IAWPL TSSSSLPEES ACPLSPTSPTG GSPTPYGEDH AAATPASPLV LLPLETRPAE DPQPSGSPHP VKPLTAAPVE
1201   ASPDRKQSR T SLSTALSSGL ERLKTVTSGG IQSVLPASQL GSTVDTKRLK DSAVLDQSAK YYHLTHDELI GLLLQREREL
1281   SQRDEHVQEL ESYIDRLLVR IMETSPTLLQ ISPGPSK
  
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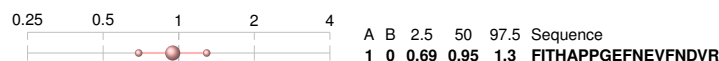


5.608 "PREDICTED: similar to capping protein (actin filament) muscle Z-line, alpha 1 [Rattus norvegicus]"

Protein Accession	gij109467357
Mean Expression Ratio	0.957
Median Expression Ratio	0.956
Credible Interval	(0.712, 1.28)
Associated Peptides	1
Associated Spectra	1
Coverage	0.063
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.887
Avg..iTRAQ.Ratio....116.114.	0.8
Avg..iTRAQ.Ratio....117.114.	0.98

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1   MADFEDRVSD EEKVRIAAK* ITHAPPGEFN EVFNDVRLLL NNDNLLREGA AHAF AQYNMD QFTPVKIEGY DDQVLITEHG
81  DLGNSRFLDP RNKISFKFDH LRKEASDPQP EDVDGGLKSW RDSCDSALRA YVKDHYSNGF CTVYAKTIDG QQTIIACIES
161 HQFQPKNFWN GRWRSEWKFT ITPPTAQVVG VLKIQVHYEY DGNVQLVSHK DVQDSVTVSN EVQTAKEFIK IIESAENEYQ
241 TAISENYQTM SDTTFKALRR QLPVTRTKID WNKILSYKIG KEMQNA
  
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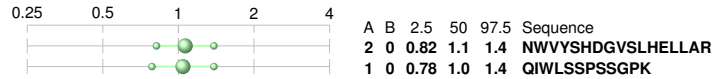
5.609 "PREDICTED: similar to Frataxin, mitochondrial precursor (Fxn) [Rattus norvegicus]"

Protein Accession	gij109463707
Mean Expression Ratio	1.05
Median Expression Ratio	1.05
Credible Interval	(0.82, 1.35)
Associated Peptides	2
Associated Spectra	3
Coverage	0.139
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.17
Avg..iTRAQ.Ratio....116.114.	1.23
Avg..iTRAQ.Ratio....117.114.	1.02

NHLBI Zile/Grant, Aged Rat

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1      MWTFGRRAAA GLLPRTASRA SAWVRNPRGR ERIGTCGRRG LHV TANADAI RSHLNLHLYL GQILNIKKQS VCVVHLRNSG
81     TLGNPSSLDE TAYERLAEET LDALAEFFED LADKPYTLKD YDVSFGDGLV TIKLGGDLGT YVINKQTPNK QIWLSSPSSG
161    PKRYDWTGKN WVYSHDGVSL HELLAEELTE ALNTKLDLSS LAYSGKGT
  
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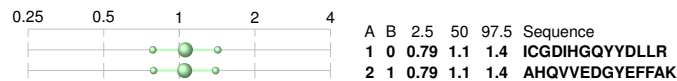


5.610 "protein phosphatase 1, catalytic subunit, alpha [Rattus norvegicus]"

Protein Accession	gi 13928710	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.8, 1.36)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.0848	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.993	1.00
Avg..iTRAQ.Ratio....116.114.	0.949	0.91
Avg..iTRAQ.Ratio....117.114.	0.912	1.10

```

1      MSDSEKLNLD SIIGRLLEVQ GSRPGKNVQL TENEIRGLCL KSREIFLSQP ILLELEAPLK ICGDIHGQYY DLLLFEYGG
81     FPPESNYLFL GDYVDRGKQS LETICLLLAY KIKYPENFFL LRGNHECASI NRIYGFYDEC KRRYNIKLRK TFTDCFNCLP
161    IAAIVDEKIF CCHGGLSPDL QSMEQIRRI RPTDVPDQGL LCDLLWSDPD KDVQGWGEND RGVSFTEGAE VVAKFLHKHD
241    LDLICRAHQV VEDGYEFFAK RQLVTLFSAP NYCGEFDNAG AMMSVDETLM CSFQILKPAD KNKGKYGQFS GLNPGGRPIT
321    PPRNSAKAKK
  
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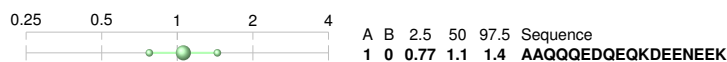
5.611 immunoglobulin binding protein 1 [Rattus norvegicus]

Protein Accession	gi 13928860	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.78, 1.40)	
Associated Peptides	1	

Associated Spectra	1
Coverage	0.0529
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.05
Avg..iTRAQ.Ratio....116.114.	1.08
Avg..iTRAQ.Ratio....117.114.	0.95

```

1      MAASEEELL  PRLPELFETS  KKLLEELEVA  TEPTGSRTIQ  DKVSKGLELL  EKAAGMSQL  DLFSRNEDLE  EIASIDLKYL
81     MVPALQGALT  MKQVNPSKRL  DHLQRAREHF  IHFLTQCHCY  HVAEFQLPQT  KNNSAENNTA  RSSMAYPNLV  AMASQRQAKI
161    ERYKQKKEVE  HRLSALKSAV  ESGQADDERV  REYLLHLRR  WIGISLEEIE  SIDQEIKILK  DKDSPREESA  CQSSLPEKPP
241    MKPFILTRNK  AQAKVFGTGY  PSLATMTVSD  WYEQHQKYGA  LPDRGIKAPP  SADPQR  AAQQ  QEDQEQKDEE  NEEFALHRMR
321    EWDDWKDTHP  RGYGNRQNMG
    
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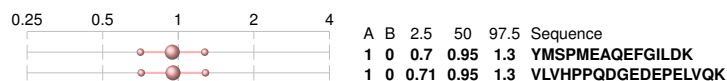


5.612 "PREDICTED: similar to Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial precursor"

Protein Accession	gij109513095
Mean Expression Ratio	0.957
Median Expression Ratio	0.956
Credible Interval	(0.738, 1.26)
Associated Peptides	2
Associated Spectra	2
Coverage	0.121
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.936
Avg..iTRAQ.Ratio....116.114.	0.955
Avg..iTRAQ.Ratio....117.114.	0.909

```

1      MWPRVLLRDG  RAAAGGCRAL  LSRFAVRFSP  PWSTGSDSPL  RSNLHGATR  AFPLIPIVVE  QTGRGERAYD  IYSRLLRERI
81     VCVMGPIDDS  VASLVIAQLL  FLQSESNKKP  IHMYINSPGG  VVTAGLAIYD  TMQYILNPIC  TWCVGGQAASM  GSLLLAAGSP
161    GMRHSLPNSR  IMIHQPSSGA  RGQATDIAIQ  AEEIMKLRQ  LYNIYAKHTK  QSLQVIESAM  ERDRYMS PME  AQEFGILDKV
241    LVHPPQDGED  EPELVQKETT  TAPADPPAPA  GT
    
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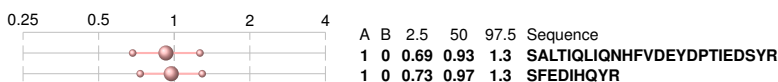


5.613 PREDICTED: similar to GTPase HRas precursor (Transforming protein p21) (p21ras) (H-Ras-1) (c-H-ras)

Protein Accession	gij109463189
Mean Expression Ratio	0.956
Median Expression Ratio	0.957
Credible Interval	(0.728, 1.25)
Associated Peptides	2
Associated Spectra	2
Coverage	0.109
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.925
Avg..iTRAQ.Ratio....116.114.	0.973
Avg..iTRAQ.Ratio....117.114.	0.896

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1      MGRRCPRMEP SLHLGLRQLG VPANSVFLWY SASAVQTVLD SRTREAPPGP PETLRPAAIT LRPRGHKDR VGPQPGPSAP
81     SYSSRSCSHL LPTPSASSHP SVKAPWPLVE GGAGAPGLAA PVEAMTEYKL VVVGAGGVGK SALT IQLIQN HFVDEYDPTI
161    EDSYRKQVVI DGETCLLDIL DTAGQEEYSA MRDQYMRTE GFLCVFAINN TKSFEDIHQY REQIKRVKDS DDVPMVLVGN
241    KCDLAARTVE SRQAQDLARS YGIPYIETSA KTRQGVEDAF YTLVREIRQH KLRKLNPPDE SGPGCMSCKC VLS
  
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5.614 annexin 1 [Rattus norvegicus]

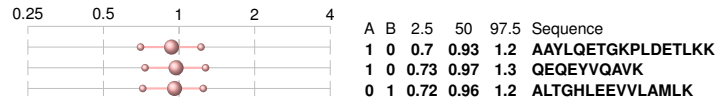
Protein Accession	gij6978501	
Mean Expression Ratio	0.955	
Median Expression Ratio	0.957	
Credible Interval	(0.745, 1.22)	
Associated Peptides	3	
Associated Spectra	3	
Coverage	0.121	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.988	0.728
Avg..iTRAQ.Ratio....116.114.	0.788	0.951
Avg..iTRAQ.Ratio....117.114.	1.12	0.95

NHLBI Zile/Grant, Aged Rat

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1      MAMVSEFLKQ ACYIEKQEQE YVQAVFSYKG GPGSAVSPYP SFNPSSDVAA LHKAIMVKGV DEATIIDILT KRTNAQRQQI
81     KAAYLQETGK PLEDETLKKAL TGHLEEVVLA MLKTPAQFDA DELRAAMKGL GTDEDTLIEI LTRSNQQIR EITRVYREEL
161    KRDLAKDITS DTSGDFRNAL LALAKGDRCE DMSVNQDLAD TDARALYEAG ERRKGTDVNV FNTILTRSY PHLRKFVQNY
241    RKYSQHD MNK ALDLELKGDI EKCLTTIVKC ATSTPAFFAE KLYEAMKGAG TRHKTLIRIM VSRSEIDMNE IKV FYQKKYG
321    IPLCQAILDE TKGDYEKILV ALCGGN

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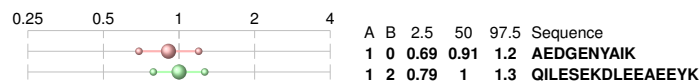
5.615 tubulin cofactor a [Rattus norvegicus]

Protein Accession	gij61557414	
Mean Expression Ratio	0.958	
Median Expression Ratio	0.957	
Credible Interval	(0.753, 1.21)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.241	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.00	1.07
Avg..iTRAQ.Ratio....116.114.	0.66	1.18
Avg..iTRAQ.Ratio....117.114.	0.758	1.02

```

1      MADPRVRQIK IKTGVVKKRLV KEKVMYEKEA KQEQEKIEKM KAEDGENYAI KQAEILQES RMMIPDCQRR LEAAYTDLRQ
81     ILESEKDLLE AE EYF EARIV LDSVKLEA

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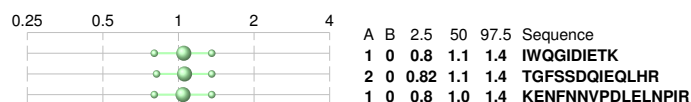
5.616 PREDICTED: similar to tescalcin [Rattus norvegicus]

Protein Accession	gij109495987	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.05	
Credible Interval	(0.834, 1.31)	
Associated Peptides	3	

Associated Spectra	4
Coverage	0.182
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.19
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	1.05

```

1      MGAHSASEE VRELEKGTGF SSDQIFQLHR RFKQLSGDQP TIRKENFNNV PDLELNPIRS KIVRAFFDNR NLRKGSSGLA
81     DEINFEDFLT IMSYFRPIDT TLGEEQVELS RKEKLFKLFH MYDSDSDGRI TLEEYRNVE ELLSGNPHIE KESARSIADG
161    AMMEAASVCV GQMEPDQVYE GITFEDFLK IWQGIDIETKM HIRFLNMETI ALCH
    
```



5.617 "calponin 3, acidic [Rattus norvegicus]"

Protein Accession	gi 9506501	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.04	
Credible Interval	(0.798, 1.37)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.0364	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.24	1.55
Avg..iTRAQ.Ratio....116.114.	0.977	0.905
Avg..iTRAQ.Ratio....117.114.	1.12	1.02

```

1      MTHFNKGPSY GLSAEVKMKI ASKYDQAAE DLRNWIEEVT GMGIGTNFQL GLKDGIIICE LINKLQPGSV KKVNESSLNW
81     PQLNIGNFI KAIQAYGMKP HDIFEANDLF ENGNMTQVQT TLVALAGLAK TRGFHTTIDI GVKYAEKQTR RFDEGKLGAG
161    QSVIGLQMG T NKCASQAGMT AYGTRRHLYD PKMQTDRKPFQ QTTISLQMG T NKGASQAGMS APGTRRDIYD QKLTLPVDN
241    STISLQMG T N KVASQKGM SV YGLGRQVYDP KYCAAPTEPV IHNGSQGTGT NGSEISDSDY QAEYPDEYHG EYPDEYPR EY
321    QYGGDDQGIDY
    
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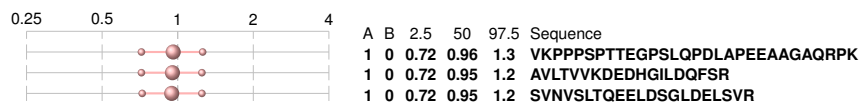


5.618 A kinase (PRKA) anchor protein 2 [Rattus norvegicus]

Protein Accession	gi 58865524
Mean Expression Ratio	0.957
Median Expression Ratio	0.957
Credible Interval	(0.752, 1.22)
Associated Peptides	3
Associated Spectra	3
Coverage	0.0805
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.99
Avg..iTRAQ.Ratio....116.114.	0.877
Avg..iTRAQ.Ratio....117.114.	1.07

```

1    MEIGVSVAEC KSVPGITSTP HSKDHSSPFY SPSHNGLLTD HHESLDNDVA REIQYLDEVL EANCDDSSVD GTYNGISSPE
81   PGAAAILVSSL GSPAHSATKV EPIEKASGRQ LPPHIELSRG PSDSMAEGER ANGHSTDDQPQ DMLGNSLQAP ASPSSSTSSH
161  CSSRDGEFTL TTLKKEAKFE LRAFHEKPKP SKLFEEDHEE KEQFCIRKVR PSEEMIELEK ERRELIRSOA VKKNPGIAAK
241  WNNFPQKTI  EEQLDEEHLE SHRKYKERKE KRAQQEQLQL QQQQQQLLQ LQQLQQQQQQ QLSLTSQLCTA PAAHEHLDSI
321  EHTKEDVTE  QIDFSAARKQ FQQMENSRT LAKGQSTPRL FSIKFFYKPL GSINSDKPP T ILRPATIGGT VEDSSTQAAK
401  EQKALCVSES QSAGAGTGNA ATQGKEGPYS EPSKRGPLSK LWAEDEGFTS ARAVLTVVKD EDHGILDQFS RSVNVSILTQE
481  ELDSGLDELS VRSQDTTVLE TSNDFSMND ISDSGASNET PNALQENSLA DFSLPTTPQT DNPSEGREGV SKSFSHDGFY
561  SPSTTLGDSP SVDDPLEYQA GLLVQNAIQQ AIAEQVDKAE VHTSKEGSEQ QEPGAMVEEA GSQAPGSEKP QGMFAPPQVS
641  SPVQEKRDVL PKILPGEDKT LREKGPSQPP TAVQPSGPVN MKETRPEGGY FSKYSEAAEL RSTASLLATQ ESDVMVGPFK
721  LRSRKQRTLS MIEEEIRAAQ EREELKRQR QVRQSTPSR AQNAPSLPSR TICYKTAPGK IEKVKPPSP TTEGSLQPD
801  LAPEEAAGA RPKNLMQTLM EDYETHKSKR RERMDDSSVL EATRVNRRK ALALRWEAGI YANQEEEDNE
    
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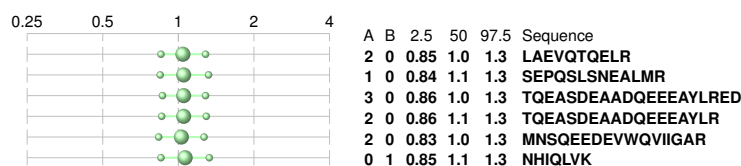


5.619 diablo [Rattus norvegicus]

Protein Accession	gi 56605642	
Mean Expression Ratio	1.05	
Median Expression Ratio	1.04	
Credible Interval	(0.888, 1.24)	
Associated Peptides	6	
Associated Spectra	11	
Coverage	0.283	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.17	1.08
Avg..iTRAQ.Ratio....116.114.	1.18	1.06
Avg..iTRAQ.Ratio....117.114.	1.01	1.09

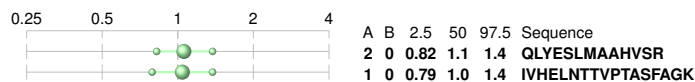
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1      MAALRSWMTR SVTFLFRYGQ RFPVSANSKK RCFSELIRPW HKTMLTGFV TLCAPVIAQK SEPQSLNEA LMRRAVSLVT
81     DSTSTFLSQT TYALIEAITE YTKAVYTLVS LYRQYTSLLG KMNSQEEDEV WQVIIGARVE MTSKQQEYLK LETTWMTAVS
161    LSEMAAEAAY QTGADQASIT ARNHIQLVKS QVQEVRLSQ KAETKLAEVQ TQELRQKTQE ASDEAADQEE EAYLRED
    
```



5.620 "PREDICTED: similar to CG15881-PA, isoform A [Rattus norvegicus]"

Protein Accession	gij109493360
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.82, 1.33)
Associated Peptides	2
Associated Spectra	3
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.16
Avg..iTRAQ.Ratio....116.114.	1.3
Avg..iTRAQ.Ratio....117.114.	0.976

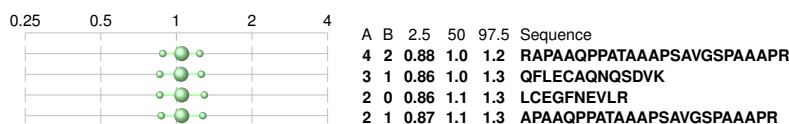


5.621 PREDICTED: similar to coiled-coil-helix-coiled-coil-helix domain containing 2 (predicted) [Rattus n

Protein Accession	gij109487557
Mean Expression Ratio	1.05

Median Expression Ratio	1.04	
Credible Interval	(0.896, 1.22)	
Associated Peptides	4	
Associated Spectra	15	
Coverage	0.312	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.01	1.28
Avg..iTRAQ.Ratio....116.114.	1.15	0.703
Avg..iTRAQ.Ratio....117.114.	1.11	1.09

1 MPRDSRSRTS RVTTPASRAP QMRAAPRAP AAQPPATAAA PSAVGSPAAA PQPGLMAQM ATTAAGVAVG SAVGHHTLGH
 81 ITGGFSGGAN AEPARPDITY QEPQGAPLQN QHSFGPCSLE IKQFLECAQN QSDVKLCEGF NEVLRQCRIA NGLI



5.622 eukaryotic translation initiation factor 4H [Rattus norvegicus]

Protein Accession	gij55741853
Mean Expression Ratio	0.957
Median Expression Ratio	0.958
Credible Interval	(0.727, 1.25)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0524
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.967
Avg..iTRAQ.Ratio....116.114.	0.883
Avg..iTRAQ.Ratio....117.114.	0.99

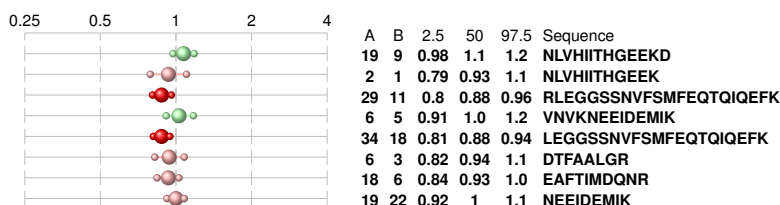
1 MADFDTYDDR AYSSFGGGRG SRGSAGGHGS RSQKELPTEP PYTAYVGNLP FNTVQGDIDA IFKDLIRSIV RLVRDKDSDK
 81 FKGFCYVEFD EVDSLKEALT YDGALLGDRS LRVDAEGRK QDKGGFGFRK GGPDDRGMGG SREPRGGWDS RDDFSSGYRD
 161 DFLGGRGGRS PGDRRAGPPM GSRFRDGPPL RGSNMDFREP TEEERAQRPR LQLKPRTVAT PLNQVANPNS AIFGGARPRE
 241 EVVQKEQE



5.623 "myosin regulatory light chain 2, ventricular/cardiac muscle isoform [Rattus norvegicus]"

Protein Accession	gi 78214305	
Mean Expression Ratio	0.958	
Median Expression Ratio	0.958	
Credible Interval	(0.887, 1.03)	
Associated Peptides	8	
Associated Spectra	208	
Coverage	0.4	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	0.69
Avg..iTRAQ.Ratio....116.114.	0.801	1.10
Avg..iTRAQ.Ratio....117.114.	1.01	0.896

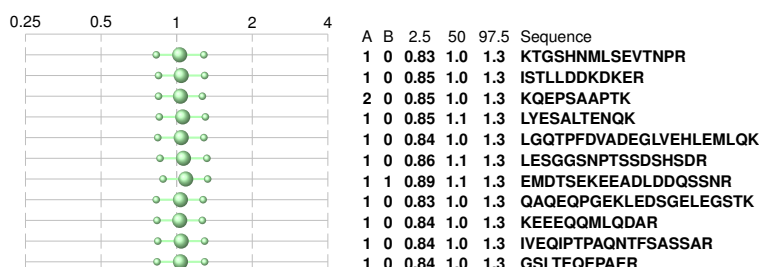
1 MSPKKAKKRL EGGSSNVFSM FEQTQIQEFK EAFTIMDQNR AGFIDKNDLR DTFAALGRVN VKNEEIDEMI KEAPGPINF
 81 VFLTMFREKL KGAGPEETLL NAFKVFAPRR RITGADCQVE MLTTQAERFS KEETDQMAA FPPNVTGNLD YK~~NLVHIITH~~
 161 ~~GEEKD~~



5.624 "PREDICTED: similar to protein phosphatase 1, regulatory (inhibitor) subunit 12B isoform b [Rattus n"]

Protein Accession	gi 109497879	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.901, 1.21)	
Associated Peptides	11	
Associated Spectra	13	
Coverage	NA	

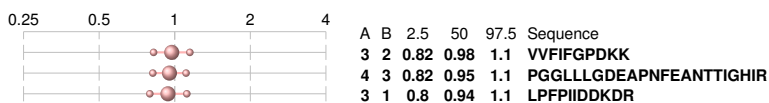
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.14	1.48
Avg..iTRAQ.Ratio....116.114.	0.935	1.46
Avg..iTRAQ.Ratio....117.114.	1.16	1.59

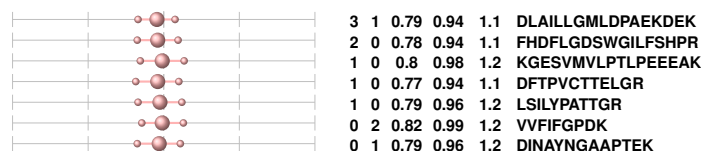


5.625 peroxiredoxin 6 [Rattus norvegicus]

Protein Accession	gi 16758348	
Mean Expression Ratio	0.959	
Median Expression Ratio	0.958	
Credible Interval	(0.85, 1.08)	
Associated Peptides	10	
Associated Spectra	28	
Coverage	0.585	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.918	0.929
Avg..iTRAQ.Ratio....116.114.	1.03	0.982
Avg..iTRAQ.Ratio....117.114.	0.868	0.87

1 M P G G L L L G D E A P N F E A N T T I G H I R F H D F L G D S W G I L F S H P R D F T P V C T T E L G R A A K L A P E F A K R N V K L I A L S I D S V E D H F
81 A W S K D I N A Y N G A A P T E K L P F P I I D D K R D L A I L L G M L D P A E K D E K G M P V T A R V V F I F G P D K E L K L S I L Y P A T T G R N F D E I
161 L R V V D S L Q L T A S N P V A T P V D W K K G E S V M V L P T L P E E E A K Q L F P K G V F T K E L P S G K K Y L R Y T P Q P





5.626 PREDICTED: similar to Anionic trypsin II precursor (Pretrypsinogen II) [Rattus norvegicus]

Protein Accession	gi 109471955	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.843, 1.28)	
Associated Peptides	1	
Associated Spectra	8	
Coverage	0.0407	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.968	1.14
Avg..iTRAQ.Ratio....116.114.	0.94	1.08
Avg..iTRAQ.Ratio....117.114.	0.935	1.49

```

1      MRALLVVLV  GAAVAFPVDD  DDKIVGGYTC  QEHSVPYQVS  LNSGYHYCGG  SLINDQWVVS  AAHCYKSRIQ  VRLGEHNINV
81     LEGDEQFVNA AKIHKPNFD  RKTLNNDIML  ILLSSPVKLN  ARVATVALPS  SCAPAGTQCL  ISGWGNTLSF  GVNDPDLQ
161    LDAPLLPQAD  CEASYPGKIT  NNMVCAGFLE  GGRDSCQGDS  GGPVVCNGEL  QGIVSWGYGC  ALPDNPGVYT  KVCNYVDWIQ
241    DTIAVN
  
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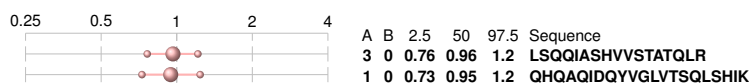
5.627 reticulon 2 (Z-band associated protein) [Rattus norvegicus]

Protein Accession	gi 42476339
Mean Expression Ratio	0.96
Median Expression Ratio	0.959
Credible Interval	(0.762, 1.21)
Associated Peptides	2
Associated Spectra	4
Coverage	0.081

Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.906
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	1.01

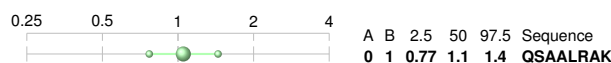
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1      MGQVLPVFAH CKEAPSTASS TPDSTEGGND DSDFRELHTA REFSEDEEEE TTSQDWGTPR ELTFSYIAFD GVVGSGGRRD
81     SVVRRPRPQG RSVSEPRDPP PQPSLGDLSL SIPSLSQSPE PGRRGDDPTV PPAERPLEEL RLRLDQLGWA VRSAGSGEDS
161    ATSSSTPLEN EEPDGLLEASE AGETNLELRL AQLHLQFEG LTPQLSPSSG IPQAHTPSPQ RSQDLNTGPD EPLPNGEGEH
241    WRLLQEPEIT AQCLNSTDQS EFTLEPLLVL ADLLYWKDTR TSGAIFTGLM ASLLCLLHFS IVSVAHLAL LGLCATISLR
321    VYRKVLQAVH RGDGTNPFQA YLDMDLTLTR EQTERLSQQL ASHVVSTATQ LHHFFLVEDL VDSLKLALLF YILTFVGAIF
401    NGLTLVILGV VALFTVPLLY RQHQAQIDQY VGLVTSQLSH IKAKIRAKIP GTGTLAPAAS VSGSKAKAE
  
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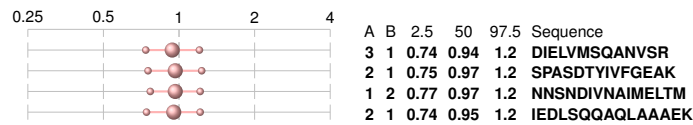
5.628 PREDICTED: similar to cytoplasmic FMR1 interacting protein 2 [Rattus norvegicus]

Protein Accession	gij109488018
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.775, 1.41)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	0.774
Avg..iTRAQ.Ratio....117.114.	1.45



5.629 PREDICTED: similar to nascent polypeptide-associated complex alpha polypeptide [Rattus norvegicus]

Protein Accession	gij109481411
Mean Expression Ratio	0.959
Median Expression Ratio	0.959
Credible Interval	(0.776, 1.18)
Associated Peptides	4
Associated Spectra	13
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.86
Avg..iTRAQ.Ratio....116.114.	0.844
Avg..iTRAQ.Ratio....117.114.	0.91



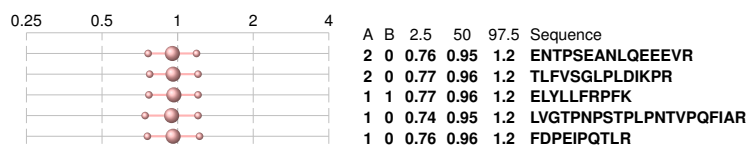
5.630 PREDICTED: similar to RNA binding protein gene with multiple splicing isoform 1 [Rattus norvegicus]

Protein Accession	gij109504262	
Mean Expression Ratio	0.96	
Median Expression Ratio	0.959	
Credible Interval	(0.798, 1.15)	
Associated Peptides	5	
Associated Spectra	8	
Coverage	0.290	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.01
Avg..iTRAQ.Ratio....116.114.	0.985	0.868
Avg..iTRAQ.Ratio....117.114.	0.96	0.604

NHLBI Zile/Grant, Aged Rat

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1      MNGGGKAEKE NTPSEANLQE EEVRTLFVSG LPLDIKPREL YLLFRPFKGY EGSLIKLTSK QPVGFSVSDS RSEAEAAKNA
81     LNGIRFDPEI PQTLELEFAK ANTKMAKNL VGTNPSTPL PNTVPQFIAR EPYELTVPAL YPSSPEVWAP YPLYPAELAP
161    ALPPAAFTY PASLHAQDLH GGRENCLLV LCLAHARVRC VHTSTLNKHS KFFGVVGLVR WVFLSRGKAQ HTCLLSTSSA
241    N
  
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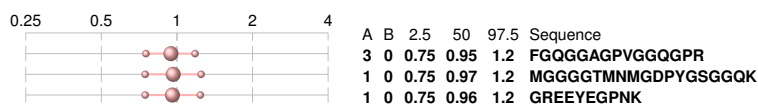


5.631 NonO/p54nrb homolog [Rattus norvegicus]

Protein Accession	gi 70778983
Mean Expression Ratio	0.96
Median Expression Ratio	0.959
Credible Interval	(0.776, 1.19)
Associated Peptides	3
Associated Spectra	5
Coverage	0.063
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.987
Avg..iTRAQ.Ratio....116.114.	0.924
Avg..iTRAQ.Ratio....117.114.	0.986

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1      MSRDRFRSRG GGGGGFHRRG GGGGRGGLHD FRSPPPGMGL NQNRGPMGPG FGGPKPPLPP PPPHQQQQP PPQQPPPPQP
81     PPHQPPPHQ PPHQPPPPP QESKPVVPQG PGSAPGVSTA PPPAVSAPPA NPPTTGAPPG PGPPTPPPA VPSTAPGPPP
161    PSTPSSGVST TFPQTGGPPP FPAGGAGPGP KQPGPGGPK GGMPPGPKP GGGPGMGAPG GHPKPPHRGG GEPRGGRQHH
241    APYHQHHQG PPPGGPGPRT EEKISDSEGF KANLSLRRP GEKTYTQRCR LFGVGNLPADI TEDEFKRLFA KYGEPGEVFI
321    NKGKGFIFIK LESRALAEIA KAELDDTPMR GRQLRVRFAT HAAALSVRNL SPYVSNELLE EAFSQFGPIE RAVVIVDDRG
401    RSTGKGI VEF ASKPAARKAF ERCSEGVFLL TTTPRPVIVE PLEQLDDEDG LPEKLAQKNP MYQKERETPP RFAQHGTFEY
481    EYSQRWKS LD EMEKQREQV EKNMKDAKDK LESEMEDAYH EHQANLLRQD LMRRQEELRR MEELHSQEMQ KRKEMQLRQE
561    EERRRREEM MIRQREMEEQ MRRQREESYS RMGYMDPRER DMRMGGGGTM NMGDPYGGGQK FFPPLGGGG GIGYEANPGV
641    PPATMSGSM GSDMRTERFG QGGAGPVGGQ GPRGMGPSTP AGYGRGREY EGPNKPRF
  
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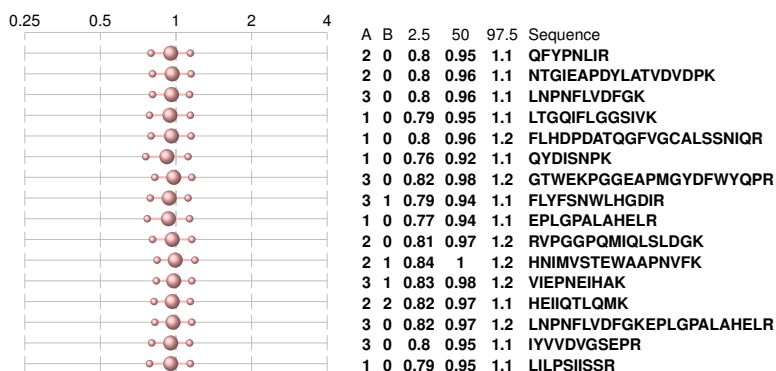


5.632 selenium binding protein 2 [Rattus norvegicus]

Protein Accession	gi 18266692	
Mean Expression Ratio	0.959	
Median Expression Ratio	0.959	
Credible Interval	(0.869, 1.06)	
Associated Peptides	16	
Associated Spectra	38	
Coverage	0.422	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	0.898
Avg..iTRAQ.Ratio....116.114.	1.04	1.01
Avg..iTRAQ.Ratio....117.114.	0.88	1.17

```

1   MATKCTKCGP GYATPLEAMK GPREEIVYLP CIYRNTGIEA PDYLATVDVD P1SPHYSQVI HRLPMPHLKD ELHHS1GWNTC
81  SSCFGDSTKS RDKLILPSII SSRIYVVDVG SEPRAPKLHK VIEPNEIHAK CNLGNLHTSH CLASGEVMIS SLGDPQGN1GK
161 GGFVLLDGET FEVKGTWEKP GGEAPMGYDF WYQPRHNIMV STEWAAPNVF1 DGFNPAHVE AGLYGSHIHV WDWQRHEIIQ
241 TLQMKDGLIP LEIRFLHDPD ATQGFVGCAL SSNIQRFYKN EGGTWSVEKV IQVPSKKVKG WMLPEMPGLI TDILLSLDD1DR
321 FLYFSNWLHG DIRQYDISNP KPRLTGQIF LGG1SIVNGGS VQVLEDQELT CQPEPLVVKG KRVPGGPQMI QLSLDGKRLY
401 VTTSLYSAWD KQFYPNLIFE GSVMLQIDVD TANGGLKLN1P NFLVD1FCKEP LGPALAHEL1R YPGGDCSSDI WI
  
```



5.633 catalase [Rattus norvegicus]

Protein Accession	gi 6978607	
Mean Expression Ratio	0.96	
Median Expression Ratio	0.959	
Credible Interval	(0.735, 1.26)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	0.0721	

Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	0.806
Avg..iTRAQ.Ratio....117.114.	0.96

```

1      MADSRDPASD QMKQWKEQRA P QKPDVLTG GGNPIGDKLN IMTAGPRGPL LVQDVVFTDE MAHFDRERIP ERVHVAKGAG
81     AFGYFEVTHD ITRYSKAKVF EHIGKRTPIA VRFSTVAGES GSADTVRDPR GFAVKFYTED GNWDLVGNNT PIFFIRDAML
161    FPSFIHSQKR NPQTHLKDDP MVWDFWNSLCP ESLHQVTFLE SDRGIPDGHR HMNGYGSHTF KLVNANGEAV YCKFHYKTDQ
241    GIKNLPVEEA GRLAQEDPDY GLRDLFNAIA SGNYPSTWTFY IQVMTFKEAE TFPFNFFDLT KVWPHKDYPL IPVGKLVLNR
321    NPANYPFAEVE QMAFDPSNMP PGIEPSPDKM LQGRLFAYPD THRHRLGPNY LQIPVNCOPYR ARVANYQRDG PMCMHDNQGG
401    APNYYPNSFS APEQQGSAL E H S Q C S A D V K R F N S A N E D N V T Q V R T F Y T K V L N E E E R K R L C E N I A N H L K D A Q L F I Q R K A V K
481    N F T D V H P D Y G A R V Q A L L D Q Y N S Q K P K N A I H T Y V Q A G S H I A A K G K A N L
    
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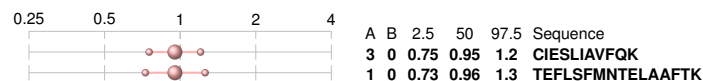


5.634 S100 calcium binding protein A11 [Rattus norvegicus]

Protein Accession	gi 51854249
Mean Expression Ratio	0.96
Median Expression Ratio	0.96
Credible Interval	(0.766, 1.21)
Associated Peptides	2
Associated Spectra	4
Coverage	0.276
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.95
Avg..iTRAQ.Ratio....116.114.	0.933
Avg..iTRAQ.Ratio....117.114.	1.03

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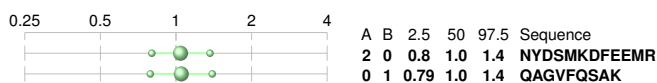
1      MPTETERCIE SLIAVFQKYS GKDGN SCHLS KTEFLSFMNT ELAAFTKNQK DPGVLD RMMK KLDLNSDGQL DFQEFNLNIG
81     GLAIACHESF LQTSQKRI
    
```



5.635 "cytochrome c oxidase, subunit VIc [Rattus norvegicus]"

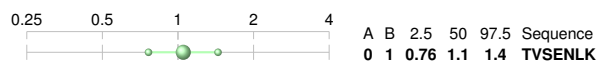
Protein Accession	gi 9506509	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.81, 1.33)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	0.323	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.876	0.927
Avg..iTRAQ.Ratio....116.114.	1.14	0.787
Avg..iTRAQ.Ratio....117.114.	1.21	1.33

1 MRGLLAKRLR VHIVGAFAVA LGVAAAYKFG VAEPRKKAYA DFYRNYDSMK DFEEMRQAGV FQSAK



5.636 PREDICTED: similar to minichromosome maintenance deficient 8 [Rattus norvegicus]

Protein Accession	gi 62645914	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.771, 1.41)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	NA	
Experiment	B	
Avg..iTRAQ.Ratio....115.114.	0.91	
Avg..iTRAQ.Ratio....116.114.	1.01	
Avg..iTRAQ.Ratio....117.114.	1.13	

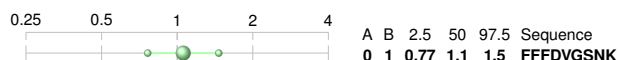


5.637 PREDICTED: similar to Transcriptional activator protein Pur-alpha (Purine-rich single-stranded DNA-

Protein Accession	gij109507148
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.771, 1.42)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0305
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.951
Avg..iTRAQ.Ratio....116.114.	0.842
Avg..iTRAQ.Ratio....117.114.	1.32

```

1   MADRDSGSER GGGGGGSGGG GGAPGGLQHE TQELASKRVD IQNKRFLYLDV KQNAKGRFLK IAEVGAGGNK SRLTLSMSVA
81  VEFRDYLGDF IEHYAQLGPS QPDLAQAQD EPRRALKSEF LVRENKYYM DLKENQGRGF LRIRQTVNRR PGLGSTQGQT
161 IALPAQGLIE FRDALAKLID DYGVEEPAE LPEGTSLTVD NKR FFDVGS NRYGVFMRVS EVKPTYRNSI TVPYKVVAKF
241 GHTFCKYSEE MKKIQEKQRE KRAACEQLHQ QQQQQQBEET AATLLQGE EGEED
    
```



5.638 restin [Rattus norvegicus]

Protein Accession	gij38505168
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.767, 1.40)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0136
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.13

Avg..iTRAQ.Ratio....116.114. 1.29
 Avg..iTRAQ.Ratio....117.114. 1.25

```

1      M S M L K P S G L K   A P T K I L K P G S   T A L K T P A A A A   A P L E K T V P S E   K A S G P P S S E T   Q E E F V D D F R V   G E R V W V N G N K   P G F I Q F L G E T
81     Q F A P G Q W A G I   V L D E F I G K N D   G S V A G V R Y F Q   C E P L K G I F T R   P S K L T R K V Q A   E D E A N G L Q T A   H A R A A S P L S T   A A A T M V S S S P
161    A T P S N I P Q K P   S Q P V A K E T S A   T P Q I S N L T K T   A S E S I S N L S E   A G S V K K G E R E   L K I G D R V L V G   G T K A G V V R F L   G E T D F A K G E W
241    C G V E L D E P L G   K N D G A V A G T R   Y F Q C Q P K Y G L   F A P V H K V T K I   G F P S T T P A K A   K A A A V R R V M A   T T P A S L K R S P   S A S S L S S M S S
321    V A S S V S S K P S   R T G L L T E T S S   R Y A R K I S G T T   A L Q E A L K E K Q   Q H I E Q L L A E R   D L E R A E V A K A   T S H V G E I E Q E   L A L A R D G H D Q
401    H V L E L E A K M D   Q L R T M V E A A D   R E K V E L L N Q L   E E E K R K V E D L   Q F R V E E E S I T   K G D L E T Q T K L   E H A R I K E L E Q   S L L F E K T K A D
481    K L Q R E L E D T R   V A T V S E K S R I   M E L E K D L A L R   V Q E V A E L R R R   L E S S K P P G D V   D M S L S L L Q E I   S A L Q E K L E V T   H T D H Q N E V T S
561    L K D H F G T R E E   M F Q K E I K A L H   A A T E K L S K E N   E S L R S K L D H A   N K E N S D V I A L   W K S K L E T A I A   S H Q Q A M E E L K   V S F S K G I G T D
641    S A E F A E L K T Q   I E R L R L D Y Q H   E I E S L Q S K Q D   S E R S A H A K E M   E S M K A K L M K I   I K E K E D S L E A   V K A R L D T A E D   Q H L V E M E E M L
721    S K L Q E A E I K K   E K F A S A S E A E   V S T Q T S M Q D T   V N K L H Q K E E Q   F N M L S S E L E K   L R E N L T D M E A   K F K E K D E R E D   Q L V K A K E K L E
801    N D I A E I M K M S   G D N S Q L T K M   N D E L R L K E R S   V E E L Q L K L T K   A N E N A S L L Q K   S I G E V T L K A E   Q S Q Q E A A K K H   E E E K K E L E N K
881    L L E L E K K M E T   S H Y Q C Q D L K A   K Y E K A S S E T K   I K H E E I L Q N F   Q K M L V D T E D K   L K A A Q E A N R D   L M Q D M E E L K S   Q A D K A K A A Q T
961    A E D A M Q I M E Q   M T K E K T E T L A   S L E D T K Q T N A   K L Q S E L D T L K   E N N L K T V E E L   N K S K E L L N E E   N Q K M E E F K K E   I E T L K Q A A A Q
1041   K S Q Q L S A L Q E   E N V K L A E E L G   R T R D E V T S H Q   K L E E E R S V L N   N Q L L E M K K S L   P S N T L R E S E Y   R K D A D E E K A S   L Q K S I S L T S A
1121   L L T E K D A E L E   K L R N E V T V L R   G E N A S A K S L H   S V V Q T L E S D K   V K L E L K V K N L   E L Q L K E N K R Q   L S S S S G N T D V   Q T E D E R A Q E
1201   S Q Q M I D F L N S   V I V D L Q R K N Q   D L K M K V E M M S   E A A L N G N G E D   P N S Y D S D D Q E   K Q S K K K P R L F   C D I C D C F D L H   D T E D C P T Q A Q
1281   M S E D P P H S T H   H G S R S E E R P Y   C E I C E M F G H W   A T N C N D D E T F
    
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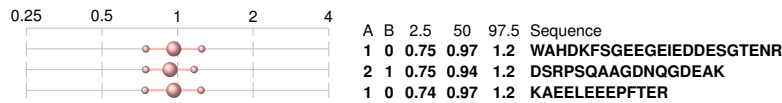
5.639 thyroid hormone receptor associated protein 3 [Rattus norvegicus]

Protein Accession	gj 57527425	
Mean Expression Ratio	0.96	
Median Expression Ratio	0.96	
Credible Interval	(0.771, 1.19)	
Associated Peptides	3	
Associated Spectra	5	
Coverage	0.0557	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.893	1.32
Avg..iTRAQ.Ratio....116.114.	0.915	1.07
Avg..iTRAQ.Ratio....117.114.	0.957	0.913

NHLBI Zile/Grant, Aged Rat

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1      MSKTNKSKSG SRSSRSRSAS RSRRSRFSKS RSRRSRSVRS RRRLSSRSR SRSYSPAHR ERNHPRVYQN RDFRGHNRGY
81     RRPYYFRGRN RGFYPWQYN RGGYGNYSRN WQNYRQAYSP RRGRSRSRSP KRRSPSPRSR SHSRNSDKSS SDRSRRSSSS
161    RSSSNHSRVE SSKRKSTKEK KSSSKDSRPS QAAGDNQGDE AKEQTFSGGT SQDIKGSSESS KPWPDPATYTG TGSASRASVS
241    DLSFRERSPA LKSPLQSVVV RRRSPRSPV PKPSPPLSNA SQMGSSMSGG AGYQSGAHQG PFDHSGSLS PSKSPVGKS
321    PPAATGSAYGS SQKESASAAG GAAYTKRYLE EQKTENGKDK EQKQTNKDKE KLKEKGGFSD ADVKMKSDPF APKDTTEKPF
401    RGSQSPKRYK LRDDFEKKMA DFHKEEMDEQ DKDKCKGRKE PEFDDEPKFI SKVIAGASKN QEEKSGKWE SLHAGKEKQR
481    KAEELIEEPPF TERSRKEERG GSKRSESGHR GFVPEKNFRV TAYKAVQEK SPPPRKTSE SRDKLGNKGD FSSGKSSFSI
561    TREAQVNVRM DSFDEDLARP SGLLAQERKL CRDLVHSNKK EQEFRSIFQH IQSAQSQRSP SELFAQHIVT IVHHVKHHFF
641    GSSGMTLHER FTKYLKRGNE QEAAKTKKSP EIHRRIDISP STFRKHGLTH EELKSPREP YKAEKGYKDD PVDLRLDIER
721    RKKHKERDLK RGKSRRESVDS RDSSHSRERS TEKTEKTHKG SKKQKHHRA RDRSRSSSSS SQSSHSYKAE EYPEEAEDRE
801    ESTTGFDKSR LGTKDFVGNP ERGGRARGTF QFRARGRGWG RGNYSGNNNN NSNNDFOKRS REEWDPEYT PKSKYYLHD
881    DREGEGSDKW MSRGRGRGAF PRGRGRFMFR KSSTSPKWAH DKFSGEEGEI EDDESGTENR EEKDSLQPSA E
    
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5.640 "PREDICTED: similar to procollagen, type XV [Rattus norvegicus]"

Protein Accession	gij109474895
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.772, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0112
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.42
Avg..iTRAQ.Ratio....117.114.	1.26

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1      MTHRRTAQGR RPRWLLSIIS TLLSTVLQTR AATGSASQDH LDLTELIGVP LPSSVSFVTG YGGFPAYSFR PGANVGRPAR
81     TLIPSTFFRD FAIGVAVKPS SAQGGVLFV TDAFQKVIYL GLRLSRVEDG RQRVILYYTE PGSHVSQEA AFSVPVMTNR
161    WNRFAVTVQG EEAVLFMDCE EHSQVLFQRS SRPLTFEPPA GIFVGNAGAT GLERFTGSIQ QLI IYSDPRT PEELCEAQES
241    SASGEASGFQ EMDEVAEIME AVTYTQAPPK EAHVDPISMP PTSSPTEDT ELSGEPVPEG TPGTDL SITG HSSPEQSSGE
321    ILNDTLEVRT VDGNPSTDGG SGDGALLNVT DGGGLSATAT GETRVVPTTA LEVENGSMP T GSPTLAMFTQ SFREVDMDDL
401    ENLTTASGDG EVPTSTDVDT EAGTLP TGGP TLKPREATL GSLGEWSTT VVSKVPLNAP EEEEASGTAI DSLDAFTPTV
481    VLEQASGTPT DIQAALTTT APEQVFTAAP TDGEDLVTST EESDEEGSGS TLP IGPPLSK PTVTPERQVT LAGVEAEGSD
561    PVWGVVGVSG SGIIVGNEDL LRGP PGGPPG PGSPGIPGPK GTDV FVGVPPG SPGEDGAPGE PGPQGPPEGQP GLDGASGQPG
641    MKGEKARGP NGSVGEKGD P GSRGLPGPPP KNGEVGIPGA MGPPGPPGPP GPPPGCTTK LGFEIEGSD TQLLSKPRIS
721    GPSSPSGPKG EKGEQKAGE RGTDGISTMG PPGPRGPPGR VEVLSSSLIN ITNGSMNFS D IPELMGPPGP DGVPGLPGFP
801    GPRGPKGDTG VPGFPGLKGE QGEKGEPGA I LTGDIPL EMV KGRKGEPPGVH GAPGPMGPKG PPGHKGEFGL PGRGRPGLN
881    GLKGAKGDRG IMLPGPPGLP GPPGPPGPPP AVVNIKGA V PIPARPHCKT PVGTAHPGDP ELVTFHGKVG EKGSWGLPGT
961    KGEKGDQGAQ GPPGPPVDP A YLRHFLNSLK GENGDAAFRG ESSHNLVSG PPGLPGHPGL AGQKGEAVVG PQGPPGIPGL
1041   PGPFGFRPG VPGPPGPPG P GPPAILGAA VPLPGPPGPP GQPLPGSRN LVTALSDMGD MLQKAHLVIE GTFIYLRESG
1121   EFFLRVRDGW KKLQGLGELIP IPADSPPPPA LSSNPYQPP PLNPILSANY ERPVLHLVAL NTPVAGDIRA DFQCFQARA
1201   AGLLSTFRGF LSSHLQDLST VVRKAERFSL PIVNLKQV L FNNWDSIFSG DGGQFNTHIP IYFVGDGRV M TDP SWPQKVV
1281   WHGSNPHGVR LVDKYCEAWR TDMAVTGFA SPLSTGKILD QKAYSCANRL I VLCIENSFM TDARK
    
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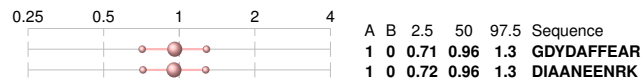


5.641 PREDICTED: similar to SH3 domain-binding glutamic acid-rich-like protein [Rattus norvegicus]

Protein Accession	gij109511015
Mean Expression Ratio	0.96
Median Expression Ratio	0.96
Credible Interval	(0.731, 1.25)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0541
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.00
Avg..iTRAQ.Ratio....116.114.	0.824
Avg..iTRAQ.Ratio....117.114.	0.949

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1      MVTRSGSQVG VTGCQANEGR WPVRKAWPAN LPEALKGART ARLPQVESSN KSGTWKSRT R LQAAYLLKEL VLRLERELNG
81     ATREGWGGKP PFETEGFEDG FWYLALNSCG DCYNVTLQRQ FGLVEGTDGP VSINGAEELR EANLKLEVTL NVLSEQVSSG
161    TSQHFYKLCN YYGSLRNDVN EPEPSGVWGW DCSAGSSLKA AAGGGGALAS SFHLPPPSRS NLCLAGSSVA RFQPLLQLFP
241    SPFQDSGDRP EALVSRMVIH VYIASSSGST AIKKKQDVL CFLEANKIGF EEKDIAANE E NRRWMRENVP EDSRPPTGYP
321    LPPQIFNESQ YRGDYDAFFE AFENNAVYAF LGLTAPPGSK EAEAQAQQA
    
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5.642 ADP-ribosylation-like factor 6 interacting protein 5 [Rattus norvegicus]

Protein Accession	gij12083627	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.803, 1.34)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.0585	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.91	1.13

Avg..iTRAQ.Ratio....116.114.	1.03	1.10
Avg..iTRAQ.Ratio....117.114.	1.05	1.78

1 MDVNIAPLRA **WDDFFPGSDR** FARPDFRDIS KWNDRVSNL LYYQTNYLVV AAMMISIVGF LSPFNMILGG IVVVLVFTGF
 81 VAAAHNKDVL RRMKKRYPT FVMVMLASY FLISMFGGVM VFVFGITFPL LLMFIHASLR LRNLKNQLEN KMEGIGLKRT
 161 PMGIVLDALE QQEEGINRLT GCISKVKE



5.643 PREDICTED: similar to dystonin isoform b [Rattus norvegicus]

Protein Accession	gj 109485920
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.773, 1.40)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.967
Avg..iTRAQ.Ratio....116.114.	0.968
Avg..iTRAQ.Ratio....117.114.	1.19



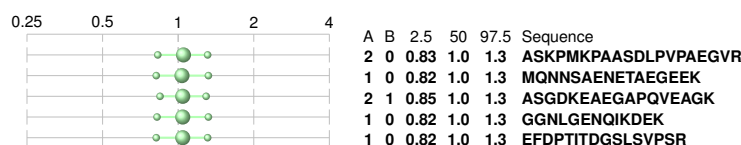
5.644 caldesmon 1 [Rattus norvegicus]

Protein Accession	gj 6978589
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.861, 1.25)

Associated Peptides	5	
Associated Spectra	8	
Coverage	0.154	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.18	0.86
Avg..iTRAQ.Ratio....116.114.	0.816	0.958
Avg..iTRAQ.Ratio....117.114.	1.39	1.43

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1      MLSRSGSQGR RCLATLSQIA YQRNDDDEEE AARERRRRAR QERLRQKQEE ESLGQVTDQV EAHVQNSAPD EESKPATANA
81     QVEGDEEAAL LERLARREER RQKRLQEALE RQKEFDPTIT DGSLVSPSR MQNNSAENET AEEGEEGGESR SGRYEMEETE
161    VVITSYQKNS YQDAEDKKKE EKEEEEEEEK LKGGNLGENQ IKDEKIKKKD EPKEEVKNFL DRKKGFTEVK AQNGEFMTHK
241    LKQTENAFSP SRSGGRASGD KEAEGAPQVE AGRLEELRR RRGETESEEF EKLKQKQQEA ALELEELKKK REERRKVLEE
321    EEQRRKQEEA DRKAREEEEE RRLKEEIERR RAEAAEKRQK MPEDGLSEDK KPFKCFTPKG SSLKIEERAE FLNKSSVQKSG
401    VKSTHQAAVV SKIDSRLEQY TNAIEGTKAS KPMKPAASDL VVPAEGVNI KSMWEKGSVF SSPSASGTPN KETAGLKVGV
481    SSRINEWLTK SPDGNKSPAP KPSDLRPGDV SGKRNLWEKQ SVDKVTSPTK V
  
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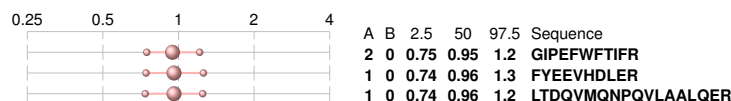


5.645 nucleosome assembly protein 1-like 4 [Rattus norvegicus]

Protein Accession	gi 58865912
Mean Expression Ratio	0.959
Median Expression Ratio	0.96
Credible Interval	(0.773, 1.2)
Associated Peptides	3
Associated Spectra	4
Coverage	0.101
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.93
Avg..iTRAQ.Ratio....116.114.	0.915
Avg..iTRAQ.Ratio....117.114.	1.08

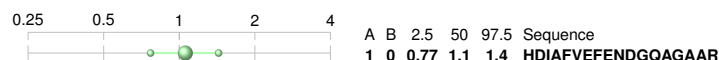
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1      MAENSLSDGG PADSVEAAKN ASNTEKLTDQ VMQNPQVLAA LQERLDNVSH TPSSYIETLP KAVKRRINAL KQLQVRCCAHI
81     EAKFYEEVHD LERKYAALYQ PLFDKRREFI TGDVEPTDAE SAWSENEED DLKLAGDMMNK VVIAEKEAAA VEELNPKGIP
161    EFWTIIFNV DMLSELVQEY DEPILKHLQD IKVKFSDPGQ PMSFVLEFHF EPNDYFTNPV LTKTYKMKSE PDKADPFSFE
241    GPEIVDCDGC TIDWKKGKNV TVKTIKKKQK HKGRGTVRTI TKQVPNESFF NFFSPLKASG DGSELDEDSE FTLASDFEIG
321    HFFRRIVPR AVLYFTGEAI EDDDNFEEGE EGEEELEGD EGEDEDDAD VNPKKEPIQP AECKQQ
  
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5.646 PREDICTED: similar to U2 small nuclear ribonucleoprotein B [Rattus norvegicus]

Protein Accession	gij109468893
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.776, 1.40)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.40
Avg..iTRAQ.Ratio....116.114.	1.20
Avg..iTRAQ.Ratio....117.114.	1.13



5.647 "PREDICTED: similar to Cofilin-2 (Cofilin, muscle isoform) [Rattus norvegicus]"

Protein Accession	gij109478222
Mean Expression Ratio	0.962
Median Expression Ratio	0.961
Credible Interval	(0.756, 1.23)
Associated Peptides	2
Associated Spectra	4
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.952
Avg..iTRAQ.Ratio....116.114.	0.965

Avg..iTRAQ.Ratio....117.114. 0.961

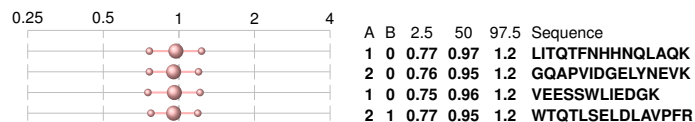


5.648 nuclear distribution gene C homolog [Rattus norvegicus]

Protein Accession	gij8394272	
Mean Expression Ratio	0.962	
Median Expression Ratio	0.961	
Credible Interval	(0.794, 1.17)	
Associated Peptides	4	
Associated Spectra	7	
Coverage	0	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.06	1.07
Avg..iTRAQ.Ratio....116.114.	0.95	0.542
Avg..iTRAQ.Ratio....117.114.	0.937	1.14

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1      MPKSDPFGFD MSVSSSKKKK PRRRRMSGGA SETSQVCSH EGCEEPGKYR APKAPDVLDD YFWFCQKHVR EYNLKNFFD
81     GTTEAELNAQ QSKDKVWERT TKPLGDPEAR AWARLGIEDP HQVLGKNATQ NPGKGPAAGR RLPPTERRAL EILEAKDTWT
161    KPEVRKAYKA LIKVLHPDMN GGDRSQEEQL QLVVWAWDQL KGSRNFKD
    
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5.649 PREDICTED: similar to Amyloid beta A4 precursor protein-binding family B member 1-interacting prote

Protein Accession [gij109505301](#)

Mean Expression Ratio	0.966
Median Expression Ratio	0.961
Credible Interval	(0.719, 1.30)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0151
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.954
Avg..iTRAQ.Ratio....116.114.	0.928
Avg..iTRAQ.Ratio....117.114.	0.791

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1      MGESNEDIDQ MFSTLLGEMD LLTQSLGVDL LPPAEPKPPR EEFNFSVGFK DLNESLNALE DQDLDALMAD LVADISEAEQ
81     RTIQAQKESQ QNQGHSALLE ASDGQGTAPR GYGANAADF VSDYEEALPP PPADPMLDLL PPPPPPPPKP LSKEEEAALA
161    KADKIKLALQ KLKEAKVKKL VVKVHMGDNS TKSLMVDLQ LARDVLDNLF EKTHCDCNVD WCLYEIYPQL QIERIFEDHE
241    NVVEVLSDWT RDTEENRVLF EKEEKYAVFK NPQNFYLDNK GKKEKESNEK MNAKNKEYLL EESFCGTSII VPELEGALYL
321    KEDGKKSQRK RYFLLRASGI YYVPKGTKT SRDLACFIQ ENVNIYYGIQ CKMKYKAPTQ HCFVLKHPQI QKESQYIKYL
401    CCDDARTLSQ WVMGIRIAKY GKTLYDNYQR AVARAGLASR WTNLGTATTP AQPAAGLKTG TSQPNGPMPQ AAPSPGPPPLR
481    ETLTQTETTK DEKQGLANHS PGASRENHRP KSSLLPPPPP VRRSSDTCSG PALPPKAKGP GSCTFFTAQPE NFLPPPPPPP
561    PQEDDNSMLL PPPPLAYLD EPPDFVPPPP PPATVEDSAL PPPPPPPCL SQEMTKSSPL PAKKLPVPPK RQENQGLPGA
641    PRNTEQDFMS DLMKALQKKR GNVV

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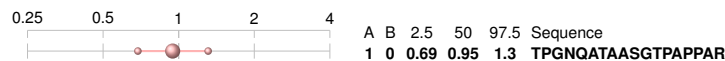
5.650 PREDICTED: similar to Y-box-binding protein 2 (Germ cell-specific Y-box-binding protein) (FRGY2 hom

Protein Accession	gij109491139
Mean Expression Ratio	0.96
Median Expression Ratio	0.961
Credible Interval	(0.711, 1.30)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0501
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.858
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	0.867

NHLBI Zile/Grant, Aged Rat

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1      MSEAEA AVVA TAAPAA TVPA TAAGVV AVVV PVPAGE PQKA GGGAGG GGGGA ASGPAAG TPS APGPR TPGNQ ATAASG TPAP
81     PARSQADKPV LAIQVLGTVK WFNVRNGYGF INRNDTKEDV FVHQTAIKRN NPRKFLRSVG DGETVEFDVV EGEKGAEAAAN
161    VTGPGGVPVK GSRYAPNRRR FRRFIPRPRP AAPPMMVAEA PSGGTEPGSE GERAEDSGQR PRRRRPPFFF YRRRFVRGPR
241    PPNQQQPIEG SDGVPEKETT PLEGDQQQGD ERVPPRFRP RYRRFRFRP PQQPTEGGD GETKPSQGPT DGSRPEPQRP
321    RNRPFYFQRRR QQPPGPRQPI AAETSAPINS GDPPTTILE
  
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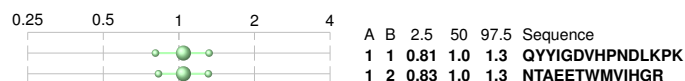


5.651 "cytochrome b5, outer mitochondrial membrane isoform [Rattus norvegicus]"

Protein Accession	gi 13399338	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.833, 1.30)	
Associated Peptides	2	
Associated Spectra	5	
Coverage	0.192	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	0.924
Avg..iTRAQ.Ratio....116.114.	1.12	1.05
Avg..iTRAQ.Ratio....117.114.	0.983	1.02

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1      MATPEASGSG RNGQGS DPAV TYRLEE VAK RNTAEETW MV IHGIVYDITR FLSEHPGGEE VLLEQAGADA TESFEDVGH S
81     PDAREMLKQY YIGDVHPNDL KPKDGD KDP S KNNSCQSSWA YWIVPIVGA I LIGFLYRHF W ADKSS
  
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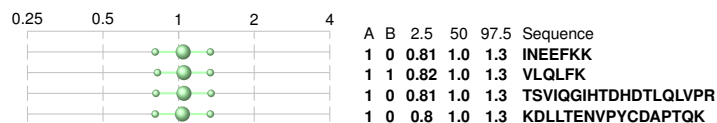


5.652 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gi 109490735	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.837, 1.29)	
Associated Peptides	4	

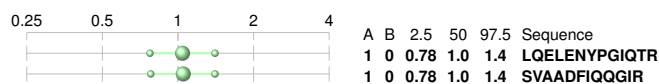
Associated Spectra	5	
Coverage	0.368	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	0.878
Avg..iTRAQ.Ratio....116.114.	1.11	1.00
Avg..iTRAQ.Ratio....117.114.	1.17	1.13

1 MRSVSGCARA VIGCQEGAAS EAESAAWAAM GQPAKVLQLF KTLHRTRQQV FKNDKRALEA ARVKINEEFK KHKNETSPEK
 81 IKEMLKIGSD VELLRLTSVI QGIHTDHDTL QLVPRKDLLT ENVPYCDAPT QRL



5.653 "PREDICTED: similar to 3-hydroxybutyrate dehydrogenase, type 2 [Rattus norvegicus]"

Protein Accession	gij109465587
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.795, 1.35)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.12
Avg..iTRAQ.Ratio....116.114.	1.26
Avg..iTRAQ.Ratio....117.114.	1.06



5.654 actin-related protein M2 [Rattus norvegicus]

Protein Accession	gi 62078603
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.774, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0159
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	0.785
Avg..iTRAQ.Ratio....117.114.	1.09

```

1      MFNPLVLDSP SVIFDNGSGL CKAGLSGEIG PRHVTSSVVG YPKFKASPTG ACQKKYFVGE EALFKQETLR LQSPIERGLI
81     TSWDDIEKLW RHLFEWELGV KPSERPVLMT EPSLNPRENR EKTAEVFMET FEVPAFYLSL QAVLALYSSA CVTGLVVDSG
161    DGVTCTVPIF EGYSLPHAVS KLFVAGK1DIT ELLTRLLLAS GRAFPCPLDK ALVDDIKEKL CYVALEPEEE LSRRAEDVLR
241    EYKLPDGNVI YIGDQLYQAP EVLFSPDQLG THGPGLAQMA SNSIAKCDAD IQKTLFGEIV LSGGSTLFQG LDDRLLKELE
321    QLASKGVPIK ITAPPDRWFS TWIGASIVTS LSSFKQMWIT AADFKEFGVS VVQRRCF
  
```



5.655 cAMP responsive element binding protein 1 isoform A [Rattus norvegicus]

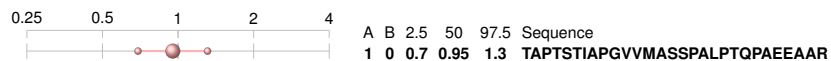
Protein Accession	gi 19745186
Mean Expression Ratio	0.96
Median Expression Ratio	0.962
Credible Interval	(0.709, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0887
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.763
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	1.12

NHLBI Zile/Grant, Aged Rat

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1      MTMDSGADNQ QSGDAAVTEA ESQQMTVQAO PQIATLAQVS MPAAHATSSA PTVTLVQLPN GQTVQVHGVI QAAQPSVIQS
81     PQVQTVQIST IAESEDSQES VDSVTDSQKR REILSRRPSY KKILNDLSSD APGVPRIEEE KSEETSAPA ITTVPVPTPI
161    YQTSSGQYIA ITQGGAIQLA NNGTDGVQGL QTLTMTNAAA TQPGTTILQY AQTTDGOQIL VPSNQVVVQA ASGDVQTYQI
241    RTAPTSTIAP GVVMASSPAL PTQPAEEAAR KREVRMLMKNR EAARECRRKK KEYVKLENR VAVLKNQNKI LIEELKALKD
321    LYCHKSD

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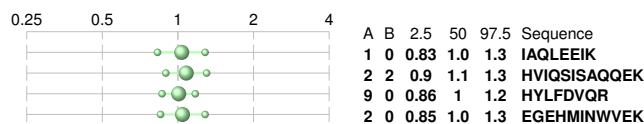
5.656 "ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1 [Rattus norvegicus]"

Protein Accession	gi 19705465	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.886, 1.22)	
Associated Peptides	4	
Associated Spectra	16	
Coverage	0.152	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.00	1.04
Avg..iTRAQ.Ratio....116.114.	1.15	1.05
Avg..iTRAQ.Ratio....117.114.	0.986	1.51

```

1      MLSRVLSAA ATAAPCLKNA AVLGPGVLQA TRVFHTGQPR LAPLPPLEPY GGKVRGLLIP EEFFQFLYPK TGVTPYVVG
81     TGLSLYFLSK EIYVITPETF STISVVGLIV YVIKKYGASI GEFIDKLNEE KIAQLEEIKQ SSMKQIQDAI NREKAQQALV
161    QKRHYLFDVQ RNNIALALEV TYRERLHKAY KEVKNRLDYH ISVQDMMRRK EGEHMINWVE KHVIQSISAQ QEEETIAKCI
241    GDLKMLAKKA QAQPIM

```



5.657 complement factor I [Rattus norvegicus]

Protein Accession	gi 13162353
Mean Expression Ratio	1.04
Median Expression Ratio	1.04

Credible Interval	(0.772, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0166
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	1.21
Avg..iTRAQ.Ratio....117.114.	1.18

```

1      MKLALLLLLL LNPFLSSSKN TPASGQPQED LVEQKCLLKN YTHHSCDKVF CQPWQKCI EG TCACKLPYQC PKAGTPVCAT
81     NRGYPTYCH LKSFECLHPE LFSNNGTCT AEEKFNVSLI YGSTDTEGIV QVKLVDQDEK MFICKNSWST VEANVACFDL
161    GFPLGVRDIQ GRFNIPVNHK INSTECLHVR CQGVETSLAE CTFTKSSKA PHGLAGVVCY TQDADFPTSQ SFQCVNGKRI
241    PQEKACDGVN DCGDQSDDEL CKGCRGQAF L CKSGVCIPNQ RKCNGEVDCI TGEDESGCEE DRKNKIHKGL ARSQGGETE
321    IETEETEMLT PDMDTERKRI KSLLPKLS CG VKRNTHIRRK RVVGGKPAEM GDYPWQVAIK DGDRITCGGI YIGGCWILTA
401    AHCVRPSRYR NYQVWTSLLD WLKPNSQLAV QGVSRRVVHE KYNGATYQND IALVEMKKHP GKKECELINS VPACVPWSPY
481    LFPQNDRCII SGWGREKDNQ KVISLRWGEV DLIGNCSR FY PGRYYEKEMQ CAGTSDGSID ACKGDSGGPL VCKDVNNVTY
561    VWGIVSWG EN CGKPEFPVGY TRVASYFDWI SYYVGRPLVS QYNV
  
```



5.658 "heat shock 27kD protein family, member 3 [Rattus norvegicus]"

Protein Accession	gi 13929052
Mean Expression Ratio	0.958
Median Expression Ratio	0.962
Credible Interval	(0.708, 1.28)
Associated Peptides	1
Associated Spectra	1
Coverage	0.112
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.00
Avg..iTRAQ.Ratio....116.114.	0.885
Avg..iTRAQ.Ratio....117.114.	0.824

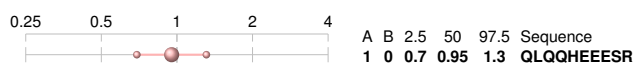
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1      MAKIILRHLI ETPVRYQEEF EARGLEDCR L DHALYALPGP TIEDLRKARG TPKALAEDSD SAETPPGEGK SRFQILLD VV
81     QFLPEDIIIQ TFEGLLLIKA QHGTRMDEHG FISRSFTRQY KLPDGVETKD LSAILCHDGI LVVEVKDPLE TK
  
```



5.659 PREDICTED: similar to mitochondrial ribosomal protein S31 [Rattus norvegicus]

Protein Accession	gij109503542
Mean Expression Ratio	0.962
Median Expression Ratio	0.962
Credible Interval	(0.712, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	0.905
Avg..iTRAQ.Ratio....117.114.	0.789



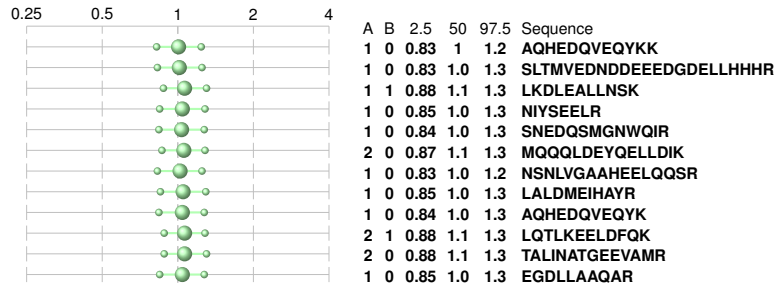
5.660 lamin A isoform C2 [Rattus norvegicus]

Protein Accession	gij50355947	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.91, 1.19)	
Associated Peptides	12	
Associated Spectra	17	
Coverage	0.227	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	1.02
Avg..iTRAQ.Ratio....116.114.	1.13	1.05
Avg..iTRAQ.Ratio....117.114.	1.15	1.01

NHLBI Zile/Grant, Aged Rat

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1      METPSQRRT  RSGAQASSTP  GRPLGSHGCR  RRRTRCSSMT  VWPCTSIACA  PWRRTTRGCA  FASLSLKRWS  AERCPASRRP
81     TSELGDARKT  LDSVAKERAR  LQLELSKVR  EFKELKARNT  KKEGDLAAQ  ARLKDLAALL  NSF EAALSTA  LSEKRTLEGE
161    LHDLRGQVAK  LEAALGEAKK  QLQDEMLRRV  DAENRLQTLK  EELDFQKNY  SEELLETKRR  HETRLVEIDN  GKQREFESRL
241    ADALQELRAQ  HEDQVEQYKK  ELEKTYSAKL  DNARQSAERN  SNLVGAAHEE  LQQSIRIDS  LSAQLSLQK  QLAAKEAKLR
321    DLDSLARER  DTSRRLAEK  EREMAEMRAR  MQQQLDEYQE  LLDIKLALDM  ETHAYKLE  GEEERLRLSP  SPTSQRSRGR
401    ASSHSSSQG  GGSVTKKRL  ESSESRSFS  QHARTSRVA  VEEVDEEGF  VRLRNKSNED  QSMGNWQIRR  QNGDDPLMTY
481    RFPFKFTLKA  GQVVTIWSG  AGATHSPPTD  LVWKAQNTWG  CGSSLRALI  NATGEEVAMR  KLVRSLTMVE  DNDDEEDGD
561    ELLHHHGH  GSH  CSSSGDPAEY  NLPSAPCCAG  HVGSLLTRLP  VAQDRRWADP  SPLALLPPVS  QSLEASAVWG  AVGVAASGTT
  
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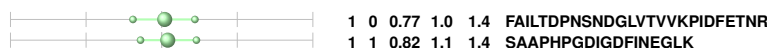
5.661 cadherin 2 [Rattus norvegicus]

Protein Accession	gi 13786162	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.813, 1.33)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	0.0486	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.933	1.15
Avg..iTRAQ.Ratio....116.114.	0.92	1.24
Avg..iTRAQ.Ratio....117.114.	1.20	1.23

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1      MCRIAGAPRT  LLPLLAALLQ  ASLEASGELA  LCKTGFPEDV  YSAVLPKDVH  EGQPLLNVKF  SNCNRKRKQV  YESSEPADFK
81     VDEEDGTVYAV  RSFPLSAEQ  KFLIYAQDKE  TQEKWQAVN  LSLEPSLTEE  PMKEPHEIE  IVFPRQLAKH  SGRLQRQKRD
161    WVIPPINLPE  NSRGFFPQEL  VRIRSDRDN  LSLRYSVTGP  GADQPPTGIF  IINPISGQLS  VTKPLDRELI  ARFHLRAHAV
241    DINGNQVENP  IDIVINVIDM  NDNRPFLHQ  VWNQSVPEGS  KPGTYVMVT  AIDADDPNAL  NGMLRYRILS  QAPSTPSNM
321    FTINNETGDI  ITVAAGLDRE  KVQQYTLIIQ  ATDMEGNPTY  GLSNTATAVI  TVTDVNDNPP  EFTAMTFYGE  VPENRVDVIV
401    ANLTVTDKQD  PHTPAWNAAY  RISGGDPTGR  FAILTDPNSN  DGLVTVVVKPI  DFETNMFVL  TVAAENQVPL  AKGIQHPPQS
481    TATVSVTVID  VNENPYFAPN  PKIIRQEEGL  HAGTMLTTLT  AQDPDRYMQQ  NIRYTKLSDP  ANWLKIDPVN  GQITTIIVLD
561    RESPNVKNNI  YNATFLASDN  GIPPMSTGTF  LQIYLLDIND  NAPQVLPQEA  ETCETPEPNS  INITALDYDI  DPNAGPFADF
641    LPLSPVTIKR  NWTITRLKGD  FAQLNLKIKF  LEAGIYEVPI  VITDSGNPPK  SNISILRVKV  CQCDSNGDCT  DVDRIVGAGL
721    GTGAI IAILL  CIIILLILVL  MFVVMKRRD  KERQAKQLLI  DPEDDVRDNI  LKYDEEGGGE  EDQDYDLSQL  QQPDTVEPDA
801    IKPVGIRRLD  ERPIHAEPQY  PVRSAAPHGP  DIGDFINEGL  KAANDNPTAP  PYDSLVLVFDY  EGSGSTAGSL  SSLNSSSSGG
881    DQDYDYLNDW  GPRFKKLADM  YGGGDD
  
```





5.662 v-crk sarcoma virus CT10 oncogene homolog (avian)-like [Rattus norvegicus]

Protein Accession	gij56605658	
Mean Expression Ratio	0.962	
Median Expression Ratio	0.962	
Credible Interval	(0.732, 1.26)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.0363	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.14	0.95
Avg..iTRAQ.Ratio....116.114.	0.852	0.767
Avg..iTRAQ.Ratio....117.114.	0.781	0.872

```

1      MSSARFDSSD  RSAWYMGVPS  RQEAQTRLQG  QRHGMFLVRD  SSTCPGDYVL  SVSENSRVSH  YIINSLPNRR  FKIGDQEFDH
81     LPALLEFYKI  HYLDTTLLIE  PÄPRYPNPPM  GSVSAPNLST  AEENLEYVRT  LYDFPGNDÆE  DLFFKKGELL  VIEKPEEQW
161    WSARNKDGRT  GMIPVPYVEK  LVRSSPHGKH  GNRNSNSYGI  PEPAHAYAQP  QTTTPLPTVA  STPGAAINPL  PSTQNGPVFA
241    KAIQKRVPÇA  YDKTALALEV  GDIVKVTRMN  INGQWEGEVN  GRKGLFPFTH  VKIFDPQNPD  DNE
    
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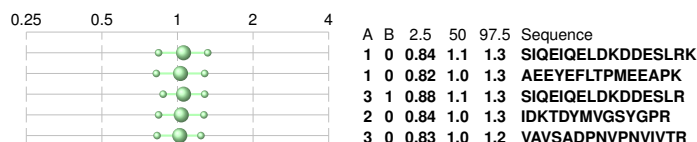
5.663 Rho GDP dissociation inhibitor (GDI) alpha [Rattus norvegicus]

Protein Accession	gij55742827	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.872, 1.23)	
Associated Peptides	5	
Associated Spectra	11	
Coverage	0.304	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.06	1.21
Avg..iTRAQ.Ratio....116.114.	0.998	0.946

Avg..iTRAQ.Ratio....117.114. 1.12 2.07

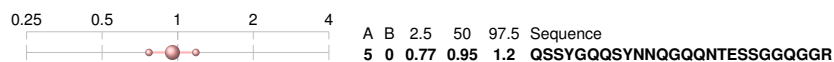
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1 MAEQEPTAEQ LAQIAAENEE DEHSVNYKPP AQKSIQEIQEQ LDKDDESLRK YKEALGRVA VSADPNVNV IVTELTLVCS
81 TAPGPLELDL TGDLESFKKQ SFVLKEGVEY RIKISFRVNR EIVSGMKYIQ HTYRKGVKID KTDYMGVGSYG PRAEYEFLT
161 PMEEAPGML ARGSYNIKSR FTDDDKTDHL SWEWNLTIKK EWKD
    
```



5.664 "PREDICTED: similar to TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Ra"]

Protein Accession	gij109488702
Mean Expression Ratio	0.964
Median Expression Ratio	0.962
Credible Interval	(0.765, 1.21)
Associated Peptides	1
Associated Spectra	5
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.957
Avg..iTRAQ.Ratio....116.114.	1.10
Avg..iTRAQ.Ratio....117.114.	0.8



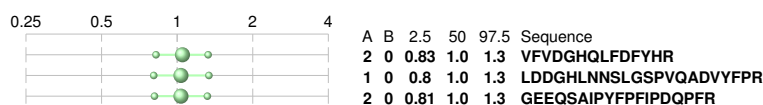
5.665 PREDICTED: similar to Galectin-5 (RL-18) [Rattus norvegicus]

Protein Accession	gij109500090
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Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.845, 1.28)
Associated Peptides	3
Associated Spectra	5
Coverage	0.172
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.05
Avg..iTRAQ.Ratio....116.114.	1.31
Avg..iTRAQ.Ratio....117.114.	1.04

```

1      MPGPTKGPSTG TVAAHLSSLL ISVVIQCTGP THLPRRQATA LPGLQPWSNG RRAGHAEQAA VPGPRPRPVP GPRFPSRALP
81     FLNATPGRRT AALATVIPSP PRPPRRTPPL PLPGLRPRQP GACARAGVCA RPARTRARRR VPGARCRNMA GSVADSDAVV
161    KLDDGHLNNS LGS9VQADVY FPRLIVFFCG HIKGGMRPGK KVLVMGIVDL NPESFAISLT CGDSEDPAD VAIELKAVFT
241    DRQLLRNSCI SGERGEEQSA IPYFFPIPDQ PFRVEILCEH PRFRVFVDGH QLFDFYHRIQ TLSAIDTIKI NGDLQITKLG
  
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5.666 PREDICTED: similar to Huntingtin interacting protein K [Rattus norvegicus]

Protein Accession	gij109470715
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.775, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	0.102
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.27
Avg..iTRAQ.Ratio....116.114.	1.16
Avg..iTRAQ.Ratio....117.114.	1.35

```

1      MNTDREVVVD ANTLVKMPSQ SFGLFSKIRS SWPICGSLLR RRGEIEMATE GDVELELETE TSGPERPPEK PRKHDGSAAD
81     LERVTDYAEK KEIQSSNLET AMSVIGDRRS REQKAKQERE KELAKVTIKK EDLELIMTEM EISRAAAERS LREHMGNVVE
161    ALIALTN
  
```



5.667 septin 9 isoform 2 [Rattus norvegicus]

Protein Accession	gi 28849875
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.82, 1.34)
Associated Peptides	1
Associated Spectra	3
Coverage	0.0284
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.20
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	1.21

```

1      MERDRITALK R SFEVEEIEP PNSTPPRRVQ TPLLRTVAS SSQKFQDLGV KNSEPAARLV DTLSQRSPPK SLRRVDLAGA
81     KAPEPMSRRT ELSIDISSKQ VESTASTPGP SRFGKRAEV LGHKTPEPVP RRTEITIVKP QESGLRRVET PASKAPEGSA
161    MPVTDAAPKR VEIQVFKPAE APNCP LPPQT LENSEAPMSQ LQSRLEPRPP VTEVPYRNQE DSEVAPSCVV DMADNPRDAM
241    LKQAPVSRNE KAPVDFGYVG ID SILEQMRR KAMKQGFEN IMVVGQSGLG KSTLINTLFK SKISRKSVQP ISEERIPKTI
321    EIKSITHDIE EKGVRMCLTV IDTPGFGDHI NNENCWQFIM KFINDQYEKY LQEEVNIINRK KRIPDTRVHC CLYFIPATGH
401    SLRPLDIEFM KRLSKVVNIV PVIKADTLT LEERVYFKQR ITSDLLSNGI DVYYPQKEFDE AEDRLVNEKF REMIPFAVVG
481    SDHEYQVNGK RILGRKTKWG TIEVENTTHC EFAYLRDLI RTHMQNIKDI TSNIHFEAYR VKRLNEGNSA MANGIEKEPE
561    TQEM
    
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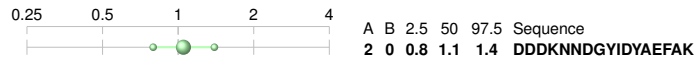


5.668 stem cell derived neuronal survival protein precursor [Rattus norvegicus]

Protein Accession	gi 21245096
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.795, 1.37)
Associated Peptides	1
Associated Spectra	2
Coverage	0.117
Experiment	A

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 Avg..iTRAQ.Ratio....116.114. 1.11
 Avg..iTRAQ.Ratio....117.114. 1.29

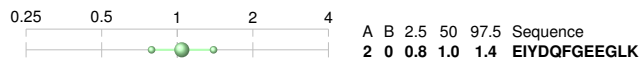
1 MASLQLLRGP FLCVLLWAF C VPGARAQEHG AGVHHGSVGL DKSTVHDQEH IMEHLEGVIN QPEAEMSPQE LQLHYFKMHD
 81 YDGN SLLDGL ELSTAITHVH KEEGSEQVPP MSEDELISII DGVL R DDDKN NDGYIDYAEF A K SLQ



5.669 "DnaJ (Hsp40) homolog, subfamily B, member 4 [Rattus norvegicus]"

Protein Accession	gi 61556870
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.787, 1.36)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0356
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.15
Avg..iTRAQ.Ratio....116.114.	1.12
Avg..iTRAQ.Ratio....117.114.	1.16

1 MGKDYYHILG IEKGATDEDI KKAYRKQALK FHPDKNKSPQ AEEKFKEVAE AYEVLSDPKK REIYDQFGEE GLKGGAGGTD
 81 GQGGTFRYTF HGDPHATFAA FFGGANPFEI FFGRRMGGGR DSEEMEIDGD PFSAFGFSMN GYPRDRNSVG PSRLKQDPP I
 161 IHELKVSLEE IYSGCTKRMK ISRKRLNPDG RSYRSEDKIL TIEIKKGWKE GTKITFPREG DETPNSIPAD IVFIIKDKEH
 241 PKFKRDGSNI VYTAKISLRE ALCGCSINVP TMDGRNIPMS VTDIVKPGMR RRIIGYGLPF PKNPDQRGDL LIEFDVSFPD
 321 VISAASKEIL RKHLPAS

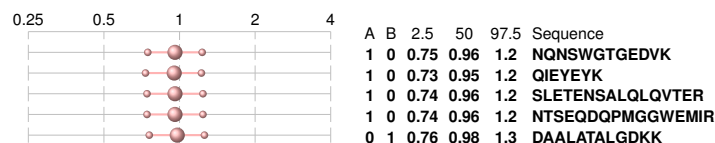


5.670 lamin B1 [Rattus norvegicus]

Protein Accession	gj 16758782	
Mean Expression Ratio	0.962	
Median Expression Ratio	0.963	
Credible Interval	(0.775, 1.19)	
Associated Peptides	5	
Associated Spectra	5	
Coverage	0.107	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	0.82
Avg..iTRAQ.Ratio....116.114.	0.954	0.962
Avg..iTRAQ.Ratio....117.114.	0.998	1.20

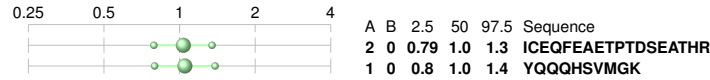
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1   MATATPVQQR AGSRASAPAT PFSPTRLSRL QEKEELRELN DRLAVYIDKV RSLETENSAL QLQVTEFEV RGRELTGLKA
81  LYETELADAR RALDDTARER AKLQIELGKF KAEHDQLLLN YAKKESDLG A QIKLREYEA ALNSKDAALA TALGDKKSLE
161 GDLEDLKDQI AQLEASLSAA KKQLADETLL KVDLENRCQS LTEDLEFRKN MYEEINETR RKHETRLVEV DSGRQIEEYK
241 KLAQALHEMR EQHDAQVRLY KEELEQTYHA KLENARLSSE MNTSTVNSAR GGMMESRMRI ESLSSQLSNL QKDSRACLER
321 IQELEDMLAK ERDNSRRMLS DKEREMAEIR DQMQQQLNDY EQLLDVKLAL DMEISAYRKL LEGEEERLKL SPSPSSRVTV
401 SRASSRSVR TTRGKRKRV DVEESEASSV SISHSASATG NVCIEEIDVD GKFIRLKNTS EQDQPMGGWE MIRKIGDTSV
481 SYKYTSRYVL KAGQTVTVWA ANAGVTASPP TDLIWKNQNS WGTGEDVKVV LKNSQGEVA QRSTVFKTTI PEEEEEEEE
561 PIGVPLEEER FHQQTTPRAS NKSCAIM
  
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5.671 PREDICTED: similar to Peroxisomal biogenesis factor 19 (Peroxin-19) (Peroxisomal farnesylated prote

Protein Accession	gj 109499074	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.812, 1.33)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	NA	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.10	
Avg..iTRAQ.Ratio....116.114.	1.01	
Avg..iTRAQ.Ratio....117.114.	1.32	



5.672 podocalyxin-like [Rattus norvegicus]

Protein Accession	gij20301990
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.765, 1.41)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0371
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	1.26
Avg..iTRAQ.Ratio....117.114.	1.41

```

1      MRPTLALSAL LLLQLLLLST PLSLQDNGNK TDTSDITSID QNQDKPATNQ PSNATPKSSV QPPTPTSIST SSPDPKATQS
81     SNSSVTTSD STTDRSSST STVPTTSNSG QTVSSGGKSS DKITTALPTT LGPVNASSQP TDLNTSTKLP STPTNSTAS
161    PHQPVSHSEG QHTTVQSSSA SVSSSDNTTL LWILTTSKPT GTSEGTQPIA ISTPGITTPV STPLQPTGSP GGTESVPTTE
241    EFTRSTSSWT PVVSGQPSTP SSTWTSGSYK LKCDPAIKPH EELLILNLTR DSFCKGSPPN ERFLELLCHS AKASFKPAED
321    SCALELAPIL DNQAVAVKRI VIETKLSPKA VFELLKDKWD DLTEAGVIDI HLGKREGPPEV NEDRFSPLPI ITIVCMASFL
401    LLVAALYGCC HQRISQRKDQ QRLTEELQTV ENGYHDNPTL EVMETPSEMQ EKKVVNLNGE LGDSWIVPLD NLTRREDLDEE
481    EDTHL
    
```



5.673 PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein G (hnRNP G) (RNA-binding motif protei

Protein Accession	gij109471751
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.794, 1.36)

Associated Peptides	1
Associated Spectra	2
Coverage	0.0291
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	0.951
Avg..iTRAQ.Ratio....117.114.	1.3

```

1      MVEADRPGLK FIGGLNTEFN EKALEAVFGK YGRIVEILLM KDRETNKSRG FAFVTFESPA DAKDVARDMN GKSLDGKAIK
81     VEQATKPSFE SGRGPPPPP RSRGPPRGLR GSGGTRGPP SRGGYDDGG YSMNFMSSS RGPLPVKRG PPRSGGPPPK
161    RSTPSGPVRS SSGMGGMPV SRGRDSYGGP PRREPLSRR DVYLSRDDG YSTKDSYSSR DYLSRRDTRD YAPPPRDYTY
241    RDYSHSSSRD DYPSRGGYDR DGYGRDREYS DHPSSGGSYRD SYESYGNSSC APPTRGPPPS YGGSSRYDDY SSSRDGYGGS
321    RDSYSSSRSD LYSSDRDRVG RQERGLPPSM ERGYPPPRDF YSSSSRGAPR GGGRGGSRSD RGGGQKQILE TNKTLDQGLH
401    AEKHKMESLC HNYQGLIREK LCYLKFSVL SPSFSLCSCE EKVKHD
  
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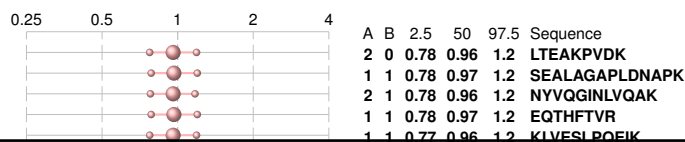


5.674 "ribosomal protein, mitochondrial, L12 [Rattus norvegicus]"

Protein Accession	gi 71361655	
Mean Expression Ratio	0.964	
Median Expression Ratio	0.963	
Credible Interval	(0.811, 1.14)	
Associated Peptides	5	
Associated Spectra	11	
Coverage	0.196	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.908	0.91
Avg..iTRAQ.Ratio....116.114.	0.952	0.977
Avg..iTRAQ.Ratio....117.114.	0.92	0.9

```

1      MPRAAAGESS DPVLFPPGDC VCASRRLVN IRSQPSRPGR QGLVARAARP ARLLPDRASL PLRAACDLPA CGAMLPAAAA
81     AASRLWGPRL GLGGSALRLV RQQMPGVCVA RQLRSSSHRR SEALAGAPLD NAPKEYPPKI QQLVQDIASL TLEISDLNE
161    LLKKTLLKIQD VGLMPMGGMV PGAVPAAAPA PEAAEEDLPP KQKEQTHFTV RLTEAKPVDK VKLIKEIKNY VQGINLVQAK
241    KLVESLPQEI KANVAKAEAE KIKAALEAVG GTVVLE
  
```



5.675 PREDICTED: similar to cullin 4B [Rattus norvegicus]

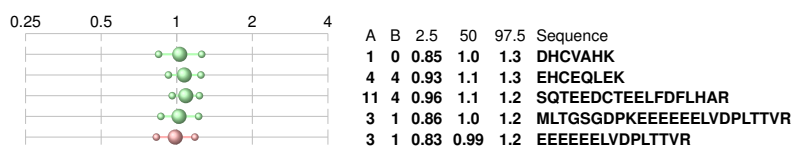
Protein Accession	gij62666420
Mean Expression Ratio	0.962
Median Expression Ratio	0.964
Credible Interval	(0.72, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.715
Avg..iTRAQ.Ratio....116.114.	0.965
Avg..iTRAQ.Ratio....117.114.	0.585



5.676 ubiquinol-cytochrome c reductase hinge protein [Rattus norvegicus]

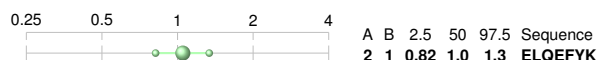
Protein Accession	gij57164091	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.916, 1.18)	
Associated Peptides	5	
Associated Spectra	32	
Coverage	0.64	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	0.87
Avg..iTRAQ.Ratio....116.114.	1.25	1.18
Avg..iTRAQ.Ratio....117.114.	1.01	0.891

1 MGLEDERKML TGSGDPKKEE EEELVDPLTT VREHCEQLEK CVKARERLES CDRRVSSRSQ TEEDCTEELF DFLHARDHCV
 81 AHFLFKSLK



5.677 PREDICTED: similar to CD9 antigen [Rattus norvegicus]

Protein Accession	gij109474240	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.807, 1.33)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.20	1.26
Avg..iTRAQ.Ratio....116.114.	0.936	0.863
Avg..iTRAQ.Ratio....117.114.	0.996	1.48



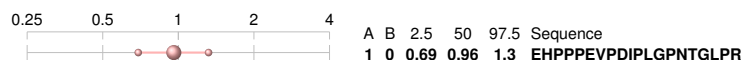
5.678 PREDICTED: similar to muscle specific protein [Rattus norvegicus]

Protein Accession	gij109457584	
Mean Expression Ratio	0.964	
Median Expression Ratio	0.964	
Credible Interval	(0.718, 1.30)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0358	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.896	
Avg..iTRAQ.Ratio....116.114.	0.886	

Avg..iTRAQ.Ratio....117.114. 0.897

```

1      MYENYAHTRV TDFLSVNP SK EANLLMQNLN KLQAPEEKLD FLFKKYAELL DEHRTEQKKL KLLKQQAQT QREKDLQSE
81     HNRAILARSK LESLCRELQR HNKTLKEETL QRAREEEER KEITSHFQST LTDIQTQIEQ QSERNMKLCQ ENTELAEKLK
161    SIIDQYELRE EHLDKIFKHR ELQQKLVD AK LEEAQELMQE AEERHRREKE YLLNQAAEWK LQAKVLKEQE TVLQAQLTLY
241    SGRFEEFQST LTKSNEVFAT FKQEMDN TTK KMKKLEKDTA TWKARFENCN KALLDMIEEK ALRAKEYECF VMKIQRLENL
321    CRALQEERKE LYKKIRDAKM SEKEDQVQHT SDEEPESKVS EDKQMDVEAA NGVQNAVKNL ATAFAILHHP EFTPDQSRER
401    QPAVNGPPGG SDLTHQHT EP AHLNHPNPSS VSGSPQPPVG SQAGSEGGCE AAPAPTACCT PAEAEELQSQG LSAGNPPDPK
481    PQKPEAKASG QVPLSPAQGS LAVVEAKCDI SPSPESERDP AVVPGCESK E HPPPEVVDIP LGPNTGLPRE PDACLNGVE
  
```



5.679 "casein kinase 2, beta subunit [Rattus norvegicus]"

Protein Accession	gi 78214347
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.787, 1.37)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0512
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.09
Avg..iTRAQ.Ratio....116.114.	1.22
Avg..iTRAQ.Ratio....117.114.	1.16

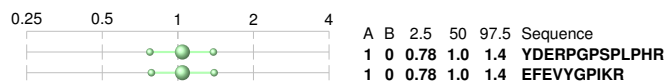
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1      MSSSSEVSWI SWFCGLRGNE FFCEVDEYI QDKFNLTGLN EQVPHYRQAL DMILDLEPDE ELEDNPNQSD LIEQAAEMLY
81     GLIHARYILT NRGIAQM L EK YQGGDFGYCP RVYCENQFML FIGLSDIPGE AMVKLYCPKC MDVYTPKSSR HHHTDGAYFG
161    TGFPHMLFMV HPEYRPKRPA NQFVPRLYGF KIHPMAYQLQ LQAASNFKSP VKTIR
  
```



5.680 PREDICTED: similar to U1 small nuclear ribonucleoprotein 70 kDa [Rattus norvegicus]

Protein Accession	gij62639737
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.794, 1.35)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.13
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	1.20



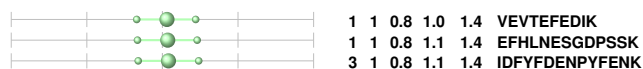
5.681 PREDICTED: similar to SET protein (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template-activating

Protein Accession	gij109470999
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.818, 1.32)
Associated Peptides	3
Associated Spectra	8
Coverage	0.175
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.10
Avg..iTRAQ.Ratio....116.114.	0.838
Avg..iTRAQ.Ratio....117.114.	1.03

```

1   MAPKQQSAIL PQLKKPRPIA ALKLEDKSAS PSLKGEKEQ QEEMEHINDV QNEIDRLNEQ ASEEILRVKQ KYNKLRQPF
81  QKRSELIAKI PNFVTTTFVN HPQVSALLGE EVEEALLYLT RVEVTEFEDI FSGYRDFYF DENPYFENKV LSKFHLNES
161 GDPSSKSTEI KWKSGKDLTK RSSQMKNKAS RKRQPEESES FSAWFTDRSD DG
    
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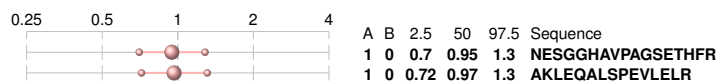




5.682 bolA-like 1 [Rattus norvegicus]

Protein Accession	gi 115392007
Mean Expression Ratio	0.962
Median Expression Ratio	0.964
Credible Interval	(0.733, 1.26)
Associated Peptides	2
Associated Spectra	2
Coverage	0.234
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.871
Avg..iTRAQ.Ratio....116.114.	0.958
Avg..iTRAQ.Ratio....117.114.	0.974

1 MLSARLARCM VSMATRACVS RGSAGSAAGG PVEAAIRAKL EQALSPEVLE LRNESGGHAV PAGSETHFRV AVVSSRFEGM
 81 SPLQRHRLVH EALSEELAGP VHALAIQAKT PAQWRENPLQ DISPPCLGGS KKTRGTS



5.683 alpha actinin 4 [Rattus norvegicus]

Protein Accession	gi 77539778
Mean Expression Ratio	0.966
Median Expression Ratio	0.964
Credible Interval	(0.724, 1.30)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0121
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.738
Avg..iTRAQ.Ratio....116.114.	0.621

Avg..iTRAQ.Ratio....117.114. 0.64

```

1      MVDYHAANQA YQYGFSSGGN GTGGGGMGD YMAQEDDWR DLLLDPAWEK QQRKTFTAWC NSHLRKAGTQ IENIDEDFRD
81     GLKMLLLEV ISGERLPKPE RGMRVHKIN NVNKALDFIA SKGVKLVSIG AEEIVDGNK MTLGMIWTII LRFIQDISV
161    EETSAKEGLL LWCQRKTAPY KNVNVQNFHI SWKDGLAFNA LIHRRPELI EYDKLRKDDP VTNLNNAFEV AEKYLDPKM
241    LDAEDIVNTA RPDEKAIMTY VSSFYHAFSG AQAETAANR ICKVLAVNQE NEHLMEDYER LASDLLLEWIR RTIPWLEDRV
321    POKTIQEMQQ KLEDFRDYRR VHKPPKVQEK CQLEINFNTL QTKLRLSNRP AFMPSEGRMV SDINNGWQHL EQAEKGYEEW
401    LLNEIRRLER LDHLAEKFRQ KASIHEAWTD GKEAMLKHRD YETATLSDIK ALIRKHEAFE SDLAAHQDRV EQIAAIAQEL
481    NELDYDSDHN VNTRCQKICD QWNLGSLTH SRREALEKTE KQLETIDQLH LEYAKRAAPF NNWMEAMED LQDMFIVHTI
561    EEIEGLISAH DQFKSTLPDA DREREAILAI HKEAQRIAES NHIKLSGSPN YTSVTPQIIN SKWEKVQQLV PKRDHALLEE
641    QSKQQSNEHL RRQFASQANM VGPWIQTKME EIGRISIEMN GTLEDQLSHL KQYERSIVDY KPNLDLLEQQ HQLIQEALIF
721    DNKHTNYTME HLRVGEWQLL TTIARTINEV ENQILTRDAK GISQEQMQEF KASFNFDKD HGGALGPEEF KACLISLGYD
801    VENDRQGDAA FNRMISVVDP NMSGVTFQA FIDFMSRETT DTDADQVIA SFKVLGADKN FITAEELRRE LPPDQAEYCI
881    ARMAPYQGPD AAPGALDYKS FSTALYGESD L
    
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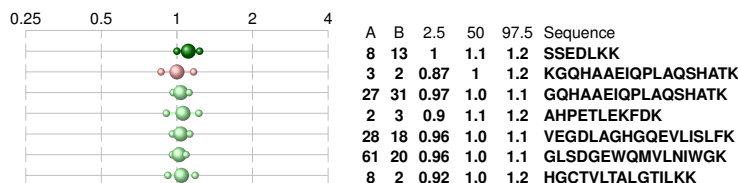


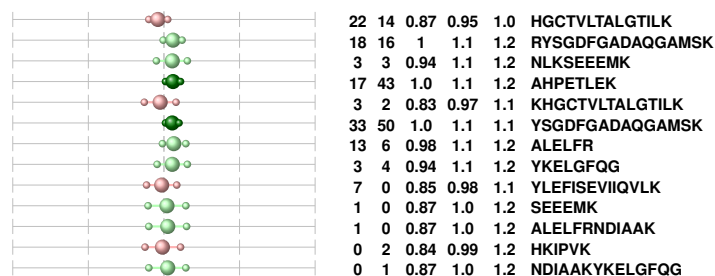
5.684 myoglobin [Rattus norvegicus]

Protein Accession	gj 11024650	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.981, 1.10)	
Associated Peptides	20	
Associated Spectra	488	
Coverage	0.974	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.01	1.02
Avg..iTRAQ.Ratio....116.114.	1.05	0.906
Avg..iTRAQ.Ratio....117.114.	1.08	1.01

```

1      MGLSDGEWQM VLNIWGWKEG DLAGHGQEV L ISLFAHPET LEKFDKFKNL KSEEBMKSS DLKKGCTVL TALGTILKKK
81     GQHAAEIQPL AQSHATKHKI PVKYLEFISE V IIVQLFKRY SGDFGADAQG AMSKALELPR NDIAAKYKEL GFQG
    
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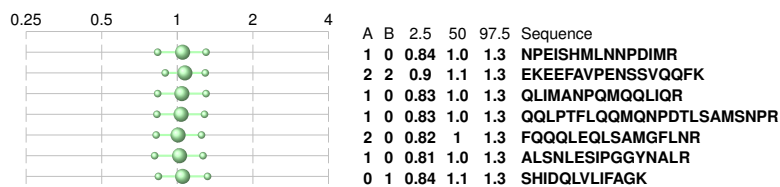


5.685 ubiquilin 1 [Rattus norvegicus]

Protein Accession	gi 48675852	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.882, 1.22)	
Associated Peptides	7	
Associated Spectra	11	
Coverage	0.198	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.986	1.44
Avg..iTRAQ.Ratio....116.114.	1.00	1.21
Avg..iTRAQ.Ratio....117.114.	1.06	0.974

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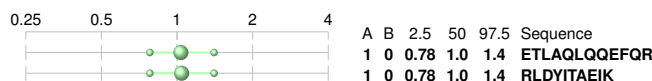
1      MAESAESGGP PGAQDSAADS GPAEPKIMKV TVKTPKEKEE FAVPENSSVQ QFKEEISKRF KSHIDQLVLI FAGIILKDQD
81     TLSQHGHDG LTVHLVIKTQ NRPQDNSAQQ TNTTGNVTS SPAPDSNPTS GPAANSSFGL GGLGGLAGLS SLGLNTTNFS
161    ELQSQMQRQL LSNPEMMVQI MENPFVQSMI SNPDLMRQLI MANPQMQLI QRNPEISHML NNPDIMQTL ELARNPAMMQ
241    EMMRNQDRAL SNLESIPGGY NALRRMYTDI QEPMLNAAQE QFGGNPFASL VSSPSSAEGT QPSRTENRDP LPNPWAPQTP
321    QSSPASGSTG STTNTVSTSA GNATSTPAGQ GTSQPNLVPF AGASMFNTPG MQSLLQQITE NPQLMQNMLS APYMRSMMS
401    LSQNPDLAAQ MMLNPLFAG NPQLQEQMRQ QLPFTLQQMQ NPDTLSAMSN PRAMQALLQI QQGLQTLATE APGLIPGFPT
481    GLAAGNSGGP AGTTAPSTAP GEDTNPQGGG AEPGHQQFIO QMLQALAGVN PQLQSEVRF QQQLQLSAM GFLNREANLQ
561    ALIATGGDIN AAIERLLGSQ PS
    
```



5.686 MHC class II region expressed gene KE2 [Rattus norvegicus]

Protein Accession	gi 47059193
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.796, 1.36)
Associated Peptides	2
Associated Spectra	2
Coverage	0.173
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	1.27
Avg..iTRAQ.Ratio....117.114.	1.09

1 MAELIQKKLQ GEVEKYQQLQ KDLSKSMGR QKLEAQLTEN NIVKEELALL DGSNVVFKLL GPVLVKQELG EARATVGKRL
 81 **DYITAEIFRY** ESQLRDLERQ SEQQR**ETLAQ** **LQQEFQ**PAQN AKAPGKA



5.687 Fas (TNFRSF6)-associated via death domain [Rattus norvegicus]

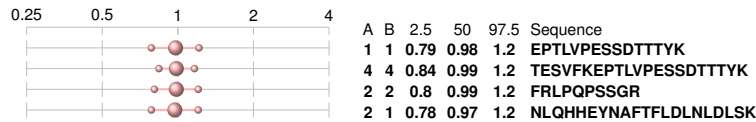
Protein Accession	gi 23097354	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.83, 1.29)	
Associated Peptides	2	
Associated Spectra	5	
Coverage	0.188	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.16	1.14
Avg..iTRAQ.Ratio....116.114.	1.26	0.639
Avg..iTRAQ.Ratio....117.114.	1.12	0.823

1 MDPFLVLLHS LSSSLSGNDL TDLKFLCRER VSKRKLERYQ **SGLDIFSVLL** **EQNDLERGHT** GLLRELLASL GRHDLQR**ED**
 81 **DPEAGATTAA** **TPGEADLR**VA FDIVCNVGR DWKRLARELK VSEAKIDGIE ERYPRSLSDR VRETLRVWKN VEKENASVAG
 161 LVKALRACRL NLVADLVEEA LMAQGSVSKS DDTSSALRDS TVSFSETP



5.688 "PREDICTED: similar to NADH-ubiquinone oxidoreductase 9 kDa subunit, mitochondrial precursor (Comple"

Protein Accession	gij109497874	
Mean Expression Ratio	0.965	
Median Expression Ratio	0.965	
Credible Interval	(0.815, 1.14)	
Associated Peptides	4	
Associated Spectra	17	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.9	1.04
Avg..iTRAQ.Ratio....116.114.	1.07	0.858
Avg..iTRAQ.Ratio....117.114.	1.04	0.797



5.689 "casein kinase II, alpha 1 polypeptide [Rattus norvegicus]"

Protein Accession	gij16758674	
Mean Expression Ratio	0.963	
Median Expression Ratio	0.965	
Credible Interval	(0.714, 1.30)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0384	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.936	

Avg..iTRAQ.Ratio....116.114. 0.838
 Avg..iTRAQ.Ratio....117.114. 0.87

```

1      MSGPVPSPRAR VYTDVNTHRP REYWDYESHV VEWGNQDDYQ LVRKLGKRGKY SEVF EAINIT NNEKVVVKIL KPVKKKKIKR
81     EIKILENLRG  GPNIITLADI VKDPVSRTPA LVFEHVNNTD FKQLYQTLTD YDIRFYMYEI LKALDYCHSM GIMHRDVKPH
161    NVMIDHEHRK  LRLIDWGLAE FYHPGQEQYV RVASRYFKGP ELLVDYQMYD YSLDMWSLGC MLASMIFRKE PFFHGHDNID
241    QLVR IAKVLG  TEDLYDYIDK YNIELDPRFN DILGRHSRKR WERFVHSENO HLVSP EALDF LDKLLRYDHQ SRLTAREAME
321    HPYFYTVVKD  QARMSSAGMA GGSTPVSSAN MMSGISSVPT PSPLGPLAGS PVIAAANSLG IPVPAAGAQQ Q
    
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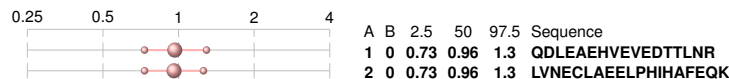


5.690 PREDICTED: similar to BoIA-2 protein [Rattus norvegicus]

Protein Accession	gij109462876
Mean Expression Ratio	0.965
Median Expression Ratio	0.965
Credible Interval	(0.755, 1.24)
Associated Peptides	2
Associated Spectra	3
Coverage	0.419
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.963
Avg..iTRAQ.Ratio....116.114.	1.1
Avg..iTRAQ.Ratio....117.114.	0.919

```

1      MELSADYLRE KLRQDLEAEH VEVEDTTLNR CATSFRVLVV SAKFEGKPLL QRHRLVNECL AEELPHIHAF EQKTLTPEQW
81     TRQRQE
    
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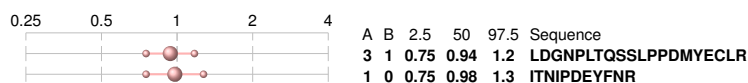


5.691 lumican [Rattus norvegicus]

Protein Accession	gi 13591983	
Mean Expression Ratio	0.963	
Median Expression Ratio	0.965	
Credible Interval	(0.772, 1.20)	
Associated Peptides	2	
Associated Spectra	5	
Coverage	0.0917	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.11	0.61
Avg..iTRAQ.Ratio....116.114.	1.01	0.449
Avg..iTRAQ.Ratio....117.114.	1.06	1.13

```

1      MNVCTFTLVL ALVGSVSGQY YDYDAPLFMY GELSPNCAPE CNCPHSYPTA MYCDDLKLS VPMVPPGIKY LYLRNNQIDH
81     IDEKAFENVT DLQWLILDHN LLENSKIKGR VFSKLRQLKK LHINYNLLE SVGPLPKSLQ DLQLANNKIS KLGSPDGLVN
161    LTFIYLQHNQ LKEEAVSASL KGLKSLEYLD LSFNQMSKLP AGLPTSLLTL YLDNNKITNI PDEYFNF FTG LQYLRLSHNE
241    LADSGVPGNS FNISSLELD LSYNKLKSIPTV NENLENY LEVNKLEKFD VKSFCKILGP LSYSKIKHLR LDGNPLTQSS
321    LPPDMYECLR VANEITVN
  
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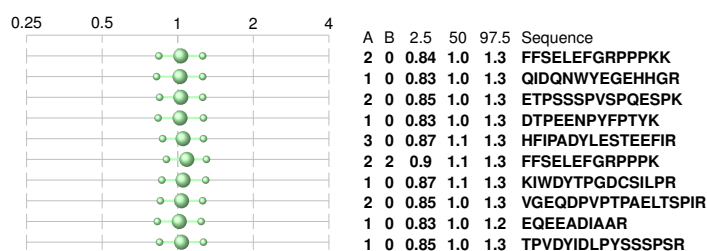
5.692 PREDICTED: similar to sorbin and SH3 domain containing 1 isoform 3 [Rattus norvegicus]

Protein Accession	gi 109463865	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.904, 1.19)	
Associated Peptides	10	
Associated Spectra	18	
Coverage	0.1	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	1.03
Avg..iTRAQ.Ratio....116.114.	1.01	1.42
Avg..iTRAQ.Ratio....117.114.	1.15	1.18

NHLBI Zile/Grant, Aged Rat

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1      MDQTKRRQLP FIVPAQFFDL PERLPNVVSG CTVYPFVST ADPLRARTIS AVKIIPVKTV KSPSGLVLP DMDPTKICTG
81     KGTVTLRASS SYRETPSSSP VSPQESPKHE NKSGLEPEDH SADEWKLSSS ADANGNAQPS PLAACKGYRSV HPSLLADKPQ
161    DATSSSPAPS EVIVVPLYLV NDRGQGGQEG TARTPASLGP LGCIHTVPAT TPAASPLTFP TLDDFIPPHL QRRPHHSQPA
241    SACGSLSPAS QTPPPSPPPP LVPIPEDLH RGLEPDLPGA VSSDGSPLL NEVSSSHIDT DSQVFPPTSK PSSAYPSTI
321    VNPTIVLLQH NREQQKRLSS LSDPASERRV GEQDPVPTFA ELTSPIRAAE RRAKDDSRV VRSAQDLSSV SMDEVGILR
401    NTERSKDWYK TMFKQIHKLN RDTPEENPYF PTYKFPPELPE IQNSEEDNP YTPTYQFPAS TSPSKSEDDDD SDLHSPRYSF
481    SEDTKSPLSV PRSKSEMNYI DGEKVVKRSA TLP LPARSSS LKSSPERNDW EPPDKKVDTR KYRAEPKSIY EYQPGKSSVL
561    TNEKMSRDIS FEEIDLKNEP WYKFFSELEF GRPPPKKIWD YTPGDCSILP FGDRKTNLEK DLNLCQAELE ADLEKVEVTN
641    KSPTAHVQPS SAVSPTPDIT SEPPGYIYSS DFHAVKRESG GTPGGLASLE NERQIYKSVL EGGDIPLQGL SGLKRPSSSA
721    STKDSSEPRH FIPADYLEST EEFIRRHDD KEKLLAQRR LKRQEAEADI AARRHTGVI THHQFITNER FGDLLNIDDT
801    AKRKSGLEMR PARAKDFDKA QTLKELPLQK GDIVYIYQI DQNWYEGEHH GRVGIFPRTY IELLPPAEKA QPRKLAPVQV
881    LEYGEAIAKF NFNQDTQVEM SFRKGERITL LRQVDENWYE GRIPGTSRQG IFPITYVDVL KRPLVK TPVD YIDLPYSSSP
961    SRSATVSPQC TSHSKLIMPA PSSLPHPRA LSPEMHAITS EWISLTVGVP GRRSLAMTPP LPPLPEASVY DMDRLALSAR
1041   ARPSLPLSLP YSSWSDHSTL RSVVSPVALP PPHKACSRAP SAQAPLHING DGGIHIRQDG FSQPPLGNSD RVISELSDAF
1121   SSQSKRQWR EDGPYDRKAE SEAGERCPGG PKISKKSCLK PSDVVRCLSS EQRLSEFHTP EDSQSFKPLS SPFFAWAEGP
1201   FELHRGV EAD RKAQSGVSQ QPQAQQRRLT PDRSQPSQDL CSYQALYSYV PQNDDELELR DGDIVDVM EK CDDGWFVGTG
1281   RRTRQFGTFP GNYVKPLYL
  
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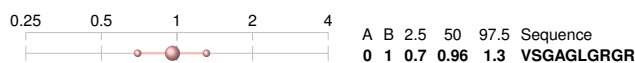


5.693 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gij109475049
Mean Expression Ratio	0.963
Median Expression Ratio	0.965
Credible Interval	(0.718, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0402
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.639
Avg..iTRAQ.Ratio....116.114.	1.27
Avg..iTRAQ.Ratio....117.114.	0.614

```

1      MDLELRRDDI LKKETPASAR RFACSRPPPP AEQPPSARPG CHRPLLLLRL LFPAAYDPGR NYFVPEPLEN SNPGRTIAPH
81     EAGLQHKAPP ARFPTPTRPR PSRTPRARAQ QQARRRPRGEH SRERAAGETS RVSGAGLGRG RLPCSPAWRR LPGWVERSAP
161    LRFNHGPKSS VWRERSRVAR ELEPAAGQPR CAPTRLPEAA GLREAVTPAG RAGQSGARPS RRGDGTGAR AGARVVTD SA
241    KAAGR GAGS
  
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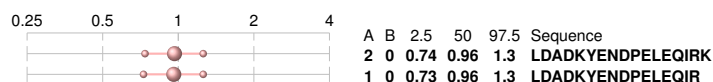


5.694 androgen-responsive gene encoding an ARD-like protein [Rattus norvegicus]

Protein Accession	gi 40018538
Mean Expression Ratio	0.965
Median Expression Ratio	0.965
Credible Interval	(0.759, 1.22)
Associated Peptides	2
Associated Spectra	3
Coverage	0.095
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.957
Avg..iTRAQ.Ratio....116.114.	1.01
Avg..iTRAQ.Ratio....117.114.	1.02

```

1   MVQAWYMDSE TADPRMPHRA QPDRPVGLEQ LRTLGVLYWK LDADKYENDP ELEQIRKTRN YSWMDIITIC KDSLPNYEEK
81  IKMFFEEHLH LDEEIRYILE GSGYFDVRDK EDKWIRISME KGDMITLPAG IYHRFTLDEK NYVKAMRLFV GEPVWTPYNR
161 AAXHFDARVQ YVKFLEGTA
    
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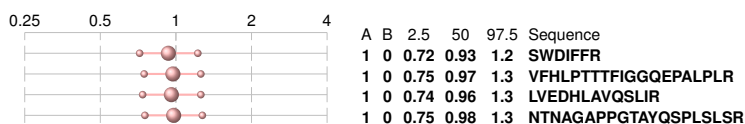


5.695 hypothetical protein LOC360975 [Rattus norvegicus]

Protein Accession	gi 62945278
Mean Expression Ratio	0.965
Median Expression Ratio	0.965
Credible Interval	(0.776, 1.22)
Associated Peptides	4
Associated Spectra	4
Coverage	0.0587
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.19
Avg..iTRAQ.Ratio....116.114.	0.854
Avg..iTRAQ.Ratio....117.114.	0.91

```

1      MFHLRTCAAK LRPLTASQTV KTFSSQNKPAE IRTFQQIRCY SAPVAEEPFL SGTSSNYVEE MYCAWLENPK SVHKSWDIFF
81     RNTNAGAPPG TAYQSPLSLR KSSLATMAHA QSLVEAQPNV DKLVEDHLAV QSLIRAYQIR GHHVAQLDPL GILDADLDSS
161    VPADIISSTD KLGfyGLHES DLDKVFHLPT TTFIGGQEPa LPLLEIIRRL EMAYCQHIGV EFMFINLEQ CQWIRQKFET
241    PGIHQFTNEE KRTLLARLVR STRFEEFLQR KWSSEKRFGL EGCEVLIPAL KTIIDMSSAN GVDYVIMGMP HRGRLNVLAN
321    VIRKELEQIF CQFDSKLEAA DEGSQDMKYH LGMYHRRINR VTDNRNITLSL VANPNSHLEAA DPVVMGKTKA EQFYCGDTFEG
401    KKVMSILLHG DAAFAGQGIV YETFHLSLDP SYTHGTVHV VVNNQIGFTT DPRMARSSPY PTDVARVVNA PIFHVNSDDP
481    EAVMYCKVA AEWRNTFHKD VVVDLVCYRR NGHNEMDEPM FTQPLMYKQI RKQKPVLPKY AELLVSQGVV NQPEYEEIS
561    KYDKICEEAF TRSKDEKILH IKHWLDSPPW GFFTLDGQPR SMTCPSTGLE EDILTHIGNV ASSVPVENFT IHGGLSRIK
641    TRRELVTNRT VDWALAEYMA FGSLLEKGIH VRLSGQDVER GTFSHRHHVL HDQNVDKRTC IPMNHLPNQ APYTVCNSSL
721    SEYGVGLFEL GFAMASPNAL VLWEAQGFDF NNMAQCIIDQ FICPGQAKWV RQNGIVLLLP HMEGGMGPEH SSARPERFLQ
801    MCNDPDPVLP NLQENFDIS QLYDCNWIVV NCSTPGNFFH VLRRQILLPF RKPLIVFTPK SLLRHPEART SFDEMLPGTH
881    FQRVIPEDGP AAQNPKVKR LLFCTGKVYV DLTRERKARD MAEEVAITRI EQLSPFPFDL LLKEAQKYPN AELAWCQEEH
961    KNQGYDYVVK PRLRRTIDRA KPVVYAGRDP AAAPATGNKK THLELQRFLL DTAFLDLDAFK KFS
    
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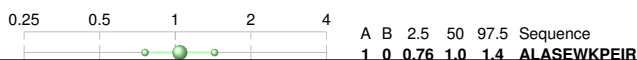


5.696 neural cell adhesion molecule 1 [Rattus norvegicus]

Protein Accession	gi 13928706
Mean Expression Ratio	1.03
Median Expression Ratio	1.04
Credible Interval	(0.763, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0128
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	0.953
Avg..iTRAQ.Ratio....117.114.	1.53

```

1      MLRTKDLIWT LFFLGTAVSL QVDIVPSQGE ISVGESKFFL CQVAGDAKDK DISWFSPNGE KLSPNQQRIS VVWNNDDSSST
81     LTIYNANIDD AGIYKCVVTA EDGTQSEATV NVKIFQKLMF KNAPTPQEFK EGEDAVIVCD VVSSLPPTII WKHKGRDVIL
161    KKDVRFIVLS NNYLQIRGIK KTDEGTYRCE GRILARGEIN FKDIQVIVNV PFTVQARQSI VNATANLGQS VTLVCDADGF
241    PEP TMSWTKD GEPIENEED DEKHIFSDDS SELTIRNVDK NDEAEYVCIA ENKAGEQDAS IHLKVFAPPK ITYVENQTAM
321    ELEEQVTLTC EASGDP PPSI TWRTSTRNIS SEEKASWTRP EKQETLDGHM VVRSHARVSS LTLKSIQYTD AGEYICTASN
401    TIGQDSQSMY LEVQYAPKLQ GPVAVYTWEG NQVNITCEVF AYPSATISWF RDGQLLPSSN YSNIKIYNTD SASYLEVTPD
481    SENDFGNYNC TAVNRIGQES LEFILVQADT PSSPSIDRVE PYSSTAQVQF DEPEATGGVP ILKYKAEWKS LGEEAWHSKW
561    YDAKEANMEG IVTIMGLKPE TRYAVRLAAL NGKGLGEISA ATEFKTQPVR EPSAPKLEGG MGEDGNSIKV NLIKQDDGGS
641    PIRHYLVKYR ALASEWKPEI LPSGSDHVM LKSLDWAAY EVYVVAENQQ GKSKAAHFVF RTSAPPTAIP ANGSPTAGLS
721    TGAIVGILIV IFVLLLVVMD ITCYFLNKCQ LLMCIAVNLC GKAGFGAKGK DMEEGKAAFS KDESKEPIVE VRTEEBERTPN
801    HDGGKHTEPN ETTPLTEPEK GPVETKSEPO ESEAKPAPTE VKTVPNEATQ TKENESKA
    
```



5.697 PREDICTED: similar to A-kinase anchoring protein-associated sperm protein [Rattus norvegicus]

Protein Accession	gij109466262
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.767, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0167
Experiment	B
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Avg..iTRAQ.Ratio....116.114.	0.862
Avg..iTRAQ.Ratio....117.114.	1.47

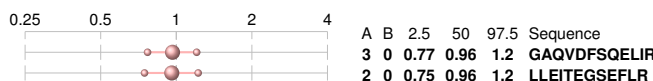
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1      MPDEKSEGID SITNTTVVRG GGPRLRCEAD CIREDEQNIC SAGSALQLRL ETLVTATTGR TSAPCSPRLC ACAAQVANKP
81     HATIARSRCC GRIGLSFQEG AEQPVRSGAR RGPFRRLRC ADPASPHAAQ RIVPGRGLP RAMPLPDTMF CAQQIHIPPE
161    LPDILKQFTK AAIRTQPADV LQWSAGYFSA LSRGDPLPVK DRIEMPVATQ KTDGTGLTQGL LKVLHKQCSH KQYVELADLE
241    KWKKNLCLPV EKFRIVDLD PSEDKMEWIK FLALGCSSLG GTLNTAMKNV CEILTSDPEG GPARIPEFET AYIYQYLSAL
321    DPEFSAVETE TYLANLRDTS ESRKNGMIGL SDFVIGKKPV
  
```



5.698 PREDICTED: similar to HESB like domain containing 1 [Rattus norvegicus]

Protein Accession	gij62651064
Mean Expression Ratio	0.965
Median Expression Ratio	0.965
Credible Interval	(0.775, 1.20)
Associated Peptides	2
Associated Spectra	5
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	0.972
Avg..iTRAQ.Ratio....117.114.	0.963

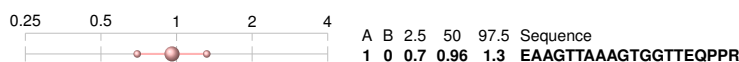


5.699 squamous cell carcinoma antigen recognized by T-cells 1 [Rattus norvegicus]

Protein Accession	gi 13928810
Mean Expression Ratio	0.966
Median Expression Ratio	0.965
Credible Interval	(0.721, 1.3)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0248
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	0.835
Avg..iTRAQ.Ratio....117.114.	1.04

```

1      MGSSKKHRGE KEAAGTTAAA GTGGTTEQPP RHREHKKKHK RSSGGGSSGG ERRKRSRERG AERGSRRGA EAEARSGAHG
81     RERSQAEPSE RRVKREKRDE GYEAAAASSKA SSGDASSLSI EETNKLRRAKL GLKPLEVNAV KKEAGTKEEP VAADVNPMA
161    LRQREELREK LAAAKEKRLL NQKLGKIKTL GEDDPWLDDT AAWIERSRQL QKEKDLAEKR AKLLEEMDQE FGVSTLVEEE
241    FEQRRQDLYS ARDLQGLTVE HAIDSFREGE TVVLTLDKDG VLQEGEDVLV NVNMVDKERA DKNVELRKKK PDYLPYVEDE
321    SVDDLAQQKP RSILAKYDEE LEGERPHSFR LEQGGMADGL RERELEEIRT KLRLQAQSLN TVGPRLASEY LSPEEMVTFK
401    KTKRRVKKIR KKEKEVIMRA DDLLPLGEDQ TQGDGFGSRL RGRGRRRVPE VEEEALEDEE KDPVAQPPPS DDTRVENMDI
481    SDEEDGGALP SGPPLEEDEE AELELQKQLE KGRRLRQLQQ LQQLRDSGK VLEIVKKLES RQRGWEEED PERKGTIVFN
561    ATSEFCRTLG EIPTYGLAGN REEQEELMDF ERDEERSANG GSESDGEENI GWSTVNLDEE KQHQDFSASS TTILDEEPIV
641    NRGAAAALLL CQNKGLLETT VQKVARVKAP NKSLSAVYC IEDKMAIDDK YSRREEYRGF TQDFKEKDG YKPDVKIEYVD
721    ETGRKLTPEK AFRQLSHRFH GKSGGKMKTE RRMKKLDEEA LLKKMSSSDT PLGTVALLQE KQKAQKTPYI VLSGSGKSMN
801    ANITTK
    
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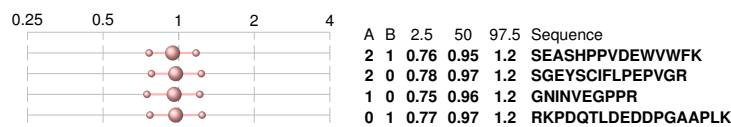


5.700 basigin [Rattus norvegicus]

Protein Accession	gi 7709992	
Mean Expression Ratio	0.965	
Median Expression Ratio	0.966	
Credible Interval	(0.8, 1.17)	
Associated Peptides	4	
Associated Spectra	7	
Coverage	0.213	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.95	0.751
Avg..iTRAQ.Ratio....116.114.	0.86	0.905
Avg..iTRAQ.Ratio....117.114.	1.07	1.17

```

1      MAAALLLALA FTFLSQGAC AAAGTIVTSV QEVDSKTQLT CFLNSSGIDI VGHRWMRGGK VLQEDTLPDL QMKYTVDADD
81     RSGEYSCIFL PEPVGRGNIN VEGPPRIKVG KKSEHASEGE FVKLICKSEA SHPPVDEWVW FKTSDTGDQT ISNGTEANSK
161    YVLIISTPELS ELIISDLDMN VDPGTYVCNA TNSQGSARET ISLRVRSRLA ALWPF LGIVA EVLVLVTIIF IYEKRKPDQ
241    TLDEDDPGAA PLKGS GSHLN DKDKNVRQRN AT
  
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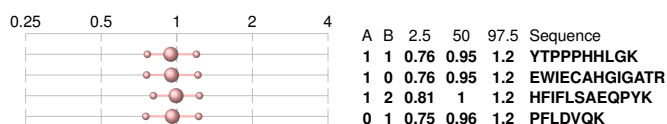


5.701 NADH dehydrogenase (ubiquinone) Fe-S protein 5b [Rattus norvegicus]

Protein Accession	gi 72086149	
Mean Expression Ratio	0.967	
Median Expression Ratio	0.966	
Credible Interval	(0.8, 1.17)	
Associated Peptides	4	
Associated Spectra	7	
Coverage	0.396	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.95	0.86
Avg..iTRAQ.Ratio....116.114.	1.08	0.789
Avg..iTRAQ.Ratio....117.114.	0.982	0.933

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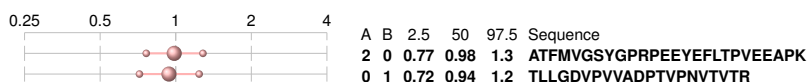
1      MPFLDVQFRL GISLDRHFIF LSAEQPYKNA ARCHAFEKEW ICAHGIGAT FAKKECKIEY EDFEFCFLRF KTIRRMHEIK
81     KQREKLMKEG KYTPPPHHLG KEEPRP
  
```



5.702 "Rho, GDP dissociation inhibitor (GDI) beta [Rattus norvegicus]"

Protein Accession	gj 57527565	
Mean Expression Ratio	0.967	
Median Expression Ratio	0.966	
Credible Interval	(0.762, 1.24)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	0.235	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.22	0.519
Avg..iTRAQ.Ratio....116.114.	1.01	0.705
Avg..iTRAQ.Ratio....117.114.	1.32	0.946

1 MTEKDEQPQL EEGEDELDSK LNYKPPPPQKS LKELQEMDKD DESLTKYKKT LLGDVPVVAD PTPVNVTVTR LSLVCDSPAG
 81 PITMDLTGDL KALKKDTFVL KEGIEYRVKI NFKVNKDIVS GLKYVQQTYR NGMKVDKATF MVGSYGPRPE EYEFLLTPVEE
 161 APKGLARGT YHNKSFFTTDD DKQDHLTWEW NLAIKKDWTD



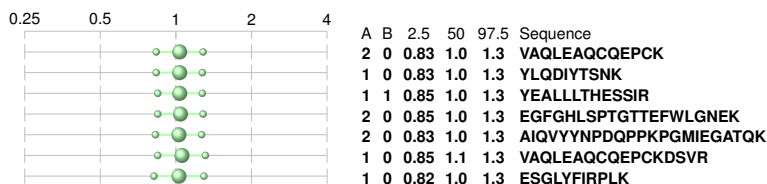
5.703 "fibrinogen, gamma polypeptide [Rattus norvegicus]"

Protein Accession	gj 61098186	
Mean Expression Ratio	1.04	
Median Expression Ratio	1.04	
Credible Interval	(0.88, 1.22)	
Associated Peptides	7	
Associated Spectra	11	
Coverage	0.215	

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.1	0.784
Avg..iTRAQ.Ratio....116.114.	1.30	1.03
Avg..iTRAQ.Ratio....117.114.	0.933	0.807

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1      MNWSLQLRSF ILCWALLLLS PTGLAQYTAT RDNCCILDER FGSYCPTTCG ISDFLNSYQT DVDTDLQTL E NILQRAENRT
81     TEAKELIKAI QVYYNPDQPP KPGMIEGATQ KSKMVEEIL KYEALLLTHE SSIRYLQDIY TSNKQKITNL KQKVAQLEAQ
161    CQEPCKDSVR IHDTTGKDCQ DIANKGAKES GLYFIRPLKA TQQFLVYCEI DGSGNGWTVL QKRLDGSVDF KKNWIQYKGG
241    FGHLSPTGTT EFWLGNEKIH LISMQSTIPY ALRIQLKDW SGRSTADYAM FRVGPESDKY RLTAYYFIGG DAGDAFDGYD
321    FGDDPSDKFF TSHNGMHFST WDNDNDKFE G NCAEQDGSW WMNKCHAGHL NGVYYQGGTY SKSSTPNGYD NGIIWATWKT
401    RWYSMKETTM KIIPFNRLSI GDGQQHHMGG SKQVGD M
    
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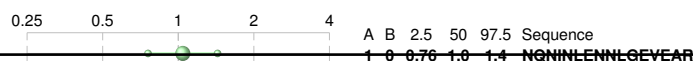


5.704 "keratin complex 1, acidic, gene 18 [Rattus norvegicus]"

Protein Accession	gij 68534953
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.764, 1.40)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0378
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.12
Avg..iTRAQ.Ratio....116.114.	1.04
Avg..iTRAQ.Ratio....117.114.	1.52

```

1      MSFTTRSTTF STNYSRLGSV RTPSQVRPA SSAASVYAGA GSGSRSISVS RSVWGGSVGS AGLAGMGVQ TEKETMQDLN
81     DRLASYLDKV KNLETENRRL ESKIREYLEK RGPQGVRDWG HYFKTIEDLR AQIFANSVDN ARIVLQIDNA RLAADDFRVK
161    YETELAMRQS VESDIHGLRK VVDDTNITRL QLETEIEALK EELLFMKKNH EEEVQGLEAQ IASSGLTVEV DAPKSQDLSK
241    IMADIRAQYE QLAQKNREEL DKYWSQQIEE STTVVTTKSA EIRDAETLL ELRRTLQTL E IDLDSMKNON INLENNLGEV
321    EAFYRVQMEQ LNGVLLHLES ELAQTRAEGQ RQTQYEYALL NIKVKLEAEI ATYRRLELDG DDFSLNDALD SSNSMQTVQR
401    TTTRKVVGDG VVSETNDRV LRH
    
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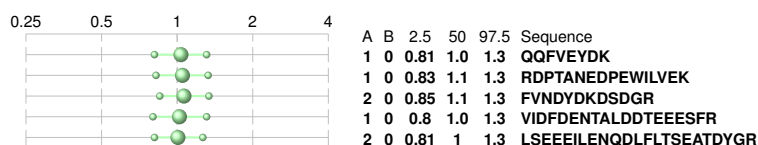


5.705 reticulocalbin 2 [Rattus norvegicus]

Protein Accession	gj 8394171
Mean Expression Ratio	1.03
Median Expression Ratio	1.04
Credible Interval	(0.852, 1.25)
Associated Peptides	5
Associated Spectra	7
Coverage	0
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	1.26

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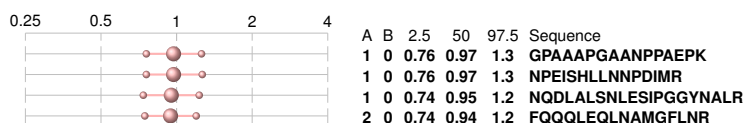
1   MTRHAIGTPE QLRDPNYMPP LYRAIPLGVQ HVLAMFVSNV TPAAIIAGAA GFGFGSNSPD FPELLYLIQM SMLFAGVATL
81  LQTLTLGPGV AGLPIVQGTS FAFIPIMIPL VAGKGV DGLA ALFGGVVIGG MFHAFGLGLFI GKIRFALPPL VTGLVVVTMIG
161 LALVKVGIQY AAGGVPAIGT PAYGSLNWS AALVVIFVTL GIKFFTRGML SISAVLIGLI VGYIYALAVG MLSFGDISGS
241 WSRSAAFALP NPLKYGFEPF AAATIGFCLM AFISAIETVG DVAGITKGGG GREATDREIQ GATYADGIGS AVAGLFGGLP
321 NTSFSQNVGL IAMTGVMRSH VVTVGALFLI LCGLVPKVGG VIRTIPIEVL GGGVIVMFGM VVAAGMSMLS DVDWNRNMV
401 IFAISISIGL GLQLEPGAVQ HLPDTAKILL TSGLLPAALI AIVLNLLLPE ELAEESTEEV SGLSGSSKG KLPHTPKTLH
    
```



5.706 PREDICTED: similar to ubiquilin 2 [Rattus norvegicus]

Protein Accession	gj 62666715
Mean Expression Ratio	0.963
Median Expression Ratio	0.966
Credible Interval	(0.782, 1.19)
Associated Peptides	4
Associated Spectra	5
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.02
Avg..iTRAQ.Ratio....116.114.	1.04

Avg..iTRAQ.Ratio....117.114. 1.01

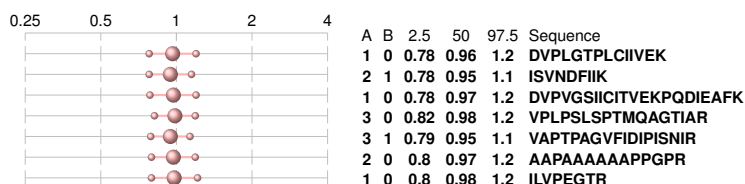


5.707 PREDICTED: similar to dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase

Protein Accession	gij109484674	
Mean Expression Ratio	0.967	
Median Expression Ratio	0.966	
Credible Interval	(0.838, 1.12)	
Associated Peptides	7	
Associated Spectra	15	
Coverage	0.143	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.975	0.799
Avg..iTRAQ.Ratio....116.114.	0.982	0.785
Avg..iTRAQ.Ratio....117.114.	1.12	0.614

```

1      MAAMIGTWSG SISPSVGLDG CSNQSPAFVL TDKAEINLVF EKDESERLL KNPGYRKSRA ALGEVTPETA EPLGRGVGGS
81     MWRVCARRVQ SAVPRAGFRA RWATLKGPRT GPAAVRCGSG IPSYGVRSIC GWSYGSATVP RNRILQQLG SPSRRSYSLP
161    PHQKVPLPSL SPTMQAGTIA RWEKKEGEKI SEGDLIAEVE TDKATVGFES LEECYMAKIL VPEGTRDVPV GSIIICITVEK
241    PQDIEAFNY TLDSATAATQ AAPAPAAAPA AAPAAPSASA PGSSYPVHMV IVLPALSPMT TMGTVQRWEK KVGEKLSEGD
321    LLAEIETDKA TIGFEVQEEG YLAKILVPEG TRDVPLGTPL CIIVEKQEDI AAFADYRPTV VTSLKQPAPP PVPPPVAAVP
401    PIPQPLAFTP SAAPAGPKGR VEVSP LAKKL AAEKGIDLTV VKGTGPEGRI IKKDIDSFVP TKAAPAAAAA APPGPRVAFT
481    PAGVFIDIPV SNIRVIAQR LMQSKQTIPH YLSVDVNMG EVLLVRKELN KMLEGKGIS VNDFITFASA LACLKVPEAN
561    SSWMDTVIRQ NHVVDVSVAV STPAGLITPI VFNAHIKGLE TIASDVVSLA SKAREGKLP HEPQGGFTTI SNLGMFGIKN
641    FSAIINPPQA CILAIGASED KLIPADNEKG FDVASVMSVT LSCDHRVVDG AVGAQWLAEF KKYLEKPVMT LL
    
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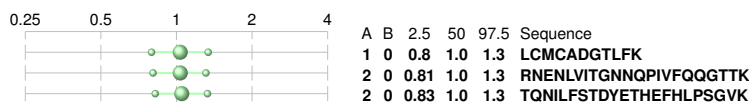


5.708 PREDICTED: similar to Beta-sarcoglycan (Beta-SG) (43 kDa dystrophin-associated glycoprotein) (43DAG)

Protein Accession	gij109499619
Mean Expression Ratio	1.03
Median Expression Ratio	1.04
Credible Interval	(0.835, 1.28)
Associated Peptides	3
Associated Spectra	5
Coverage	0.144
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.04
Avg..iTRAQ.Ratio....116.114.	1.20
Avg..iTRAQ.Ratio....117.114.	1.11

```

1      MQPASDSRWR VTGLQGSEPT QTLAHSGLS EGWRGRKAW PSQGVSPFPV PERKRGLRRA KMAAAAAAAAA ATEQQGSNGP
81     VKKSMREKAV ERRNVNKEHN SNFKAGYIPI DEDRLHKTGL RGRKGNLAIC VIVLLFILAV INLLITLVIW AVIRIGPNGC
161    DSLEFHESGL LRFKQVSDMG I IHPLYKSTV GGRRNENLVI TGNNQPIVFQ QGTTLSVEK NKTSITSDIG MQFFDPR QQN
241    ILFSTDYETH EFHLPSSGVS LNVQKASTER ITSNNATSDLN IKVDGRAIVR GNEGVFIMGK TIEFHMRGDV ELKAENSIIL
321    NGTVMVSPTR LPSSSGGDQS GSGDVVRYKL LCMCADGTLFK VQVTSHNMGC QVSDNFCGNT H
  
```



5.709 drebrin-like [Rattus norvegicus]

Protein Accession	gij13786198
Mean Expression Ratio	1.04
Median Expression Ratio	1.04
Credible Interval	(0.776, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0323
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.12
Avg..iTRAQ.Ratio....116.114.	1.25

Avg..iTRAQ.Ratio....117.114. 1.16

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1      MAVNLSRNGP ALQEAYVRVY TEKSPTDWAL FTYEGNSNDI RVAGTGEGGL EELVEELNSG KVMYAFCRVK DPNSGLPKFV
81     LINWTGEGVN DVRKGACANH VSTMANFLKG AHVTINARAE EDVEPECIME KVAKASGANY SFHKESSCFQ DVGPPAPVGS
161    VYQKTNAVSE IKRVGKDNFW AKAEKEEENR RLEEKRAAE EKQRLEEERR ERELQEAARR EQRYQEQRHS AGPPSRTGEL
241    EQEVVSRSRQ EWESAGQQAP HPREIFKQKE RAMSTTSVSS SQPGKLRSPF LKQQTQPEA SYGREPTSPV SRPAAGVCEE
321    LAPSTPPSAQ TDDEPTYEVP SEQETLYEEP PPVQQPGAGS GHIDNYMQSQ DLSGQGLCAR ALYDYQAADD TEISFDPENL
401    ITGIEVIDEG WWRGYGPDGH FGMFPANYVE LIE
    
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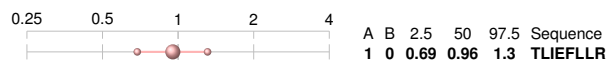


5.710 leucine aminopeptidase 3 [Rattus norvegicus]

Protein Accession	gi 58865398
Mean Expression Ratio	0.965
Median Expression Ratio	0.966
Credible Interval	(0.715, 1.30)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0154
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.832
Avg..iTRAQ.Ratio....116.114.	0.903
Avg..iTRAQ.Ratio....117.114.	1.12

```

1      MYLLPLPAAA RVALRRRLGVR GLWDRGLSTA DMTKGLVLGI YSKDKDDDVP QFTSAGENFN KLVSGRLREM LNISGPPLKA
81     GKTRTFYGLH QDFPSVVVVG LGKRSAGVDD QENWHEGKLN IRAAVAAGCR QVQDLELPSV EVDPCGDAQA AAEGAVLGLY
161    EYDDLKQKKK VAVSAKLHGS GDLEAWKGV LFASGQNLAR QLMESPANEM TPTRFAEVIE KNLKSASSKT EVHIRTKSWI
241    EEQEMGSFSL VAKGSEEPFV FLEIHYTGSP NATEAPLVFV GKGITFDSSG ISIKASANMD LMRADMGGAA TICSIAIVSAA
321    KLNLPINIIG LAPLCENMPS GKANKPGDVV RARNGKTIQV DNTDAEGRLI LADALCYAHT FNPKVIINAA TLTGAMDVAL
401    GSGATGVFTN SSWLWNKLF EASVETGDRV RMPLEFHYTR QVIDCQLADV NNLGKYRSAG ACTAAAFRE FVTHTKWAHL
481    DIAGVMTNKD EIPYLRKGM SGRPTR LIEF LLEFSKDSS
    
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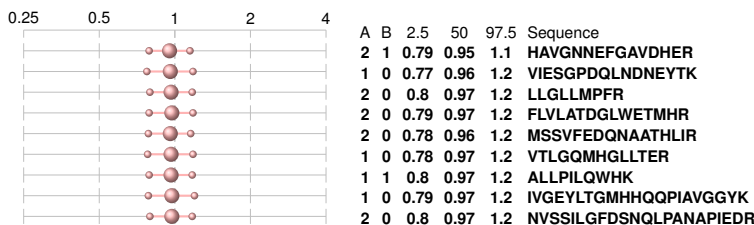


5.711 "protein phosphatase 2C, magnesium-dependent, catalytic subunit [Rattus norvegicus]"

Protein Accession	gij122427836	
Mean Expression Ratio	0.966	
Median Expression Ratio	0.966	
Credible Interval	(0.839, 1.11)	
Associated Peptides	9	
Associated Spectra	16	
Coverage	0.255	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.08
Avg..iTRAQ.Ratio....116.114.	1.08	0.769
Avg..iTRAQ.Ratio....117.114.	0.902	0.953

```

1      MPAPTQLFFP LVRNCELSRI YGTACYCHHK HLCCSPPYIP QNRLRYTPHP AYATFCRPRE NWWQYTQRR YASTPQKFFL
81     TPPQVNSILK ANEYSFKVPE FDGKNVSSIL GFDSNQLPAN APIEDRRSAA TCLQTRGMLL GVFDGHAGCA CSQAVSERLF
161    YYIAVSLPH  ETLLEIENAV ESGRALLPIL QWHKHPNDYF SKEASKLYFN SLRTYWQELI DLNTGESADI DVKEALINAF
241    KRLDNDISLE AQVGDPSNFI NYLVLRVAFS GATACVAHVD GVDLHVANTG DSRAMLGVQE EDGSWSAVTL SNDHNAQNER
321    ELERLLEHP  KNEAKSVVKQ DRLLGLLMPF RAFGDVKFKW SIDLQKRVIE SGPDQLNDNE YTRFIPPNYH TPPYLTAEPF
401    VTYHRLRPQD KFLVLATDGL WETMHRQDVV RIVGEYLTGM HHQQPIAVGG YKVTLGQMHG LLTERRAKMS SVFEDQNAAT
481    HLIHRAVGNN EFGAVDHERL SKMLSLEPEEL ARMYRDDITI IVVQFNESHVV GAYQNQEQ
    
```



5.712 "PREDICTED: similar to guanine nucleotide binding protein (G protein), gamma 12 [Rattus norvegicus]"

Protein Accession	gij109473637
Mean Expression Ratio	0.966
Median Expression Ratio	0.967
Credible Interval	(0.714, 1.3)
Associated Peptides	1
Associated Spectra	1
Coverage	0.222

Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.813
Avg..iTRAQ.Ratio....116.114.	0.906
Avg..iTRAQ.Ratio....117.114.	1.03

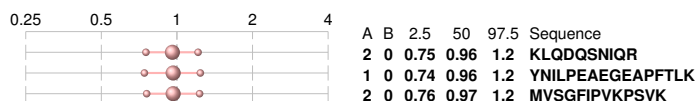
1 MSSKTASTNS TAQARRTVQQ LRLEASIERI KVKASADLM SYCEEHARSD PLLMG IPTSE NPFKDKKTCI IL



5.713 pregnancy-zone protein [Rattus norvegicus]

Protein Accession	gi 21955142
Mean Expression Ratio	0.966
Median Expression Ratio	0.967
Credible Interval	(0.778, 1.19)
Associated Peptides	3
Associated Spectra	5
Coverage	0.026
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	0.97
Avg..iTRAQ.Ratio....117.114.	0.93

1 MRRNQLPIPV FLLLLLLLPR DATAATGKPR YVVLVPSELY AGVPEKVCVH LNHLNETVTL NVTLEYGVQY SNLLIDQAVD
81 KSSSYCSSFT ISRP LSPSAL IAVEIKRGPTH HFIKKKSMWI TKAESPVFVQ TDKPIYKPGQ TVKFRVVSVD ISFRPVNETF
161 PVVYIENPKR NRIFQWQNV D LPGAHLQLSF PLSVEPALGI YKVVVQKDSG KKIEHSFEVK EYVLPKFEVQ VKMPKTM A FL
241 EEELVVTACG LYTYGKVPVG LVTMKVCRKY TQSYSNCHGQ HSKSICEEFS RQADEKGCFR QVVKTKVFP RQKGYDMKIE
321 VEAKIKEDGT GIELTGTGSC EIANTLSK LK FTKANTFYRP GLPFFGQVLL VDEKGPPIPN KNLTVQVNSV RSQFTFTTDE
401 HGLANILIDT TNFTFSFMGI RVIYKQNNIC FDNWVDEYH TQADHSAARI FSPRSYIQL ELVLGTLACG QTQEIRIHFL
481 L NEDALKDAK DLTFYLIKA RGSIFNSGSH VFPLEQGVK GVVSFPIRVE PGMAPVAKLI VYIILPNEEL IADVQKFIDIE
561 KCFANTVNL S FPSAQSLPAS DTHLTVKATP LSLCALTAVD QSVLLKPEA KLS PQSIYNL LPQKAEQGAY LGPLPYKGG E
641 NCIKAEDITH NGIVYTPKQD LNDNDAYSVF QSIGLKIFTN TRVHKPRYCP MYQAYPPLPY VGE PQALAMS AIPGAGYRSS
721 NIRTSSMMM GASEVAQEVE VRETVRKYFP ETWIWDMVPL DLSDGDELFP KVPDTITWEK ASAFCLSGTT GLGLSSTISH
801 KVFQPPFLEL TLPYSVVRGE AFILKATVLN YMPHCIRIHV SLEMSPDFLA VPVGS HEDSH CICGNERKTV SWAVTPKSLG
881 EVNFTATAEA LQSP ELCGNK VAEVPALVQK DTVVKPVIVE PEGIEKEQTY NTL LCPQDAE LQENWTL DLP ANVVEGSARA
961 TQSVLGDILG SAMQNLQNL QMPYGCGEQN MVLVFPNIYV LEYLN ETQQL TEAIKSKAIS YLISGYQRQL NYQHS DGSYS
1041 TFGDRGMRHS QGNTWLTA FV LKAFQAQSY IYIEKTHITN AFNWL SMKQR ENGCFQSGS LLNNAMKGGV DDEVTLSAYI
1121 TIALLEMLP VTHSVVRNAL FCLETAWASI SNSQESHVYT KALLAYAFAL AGNRKRSEV LESLNKDAVN EESVHWQRP
1201 KNVEENVREM RSFSYKPRAP SAEVEMTAYV LLAYLTSASS RPTRDLSSD LTTASKIVKW ISKQNSHGG FSS TQDTVVA
1281 LQALSKYGAA TFTKS NKEVS VTIESSGTVS GTLHVNNGR LLLQEVRLAD LFGNYITKVS GSGCVYLQTS LKYNILPEAE
1361 **GEAPFTLVN** TLPLNFDKAE HHRKFQIHIN VSYIGERFNS NMVIVDVK **NV SGFIPVKPSV** KKLQDQSNIQ RTEVNTNHVL
1441 IYIEKLTNQT MGFSFAVEQD IPVKNLKPA P VKVYDYETD EFAIEEYSAP FSSDSEQGNA



5.714 "myosin, heavy polypeptide 4, skeletal muscle [Rattus norvegicus]"

Protein Accession	gij106879208
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.795, 1.35)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0201
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.39
Avg..iTRAQ.Ratio....117.114.	1.9

1	MSSDAEMAVF	GEAAPYLRS	EKERIEAQNK	PFDKSSVVF	VDAKESYVKA	TVQSREGGKV	TAKTEGGATV	TVKEDQVFSM
81	NPPKYDKIED	MAMMTHLHEP	AVLYNLKERY	AANMIYTYSG	LFCVTVNPYK	WLPVYNPEV	AAYRGKKRQE	APPHIFSISD
161	NAYQFMLTDR	ENQSILITGE	SGAGKTVNTK	RVIQYFATIA	VTGDKKKEEA	PSGKMGGTLE	DQIISANPLL	EAFGNAKTVR
241	NDNSSRFGKF	IRIHFGATGK	LASADIETYL	LEKSRVTFQL	KAERSYHIFY	QVMSNKKPEL	IEMLLITNTP	YDFAYVSQGE
321	ITVPSIDDQE	ELMATDTAVD	ILGFTADEKV	AIYKLTGAVM	HYGNMKFKQK	QREEQAEPDG	TEVADKAAYL	TSLNSADLLK
401	ALCYPRVKVG	NEYVTKGGTV	QQVYNSVGAL	AKAMYEKMFL	WMVTRINQQL	DTKQPRQYFI	GVLDIAGFEI	FDFNLTLEQLC
481	INFPTNEKLQQ	FFNHHMFVLE	QEYKKEGIE	WEFIDFGMDL	AACIELIEKP	MGIFSILEE	CMFPKATDTS	FKNKLYEQHL
561	GKSNNFQRPK	PAKGKAEAHF	SLVHYAGTVD	YNIIGWLDKN	KDPLNETVVG	LYQKSLKTL	APLFSGGQAA	EAEAGGGKKK
641	GKKKGSSFQT	VSALEFRENLN	KLMTNLKSTH	PHFVRCLIPN	ETKTPGAMEH	ELVLHQLRCN	GVLEGIRICR	KGFPSTRILYA
721	DFKQRYKVLN	ASAIPEGQFI	DSKKASEKLL	GSIDIDHTQY	KFGHTKVFFK	AGLLGTLEEM	RDEKLAQLIT	RTQAVCRGYL
801	MRVEFRKME	RRESIFCIQY	NVRAFMMNVKH	WPWMKLYFKI	KPLLKSAETE	KEMATMKEDF	EKAKEDLAKS	EAKRKELEEK
881	MVALMQEKND	LQLQVQAEAD	GLADAEERCD	QLIKTKIQLE	AKIKELTERA	EDEEEINAEI	TAKKRKLEDE	CSELKDDIDD
961	LELTAKVEK	EKHATENKVK	NLTEEMAGLD	ENIVKLTREK	KALQEAHQQT	LDDLQAEEDK	VNTLTAKATK	LEQQVDDLEG
1041	SLEQEKLRM	DLERAKRKL	GDLKLAQEST	MDIENDKQQL	DEKLKKKEFE	MSNLQSKIED	EQALGMQLQK	KIKELQARIE
1121	ELEEEIEAER	ASRAKAEKQR	SDLSRELEEI	SERLEEAGGA	TSAQIEMNKK	REAEFQKMRR	DLEEATLQHE	ATAAALRKKH
1201	ADVAELGEQ	IDNLQRVKQK	LEKEKSELKM	EIDDLASNME	TVSKAKGNLE	KMCRTLEDQL	SEVKTKEEEO	QRLINELSAQ
1281	KARLHTESGE	FSRQDDEKDA	MVSQLSRGKQ	AFTQQIEELK	RQLEEEESKAK	NALAHALQSA	RHDCDLLREQ	YEEEQEAKAE
1361	LQRAMSKANS	EVAQWRTKYE	TDAIQRTEEL	EEAKKLAQR	LQDAEEHVEA	VNSKCASLEK	TKQRLQNEVE	DLMDVERSN
1441	AACAALDKKQ	RNFQVLAEW	KQKYETQAE	LEASQKESRS	LSTELFKVKN	AYEESLDQLE	TLKRENKIQ	QEISDLTRQI
1521	AEGGKHIHEL	EKIKKQIDQE	KSELQASLEE	AEASLEHEEG	KILRIQLELN	QVKSEIDRKI	AEKDEEIDQL	KRNHLRVVES
1601	MQSTLDAEIR	SRNDALRIKK	KMEGDLNEME	IQLNHANRQA	AEAIRNLRNT	QGMLKDTQLH	LDDALRGQDD	LKEQLAMVER
1681	RANLMQAEIE	ELRASLEQTE	RSRRVAEQEL	LDASERVQLL	HTQNTSLINT	KKKLETDISQ	IQGEMEDIVQ	EARNAAEKAK
1761	KAITDAANMA	EELKKEQDTS	AHLERMKKNM	EQTVKDLQHR	LDEAEQLALK	GGKKQIQKLE	ARVRELENEV	ENEQKRNEEA
1841	VKGLRKHERR	VKELTYQTEE	DRKNVLRQLD	LVDKQLQTKV	AYKRQAEAAE	EQSNVNLAKE	RKIQHELEEA	EERADIAESQ
1921	VNKLRLVKSRE	VHTKVISEE						

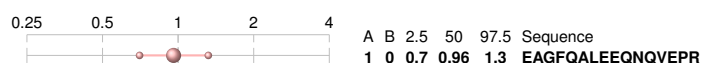


5.715 PREDICTED: similar to golgi phosphoprotein 4 [Rattus norvegicus]

Protein Accession	gij109466762
Mean Expression Ratio	0.966
Median Expression Ratio	0.967
Credible Interval	(0.716, 1.30)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0408
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.633
Avg..iTRAQ.Ratio....116.114.	1.14
Avg..iTRAQ.Ratio....117.114.	1.32

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1      MPRRMEEKPL SSMQKEAGFQ ALEEQNQVEP REPEGRQVEE EHRKALEEEE MEQVGQAEHL EEEHDPSPPE QDREWRDQRR
81     QNAAHLLDGR FQAEIEHSTK AATNFRSPYE EQLEQQRLAA RRDEEAQRLR EHQEALHQQR LHGQLLRQQQ QQQYLAREMA
161    QQKQADHEEG QQQYQLRQQA HSDAVENDVA QGAEDQGIPE EGGAYDRDN QRQDEAEGDP GNRQEFHPEPG HQEGDPEAEA
241    DRAAAQDINP ADDPNNQGED EFEEAEQVRE ENLPEESEER KQSEAKQGNV EMDEHLVMAG NPDQQEDNVD EQYQEEGEEE
321    VQEDLTTEKK RELEHNAEET YGENPDDKNN DVEEQGVFNR AHPKGRQEHY EEEDEEDGA AVAEKSHRRA EM
    
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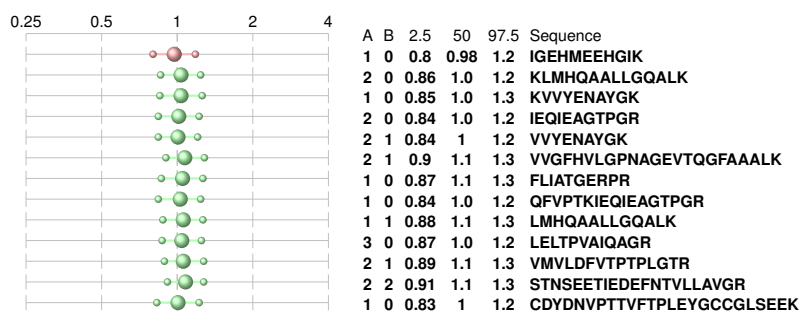
5.716 thioredoxin reductase 1 [Rattus norvegicus]

Protein Accession	gij78191795	
Mean Expression Ratio	1.03	
Median Expression Ratio	1.03	
Credible Interval	(0.922, 1.16)	
Associated Peptides	13	
Associated Spectra	27	
Coverage	0.317	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.978	1.32
Avg..iTRAQ.Ratio....116.114.	1.05	1.25
Avg..iTRAQ.Ratio....117.114.	1.10	0.918

NHLBI Zile/Grant, Aged Rat

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1      MNDKSDAPKS YDFDLIIIGG GSGGLAAAKE AAKFDKVMV LDFVTPPLG TRWGLGGTCV NVGCIPKLM HQAALLGQAL
81     KDSRNYGWKL EDTVKHDWEK MTEVQNHIG SLNWGYRVAL REKVVYENA YGKFIGPHKI MATNNKGKEK VYSAERFLIA
161    TGERPRYLGI PGDKKEYCISS DDLFSLPYCP GKTLVVGASY VALECAGFLA GIGLDVTVMV RSILLRGFDO DMANKIGEHM
241    EEHGKIFIRQ FVPTKIEQIE AGTPGLKVT AKSTNSEETI EDEFNTVLLA VGRDSCRTI GLETVGVKIN EKTGKIPVTD
321    EEQTNVPYIY AIGDILEGK1 ELTPVAIQAG RLLAQRLYGG STVKCDYDNV PTTVFTELEY GCCGLSEEKA VEKFGREENIE
401    VYHSFFWPLE WTVPSRDNNK CYAKVVCNLK DNERVVGFBV LGPNAGEVTO GFAAALKCGL TKQQLDSTIG IHPVCAEIFT
481    TLSVTKRSGG DILQSGCUG
  
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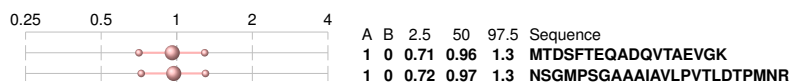


5.717 quinoid dihydropteridine reductase [Rattus norvegicus]

Protein Accession	gi 11693160
Mean Expression Ratio	0.967
Median Expression Ratio	0.967
Credible Interval	(0.74, 1.26)
Associated Peptides	2
Associated Spectra	2
Coverage	0.174
Experiment	A
Avg...iTRAQ.Ratio....115.114.	0.998
Avg...iTRAQ.Ratio....116.114.	1
Avg...iTRAQ.Ratio....117.114.	0.95

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1      MAASGEARRV LVIYGGRGALG SRCVQAFRAR NWWVASIDV ENEEASASVI VKMTDSFTEQ ADQVTAIEVGK LLGDQKVDIAI
81     LCVAGGWAGG NAKSKSLFKN CDLMWKQSIW TSTISSHLAT KHLKEGGLT LAGAKAALDG TPGMIGYGMA KGAVHQLCQS
161    LAGKNSGMPS GAAAIAVLFPV TLDTPMNRKS MPEADFSWT PLEFLVETFH DWITGNKRPN SGSLIQVVT DKGTELTPAY
241    F
  
```



5.718 "PREDICTED: similar to Myosin-binding protein C, cardiac-type (Cardiac MyBP-C) (C-protein, cardiac m"

Protein Accession	gij109468428	
Mean Expression Ratio	1.03	
Median Expression Ratio	1.03	
Credible Interval	(0.94, 1.14)	
Associated Peptides	16	
Associated Spectra	43	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.31	0.905
Avg..iTRAQ.Ratio....116.114.	0.785	0.88
Avg..iTRAQ.Ratio....117.114.	1.15	1.31



5.719 hypothetical protein LOC499417 [Rattus norvegicus]

Protein Accession	gij66730335	
Mean Expression Ratio	0.968	
Median Expression Ratio	0.967	
Credible Interval	(0.753, 1.25)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.109	

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.923	0.854
Avg..iTRAQ.Ratio....116.114.	0.905	0.739
Avg..iTRAQ.Ratio....117.114.	1.05	0.895

1 MSEEKPKEGV KTENDHINLK VAGQDGSVVO FKIKRHTPLS KLMKAYCERQ GLSMRQIRFR FDGQPINETD TPAQLEMEDE
 81 DTIDVFQQQT GGTASRASVP TPSHFDPICY



5.720 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 [Rattus norvegicus]"

Protein Accession	gi 13786158
Mean Expression Ratio	0.965
Median Expression Ratio	0.967
Credible Interval	(0.714, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0263
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.924
Avg..iTRAQ.Ratio....116.114.	0.914
Avg..iTRAQ.Ratio....117.114.	0.827

1 MVLESTMVCV DNSEYMRNGD FLPTRLQAQQ DAVNIVCHSK TRSNPENNVG LITLANDCEV LTTLTPDTGR ILSKLHTVQP
 81 KGRITFCTGI RVAHLALKHR QGKNHKMRII AFGVSPVEDN EKDLVKLAKR LKKEKVNVDI INFGEEVNT EKLTAfvNTL
 161 NGKDGtGSHL VTVPpGpSLA DALISSPILA GEGGAMLGLG ASDFFFGVDP SADPELALAL RVSMEEQRQR QEEEEARRAAA
 241 ASAAEAGIAT FGTEGERDSD DALLKMTISQ QEFGRAGLPD LSSMTEEEQI AYAMQMSLQG AEFGQAESGD IDASSAMDTs
 321 EPVKEEDDYD VMQDPEFLQS VLENLPGVDP NNEAIRNAMG SLASQATKDG KKDKKKEEEK

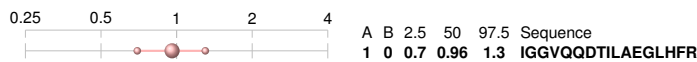


5.721 B-cell receptor-associated protein 37 [Rattus norvegicus]

Protein Accession	gij 61556754
Mean Expression Ratio	0.968
Median Expression Ratio	0.967
Credible Interval	(0.725, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0569
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.876
Avg..iTRAQ.Ratio....116.114.	0.965
Avg..iTRAQ.Ratio....117.114.	0.872

```

1      MAQNLKDLAG RLPSPGRMG TALKLLGAG AVAYGVRESV FTVEGGHRAI FFNRIGGVQQ DTILAEGLHF RIPWFQYPII
81     YDIRARPRKI SSPTGSKDLQ MVNISLRVLS RPNAQELPSM YQRLGLDYEE RVLPSIVNEV LKSVVAKFNA SQLITQRAQV
161    SLLIRRELTE RAKDFSLILD DVAITELSF S REYTAAVEAK QVAQQEAQRA QFLVEKAKQE QRQKIVQAE G EAEAAKMLGE
241    ALSKNPGYIK LRKIRAAQNI SKTIATSQNR IYLTADNLVL NLQDESFTRG SDSLIKGKK
  
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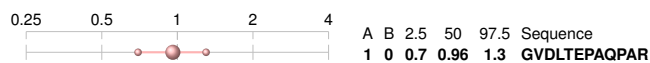


5.722 "RAB5A, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gij 12083645
Mean Expression Ratio	0.965
Median Expression Ratio	0.967
Credible Interval	(0.713, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0558
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	1.25
Avg..iTRAQ.Ratio....117.114.	1.16

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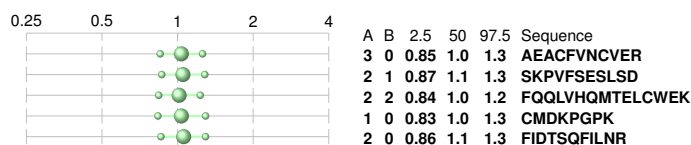
1      MANRGATRPN GPNTGNKICQ FKLVLGESA VGKSSLVLRV VKGQFHEFQE STIGAAFLTQ TVCLDDTTVK FEIWDTAGQE
81     RYHSLAPMY RGAQAIVVY DITNEESFSR AKNWVKELQR QASPNIVIAL SGNKADLANK RAVDFQEAQS YADDNSLLFM
161    ETSAKTSMNV NEIFMAIAK LPKNEPQNP ANSARGRGVD LTEPAQPARS QCCSN
  
```

5.723 translocase of inner mitochondrial membrane 8 homolog a [Rattus norvegicus]

Protein Accession	gj 16758098	
Mean Expression Ratio	1.03	
Median Expression Ratio	1.03	
Credible Interval	(0.883, 1.22)	
Associated Peptides	5	
Associated Spectra	13	
Coverage	0.577	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	0.963
Avg..iTRAQ.Ratio....116.114.	1.06	1.17
Avg..iTRAQ.Ratio....117.114.	1.11	0.674

1 MESSSSSSGS ALAAVDPQLQ HFIEVETQKQ RFQQLVHQMT ELCWEKCMDK PGPKLDSRAE ACFVNCVERF IDTSQFILNR
81 LEQTQSKPV FSESLSLSD



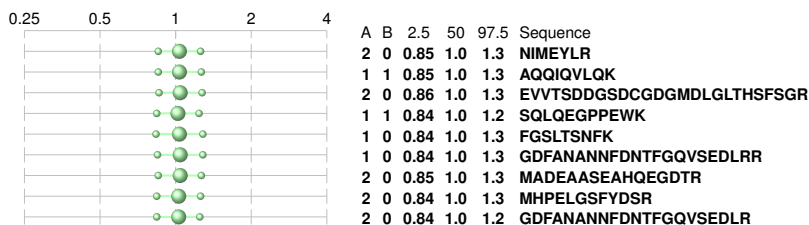
5.724 "fibrinogen, alpha polypeptide [Rattus norvegicus]"

Protein Accession	gj 56797757	
Mean Expression Ratio	1.03	
Median Expression Ratio	1.03	
Credible Interval	(0.895, 1.19)	
Associated Peptides	9	
Associated Spectra	16	
Coverage	0.143	

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	0.993
Avg..iTRAQ.Ratio....116.114.	1.29	0.945
Avg..iTRAQ.Ratio....117.114.	0.977	0.988

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1      MSLRVACLI  LSLASTVWTA  DTGTTSEFIE  AGGDIRGPRI  VERQPSQCKE  TDWPFCSDED  WNHKCPGSCR  MKGLIDEANQ
81     DFTNRINKLK  NSLFDFQKNN  KDSNSLTRNI  MEYLRGDFAN  ANNFDNTFGQ  VSEDLRRRIE  ILKRKVEKA  QQIQVLQSDV
161    RDQLIDMKRL  EVDIDIKIRS  CKGSCRSVS  REINLKDYEG  QQKQLEQVIA  KELLPAKDRQ  YLPAIKMSPV  PDLVPGSFKS
241    QLQEGPPEWK  ALTEMRQMRM  ELERPGKDG  SRGDLPGDSR  GDSATRGP  KIENPMP  GSGYWRP  SGSGSDGNW
321    SGTGSDDTG  TWGAGSSRP  SSGSNLKPS  PDWGEFSEF  GSSSPATR  YHTGKLV  GDKELL  KVTSTGTST
401    RRSCSKTIT  TVLGNDGHR  VVKEVVTSDD  GSDCGDGM  GLTHSFSG  DELSRMH  GSFYDSR  LTSNFKF
481    KTSDDIFTD  IENPSSHVP  FSSSSKTST  RKQVTKSY  ADEARSEAH  EGDYF  TTKRG  RARTMRD  VLQTHPS
561    NGIFSILPG  SSKIFSVY  QETSLGGW  IQQRM  FNRTWQDY  GFGSLN  GEFWLGN  HLLTLRGS
641    RVELEDWAG  EAYAEYH  GSEAEGY  VSSYQ  ALMEGSVE  TEYTS  FSTFDR  WEENCAE
721    GGWWYNSCA  ANLNGI  GTYDPR  YEIENG  PFRGADY  AVR  GQ
  
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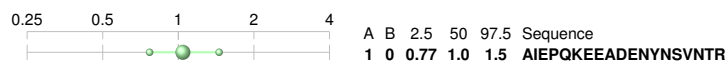


5.725 syntaxin 4A (placental) [Rattus norvegicus]

Protein Accession	gij13592099
Mean Expression Ratio	1.04
Median Expression Ratio	1.03
Credible Interval	(0.774, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0638
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	1.52

```

1      MRDRTHELRQ  GDNISDDEDE  VRVALVVHSG  AARLSSPDDE  FFQKVQTI  TMAKLES  ELEKQQ  ATPLPEES
81     QGLQNLREEI  KQLGREVRA  LKAIIEP  ADENYNS  RMKKTQ  SQQFV  CNSMQ  KNVERIRR
161    KITNAGMYS  EELEQLD  QSEVFV  KDTQV  NEISAR  QQLERT  HEIFTF  VEMQEMIN
241    IEKNILSAD  YVERGQEH  IALENQ  KKKVM  SVTVL  IGITIT
  
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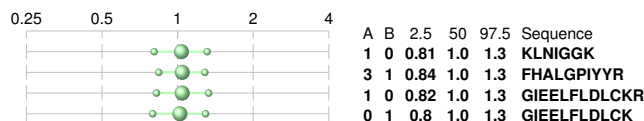


5.726 "RAB21, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gj 51948448	
Mean Expression Ratio	1.03	
Median Expression Ratio	1.03	
Credible Interval	(0.847, 1.25)	
Associated Peptides	4	
Associated Spectra	7	
Coverage	0.13	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1	1.1
Avg..iTRAQ.Ratio....116.114.	1.15	0.784
Avg..iTRAQ.Ratio....117.114.	1.13	0.966

```

1   MAAAGGGAAA AAGRAYSFV VLLGEGCVGK TSLVLRycEN KFNDKHITL QASFLTKKLN IGGKRVNLAI WDTAGQERFH
81  ALGPIYYEDS NGAILVYDVT DEDSFQKVKV WVKELRKMLG NEICLCIVGN KIDLEKERVH SIQEAESYAE SVGAKHYHTS
161 AKQNKGIEEL FLDLCKRMIE TAQVDERAKG NGSSQAGAAR RGVQIIDDEP QAQSGSGGCC SSG
    
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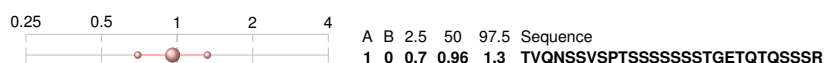
5.727 PREDICTED: similar to 82-kD FMRP Interacting Protein [Rattus norvegicus]

Protein Accession	gj 109491383	
Mean Expression Ratio	0.966	
Median Expression Ratio	0.968	
Credible Interval	(0.719, 1.29)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0466	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.95	

Avg..iTRAQ.Ratio....116.114. 0.814
 Avg..iTRAQ.Ratio....117.114. 1.24

```

1      MLSYGEINGN  AGEREISLKN  LSSDEATNPI  SRVLNGNQV  VDTSLKQTVK  TSTFGKAGIK  TKNFIQKNSM  DKKNGKSYEN
81     KSGETQAVDK  TDTIAIPNGV  ITNNSGYITN  GYMSKGADND  GSGSESGYTT  PKRRKARRNS  AKGCENLNLV  QDKIMQETSV
161    PALKQGLETL  KPDYSEQKGT  RVDGSKPIWK  YETGPGGTSR  GKPAMGDIIR  KSSDIKPGLS  SKKFDDRPKG  KHASAAASKE
241    DSWTLFKPPP  VFPVDNSSAK  IVPKISYASK  VKENLNKTVQ  NSSVSPTSSS  SSSSTGETQT  QSSSRLSQVP  MSALKSVTSA
321    SFSNGPVLAV  TDGSMYPSAG  QPLLTTAANT  LTPISTGTDS  VLQDMSLSSA  AVEQIKSSLF  IYPSNMQTVL  LSAQVDLPSQ
401    TDQQNLGDI  F  QNQWGLSFIN  EPSAGPETVI  GKSSDHKVME  VTFQGEYPAT  LVSQGA EIIP  SGTEHPVFPK  AYELEKRTSP
481    QVLGNILKPG  TTESGALSLE  PSHIGDLQKA  DTSSQGALVF  LSKDYEIENQ  NPLASPTNTL  LGSAKEQRYQ  RGLERNDSWG
561    SFDLRAAIVY  HTKEMESIWN  LQKQDPKRRI  TYNEAMDSPD  Q
    
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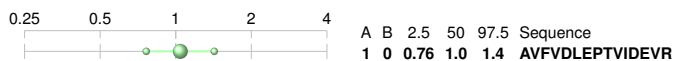


5.728 similar to Tubulin alpha-2 chain (Alpha-tubulin 2) [Rattus norvegicus]

Protein Accession	gij112984124
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.767, 1.40)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0333
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.13
Avg..iTRAQ.Ratio....116.114.	0.982
Avg..iTRAQ.Ratio....117.114.	1.46

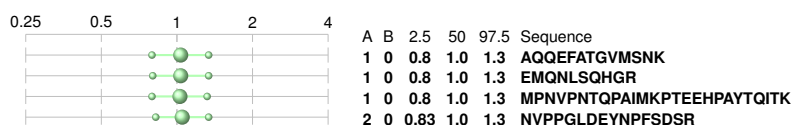
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1      MRECISIHVG  QAGVQIGNAC  WELYCLEHGI  QPDGQMPSDK  TIGGGDDSFN  TFFSETGAGK  HVPRAVFVDL  EPTVIDEVRT
81     GTYRQLFHPE  QLITGKEDAA  NNYARGHYTI  GKEIIDLVLD  RIRKLADQCT  GLQGFVLFHS  FGGGTGSGFT  SLLMERLSVD
161    YGKKSLEFS  IYPAPQVSTA  VVEPYNSILT  THTTLEHSDC  AFMVDNEAIY  DICRRNLDIE  RPTYTNLRL  ISQIVSSITA
241    SLRFDGALNV  DLTEPQTNLV  PYPRIHFPLA  TYAPVISAEK  AYHEQLSVAE  ITNACFEPAN  QMVKCDPRHG  KYMACCLLYR
321    GDVVPKDVNA  AIATIKTKRS  IQFVDWCPTG  FKVGINYQPP  TVVPGGDLAK  VQRAVCMLSN  TTAIAEAWAR  LDHRFDLMYA
401    KRAFVHWYVG  EGMEEGEFSE  AREDMAALEK  DYEEVGVDSV  EGEGEEEGEE  Y
    
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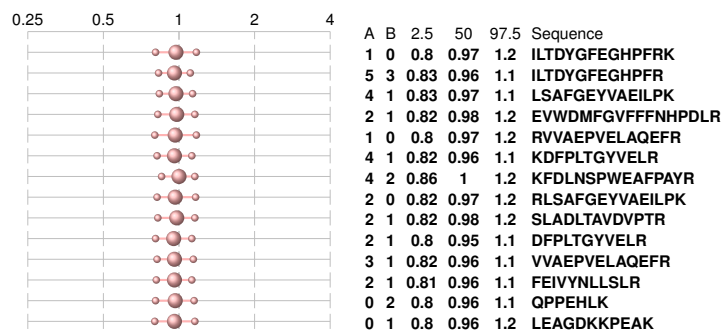
5.729 PREDICTED: similar to Secretory carrier-associated membrane protein 1 (Secretory carrier membrane p

Protein Accession	gij109465823
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.835, 1.28)
Associated Peptides	4
Associated Spectra	5
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.13
Avg..iTRAQ.Ratio....116.114.	1.17
Avg..iTRAQ.Ratio....117.114.	1.08



5.730 PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 3 [Rattus norvegicus]

Protein Accession	gij27702072	
Mean Expression Ratio	0.968	
Median Expression Ratio	0.968	
Credible Interval	(0.879, 1.07)	
Associated Peptides	14	
Associated Spectra	47	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.996	0.859
Avg..iTRAQ.Ratio....116.114.	1.11	0.928
Avg..iTRAQ.Ratio....117.114.	0.931	0.782

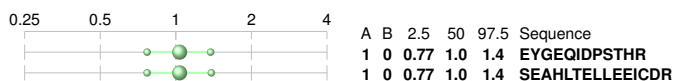


5.731 PREDICTED: similar to MIR-interacting saposin-like protein precursor (Transmembrane protein 4) (Put

Protein Accession	gij109481425
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.793, 1.34)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0885
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.18
Avg..iTRAQ.Ratio....116.114.	1.16
Avg..iTRAQ.Ratio....117.114.	1.07

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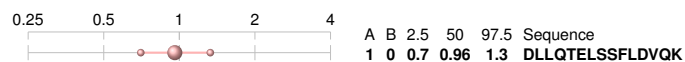
1      MNGSRRIIPWT VFAFQGVLA SEAPLKLPAR ARVWRGWL RV IFVEARTGPS DLRLGSWLGT GCWARRSLAT LNLSAGALW
81     RSPDSPVLSS QLLGLGAKVR VRLSSAWAT AAAVGAEVER PCPAKDERLG LAGPTFGGPA GNYLGSKEPG STLWRALVDE
161    LEWEIARVDP KKTIQMGSFR INPDGSQSVV EYPYARSEAH LTELLEEICD NMKEYGEQID PSTHRKNYVR VVGRNGGSSE
241    LDLQGIRIDS DISGTLKFAC ESIVEEYEDE LIEFFSREAD NVKDKLCSKR TDLCDHALHR SHDEL
    
```



5.732 S100 calcium binding protein A1 [Rattus norvegicus]

Protein Accession	gi 56090267
Mean Expression Ratio	0.97
Median Expression Ratio	0.968
Credible Interval	(0.723, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.160
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.928
Avg..iTRAQ.Ratio....116.114.	0.883
Avg..iTRAQ.Ratio....117.114.	0.908

1 MGSELETAME TLINVFHAHS GKEGDKYKLS KKELKDLLQT ELSSFLDVQK DADAVDKIMK ELDENGDGEV DFQEFVVLVA
 81 ALTVACNFF WENS



5.733 cell division cycle 42 [Rattus norvegicus]

Protein Accession	gi 61889112	
Mean Expression Ratio	0.967	
Median Expression Ratio	0.968	
Credible Interval	(0.774, 1.20)	
Associated Peptides	2	
Associated Spectra	5	
Coverage	0.115	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.988	1.11
Avg..iTRAQ.Ratio....116.114.	0.92	0.743
Avg..iTRAQ.Ratio....117.114.	0.854	1.55

1 MQTIKCVVVG DGAVGKTCLL ISYTTNKFPS EYVPTVFDNY AVTVMIGGEP YTLGLFDTAG QEDYDRLRPL SYPQTDVFLV
 81 CFSVVSPSSF ENVKEKWPPE ITRHCPKTPF LLVGTQIDLR DDPSTIEKLA KNKQKPIITPE TAEKLARDLK AVKYVECSAL
 161 TQRGLKNVFD EAILAALFPP EPKKSRRCVL L



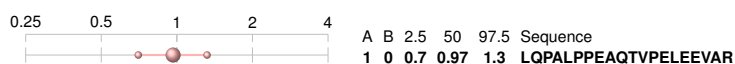


5.734 PREDICTED: similar to NFkB interacting protein 1 [Rattus norvegicus]

Protein Accession	gij109461367
Mean Expression Ratio	0.97
Median Expression Ratio	0.968
Credible Interval	(0.722, 1.3)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0242
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.9
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	0.958

```

1      MDSEAFQQR  DILLDNFQSL  AMKHMDLKQM  ELDTAAAKVD  ELTKQLESIW  SDSPAPPGTQ  AGVPSRMSRY  STSPVPEHFG
81     SRGSLQKIAA  DGVEARFGRS  ESAPSLHPYS  PLSPKGRPSS  PRTSIYLQPT  TDPYSSSLDR  APSRPRAFEE  GTGSPHGRAP
161    SPRPGTGPVR  QPGPPTPFDY  LGRAGSPRGS  PLAEGPQAFF  PERGSPRPP  AAAYDTSATF  GSPLLGAGGS  AFAPPLRAQD
241    DSTLRRRPPK  AWNESDLDDVA  YEKSSQTAS  YERLDVFRP  ASPLQLLPW  RESSLDGLGA  SGKDNITSAT  LPRNYKVSPL
321    ASDRRSDVGS  YRRSMGSAGP  SGTLPRSWQP  VSRIPMPFSS  PQRSTPRQR  PIPLSMIFKL  QNAFWEHGAS  RAVLPGSPIF
401    SRAPPPKLP  QPPPQPQLFP  QPQPMPFQS  QPQPQTPVPO  QTWSPMNEGL  LKSPAELEPE  PELEGLLAPV  LESGDADEGT
481    VTRPLSPTRL  QPALPPEAQT  VPELEEVARV  LAEIPRPLKR  RGSMEQSPAA  ALPPTHKKQY  QQIINRLFHR  HGGPFGGPE
561    PELSTITEGS  EARAGPPAPA  PPAPIPPPAP  AQSNPPEQPQ  SMEMRSVLRK  VGSPRKARRA  RLNPLVLLLD  AALTGELDVV
641    QQAVKEMNDP  SQPNEEGITA  LHNAICGANY  PIVDFLIAAG  ANVNSPDSHG  WTPLHCAASC  NDTAICTALV  QHGAAIFATT
721    LSDGATAIEK  CDPYREGYAD  CATYLADVEQ  SMGLMHNGV  YALWDYSAEF  GDELSFREGE  SVTVLRRDGP  EETDWWAAL
801    HQQEGYVPRN  YFGLFPRVKS  QRSKI
    
```



5.735 PREDICTED: similar to heterogeneous nuclear ribonucleoprotein H3 isoform a [Rattus norvegicus]

Protein Accession	gij109509819
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.796, 1.35)
Associated Peptides	1
Associated Spectra	2

Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.12
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	1.16



5.736 PREDICTED: similar to cardiomyopathy associated 1 [Rattus norvegicus]

Protein Accession	gij109485595
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.792, 1.34)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0192
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.18
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	1.17

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1      MADAQMQVVH TPTIQMRTGE DLPLPPPSAL EGLPPPPFKE SFSKFQQQRQ ANELRRLYKH IHPELRKNLE EAVAEDLAKV
81     LGSEEPTEGD VQCMRWIFEN WSLDAIGDHE RPAGKEPVSG GNVQATSRKF EEGSFTNSSD LEPGPQLSGG DVRASTRQLFE
161    TKSLDALTGQ EEATQMTMKE PAVSGDVQGT RKLFFETKPLD MLGSCPSIQD QSPLELRSEI QELKGDVKKK VKLFTQTEPLC
241    AIQDAEGAIH EVKAACREEI QSNAVRSARW LFETRPLDAF NQDPSQVRVI RGISLEEGAL PDVSATRWIF ETQPLDAIRE
321    ILVDEKDFQP SFDLFFPPGD VQHQHHLFET CALDTLKGER ETEAEAPAKE EVIPGDVVRST LWFETKPLD AFRDQVQVGH
401    LQRVDHQKGE GPVIECLSSN GTSALPLSQG VPQNNPKGD VKTFKNLFET LPLDSIGQGE PSACGNINRG QRTDSTGLSE
481    GADAPVYAMQ DSRGQLHALT SVSREQVVG G DVQGYKWMFE TQPLDRLGRS PSTVDVVRGI TRQEUVVAGDV GTTRWLFETQ
561    PLEMIHQEQQ QKREEEEGRG PGGPPPELPQ KGDVQTIKWL FETYPMSELA EKQSEVETGP VSKAEAQSC T WMFQSQSLNQ
641    AEGSGEQHLQ TSQVQAGDRQ TDSHFVETES LSAQGGQSSGR KPVRVCSRVE IPSGQVSRQK EVFQALEAGK RGVQETVLSF
721    GSIPTGSVHK FTWLFEPCPM GSLAAESVSG GNLQEEQPKV SADPGTPERQ ETAARTLRT LHATPGILHH GGILMEARGP
801    GELCLAKYVL PSPGQGRPCV QKEELVCGEL PRIVRQVLGR TDVDQQGLLV QEDTAGQLRL HPLKLPFGPD FENIEDMDPE
881    LQQLLACGLG VSMAKTGLVM QETGQGLVAL TAYSLQPQPT SRGPERSVQ LLASCIDKGE LHSLSPLRWE PPTDSSSVPV
961    TEETQRLPPT ESIIIRVTPLD STMKMGHLRV SGSTPCPPLP RAAGKVVLPN GRPGAPLQEA RKQVDISHAG QKGAASGRP
1041   EGTIAPPLGS GAPNLQEAHQ NLRLATAEAO SLHQOVLSRH AQGSDPAATS ISAQDVLQVP TPTTTQGSIM PVAGRDRARIT
1121   AVPRKVSVDN KAVPRGLPRG RVTIQDGIYA AHPVRTSDLP GAIQPSKEPE QPRDSPPQAD QGQSPREYH EPGGHSQRAW
1201   GPLGKVMPOI WPECLQAADT SLKTVPLTHH TLTPKPQAAG DSLHSHNASP PTLPAAVTEE PDHPAQGHQ KDSVQQASKP
1281   LREPLLHSHN RPAGQKTLLE SETKLSKAES TVLPRKKPPV PPKPAHLSQV HPPHRLPKPL AASASISEAG QDHPGPEPV
1361   ANPGSAKAPT IAGQCCLPLA ECSKGQKQPM RQYPLSTAS RPSGGQTSNS NSQSPESRKL TILNNDNDVS PPQKHPSSPK
1441   QQPMDGSKQR TPESPEIVQG SHQELQGLLS QVQTLKEEAA HTVNVQTLRK LFEGAPQLAG GTRQVPTAPH KTEVSVEQAF
1521   GELTRVSSKV AQLKEQTLAR LLDIEETVHK ALSIFSFQS EGHTSSPPQ SAKDLGVKKV STSNRRARPMG SNQVKEPPAV
1601   ENQEKVESRP EAQQQDEIRN HAEARGQAAV NVLPSRRLET ARAEPGLQVQ SPSCRGSSSP TFISIQSAK TLLDASSPQG
1681   SHSISGKNTH LAQDISQALL YQRDIQDQAG TKEMAIGKSV FTGQQENVLE FQTGSATSKS YGATKTVTEQ YEEMDQFGNT
1761   VLTSSTTTTIQ QAEPLMDDPR QLGLYTFPML RQFLHSPSRF NSDLAGAEIP WVPCSHFHPA AQ
    
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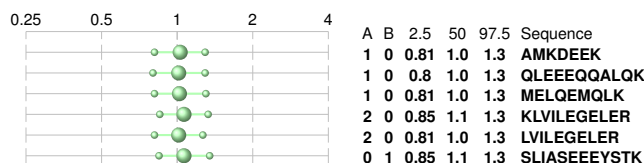


5.737 hypothetical protein LOC500450 [Rattus norvegicus]

Protein Accession	gj 66730475	
Mean Expression Ratio	1.03	
Median Expression Ratio	1.03	
Credible Interval	(0.862, 1.24)	
Associated Peptides	6	
Associated Spectra	8	
Coverage	0.176	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.995	0.683
Avg..iTRAQ.Ratio....116.114.	0.9	0.946
Avg..iTRAQ.Ratio....117.114.	0.93	0.965

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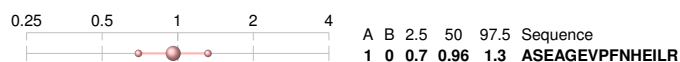
1      MDAIKKKMQM LKLDKENAID RAEQAEADKK QAEDRCKQLE EEQQALQK KL KGTEDEVEKY SESVKDAQEK LEQAEKKATD
81     AEADVASLNR RIQLVEEELD RAQERLATAL QKLEEEAKAA DESERGMKVI ENRAMKDEEK MELQEMQLKE AKHIAEDSDR
161    KYEEVAR KLV ILEGELESE ERAEVAESRA RQLEEEELRTM DQALKSLIAS EEEYSTKEDK YEEI KLEE KLKEAETRAE
241    FAERSVAKLE KTIDDLLEETL ASAKEENVEI HQTLDQTLE LNNL
    
```



5.738 PREDICTED: similar to COP9 signalosome subunit 6 [Rattus norvegicus]

Protein Accession	gj 109495350	
Mean Expression Ratio	0.967	
Median Expression Ratio	0.968	
Credible Interval	(0.724, 1.3)	
Associated Peptides	1	
Associated Spectra	1	

Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.875
Avg..iTRAQ.Ratio....116.114.	0.92
Avg..iTRAQ.Ratio....117.114.	1.03



5.739 PREDICTED: similar to seryl-aminoacyl-tRNA synthetase 2 [Rattus norvegicus]

Protein Accession	gi 34855637
Mean Expression Ratio	0.964
Median Expression Ratio	0.968
Credible Interval	(0.716, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.958
Avg..iTRAQ.Ratio....116.114.	0.952
Avg..iTRAQ.Ratio....117.114.	0.794



5.740 PREDICTED: similar to malignant T cell amplified sequence 1 [Rattus norvegicus]

Protein Accession	gij109471042
Mean Expression Ratio	0.968
Median Expression Ratio	0.968
Credible Interval	(0.72, 1.30)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0994
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.924
Avg..iTRAQ.Ratio....116.114.	0.778
Avg..iTRAQ.Ratio....117.114.	1.12

1 MFKKFDEKES VSNCIQLKTS VIKGIKSQLT EQFPGIEPWL NQIMPKKDPV KIVRCHEHME ILTVNGELLF FRQRKGFYFP
 81 TLRLLLHKYFP ILPHQQVDRG AIKFVLSGAN IMCPGLTSPG AKLYTAAVDT IVAVMAEGKE HALCVGVMMK AAADIEKINK
 161 **GIGIENIHYL NDGLWHMK**TY K



5.741 ATP synthase F0 subunit 8 [Rattus norvegicus]

Protein Accession	gij110189667
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.763, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	0.119
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.27
Avg..iTRAQ.Ratio....116.114.	1.18
Avg..iTRAQ.Ratio....117.114.	1.11

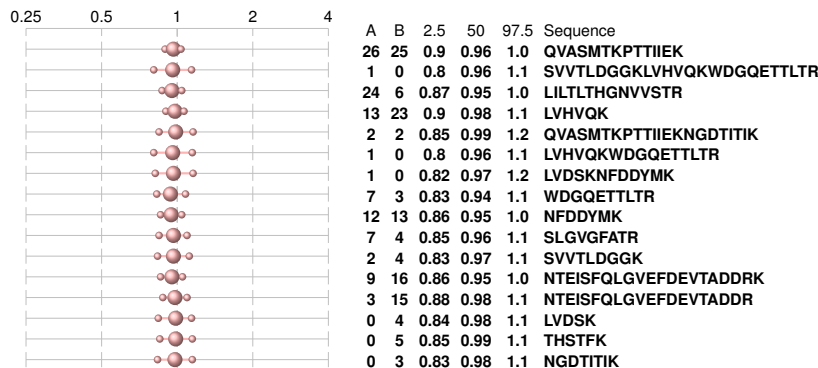
1 MPQLDTSTWF ITIISSMATL FILFQLKISS QTFFAPPSPK TMATEK**TNNP** WESKWTKIYL PLSLPPQ



5.742 heart fatty acid binding protein [Rattus norvegicus]

Protein Accession	gij 13162363	
Mean Expression Ratio	0.968	
Median Expression Ratio	0.969	
Credible Interval	(0.905, 1.03)	
Associated Peptides	16	
Associated Spectra	231	
Coverage	0.82	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.927	0.868
Avg..iTRAQ.Ratio....116.114.	0.988	0.905
Avg..iTRAQ.Ratio....117.114.	0.856	0.977

1 MADAFVGTWK LVDSKNFDDY MKSLGVGFAT RQVASMTRPT TIIKNGDTI TIKTHSTFKN TEISFQLGVE FDEVTADDRK
 81 VKSVVTLDDG KLVHVQKWDG QETTLRELS DGKLILTLTH GNVVSTRTYE KEA

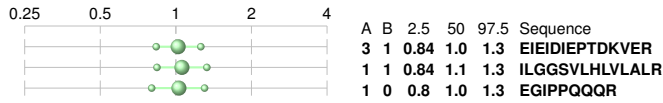


5.743 "neural precursor cell expressed, developmentally down-regulated gene 8 [Rattus norvegicus]"

Protein Accession	gij 20302051	
Mean Expression Ratio	1.03	
Median Expression Ratio	1.03	

Credible Interval	(0.844, 1.26)	
Associated Peptides	3	
Associated Spectra	7	
Coverage	0.457	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.28
Avg..iTRAQ.Ratio....116.114.	0.97	1.25
Avg..iTRAQ.Ratio....117.114.	1.04	0.872

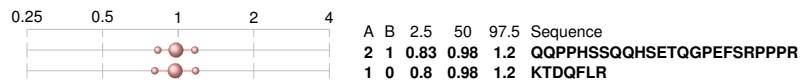
1 MLIKVKTLTG KRIEIDIEPT DKVERIKERV EEKEGIPPQQ QRLIYSGKQM NDEKTAADYK ILGGSVLHLV LALFGGGGLG
81 Q

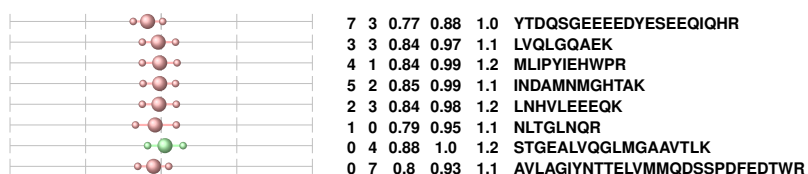


5.744 hypothetical protein LOC498909 [Rattus norvegicus]

Protein Accession	gi 78214350	
Mean Expression Ratio	0.969	
Median Expression Ratio	0.969	
Credible Interval	(0.877, 1.06)	
Associated Peptides	10	
Associated Spectra	49	
Coverage	0.471	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.993	0.9
Avg..iTRAQ.Ratio....116.114.	1.02	0.876
Avg..iTRAQ.Ratio....117.114.	0.8	0.986

1 MAATAAVSGV LRRLGWRLIQ LRCLPVARCQ SPLMPRAFHT AVGFRSSEEQ RQPPHSSQQ HSETQGPEFS RPPPRYTDQS
81 GEEEDYESE EQIQHRILTA ALEFVPDHGW TAEAIAEGAQ SLGLSSAAAS MFGSDGSELI LHFVTQCNR LNHVLEEEQK
161 LVQLGQAEKR KTDQFLRDAV ETRLRMLIPY IEHWPRALSI LLLPQNIPPS LSLLTSMVDD MWHYAGDQST DFNWYTRRAV
241 LAGIYNTTEL VMMQDSSPDF EDTWRFLDNR INDAMNMGHT AKQVKSTGEA LVQGLMGA AV TLKNLTGLNQ RR

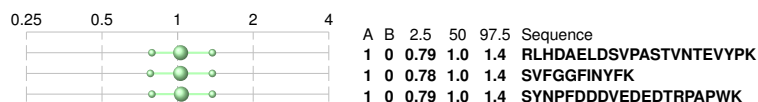




5.745 synaptosomal-associated protein 29 [Rattus norvegicus]

Protein Accession	gi 62751974
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.814, 1.32)
Associated Peptides	3
Associated Spectra	3
Coverage	0.206
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.06
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.14

1 MSGYPKSYNP FDDDVEDEDTRPAPWFDARD LPDGPDAPID RQQYLRQEVLRRAEATAAST SRSLSLMYES EKIGVASSEE
 81 LVRQRGVLEH TEKMDKMDQ DLKMSQKHIN SIKSVFGGFI NYFISKVPEP PPEQNGSIVP QPSSRLKEAI NTSKDQESKY
 161 QASHPNLRKL HDAELDSVPA STVNTEVYPK NSSLRAYHQK IDSNLDELSV GLGRLKDIAL GMQTEIEEQD DILDRLTTKV
 241 DKLDVNIKST EKKVRQL



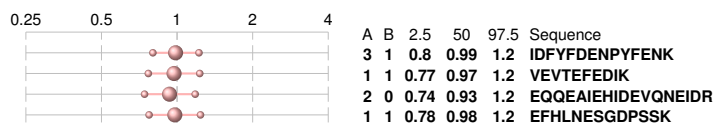
5.746 protein kinase N3 [Rattus norvegicus]

Protein Accession	gi 114145515
Mean Expression Ratio	0.97
Median Expression Ratio	0.97
Credible Interval	(0.802, 1.17)
Associated Peptides	4
Associated Spectra	10

Coverage	0.0574
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.02
Avg..iTRAQ.Ratio....116.114.	0.99
Avg..iTRAQ.Ratio....117.114.	0.987

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1   MAPKRQFAIL PQPNETQTRR CPEAGGQVDL SRPAEGSTFL VLRSDSGFRA SVHFSLSSVD REVCVSYAQL RVVVWCFPRG
81  LGSVCFLHS SCEVHNPISS MPRGSSVEQA LGSMLAVVTS TNPWIRRCMC WRSCLCGAVR FLGCVFSESQ QKSC TAVYDD
161 QSSRMGWKKK EQQEAIEHID EVQNEIDRLN EQASEEILKV EQKYNKLRQP FFQKRSELIA KIPNFVWTF VNHQPVSALL
241 GEDEEALHY LTRVEVTEFE DIKSGYRIDF YFDENPYFEN KVLSKEFHLN ESGDPSSKST EIKWKS GKER KLLAAAQ QML
321 KDSQLKVALL RMKISGLEAS GSPEPGP DLL AEELQHRLRI EAAVAAGAKN VVKLLGGQRI QDRKALAEAQ AQLQESSQKL
401 DLLRLALELL LERLPPTHSL RSRVTRELRM AMLGNPQLG TLVKPIALTG EVLAVLKVDN RVVGGQTGWGL VAEKSWDQAF
481 SISLDRVTFE EPVIERPRRL QRQRRVFSKR RGQDFLRASQ MNLSTAWGR LVMSLLPPCS SPSTVSPKGCPSAAACETS
561 SSASPSMVMR LPAPCDWAQT FPSYSNFRPV KTLPGEDMKP PPKPPRLYLQ EPAPGTPCTK RPHMDPRTVG APPLAALSTR
641 NPPQLQDFRC LAVLGRGHFG KVLVQYKGT GKYYAIKALK KQEVLRDEI DSLYCEKRIE TVGRTGHFP LLSLLACIQT
721 SSHACFVTEF LPPGDLMMQI HEDVFPPEQA CFYLACVVLG LQFLHEKRII YRDLKLDNLL LDAQGF LKIA DFGLCKEGIG
801 FGDRTSTFCG TPEFLAPEVL TQEAYTRAVD WWGLGVLLYE MLVGDTEDEV FECIVNADVP CPHFLSAQGL ELIQKLLQKS
881 PEKRLGAGER AAEIEIKVQPF FRPPFVPTLC GPADLRYFEG EFTSLPPTLT PFVPRRSLSA RQQAARDFD FVSKRFLES
    
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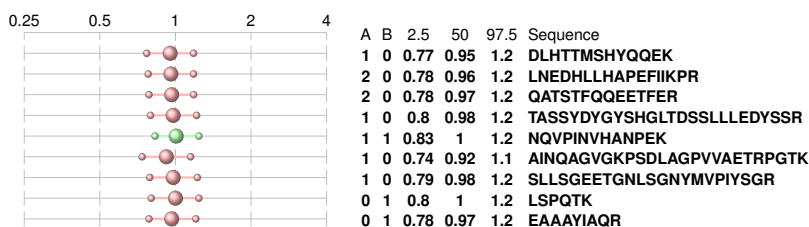


5.747 PREDICTED: similar to Myomesin-1 (Skelemin) isoform 1 [Rattus norvegicus]

Protein Accession	gij109487636	
Mean Expression Ratio	0.97	
Median Expression Ratio	0.97	
Credible Interval	(0.83, 1.13)	
Associated Peptides	9	
Associated Spectra	12	
Coverage	0.088	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.989	1.02
Avg..iTRAQ.Ratio....116.114.	0.789	0.996
Avg..iTRAQ.Ratio....117.114.	1.09	1.29


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1      MSLPFYQRSH QHYDLSYRNK DLHTTMSHYQ QENKRSAYVT HGSTAYSSRS SAAHRQESEA LRQASAASYQ QQASKAYSLG
81     TSSSQHYQGS EVSRKTASSY DYGYSHGLTD SLLLEDYSS RLSPQTKRAK RLLSGEETG NLSGNYMVPI YSGFQVHISG
161    IRDSEERIK EAAAYIAQQT LLESEEAIMA SKQSTASKQS TASKQTSKQA TSTFQQEETF EKRSRNI SIR EKAEELSLRK
241    TLEETQAYHG KLNEDHLLHA PEFIKPRSH TWVEKENVKL HCSVAGWPEP RLTWYKNOVP INVHANPEKY IIESRYGMHT
321    LEISKCDFED TAQYRASAMN VQGEVSAYAS VVVKRYGEL DDSLRLGGVS MPLSFAVTPY GYASKFEIHF DDKFDVSGFR
401    EGETMSLGR VVITPEIKHV QPEVQYWRNG APVSPSKWVQ PHWSGDRATL TFSHLNKEDE GLYTIRVRMG EYEQYSAYV
481    FVRDADAIE GAPAAPLDVV SLDANKDYII ISWKQPAVDG GSPILGYFID KCEVGTDTWS QCNDTPVKFA RFPVTGLIEG
561    RSYIFRRAV NKTGIGLPSR VSEPVAALDP AEKARLKS RP SAPWTGQIIV TEEETTEGVI PGFPTDLSVT EATRSYVVL
641    WKPPGQRGHE GIMYFVEKCD VGTEWQRVN TELPVKSPRF ALFDLVEGKS YRFRVRCNS AGVGEPEST EVTUVGDKLD
721    IPKAPGKIIP SRNTDTSVVV SWEESKDAKE LVGYIESSV VSGGWEPEN NNPVKGSRFT CHGLTTGQSY IFRVAVNA
801    GLSEYSQDSE AIEVKAAGG GVSPDVWVPL SDTPGGTDS GGAMSGASFP TSQKDALPSS KPNKPSFPSS PSNRGQKEVS
881    KVNGSVQEEL SPPSMEVASK EQSKSGPPEK KDPVAVPSP PYDITCLESE RDSMVLGWKQ PDKTGGAEIT GYVNYREVV
961    GGVPGKWR EA NIKAVSDAAY KISELKENTV YQFQVSAMNI AGLGAPSAVS ECFKCEEWI AVPGPPHSLK LSEVRKNSLV
1041   LQWKPPVYSG RTPVTGYFVD LKEASAKDDQ WRGLNEAIP NKYL RVQGLK EGISYVFRVR AINQAGVGKPSDLAGPVVAE
1121   TRPGTKEVVV NVDDDGVISL NFECQMTPK SEFVWSKDYV PSEDSRLEV ESKGNKTKMV FKDLGPDLDG TYSVDVTD
1201   GIASSYLIDE EEMKRLLALS QEHKFPVPT KSELAVEILE KGQVRFWMQA EKLSGNKVN YIFNEKEIFE GPKYKMHIDR
1281   NTGIEMFME KLQDEDEGTY TFQIQDGKAT GHSTLVLIGD VYKKLQKEAE FQRQEWIRKQ GPHFAEYLSW EVTGCNVLL
1361   KCVANIKKE THIVWYKDER EISVDEKHF KDGICTLLIT EFSKKDAGFY EVILKDDRGR DKSRLKLVDE AFQDLMTFVC
1441   RKIALSATDL KIQSTAEGIR LYSFVCIYLD DLKVNWSHNG TGIKYTDRVK SGVTGEQIWL QINEPTQNDK GKYYMELEFD
1521   KTGHQKSVDL SGQAFDEAFA EFQRLKQAAI AEKNRARVLG GLPDVVTTIQE GKALNLTCNV WGDPTPEVSW LKNEKPLTSD
1601   DHCCLKFEAG KTAFFTISGV STADSGKYGL VVKNKYGSET SDFTVSVFIP EEEARKGASE PPKGNQKSK
    
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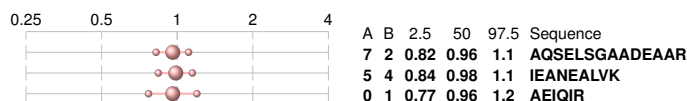


5.748 "ATP synthase, H⁺ transporting, mitochondrial F1 complex, delta subunit precursor [Rattus norvegicus]"

Protein Accession	gi 20806153	
Mean Expression Ratio	0.97	
Median Expression Ratio	0.97	
Credible Interval	(0.829, 1.13)	
Associated Peptides	3	
Associated Spectra	19	
Coverage	0.173	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.903	0.853
Avg..iTRAQ.Ratio....116.114.	0.999	0.93
Avg..iTRAQ.Ratio....117.114.	0.94	1.06

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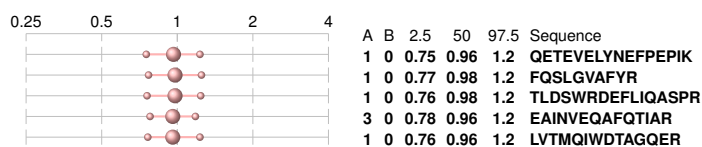
1      MLPAALLRHP GLRRLLVQAR TYAQAASPA PAAGPGQMSF TFASPTQVFF DGANVRQVDV PTLTGAFGIL ASHVPTLQVL
81     RPLVMVHAE DGTTKYFVS SGSVTYNADS SVQLLAEV V TLDMLDLGAA RANLEKQSE LSGAADEAAR AEIQIRIEAN
161    EALVKALE
    
```



5.749 "RAB7, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gij13027392
Mean Expression Ratio	0.969
Median Expression Ratio	0.97
Credible Interval	(0.795, 1.17)
Associated Peptides	5
Associated Spectra	7
Coverage	0.338
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.933
Avg..iTRAQ.Ratio....116.114.	0.97
Avg..iTRAQ.Ratio....117.114.	1.11

1 MTSRKKVLLK VIILGDSGVG KTSLMNQYVN KKFNSQYKAT IGADFLTKEV MVDDR LVTMQ IWDTAGQERF QSLGVAFYRG
 81 ADCCVLVFDV TAPNTFKTLD SWRDEFLIQA SPDPENFPF VVLGNKIDLE NRQVATKRAQ AWCYSKNNIP YFETSAKEAI
 161 NVEQAFQTIA RNALKQETEV ELYNEFPEPI KLDKNERAKA SAESCSC



5.750 "tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide [Rattus nor]"

Protein Accession	gij9507245
Mean Expression Ratio	0.972
Median Expression Ratio	0.97
Credible Interval	(0.724, 1.31)
Associated Peptides	1
Associated Spectra	1

Coverage	0.0567
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.992
Avg..iTRAQ.Ratio....116.114.	1.12
Avg..iTRAQ.Ratio....117.114.	1.01

```

1      MVDREQLVQK  ARLAEQAERY  DDMAAAMKNV TELNEPLSNE ERNLLSVAYK  NVVGARRSSW  RVISSIEQKT  SADGNEKKIE
81     MVRAYREKIE  KELEAVCQDV  LSLLDNYLIK  NCSETQYESK  VFYLMKMGDY  YRYLAEVATG  EKRA TVV ESS  EKAYSEAHEI
161    SKEHMQPTHP  IRLGLALNYS  VFYYEIQNAP  EQACHLAKTA  FDDAIAELDT  LNEDSYKDST  LIMQLLRDNL  TLWTSDQDD
241    DGGEGNN
  
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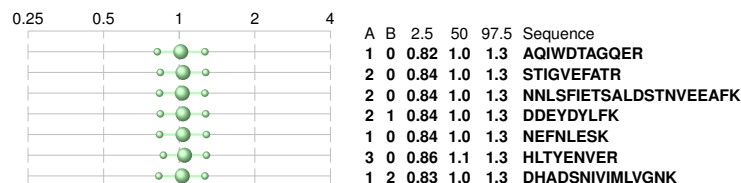


5.751 "RAB11B, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gi 14249144
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.876, 1.21)
Associated Peptides	7
Associated Spectra	15
Coverage	0.381
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	1.12

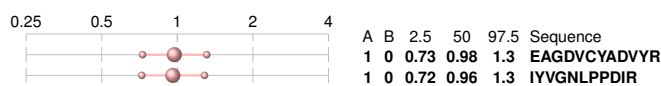
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1      MGRDDEYDY LFKVVLIGDS  GVGKSNLLSR  FTRNEFNLES KSTIGVEPAT  FSIQVDGKTI  KAQIWDTAGO  ERYRAITSAY
81     YRGAVGALLV  YDIAKHLTYE NVERWLKELR  DHADSNIVIM  LVGNKSDLRH  LRAVPTDEAR  AFAEKNNLSF  IETSALDSTN
161    VEEAFKNILT EIYRIVSQRQ  IADRAAHDES  PGNNVVDISV  PPTTDGQKPN  KLQCCQNL
  
```



5.752 "PREDICTED: similar to splicing factor, arginine/serine-rich 1 (ASF/SF2) [Rattus norvegicus]"

Protein Accession	gij109488756
Mean Expression Ratio	0.97
Median Expression Ratio	0.97
Credible Interval	(0.743, 1.26)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.931
Avg..iTRAQ.Ratio....116.114.	1.08
Avg..iTRAQ.Ratio....117.114.	0.892

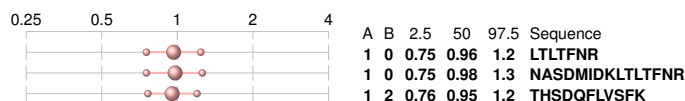


5.753 "ATP synthase, H⁺ transporting, mitochondrial F1 complex, gamma subunit [Rattus norvegicus]"

Protein Accession	gij39930503	
Mean Expression Ratio	0.968	
Median Expression Ratio	0.97	
Credible Interval	(0.783, 1.2)	
Associated Peptides	3	
Associated Spectra	5	
Coverage	0.0872	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.948	0.807
Avg..iTRAQ.Ratio....116.114.	0.956	0.726
Avg..iTRAQ.Ratio....117.114.	1.03	0.916

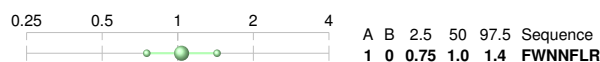
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81     EIRGPEDKKK HLIIGVSSDR GLCGAIHSSV AKQMKNDMAA LTAAGKEVMI VGIGEKIKSI LYRTHSDQFL VSPFDVGRKP
161    PTFGDASVIA LELLNSGYEF DEGSIIFNQF KSVISYKTEE KPISFSTVV AAENMSIYDD IDADVLQNYQ EYNLANIIYY
241    SLKESTTSEQ SARMTAMDNA SKNASDMIDK LTLTFNRTRO AVITKELIEI ISGAAALD
  
```



5.754 "PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa isoform 1 [Rattus]"

Protein Accession	gi 27660847
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.766, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.94
Avg..iTRAQ.Ratio....116.114.	1.51
Avg..iTRAQ.Ratio....117.114.	1.10

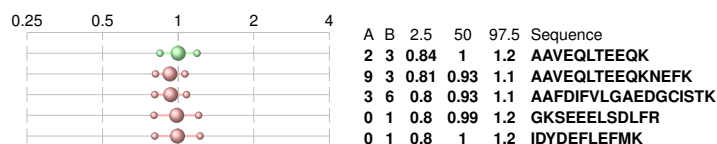


5.755 "troponin C, cardiac/slow skeletal [Rattus norvegicus]"

Protein Accession	gi 77627992
Mean Expression Ratio	0.97
Median Expression Ratio	0.971
Credible Interval	(0.851, 1.10)
Associated Peptides	5

Associated Spectra	28	
Coverage	0.348	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.939	0.78
Avg..iTRAQ.Ratio....116.114.	0.766	0.97
Avg..iTRAQ.Ratio....117.114.	0.888	1.15

1 MDDIYKAAVE QLTEEQKNEF KAAFDIFVLG AEDGCISTKE LGKVMRMLGQ NTPPELQEM IDEVDEDGSG TVDFDEFLVM
 81 MVRCKMDDSK GKSEEELSDL FFMFDKNADG YIDLDELKMM LQATGETITE DDIEELMKDG DKNNDGRIDY DEFLEFMKGV
 161 E



5.756 hypothetical protein LOC361726 [Rattus norvegicus]

Protein Accession	gi 56605818
Mean Expression Ratio	0.969
Median Expression Ratio	0.971
Credible Interval	(0.725, 1.3)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0732
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.873
Avg..iTRAQ.Ratio....116.114.	0.904
Avg..iTRAQ.Ratio....117.114.	0.912

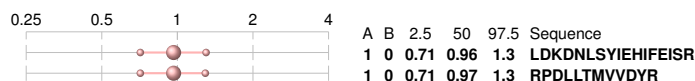
1 MAVVTLIPTL ARVLSKHSLL SPLLSVTSFR RFYRGDSPTD SQKDMIEIPL PPWQERTDES IETKRARLLY ESRKRGMLN
 81 CILLSLFAKE YLHNMTKQL NLYDRLINEP SNDWDIYYWA TEAKPAPEIF ENEVMELLRE FTKNKNKEQR LRAPDLEYLF
 161 EKPR



5.757 phosphoprotein enriched in astrocytes 15 [Rattus norvegicus]

Protein Accession	gi 61557370
Mean Expression Ratio	0.97
Median Expression Ratio	0.971
Credible Interval	(0.741, 1.26)
Associated Peptides	2
Associated Spectra	2
Coverage	0.223
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.982
Avg..iTRAQ.Ratio....116.114.	0.915
Avg..iTRAQ.Ratio....117.114.	1.05

1 MAEYGTLLQD LTNNITLEDL EQLKSACKED IPSEKSEEIT TGSAWFSFLE SHNKLDKDNL SYIEHIFEIS RRPDLLTMVV
 81 DYRTRVLKIS EEDELDTKLT RIPSARKKYD IIRQPSEEEI IKLAPPPKKA



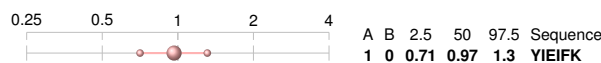
5.758 heterogeneous nuclear ribonucleoprotein H1 [Rattus norvegicus]

Protein Accession	gi 18266700
Mean Expression Ratio	0.972
Median Expression Ratio	0.971
Credible Interval	(0.728, 1.29)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0161
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.929
Avg..iTRAQ.Ratio....116.114.	0.937
Avg..iTRAQ.Ratio....117.114.	0.92

NHLBI Zile/Grant, Aged Rat

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1      MGHRYVEVFK SNNVEMDWVL KHTGPNSPDT ANDGFVRLRG LPFGCSEEEI VQFFSGLEIV PNGITLPVDF QGRSTGEAFV
81     QFASQEIAEK ALKKHKERIG HRYIEIFKSS RAEVRTHYDP PRKLMAMQRP GPYDRPGAGR GYNSIGRGAG FERMRRGAYG
161    GYGGGYDDYN GYNDGYGFGS DRFGRDLNYC FSGMSDHRYG DGGSTFQSTT GHCVHMRGLP YRATENDIYN FFSPLNQVVRV
241    HIETGPDGRV TGEADVFEFAT HEDAVAAMSK DKANMQHRYV ELFLNSTAGA SGGAYEHRYV ELFLNSTAGA SGGAYGSQMM
321    GGMGLSNQSS YGGPASQQLS GYGGGYGGQ SSMGSDYQVL QENSSDFQSN IA
  
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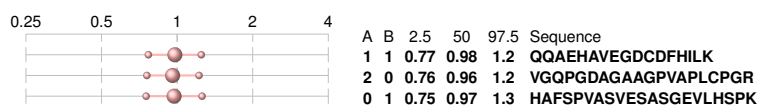


5.759 alpha-2-HS-glycoprotein [Rattus norvegicus]

Protein Accession	gi 6978477	
Mean Expression Ratio	0.973	
Median Expression Ratio	0.971	
Credible Interval	(0.785, 1.21)	
Associated Peptides	3	
Associated Spectra	5	
Coverage	0.165	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.984	0.84
Avg..iTRAQ.Ratio....116.114.	0.89	1.01
Avg..iTRAQ.Ratio....117.114.	0.876	1.16

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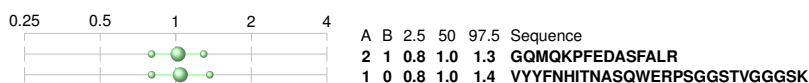
1      MKSLVLLLCF AQLWSCQSAP QGAGLGFREL ACDDPETEHV ALIAVHYLNK HLLQGFRQIL NQIDKVKVWS RRPFGQVYEL
81     EIDTLETTCH ALDPTPLANC SVRQQAEHAVY EGDCDFHILK QDGGFRVLHA QCHSTPDSAE DVRKFCPRCP ILIRFNDTNV
161    VHTVKTALAA FNAQNGTYF KLVEISRQON VFPVSTLVE FVIAATDCTG QEVTDPAKCN LLAEKQYGFC KATLIHRLGG
241    EEVSVACKLF QTQPQANAN PAGPAPTVGQ AAPVAPPAGP PESVVVGPVA VPLGLPDHRT HHDLRHAFSPVASVESSASGE
321    VLHSPKVGQQP GDAGAAGPVA PLCPGHVRYF KI
  
```



5.760 PREDICTED: similar to protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 [Rattus norv]

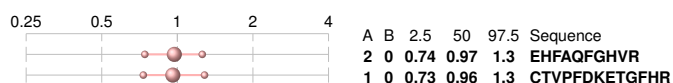
Protein Accession	gi 109483152	
Mean Expression Ratio	1.03	
Median Expression Ratio	1.03	

Credible Interval	(0.813, 1.29)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.09	0.727
Avg..iTRAQ.Ratio....116.114.	1.13	1.15
Avg..iTRAQ.Ratio....117.114.	1.14	0.618



5.761 "PREDICTED: similar to CG33714-PB, isoform B [Rattus norvegicus]"

Protein Accession	gij109478550
Mean Expression Ratio	0.97
Median Expression Ratio	0.971
Credible Interval	(0.759, 1.24)
Associated Peptides	2
Associated Spectra	3
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.94
Avg..iTRAQ.Ratio....116.114.	1.00
Avg..iTRAQ.Ratio....117.114.	1.05



5.762 reversion induced LIM [Rattus norvegicus]

Protein Accession	gi 8394189
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.787, 1.34)
Associated Peptides	1
Associated Spectra	2
Coverage	0
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.23
Avg..iTRAQ.Ratio....116.114.	1.21
Avg..iTRAQ.Ratio....117.114.	1.03

```

1      MSNAQLETAI EAAWDARDTI TSATTGETRD AIEDTLAALD SGKLRVAEKM ENGDWHVNQW AKKAVLLGFR IKDMEQQDGG
81     PQGSGWWDKV DSKFKGWDA DWKEAGFRAV PNCVVRKSAY IAPGVVLMPS FVNIGAYVDS GTMVDTWATV GSCAQIGKNV
161    HLSGGVGIGG VLEPMQAGPT IIEDNCFIGA RSEVVEGCIV REGSVLGMGV YIGQSTKILD RETGEVFYGE VPAGSVVVAG
241    SMPSKNGVHL YCAVIVKRVD EKTRSKTSIN ELLRD
  
```



5.763 cardiac ankyrin repeat protein [Rattus norvegicus]

Protein Accession	gi 7106248
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.757, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.36
Avg..iTRAQ.Ratio....116.114.	0.927
Avg..iTRAQ.Ratio....117.114.	1.29

NHLBI Zile/Grant, Aged Rat

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1      MLKNAQKDFI QRHIGPSVDE QNVMLKELGY QNLDDLIKDT VPEKILLKDD LDIGDPNSEY KALRKLKDIS KKNKIYSSFI
81     GMGYGYGTYTP YVILRNILEN PGWYTSYTPY QPEVAQGRLE MLLNFQQMII DFTGMDIANA SLLDEGTAAA EAMGLSYRIS
161    KSESKKVFVS KNCHPQTIDV IKTRAEPGLL EIIVGEDDKD IKEDIICGII QYPGTLGDIK DPSEAIKSIH KFNKGAVLAC
241    DLLALAKLKT PAELGADIAV GSSQRFGIPM GYGPHAAFF ATKDEYKRSM PGRIVGVSV D RHGKKAYRLA LQTRQHIRR
321    DKATSNICTA QALLAIVSAA YAVYHGFQGI KKAESVSQL TKNFADKLLQ SGYELYSNEF FDTVTTIKTLD KTEKIYNAL
401    DQGVNIRKVN SEMLAVSFDE RKNLYRANQL LKIFNCSETI KETMNESLSN IPKNLLRSTST YLDHPVFNSY HSETEMLRYL
481    KKLESDIAL NKSMIALGSC TMKLNVAEM IPVTWKEFSQ PHFSPVEQM DGYRELFDDL KNWLRSTGF SGVSLQPNAG
561    AQGEFAGLMV IRKFHEKNGE TNRNVCLIPS SAHGTPASA QMVGKVVVV KCDQYGNVDY EDLKNKAEH SENLAALMVT
641    YPSTHGVEE KITDICELIH NHGGQVYMDG ANLNALVIA KPGNFGPDVC HINLHKTFCI PHGGGGPGMG PIACKKHLEI
721    FLPKHSVIKD CGPVTGMGAV SAAPWSSSI LSIWMIKMG SEGLRKAS QVAILNANYI AHKLKDSFPI LYKGSNGVA
801    HECIDIIRTI KSETGITTEED IAKRLIDFGY HAPTMSWPVA GTMMIEPTES ESLSEIDKFC STLIKIKQEI DKIQSGEYDK
881    TDNPLKNAPH THVELTSNWK DHKYEREEAA YPSEFLRTNK YWPPVGRVDN VYGDKNLFC T CPSMEEYEDT AA
  
```



5.764 PREDICTED: similar to 60S acidic ribosomal protein P1 [Rattus norvegicus]

Protein Accession	gij109475161	
Mean Expression Ratio	0.973	
Median Expression Ratio	0.972	
Credible Interval	(0.763, 1.24)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.182	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.946	0.613
Avg..iTRAQ.Ratio....116.114.	1.11	1.02
Avg..iTRAQ.Ratio....117.114.	1.08	0.89

```

1      MTFISELTWI YSAFILHDNK VIQDKIDALI KAAGVNVEPF WPGLFAKVL A NECQHRELMC NVGAGGLTPA AGAVPAGGTA
81     LSTTWYLS
  
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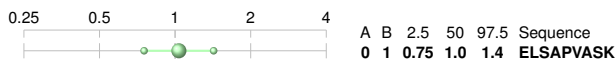


5.765 PREDICTED: similar to ring finger protein 17 long isoform [Rattus norvegicus]

Protein Accession	gij109501730
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.764, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00549
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.862
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	1.01

```

1      MAAEASSTGL ASCHLAGSKS GAPGASGCQC TRCGRKASFA SGHHHEYPCG HAFCELCLLA PQEYTTSKCT DCEVRTTVTM
81     NQGHYPVDGF IKEDSSVEAL PPKMVNNCSS GLEKTVDQLI INLEHSSSIH RNVSSPSAVM SETEEIDEAL KIAGCNSEQL
161    SNAIKMLDST QDQTRQETGS LREVVEKQFD TLIASLDSRK KSLCEELVRR TDDYLSKLVV VKSYIEEKKS DLDAAMKIAK
241    ELKSAPSLRT YCDLTQIIRT LKLNFESELS QVSSIIPRNP PRLNINCSEV ICMFNMGKI EPEDSTKCHP QENEVQGNVQ
321    KKFNSKKELC CDVYSSLEKK RVDTVVLADE APVPLQAEF PDRHLEGENK QPQKEVLVVA SPKTVAVLPQ LGSSPDVIEE
401    EIIIEENLESC FTDEPIETPR YPKKPPQKEL SAPVASK AGC PELVVFVSHVT HPCHFYVRKY SQIKDAAMLE KMKQVCSKS
481    LHLDPSTLE  LGARIFVNSI KNRMWCRCGII TEIIPTKTKN VRKPCSPTKF SVCEISLIQI FMVDFGNSEV LIITGVGDTH
561    VGPESHVGEQH ITLSDFCLLV RKSEPYSEEL LKDIPHLAHL CSLKDIPVYN SSEGWEKEAK VEFLKMNKKA AVLMKVFGE
641    DDILIVDLQK PPTNKISSDM PVSLRDALVF MELARFRSQS LRSHGENNTA LCYRPPALPE EMTEVSVMVC HINSPTDFYL
721    QLMENLDFLS LLKTIEEFYK GEDGENLEIL CPLQNQACVA KFEDGIWYRA KVIKGLPHRE VEVKYVDFGN TAKITLKDMM
801    KIKDEFLEPP EKAIKCLAF IEPKRSRSHWS KKAKEKFEEK TQDKFVTCSV IKILENGVLL VELFDSRAPG TSAVSINEQL
881    VKEGLASIEA GYTLKDNSKK HLEVWDFPSE EIISSSEINSL SPLSVNSLAN ESFQSLYNKE LPVVICNVLS PEKIYVQWLL
961    TENLLTSLEE KMVAAYEHSE WKPVKWECDM HCAVKIPAKS QWRRGQIIRM VTDTLVEVLL YDVGIELVNV IHCLRELQEN
1041   LKTMGRSLE  CSLVDIRPTG GSDKWTATAC DCLSLYLTGA IATIILQENS TTWPLPVKIF CRDEKGERVD VSKYLIRKGL
1121   ALRDRRVSKS SNSHSPEKSL EIPLEQGDSV VTKCFQINFV TNKKIADKVN EHKVPESKEK YSESRNNGFY KPPAVPNTSS
1201   FEAIVSCIGD DGTIFVVPKL SEFELIKMMD EIQSNLKCGL LLEPYFWKKG EPCAVRGSdT LWYRGKVMV VGGTIRVQYL
1281   DHGFTEKIPQ CHLYPILLYP DTPQFCIPQC LYQTLPGVNV WQPDALIELQ ELLSKREVDI HMELPDPHPW GKLSVHLYFD
1361   GMSLSYFMAY HKYCFIEHTE EIFKEKPRGQ NKRYEDENWK IRFEDLLPE MEAPILPPYL SSSLPPPEEL YAVQVKHIVS
1441   PDEVYICLDS VESCTQLNNH GTDDSGVSW EPESESLEEA LQRLNKNVET FPPLTDFSS EPCVAVRGSdT LWYRGKVMV VGGTIRVQYL
1521   KEFNPLSVLV LFDVYGSTEK LTINRLRQIP IQLMQYPAQA IKVLLAGFKP PLSDSGKTRI PYCPRWSMEA LWTMIDCLQG
1601   KQLYASSVAQ APEQIVTLYE DEQYPVHMSL VEMGLADKDE
  
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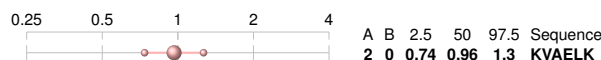
5.766 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gij109468610
Mean Expression Ratio	0.973
Median Expression Ratio	0.972
Credible Interval	(0.75, 1.27)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0195

Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.951
Avg..iTRAQ.Ratio....116.114.	1.14
Avg..iTRAQ.Ratio....117.114.	0.879

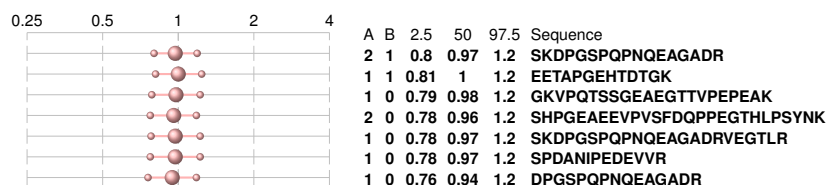
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1      MEDVGQNLLD DEDEITEIPT LEAIKQNLKY LNSDLEKDLQ RLDEANQTLT RRIQKKEESI QSLERDIALS IGRVPERDDF
81     NEIIVQKETA LKDLELEIAK LEKKNKTLK NVMELQKKIS KGTRNAVSDP ETLKKKVAEL KVKLQKSTES CAQQEKEIAK
161    MESDYQSVFQ LCEDQAHYIK KYQEILREME KEKEVMLLEK EISKAQNDSS QVVKPGSTLV ETIQSNMEKN IIKKQKRKFW
241    LRHFRYLFFM IMIVIRLLGY VFFHLQYINP DFLVDTLFML MSRSCLKWLR DILFPFLTLE VEDVLPH
    
```



5.767 PREDICTED: similar to protein kinase substrate MK2S4 isoform 2 [Rattus norvegicus]

Protein Accession	gij109498899	
Mean Expression Ratio	0.974	
Median Expression Ratio	0.972	
Credible Interval	(0.827, 1.15)	
Associated Peptides	7	
Associated Spectra	11	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.974	1.03
Avg..iTRAQ.Ratio....116.114.	1.02	0.966
Avg..iTRAQ.Ratio....117.114.	0.984	1.17

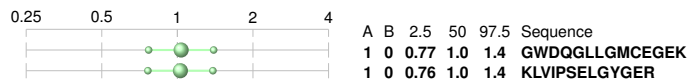


5.768 PREDICTED: similar to FK506-binding protein 2 precursor (Peptidyl-prolyl cis-trans isomerase) (PPIa)

Protein Accession	gj 62641808
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.79, 1.34)
Associated Peptides	2
Associated Spectra	2
Coverage	0.142
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.10
Avg..iTRAQ.Ratio....116.114.	1.07
Avg..iTRAQ.Ratio....117.114.	1.13

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1      MRSPALRVQ  RVLEGPMRAG  SVSRPVATKT  RLRRSDSTSG  IGSGGAARRD  MRLSWILTVL  SICLSALVTA  TGAEGKRKLQ
81     IGVKRRVDHC  PIKSRKGDVL  HMHYTGKLED  GTEFDSSLPQ  NQPFVFSLGT  GQVIKQWDQG  LLGMCEGEKR  KLVIPSELGY
161    GERGAPPKIP  GGATLVFEVE  LKTIERRSEL
    
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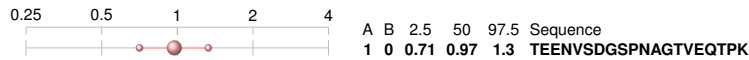


5.769 "cyclin-dependent kinase inhibitor 1B (p27, kip1) [Rattus norvegicus]"

Protein Accession	gj 50054216
Mean Expression Ratio	0.973
Median Expression Ratio	0.972
Credible Interval	(0.726, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.102
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.02
Avg..iTRAQ.Ratio....116.114.	0.933
Avg..iTRAQ.Ratio....117.114.	0.913

NHLBI Zile/Grant, Aged Rat

1 MSNVRVSNGS PSLERMDARQ TEHPKPSACR NLFQPVNHEE LTRDLEKHCR DMEEASQRKW NFDQNHKPL EGRYEWQVEE
 81 RGSLEPFYR PPRPKSACK VPAQESLDVS GSRQAVPSIG SQANSEDRHL VDQMPDSSDS PAGLAEQCPG MRKRPAEDS
 161 SSQNKRRNR EENVSDGSPN AGTVEQTPK PGLRRQT



5.770 eukaryotic translation elongation factor 1 alpha 1 [Rattus norvegicus]

Protein Accession	gi 28460696
Mean Expression Ratio	0.973
Median Expression Ratio	0.972
Credible Interval	(0.726, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0195
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.942
Avg..iTRAQ.Ratio....116.114.	0.986
Avg..iTRAQ.Ratio....117.114.	0.837

1 MGKEKTHINI VVIGHVDSGK STTGHLIYK CGGIDKRTIE KFEKEAAEMG KGSFKYAWVL DKLKAERERG ITIDISLWKF
 81 ETSKYVYVII DAPGHRDFIK NMITGTSQAD CAVLIVAAGV GEFEAGISKV GQTRHALLA YTLGVKQLIV GVNKMDSTEP
 161 PYSQKRYEEI VKEVSTYIKK IGYNPDTVAF VPIGWNGDN MLEPSANMPW FKGWVTRKD GSASGTTLE ALDCILPPTP
 241 PTDKPLRLPL QDVYKIGGIG TVPVGRVETG VLKPGMVVTF APVNVTTTEVK SVMHHEALS EALPGDNVGF NVKNVSVKDV
 321 RRGNVAGDSK NDPPMEEAGF TAQVIILNHP GQISAGYAPV LDCHTAHIAC KFAELKEKID RRSGKKLEDG PKFLKSGDAA
 401 IVDMPGKPM CVESFSDYFP LGRFAVRDMR QTVAVGVVKA VDKKAAGAGK VTKSAQKAQK AK



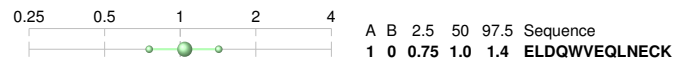
5.771 "protein phosphatase 2a, catalytic subunit, beta isoform [Rattus norvegicus]"

Protein Accession	gi 8394021
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.76, 1.38)
Associated Peptides	1

Associated Spectra	1
Coverage	0.0421
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.17
Avg..iTRAQ.Ratio....117.114.	1.17

```

1      MDDKAFTKEL DQWVEQLNEC YQLNENQVRT LCEKAKEILT KESNVQEVRC PVTVCGDVHG QFHDLMELEFR IGGKSPDTNY
81     LFMGDYVDRG YYSVETVTLV VALKVRYPER ITILRGNHES RQITQVYGFY DECLRKYGNA NVWKYFTDLF DYLPPLTALVD
161    GQIFCLHGGL SPSIDTLDHI RALDRLQEVV HEGPMC DLLW SDPDDRGGWG ISPRGAGYTF GQDISETFNH ANGLTLVSRA
241    HQLVMEGYNW CHDRNVVTIF SAPNYCYRCG NQAAIMELDD TLKYSFLQFD PAPRRGEPHV TRRTPDYFL
    
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5.772 PREDICTED: similar to Plasma retinol-binding protein precursor (PRBP) (RBP) [Rattus norvegicus]

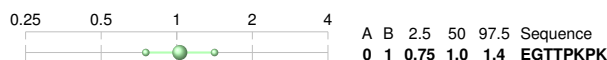
Protein Accession	gij109463849
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.762, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.06
Avg..iTRAQ.Ratio....116.114.	1.22
Avg..iTRAQ.Ratio....117.114.	1.10



5.773 PREDICTED: similar to ribosomal protein L37 [Rattus norvegicus]

Protein Accession	gij109504903
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.769, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0825
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.861
Avg..iTRAQ.Ratio....116.114.	1.01
Avg..iTRAQ.Ratio....117.114.	1.20

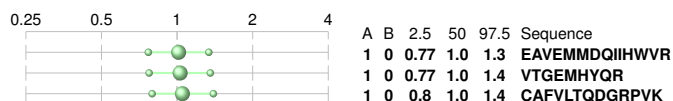
1 MTKGTSSF^GGK RRHK^THTL^CR RCGSKAY^HLQ KSTCGK^CAYP AKRR^RKYN^WS AKAKRR^NTTG TGRMR^HLKIV YRRFR^HGF^RE
 81 ^GTTP^KPK^RAA VAASS^SS



5.774 renin binding protein [Rattus norvegicus]

Protein Accession	gij13592043
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.8, 1.31)
Associated Peptides	3
Associated Spectra	3
Coverage	0.086
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	1.04
Avg..iTRAQ.Ratio....117.114.	1.22

1 MEKERETLQV WKQ^RVGQ^ELD SVIAFW^MEHS HDQ^EHGG^FFT CLGRD^GQV^YD HLK^YVWL^QGR QVW^MYCL^RYR TFER^FRR^VEL
 81 LDA^AKAG^GEF LLS^YAR^VAPP GKK^CAF^VLT^Q DGR^FV^KV^QRT IFSE^CF^YT^MA MNEL^WK^VT^GE M^HY^QRE^AV^EM MD^QI^IH^WV^RE
 161 DPAG^LGR^FQ^L SGT^LATE^PMA VPM^MLL^NL^VE QLGE^EDE^EMT DKYA^EL^GD^WC AHR^IL^QH^VQ^R DGQ^VV^LEN^VS EDG^KEL^PG^CL
 241 GRH^QNP^GH^TL EAG^WF^LL^QYA LRK^GDP^KL^QR HIID^KF^LLL^P FHSG^WD^PEH^G GLFY^FQ^DAD^D LCPT^QLE^WN^M KLW^WP^HTE^AM
 321 IAF^LM^GY^RDS GDP^ALL^NLF^Y QVA^EY^TF^HQ^F RDPE^YGE^WFG YLN^QE^GK^VAL TIK^GGF^FK^GC FHV^PRC^LAM^C EQIL^GALL^QR
 401 LGP^APL^GSL^P AVPT^REG^SK



5.775 PEST-containing nuclear protein [Rattus norvegicus]

Protein Accession	gij114145670
Mean Expression Ratio	0.973
Median Expression Ratio	0.973
Credible Interval	(0.717, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0688
Experiment	A
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Avg..iTRAQ.Ratio....116.114.	0.856
Avg..iTRAQ.Ratio....117.114.	0.896

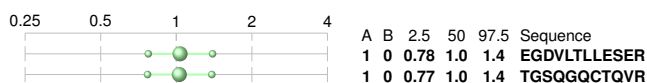
1 MGASCTATQS QFLLYTLTSS EETVGSVGDG CRGPEEEAEK PVKTKTVSSS NGGESSRSA EKRSAEDEAA DLPTKPTKMS
 81 KFGFAIGSQT ARKASAISIR LGASKPKETV PTLAPKTLV AAFPNEDEDS EPEEMPPEAK MRMKNIGRDT PTSAGPNSFN
 161 KGRHGFSNDQ KLWERNIKSH LGNVHDQDN



5.776 PREDICTED: similar to 40S ribosomal protein S28 [Rattus norvegicus]

Protein Accession	gij109481715
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.789, 1.34)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	1.21

Avg..iTRAQ.Ratio....117.114. 1.00

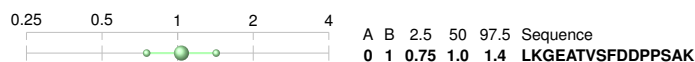


5.777 PREDICTED: similar to fusion (involved in t(12;16) in malignant liposarcoma) (predicted) [Rattus no

Protein Accession	gij109510509
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.765, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0321
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.17
Avg..iTRAQ.Ratio....116.114.	0.786
Avg..iTRAQ.Ratio....117.114.	1.11

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1   MASNDYTQQA TQSYGAYPTQ PGQGYSQSN QPYGQQSYSG YGQSADTSGY GQSSYGSSYE QTQNTGYGTQ SAPQGYGSTG
81  GYGSSQSSQS SYGQQSSYPG YGQQPAPSST SGSYGGSSQS SSYGQFPQSGG YGQQSGYGGQ QQSYGQQQSS YNPPQGYGQQ
161 NQYNSRQWRW WRGGGNYGQD DQSSMSGGDG GGGYGNQYQS GSGGGYGGG QQDRGGHGRG GGGVYNRSSG GYEPGRGGG
241 RGGRGGMGGS DRGGFNKFGG PRDQSSHDS EQDNSDNTI FVQGLGENVT IESVADYFKQ IGIKTNKKT GQPMINLYTD
321 RETGKLGEEA TVSFDDPPSA *TAIDWFDGK EFSGNLIKVS FATRRADFNR VNRRGGRGQG GPMHGGYGG GGGQQRAGDW
401 KCPNPTCENM NFSWRSECNQ CKAPKPDGPG GPGGSHMGG NYGDDRHRGR GYDRGSYRGR GDRGGGFRGG RGGDRGGGFG
481 PGRMDSRGEH RQDRRERPI
    
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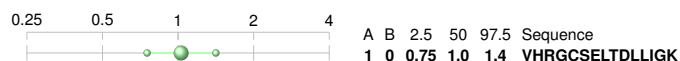


5.778 PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Rattus norvegicus]

Protein Accession	gij109486855
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.765, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0622
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.51
Avg..iTRAQ.Ratio....116.114.	1.28
Avg..iTRAQ.Ratio....117.114.	1.74

```

1      MLLNGLRIP ELEFRNRTMF ESSWESQWAA FSVDDPPVLP SEPLAAVSNA MAFLISKVFL RCTIHFGFVC APSGTSSPDG
81     AAGRRTTEWL ASLLLEKASG FSSVSLRVHR GCSELTDLLI GKRSHSSEA IPREIFGIGF EILLSLFPPG GFSLLEKPAK
161    SDDIKKVVQK ASKGPLKGIL GYTEDQVVSC DFNSNSHSST FDAGAGIALN DNFVKLISWY DNEYGYSNRV VDLMAYMASK
241    E
    
```



5.779 proteoglycan peptide core protein [Rattus norvegicus]

Protein Accession	gij9910488
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.757, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0391
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	0.994
Avg..iTRAQ.Ratio....117.114.	1.51

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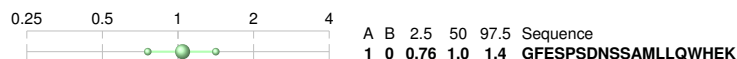
1      MRQVPVGRTR VLALAFVLVW GSSVQGYPAR RARYQWVRC PDGIFANCIE EKGPRFDLIA EESNVGPPMT DPVLMRGFPN
81     DFFPISDDYS GSGSGSGSGS GSGSGSGSGS GSGSGSGSGS GSGSGSGSGS GSGSGSGSLA DMEWEYQPTD ENNIVYFNYG
161    PFDRMLTEQN QEQPGDFII
    
```



5.780 "actin related protein 2/3 complex, subunit 5 [Rattus norvegicus]"

Protein Accession	gi 71043638
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.76, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.126
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.22
Avg..iTRAQ.Ratio....116.114.	1.22
Avg..iTRAQ.Ratio....117.114.	1.08

1 MSKNTVSSAR FRKVDVDEYD ENKFVDEEDG GDGQAGPDEG EVDSCLRQGN MTAALQAALK NPPINTKSA VKDRAGSIVL
81 KVLISFKAND IEKAVQSLDK NGVDLLMKYI YKGFESPSDN SSAMLLQWHEE FALAAGGVGS IVRVLTARKT V

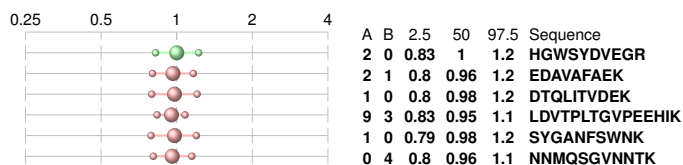


5.781 "NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) [Rattus norvegicus]"

Protein Accession	gi 68341995	
Mean Expression Ratio	0.973	
Median Expression Ratio	0.974	
Credible Interval	(0.848, 1.11)	
Associated Peptides	6	
Associated Spectra	23	
Coverage	0.371	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.967	0.828
Avg..iTRAQ.Ratio....116.114.	1.07	0.718

Avg..iTRAQ.Ratio....117.114. 0.985 0.986

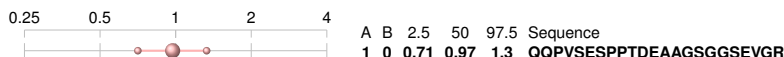
1 MAAVSMSVSL RQALLRQRAV ATAAVSVCRV PSRLNLTSTW KLADGQTRDT QLITVDEKLD VTPLTGVPEE HIKTRKVRIF
 81 VPARNNMQSC VNNTFKWKME FDRERWENP LMGWASTADP LSNMVLTFSA KEDAVAFAEK HGWSYDVEGR KVPKPKSKSY
 161 GANFSWNKRT RVSTK



5.782 "eukaryotic translation initiation factor 3, subunit 9 (eta) [Rattus norvegicus]"

Protein Accession	gij7225511
Mean Expression Ratio	0.976
Median Expression Ratio	0.974
Credible Interval	(0.726, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0289
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.925
Avg..iTRAQ.Ratio....116.114.	1.01
Avg..iTRAQ.Ratio....117.114.	1.04

1 MQDAENVAAP EAAEERAEP RQQPVSESP TDEAAGSGGS EVGR TEDAE DAEARPEPEV RAKPAAQSEE ETAASPAASP
 81 TPQSAQEPSA PGKAEAGGEQ ARHPSARAEE EGGSDGSAAE AEPRALENGE ADEPSFSDPE DFVDDVSEEE LLGDVLKDRP
 161 QEADGIDSVI VVDNVPPQVGP DRLEKLNVI HKIFSKFGKI INDYYPEEDG KTKGYIFLEY ASPAHAVDAV KNADGYKLDK
 241 QHTFRVNLFT DFDKYMTISD EWDIPEKQPF KDLGNLRYWL EEAECRDQYS VIFESGDRTS IFWNDVKDPV SIEERARWTE
 321 TYVVRWSPKGT YLAFHQHGI ALWGGDKFKQ IQRFSHQGVQ LIDFSPCERY LVTFSPLMdT QDDPQAI I IW DILTGHKRRG
 401 FHCESSAHWP IFKWSHDGKF FARMTLDTLS IYETPSMGLL DKKSLKISGI KDFSWSPPGN IIAFWVPEDK DIPARVTLMQ
 481 LPTRQEI RVR NLFNVVDCKL HWQKNGDYLC VKVDRTPKGT QGVVTNFEIF RMREKQVPVD VVEMKET I IA FAWEPNGSKF
 561 AVLHGEAPRI SVSFYHVXSN GKIELIKMFD KQANTIFWS PQGFVVLG LRSMNGALAF VDTSDCTVMN IAEHYMASDV
 641 EWDP TGRYV TSVSWSHKV DNAYLWTFQ GRLLQKNNKD RFCQLLRPR PPTLLSQDQI KQIKKDLKKY SKIFEQKDRL
 721 SQSKASKELV ERRRTMEDF RQYRKMAQEL YMKQKNERLE LRGGVDTDEL DSNVDDWEE TIEFFVT EEV IPLGSQE

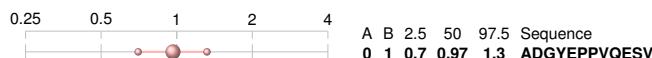


5.783 ribosomal protein S3a [Rattus norvegicus]

Protein Accession	gij8394221
Mean Expression Ratio	0.974
Median Expression Ratio	0.974
Credible Interval	(0.721, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.765
Avg..iTRAQ.Ratio....116.114.	0.689
Avg..iTRAQ.Ratio....117.114.	1.00

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1      MDMRNIAIIA HVDHGKTTLV DELLKQSGTY RENQATTERA MDSNDLERER GITIFAKPTS VVWNNTRINI VDTPGHADFG
81     GEVERILSMV DGVVLLVDAA EGPMPQTKFV TSKALKLGLR PIVVLNKVDK ADAEPDRALD ECFDLFASLD ATDEQLEFPH
161    MYASGRSGWA DAELDGPRKD LSALFELVLK HVPAPKQIEN ADKPFTMLAT TLGGDFFLGR LLTGRVETGT LKAGQSIKAM
241    SRDGKLIENF RCTKILAFRG LEQTAIDVAE AGDIVSIAGM SKATVADTLA DTSVNEAIPA QPIDPPTITV TFGINDSPLA
321    GRDGKKVQSR VIRERLMKEA ESNVAIKISD TPGGDAFEVA GRGELQMGVL IENMRREGFE LSISRPPQVLF QEIDGVRHEP
401    IEEATIDVDD EYSGAVIEKI TGTRKGELVE MKPAGAGKTR IIAHVPSRGL IGYHGFEFLTD TRGTGVINRV FHSWAPHKGT
481    IPGRRAGVLI SMENGTSAVF ALWNLEERGK MMIGAQADVY TGMII GEHSR ENDLEVNPLK GKCLTNVRAS GTDEAVRLTT
561    PMTSLSEAEI AYIDDELVE VTPNAIRLRK RYLDPPERKR MAKSA
    
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5.784 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 [Rattus norvegicus]"

Protein Accession	gij14010879	
Mean Expression Ratio	0.974	
Median Expression Ratio	0.974	
Credible Interval	(0.765, 1.24)	
Associated Peptides	1	
Associated Spectra	4	
Coverage	0.0105	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.942	0.858
Avg..iTRAQ.Ratio....116.114.	1.06	0.522

Avg..iTRAQ.Ratio....117.114. 0.954 1.48

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1      MITSAAAGIIS LLDEEEPQLK EFALHKLNAV VDNFVAEISE SVDKIEVLYE DEGFRSRQFA ALVASKVFYH LGAFEEESLNY
81     ALGAGDLFNV NDNSEYVETI IAACIDHYTK QCVENADLPE GEKKPIDQRL EGIWNKMFQR CLDDHKYKQA IGIALETRRL
161    DVFEKTILES NDVPGMLAYS LKLCMSLMQN KQFRNKVLRV LVKIYMNLEK PDFINVCQCL IFLDDTQAVS DILEKLVKED
241    NLLMAYQICF DLYESASQQF LSSVIQNLRT VGTPIASVPG STNTGTVPGP EKDSDSMETE EKTAGAVAGK TPDASPEPKD
321    QTLKMIKILS GEMAIELHLQ FLIRNNNTDL MILKNTRKDAV RNSVCHTATV IANSFMHCGT TSDQFLRDNL EWLARATNWA
401    KFTATASLGV IHKGHEKEAL QLMATYLPKD TSPGSAYQEG GGLYALGLIH ANHGGDIIDY LLNQLKNASN DIVRHGGSLG
481    LGLAAMGTAR QDVYDLLKTN LYQDDAVTGE AAGLALGLVM LGSKNTOAIE DMVGYAQETQ HEKILRGLAV GIALVMYGRM
561    EEDADALIESL CRDKDPILRR SGMYTVAMAY CGSGNKAIR RLLHVAVSDV NDDVRRAAVE SLGFILFRTP EQCP SVVSL
641    SESYNPHVRY GAAMALGVCC AGTGNKEAIN LLEPMTNDPV NYVRQALIA SALIMIQQTE ITCPKVNQFR QLYSKVINDK
721    HDDVMAKFGA ILAQGILDAG GHNVTISLQS RTGHTMPSV VGVLVFTQFW FWFPLSHFLS LAYTPTCIIG LNKDLKMPKV
801    QYKSNCKPST FAYPAPLEVP KEKEKEKVVST AVLSITAKAK KKEKEKEKKE EEKMEVDEAE KKEKEKKEKE PEPNFQLLDN
881    PARVMPAQLK VLSMTETCRY QPFKPLSIGG IILKDTSED IEELVEPVAA HGPKEIEEEEQ EPEPEPEFVEY IDD
    
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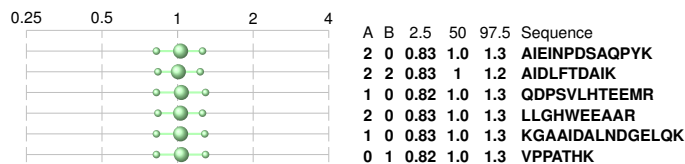


5.785 suppression of tumorigenicity 13 [Rattus norvegicus]

Protein Accession	gij13592093	
Mean Expression Ratio	1.03	
Median Expression Ratio	1.03	
Credible Interval	(0.869, 1.21)	
Associated Peptides	6	
Associated Spectra	11	
Coverage	0.182	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.995	1.11
Avg..iTRAQ.Ratio....116.114.	1.04	1.15
Avg..iTRAQ.Ratio....117.114.	0.982	0.975

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1      MDPRKVSELR AFVKMCRQDF SVLHTEEMRF LREWVESMGG KVPPATHKAK SEENTKEEKR DKTTEDNIKT EEPSSSEESDL
81     EIDNEGVIEA DTDAPQEMGD ENAEITEAMM DEANEKRGAA IDALNDGELQ KAIDLFTDAI KLNPRLAILEY AKRASVFKVL
161    QKPNAAIRDC DRATEINPDS AQPYKWRGKA HRLLGHWEEA ARDLALACKL DYDEDASAML REVQPRAQKI AEHRKRYERK
241    REEREIKERI ERVKKAREEH EKAQREEEAR RQSGSQFGSF PGGFPGGMPG NFPGGMPGMG GAMPGMAGMP GLNEILSDPE
321    VLAAMQDPEV MVAFAQDVAQN PSNMSKYQNN PKVMNLI SKL SAKFGGHS
    
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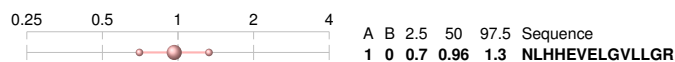


5.786 fumarylacetoacetate hydrolase domain containing 1 [Rattus norvegicus]

Protein Accession	gij68163417
Mean Expression Ratio	0.974
Median Expression Ratio	0.975
Credible Interval	(0.72, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0633
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.9
Avg..iTRAQ.Ratio....116.114.	1.08
Avg..iTRAQ.Ratio....117.114.	0.928

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1   MASTKPLSRF WEWGKNIVCV GRNYADHVKE MRSTVLSEPV LFLKPSTAYA PEGSPVLMFA YCRNLHHEVE LGVLLGRGE
81  AVPEAAANDY VAGYALCLDM TARDVQDECK KKGLPWTAK SFTSSCPVSA FVPKEKIPDP HALRLWLKVN GELRQEGKTS
161 SMIFSIPYII SYVSKIITLE EGDLIITGTP KGVGAVKEND EIEAGIDGVV SMRFKVERSK Y
  
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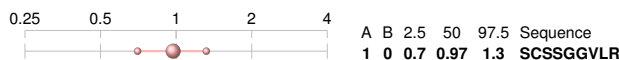


5.787 PREDICTED: similar to Fras1 protein isoform 2 [Rattus norvegicus]

Protein Accession	gij109500290
Mean Expression Ratio	0.973
Median Expression Ratio	0.975
Credible Interval	(0.716, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00223
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.973
Avg..iTRAQ.Ratio....116.114.	0.814
Avg..iTRAQ.Ratio....117.114.	0.988

NHLBI Zile/Grant, Aged Rat

1 MGVFKAFLGV ALALAEFAVL PHCEGACLYR GSSLADATIW KPDSCQNCRC HGDIVICKPV VCKNPRCAFE KGEVLWIAPN
81 QCCPQCAPRT PGSCHHEGKI REHGTEWASG PCTLCSCTYG EVRCSHQOCT PLSGCGPQELE FLAEGHCCPI CVGTGKPCSD
241 DGHVFDQGED WPLSHCAKCV CRNGLTQCFT AQCQPLFCNQ DEIVVRVPGK CCSQCSRRSC STAGQVYEHG EQWKEDACTL
161 CMCDQGGQVRC HKQACPLPRC ARGQSKARHH QCCCEECVSP VRSCSSGGVLR YQDEMWKGS ACEFCVCDQG QVTQTGCECA
321 KVACAPGEEEL VHLEGGKCCPE CISRNDYCVY EEKAEIMSSN SSEIKHVPEG KKWEEGPCKL CECREAQVTC YEPSCPPCPV
401 ATLAMAVKGQ CCPDCTPVHC HPDCLTCSHS PEHCDLQDPP TKLLQNGRCV PSCGLGFYQA GSLCLACQPQ CSTCTSSLEC
481 SSCLPPLLMQ QGQCVSTCGD GFYQDHHSCA VCHESACAGW GPTEKHCVAC RDPDLLVLRDG SCENTCGNGF YNRQGTVCAC
561 DQSCCKSCGPS SPRCLTCAEK TVLYDGTICIS ECPRGYADA TGRCKVCHVS CASCSGPAAA HCTACVHPQV LRQGHCLPSC
641 GGGFYDPDGI CGACHGSCHT CVGPEPTHCT QCKKPEAGLQ VEQHSNGENVP YGKCVSQCGA HFYLESTGLC EACHPSCLLC
721 EGKSPRNCTG CGPAHVLLAG RCLSQCPETH FNGEHTCTEC HPSRCRCHGP LESDVCVCHP HLTLSSSGRCK ASCKDEQFLN
801 LVGYCADCHP DTSQVCLKCO DTGSVCLKCO HARHLLGDHG ERRAITQQLL DIRDDNPDQ VVLCPPPGHY KERGTCKRCH PSCRSCTGCG PFSCSSCTNC
881 LVLTHIGACS STCFPGHYLD DNQACQPCNR HCRSCDSQGS CTSCRDPSPKV LFFGECQYES CAPQYYLIDIS TKTKCECDWS
961 CNACTGLPRT DCLQCMDGYV LQDGVVCEQC SPQHYRDSGS CKRCDSHCLO CQGPHECTRC EGFLLLFRAQ CVQCAKGYF
1041 ADHAERHSGA TPQGLQCSH KDRCHLQCSH FFLKSGFSGS TCVPGFSGHS SNETCTDKVY TPLSHVNGSL TSLGFSMKPL
1121 DFFLLNIHQH DGRVDDLFLH IVSTPTNGQL LLSRNGKEVQ LEKAGHFSWK DVNGKVRVYV HSKKLRKGY FSLKISDQQF
1201 FFEFQLINIQ AFSTQAPYVL RNEVLHISKG ERAAITQQLL DIRDDNPDQ VVLCPPPGHY KERGTCKRCH PSCRSCTGCG PFSCSSCTNC
1281 DELSRGLLLY AHDGSDSTSD IIVFQANDGH SFQNILFRVK NVPKNGKLLS RNTGAVYWAP EIKLASCVRV TGGYVQLETP
1361 GPSADRLQL IKKECWEGVM SPACFPQRSD SMACASLGEV VLLMNLPADS PAGPAEEGHH LPDGRMTPTV STFSQQDIDD
1441 GIWVYRHSGA TAQSDSFHQV VSTATNAQEH PQSHMFNIAI LPQALEAPKL SLGTSLHMTA REDGLSVIHP QLSLFGKAES
1521 PSKIIYINIT VPLHPNQGV I EHRGRNSPI RYFTQEEINQ GQIMYRPPAA PPHLQEFMAF SFAGLPEVSR FYFTVSDQQH
1601 TSPEMALTIH LLHSDRQPPA FQIKAPLLEL SPGGRTPLGL QLVVRDAEVV PEELFFQLQK PPQHGMLMKY TAKSSVMTSA
1681 GDTFTYDEVE RNVLYVVDHG SPAWEDNMEI SVTDGLVTT SEVKEVEVSP ENREPRLAG SLSMPTVASQ HTAITRSHL
1761 AYVDDSSPDS EIWIQLSSLP LYGVLLKTSG PDMEELSGDS NFTMEDINSK NIRYSAVFET EGQSVTDGFH FVSDDMDNDR
1841 VDNQVFTITV TPAENPPHII AFADLITVDE GGRAPLSLHH FFATEDQDNL QGDAVIKLSA LPKYGCIENT GTGDRFPGGA
1921 NSELEASFPI QDVLNENIY FQSVHESIEP THDVFSFYVS DGSRSEIHS INITIERKND EPPRMTLRPL GVRLSGVAI
2001 SNSLSLQDL DTPNNELIFV LMKKPDHGYL LLRPTASDPL ENGTVLDQGS SFTYQDILAG LVGYLPGDIY MAVDEFRSL
2081 TDGLHVDTRG MEIYIELPTS NIPHLAINRG LQLSAGSVAR ITEQHLRAD TDSEAGQLVY IVKEDPGAGH LQMTKADKLE
2161 QISVRGPIRS FTQADVVSQO IEYSHGPGEA GGSFAFKFVD VNEGKNLAD QSFVINVLED KSPVVIITNK GLVLDENSVE
2241 KITTAQLLAT DQSKPTELI YRITSQFQLG HLEHVASPGI QISSFTQADL TSRNVQYVHS SGTGKLSDAF SFVLSDDLHE
2321 VTQTFSTIHI PVDDSLPLVQ NRGMRVQEGV RKTITEFELK AVDVDTEAES ITFTIVQPPR HGTIERTAGH QRYQLTSST
2401 MEDIYQNRVS YSHDGSNSLK DRFTFTVSDG TNPFFIIEEG GEEIMTAAFP QFLVDILPVD DGTPIRVTNL GLQWLEYMDG
2481 KATNLITKKE LLTVPDPTED SOLTVEVTT PMHGIVENKL QPGRVAATFT QEHVNLGLIR YVLYEEKIQK MMSDFQFLVK
2561 DSKPNVSDN IFYIHWLIS FKYTSYNVSE KAGSVSMVQ RTGNLNQYAI VLCRTEQGT A SSSSRVSSH QQQDYVEYAG
2641 QVQFDEREDT KSCTIVIND DVFENIESFT VELSMPAYAL LGEFTQAKVI INDTEDEPTL EFDKKTIRVN ESAGFLFAP I
2721 KRQGDPSAV SAICYTVPKS AMGSSLYALE SSGDFKSRGR SVESRVLLGP GVTTSTCDVM VIDDSEYEEE EEFIALADA
2801 SNNARIGRLA VAKVLISGNP DASTVSLGNT AFTISEDAGT VKVPVIRHGT DLSTFTSVWC ATRPSDPAASA TPGVDYVPS
2881 RKVEFGPVT EQYCTLTILD DTQYVPIEGL ETFVFLSSA QGAELTKPSQ AVIAINDTFQ DVPSMQFSK LLLVKEKEGV
2961 LHPIIRSGD LSYESSVRCY TQSHSAQVME DFEERRNADS SRITFLKGEK AKNCTVYIHD DSMFEPEEQF RVYLGHPNG
3041 HWSGARIGKN SMATVTSND EDAPTEFEE AAHQVREPAQ PDATAVLSVK VIRRGDQNR SKIRCSRTRD SAQSGVDYYP
3121 KSRVLKFS PGVDHIFKVEI LSNEDREWHE SFSVLVLPDD PVEAVLGDVT TATVTILDQE AAGSLILPAP PIVVTLADYD
3201 HVEELSKEGV KKAPSPGYPL VCVTPCDPHY PRYAVMKERC SEAGINQTSV QFSWEVAAPT DGNARSPEE TITDSTPPTS
3281 VNHKVLDSIY FSRRFHVRCV AKAVDKVGHV GTPLRSNVVT IGTDSAICHT PVVAGTARGF QAQSFIAATLK YLDVKHKEHP
3361 NRHISVQIP HQDGMPLIS Tmplhnlhfl LSESIYRQQH VCSNLVTARD LRGLSEAGFL DDAGLHSTAL GPGYDRPFQF
3441 DPSVREP KTI QLYRHLNLSK CVWTFDAYD MTELDVCGG SVTADFQVRD SAQSLTVHV PLYVSYIYVT APRGWASLEH
3521 HTEMEFSEFFY DTVLWRTGIQ TDSVLSARLQ ILRIYIREDG RLVIIEFKTHA KFRGQFVIEH HTLPDVKSPI LTPDHLGGIQ
3601 FDLQLLWSAQ TFDSPHQLWR ATSSYNRKDY SGEYTIYILP CTVQPTQPVW DPGEKSLACT AHAPERFLPI IAFQQTNRPV
3681 PVVYSLNTEF QLCNNEKVF L MDPNTSDMSL AEMDYKGAFS KGQILYGRVL WNPEQNLHSA YKLQLEKVVY CTGKDGYPV
3761 FDPGTGTYNE GPQYGCIOFN KHLKHRFLLL DRSQPEVTDK YFHDVPPFAH FASELPDFQV VSSMPGVDFG TLKVDALYKV
3841 EAGHQWYLVQ IYIISPDSIS RPRVQSRSLA SLRRHQRLDV DPSGWLSDLD SLIYDNEGDQ VKNGTNMKSL NLELQEPVIA
3921 ASLSQSGASI GSALAALMLL LLLFLVACFI TRCQKQKKK QPPEDTLEEY PLNTKVDVAK KNTDKGEKNA NRQYCTVRNV
4001 NILSDSEGY TFKGAKVKKL NLEVRVHNNL QDGTVEV



5.788 PREDICTED: similar to genetic suppressor element 1 [Rattus norvegicus]

Protein Accession	gij109508225
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.762, 1.38)
Associated Peptides	1

Associated Spectra	1
Coverage	0.00689
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.15
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	1.18

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1      MSTRPQGQ LGH  CHLRDLRLLL  LRLPLTASQT  VRLTAVFMSA  WSRGQQAGSN  TGARMLVPHS  RGQAGVRKEA  KGRLAAGTDL
81     TSPNGHLG I K  LYPLVQADER  GKPYSQFRAS  DREALKTVAF  AEHEWPAKPR  RGPFRLLSSP  G RQERGGGTYP  AGCDRAGCSG
161    RSVGRRRER AG  EWAALRLG  VSSAATAAGV  SWPRPRKHLH  PERPSRRRTA  PGEISSSDKP  GRRWLRHVSG  AAQRGPGGMK
241    GMSHEPKSP S  IGMLSTATRT  TATVNPLTPS  PLNGALVPTG  SPATSSALSA  QAAPSSSFAA  ALRKLAKQAE  EPRGSSLSSE
321    SSPVSSPATN H  SSPASTPKR  VPMGPIIVPP  GGHSVPSTPP  VVTIAPTQTV  NGVWRSESRQ  DSGSRGGSSG  RERLLVEPPL
401    AQEKAAGPAI P  SHLLSTPYF  FGLSPSSVVQ  DSRFQPLNLQ  RPYVHHVPPS  TVTEDYLRSF  RPYHTAEDLR  MSSLPPLGLD
481    PATAAAYYHP S  YLTPHPPFH  PAFRMDDSYC  LSAALRSPFY  IPTPGSLPPL  HPSAMHLHLS  GVRYPPELSE  SSLAALHSER
561    ISSLSAERLQ M  DEELRRERE  REREREREAD  REREKERERE  QREKEREKEL  ERERERERER  ELERQREQRA  REKELLAAKA
641    LEPTFLPVAE L  HGLRGHTTE  ERPKPSEQLT  PTRAEKLKDT  GVQAPKPVQH  FLHPVPAPHH  TVPSLISSHG  IFSLPGSSAA
721    TALLIQR TNE  EEKWLARQRR  LRQEKEDRQS  QVSEFRQQLV  EQHLDLGRPL  VPTEAEHRPE  STRPGPNRHD  QGSREPPQHF
801    GGPFPPLISPK F  QHHTVPTAL  WNPVSLMDNT  LETRRAESHS  LHSHTAFEP  SRQAAVPLVK  VERVYCTEKA  EEPKREATP
881    LDKYQPPPPP P  PPPPREAGG  LEPQTFPHGP  GPF LAELEKS  TQTILGQQR  SLSQTFPFG  LTGSLKSGSP  YCHTTARGPD
961    PAYIYDEF LQ  QRRRLVSKLD  LEERRRREAQ  EGYYYDLDD  SYDESDEEV  RAHLRCVAEQ  PPLKLDTSSE  KLEFLQLFGL
1041   TTQQQKEELV A  QKRRKRRRM  LRERSPPSPA  IQCKRQTPSP  RLALSTRYSP  DEMNNSPNFE  EKRRFLTFN  LTHISAERK
1121   DKERLVEMLR A  MKQRALSAA  VADSVATNSS  RDSPTISLSE  PATQPAPLET  DQPAGVPASL  SDVPKAVETG  RLEQLRPQEL
1201   LRVQEPAPPS G  EKARLSEAP  GKKNLSMLH  YLRGAAPKDI  PVPLSHSING  KSKPWEPFMA  EEF AHQFHES  VLQSTQKALQ
1281   KHKGSSALLS A  EQNHKVDTS  VHYNIPELQS  SSRVPLPQHN  GQQEPPAGRK  GPPMQEVDQD  SEDDSEEEAE  EAPRHQWGI
1361   EATFEAYQEH I  EQNLERQV  LQTQCRLEA  QNYSLSLTA  E  QLSHSMALR  SQKQKMVSE  ERLQAEELDHL  RKCLALPTMH
1441   WPRGYFKGY P  R

```



5.789 PREDICTED: similar to Mimecan precursor (Osteoglycin) isoform 1 [Rattus norvegicus]

Protein Accession	gij109505532
Mean Expression Ratio	1.03
Median Expression Ratio	1.03
Credible Interval	(0.765, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.19
Avg..iTRAQ.Ratio....116.114.	1.25
Avg..iTRAQ.Ratio....117.114.	1.11



5.790 hepatoma-derived growth factor-related protein 2 [Rattus norvegicus]

Protein Accession	gij19424218	
Mean Expression Ratio	0.976	
Median Expression Ratio	0.975	
Credible Interval	(0.757, 1.25)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.0239	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.02	0.99
Avg..iTRAQ.Ratio....116.114.	0.852	0.706
Avg..iTRAQ.Ratio....117.114.	0.942	1.26

```

1      MPHAFKPGDL VFAKMKGYPH WPARIDDIAD GAVKPPPNKY PIFFFGTHET AFLGPKDLFP YDKCKDKYGK PNKRKGFNEG
81     LWEIFQNNPHA SYSAPLPVSS SDSEAPEADL GGGSDADKEK EARRVMTVTA VTTTATSGRT ESDSDSDKNS DHSGLKRKTP
161    VLKMSVSKRA RKASSDLQQA SVSPSEEDSE SPSESEKTSQ QDFTPEKKT I ARAPRRAPLG GRKKKKVPSA SDSDSRADSD
241    GAKEEPVVT A QPSPSSASS SSSASDSDV SIKKPPRGRK PAEKPPPKPR GRRSKPERPP STSSSDSDSD SGEVDRISEW
321    KRRDEERRRE LEARRRREQE EELRRRREQE REEKERRKER AERGGSSGEE LEDEEPVKKR SRKARGRGT P SSSDSEPEGE
401    LGKEGKLLAK KSQLQGSESA RKPGQKEKRG RPDEKPRARP VKVERTKRS EGLSLDRKGE KKKEPSVEER LQKLHSEIKF
481    ALKVDNPDVR RCLSAL EELG TLQVTSQILQ KNTDVVATLK KIRRYKANKD VMAKAAEVYT RLKSRVLGPK VEALQKVNKA
561    GAEKERADGE KVEEQPGEQA PELAEDEPS TDRSAPVNGE AASQKGENTE DGAQEDGQDL EDGPRGGSSE ELHDSPOQDS
641    DPARPGNEHQ DHERMQLASE SADDDDEDS
    
```



5.791 paxillin [Rattus norvegicus]

Protein Accession	gij58865866	
Mean Expression Ratio	1.03	
Median Expression Ratio	1.03	
Credible Interval	(0.755, 1.38)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0307	

Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	1.24
Avg..iTRAQ.Ratio....117.114.	1.28

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1      MDDL DALLAD LESTTSHISK RPFVFLSEEP YSYPTGNHTY QEIAVPPPPV PPSSEALNG TVLDPLDQWQ PSGSRYAHQQ
81     PPSPSPPIYSS STKNSSASNP QDSVGSLSR AGEEEHVYSF PNKQKSAEPS PTVMSSSLGS NLSELDRLLL ELNAVQRSPS
161    GFSAGMVSQV ASREPLGSWG TEGRAIILSP FFQDEAESS PLPGALSPLY GVPESNNLLG GKAGPLMKEK PKRNGGRGLE
241    DVRPSVESLL DELENSVPSF VPAITVNQGE MSSPQRVTSS QQQTRISASS ATRELDELMA SLSDFKFMAQ GKTGSSSPFG
321    GLSKPGSQLD SMLGSLQSDL NKLGVATVAK GVCGACKKPI AGQVVTAMGK TWHPEHFVCT HCQEEIGSRN FFERDGGPYC
401    EKDYHSLFSP RCYYCNGPIL DKVVTALDRT WHPEHFFCAQ CGAFFGPEGF HEKDGKAYCR KDYFDMFAPK CGGCARAILE
481    NYISALNTLW HPECFVCREC FTFPVNGSFF EHDGQPYCEV HYHERRGSLC SGCQKPITGR CITAMAKKFH PEHFVCAFCL
561    KQLNKGTFKE QNDKPYCQSC FLKLFC
  
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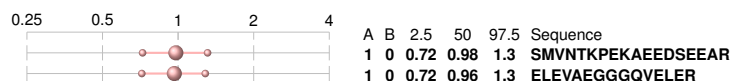


5.792 cell division cycle 37 homolog [Rattus norvegicus]

Protein Accession	gi 16758570
Mean Expression Ratio	0.973
Median Expression Ratio	0.975
Credible Interval	(0.745, 1.27)
Associated Peptides	2
Associated Spectra	2
Coverage	0.087
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.04
Avg..iTRAQ.Ratio....116.114.	0.964
Avg..iTRAQ.Ratio....117.114.	1.03

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1      MVDYSVWDHI EVSDDEDETH PNIDTASLFR WRHQARVERM EQFQKEKEEL DRGCRECKRK VAEFQRLKE LEVAEGGGQV
81     ELERLRAEAQ QLRKEERTGS RSWRTCGKKE KNMPWNVDTL SKDGFSKSNV NTKPKAEED SEEAREQKHK TFVEKYEKQI
161    KHFGMLHRWD DSQKYLSDNV HLVCEETANY LVIWCIDLEV EEKCALMEQV AHQTMVMQFI LELAKSLKVD PRACFRQFFT
241    KIKTADQQYM EGFKYELEAF KERVRGRAKL RIEKAMKEYE EEERKKRLGP GGLDPVEVYE SLPEELQKCF DVKDVQMLQD
321    AISKMDPTDA KYHMQRCIDS GLWVPNSKSG EAKEGEEAGP GDPLLEAVPK AGFEKDISA
  
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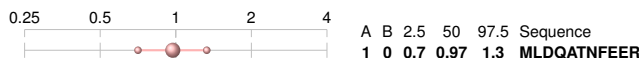


5.793 PREDICTED: similar to smoothelin isoform 1 [Rattus norvegicus]

Protein Accession	gij109499934
Mean Expression Ratio	0.976
Median Expression Ratio	0.975
Credible Interval	(0.725, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0119
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.959
Avg..iTRAQ.Ratio....116.114.	0.818
Avg..iTRAQ.Ratio....117.114.	0.988

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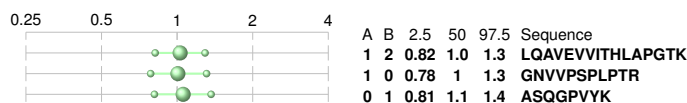
1   MADEALAGLD EGALRKLLLEV TADLAERRRI RSAIRELQRQ ELERELEGALA SKRFRAERQD NKENWLHSQQ REAEQQAALA
81  RLAGRLESMN DVEELTTLLR SAGEYEERKL IRAAIRRVRA QEIEAATLAG RLCSRLPSSG SREDSRRQAA HTLDPGKVPE
161 EEKQQQTEV REPTTPPEDT SQDVTVTLL LRAPPGGTPS SPASPDSSPT TASPEPLLEP AGAQCPAAEA PVSSEPLPHF
241 SEAFSPEPPM SPAPFSSQGR VISKPLLGST EPSDTVDSTR GSSNTKRADL AEPKPCQRSL SVLSPRQPTQ NQEP TPLAGS
321 SQFRRAGSVR DRVRKFTSDS PVVARLQDGP PRTALASFTP TRLPGPSLMS TTLASSSSSS NSSSPSPSDT SSHKKQRELA
401 HSLAQLQSCP QEEGPGGRSL APRSLENRAG GPRPCSEEPS TPPPVAVG TG EPGGSMKTF TIEIKDGRGQ ASTGRVVLPT
481 GNQRAELTLG LRAPPTLLST SSGGKNTITH VSSPGTVTRL GSVTHVTTF S HASPGNRGGC NFKMEPDPAE PPSATVEAAN
561 GTEQTLKVN KGPEGRSPLS AEELMAIEDE GILDKMLDQA TNFEEKRLIR AALRELRQRK RDQRDKERER RLREARARPG
641 ESRSNMATTE TTRHSQRAA DGSAVSTVTK TERLVHSNDG TQTARTTVE SSFVRRSENG SSSSSSTTVQ TKTFSSSSSS
721 SKKMGSI FDR EDQTSRSGS LAALEKRQAE KKKELMKAQS LPKTSASQAR KAMIEKLEKE GSSGSPGTPR TAVQRSTSFQ
801 VPNANSIQM LLDWCRAKTR GYEHVDIQNF SSSWSDGMAF CALVHNFFFE AFDYGQLSPQ NRRQNFEAMF SSAEMLVDCV
881 PLVEVEDMMI MGKKPDPKCV FTYVQSLYNH LRRHELRLRG KNV
    
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5.794 calcium-regulated heat-stable protein (24kD) [Rattus norvegicus]

Protein Accession	gij22758142	
Mean Expression Ratio	1.03	
Median Expression Ratio	1.03	
Credible Interval	(0.826, 1.28)	
Associated Peptides	3	
Associated Spectra	5	
Coverage	0.238	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.916	0.998
Avg..iTRAQ.Ratio....116.114.	0.998	0.966
Avg..iTRAQ.Ratio....117.114.	0.848	1.25

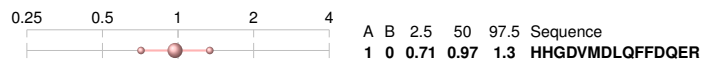
1 MSSEPPPPFQ PPTHQTSIGL LDTFRARDRS PSLRGNVVP SPLPTRRTRT FSATVRSQG PVYKGVCKCF CRSKGHGFIT
 81 PADGGPDIFL HISDVEGEYV PVEGDEVITYK MCSIPPKNK LQAVEVVITH LAPGTRHETW SGHVISS



5.795 PREDICTED: similar to Nucleoporin Nup43 [Rattus norvegicus]

Protein Accession	gij109460423
Mean Expression Ratio	0.978
Median Expression Ratio	0.975
Credible Interval	(0.727, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0339
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.24
Avg..iTRAQ.Ratio....116.114.	0.987
Avg..iTRAQ.Ratio....117.114.	0.804

1 MRGGGMAGPT GAASSGSAVA APSAVASSGH RLPHEVLSNQ NFTGRGGPEE RAVCFLLNLL AGFSMEEIYA KFVSQKISK
 81 RWRFPVPSGSL QTTEFATGS WDNEENCVSL WSIGEFGLND SDGGFEGDHQ LLCDIRHGD VMDLQFFDQE RIVAASSTGC
 161 VTVFLHHPNN QTLVSQQWP TAHYHTGPGS PSYSSAPCTG IVCDNPEIVT VGEDGRINLF RVDHKEAVRT IDNADSSTLH
 241 AVTFLRTPFI VTVNSIGQLK IWDFRQQGSE PCQILSLTGD RVPLHCVDRH PDQQHVVATG GQDGMLSIWD VRQGTMPVSL
 321 LKAHEAEMWE VHFHPSNPDH LFTCEDGSL WHWDASTNAP EKSSLFHQGG RSTFLSHSSN QASVHLSLVS SWLSTDPKAD
 401 RIEITSLLPS RTLSVNSLDV LGPCLVCGTD AESIYVTRQL FS



5.796 PREDICTED: similar to destrin [Rattus norvegicus]

Protein Accession	gij62665569
Mean Expression Ratio	1.02
Median Expression Ratio	1.02

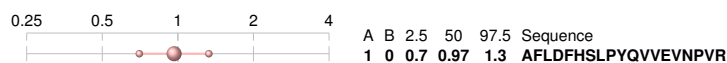
Credible Interval	(0.76, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0788
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.06
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	1.28

1 MASGVQVADE VCRIFYDMKV RKCSTPEEIK KRNKAVIFCL SADKKCIVVE EGKEILVGDV GVTITDPFKH FVGMLPEKDC
 81 RYALYDASFE TKESRKEELM FFLWAPEQAP LKSKMIYASS KDAIKKKFPF IKHEYQANGP EDLNRTSIAE KLGGLIVAF
 161 EGSPV



5.797 PREDICTED: similar to prostaglandin E synthase 2 [Rattus norvegicus]

Protein Accession	gij109469545
Mean Expression Ratio	0.974
Median Expression Ratio	0.976
Credible Interval	(0.726, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.933
Avg..iTRAQ.Ratio....116.114.	1.19
Avg..iTRAQ.Ratio....117.114.	0.834

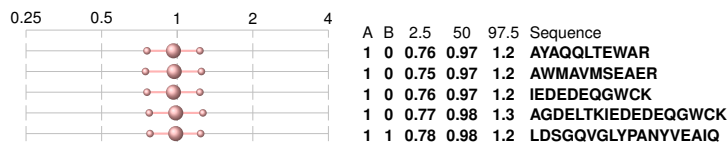


5.798 protein kinase C and casein kinase substrate in neurons 2 [Rattus norvegicus]

Protein Accession	gij76880465	
Mean Expression Ratio	0.976	
Median Expression Ratio	0.976	
Credible Interval	(0.803, 1.2)	
Associated Peptides	5	
Associated Spectra	6	
Coverage	0.119	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.01	1.08
Avg..iTRAQ.Ratio....116.114.	1.01	0.946
Avg..iTRAQ.Ratio....117.114.	0.905	1.34

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1   MSVTYDDSVG VEVSSDSFWE VGNYKRTVKK IDDGHRLLCGD LMNCLHERAR IEKAYAQQLT EWARRWRQLV EKGPPQGTVE
81  KAWMAVMSEA ERVSELHLEV KASLMNEDFE KIKNWQKEAF HKQMMGGFKE TKEAEDGFRK AQKPWAKKLLK EVDAAKKAHH
161 TACKEEKLAV SREANSKADP SLNPEQLKLL QDKIEKCKQD VLKTKDKYEK ALKELDQTFP QYMNEMEQVF EQCQQFEEKR
241 LRFREVLLE VQKHLDSLNV ASYKGIYREL EQSIKAADAV EDLRWFRANH GPGMANNWPQ FEEWSADLNR TLSRREKKKA
321 ADGVTLTGIN QTGDQSGQNK PSSNLSVPSN PAQSTQLQSS YNPFEDDDT GSSVSEKEDI KARNVSSYEK TQNYPADWSD
401 DESNPFSSST DANGDSNPFD EDTTSGTEVR VRALDYEGQ EHDLSFKAG DELTKIEDED EQGWCKGRLD SGQVGLYPAN
481 YVEAIQ
    
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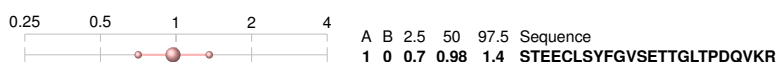
5.799 "ATPase, Ca++ transporting, cardiac muscle, fast twitch 1 [Rattus norvegicus]"

Protein Accession	gij17157987	
Mean Expression Ratio	0.977	
Median Expression Ratio	0.976	
Credible Interval	(0.724, 1.33)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0241	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.29	
Avg..iTRAQ.Ratio....116.114.	0.655	

Avg..iTRAQ.Ratio....117.114. 1.38

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1      MEAAHSKSTE ECLSYFGVSE TTGLTPDQVK RHLEKYGPNE LPAEEGKSLW ELVVEQFEDL LVRILLLAAC ISFVLAWFEE
81     GEETVTAFVE Pfvillilia NAIVGWQER NAENAIEALK EYEPemgkvy RADrksvqri KARDIVPGDI VEVAUGDKVP
161    ADIRILSIKS TTLRDQSIK TGESVSVIKH TDPVDPRAV NQDKKNMFLS GTNIAAGKAV GIVATTGVST EIGKIRDQMA
241    ATEQDKTPLQ QKLDEFGEQL SKVISLICVA VWLINIGHFN DPVHGGSWFR GAIYYFKIAV ALAVAAIPEG LPAVITTCIA
321    LGTRRMakkn AIVRSLPSVE TLGCTSVICS DKTGTLTNO MSVCKMFIID KVDGDIcslN EFSITGSTYA PEgEVlKNDK
401    PVRAGQYDGL VELATICALC NDSSLDfnet KGVYekvgea TETALTTLVE KMNVFNTEVR SLSKVERANA CNSVIRQLMK
481    KEFTLEFSRD RKSMSVYCSF AKSSRAAVGN KMFVKGaPEg VIDRCNYVRV GTRVPLTGP VKEKIMSVIK EWGTGRDTLR
561    CLALATRDTP PKREEMVLDL SAKFMEYEMD LTFVGVVGM L DPPRKEVTGS IQLCRDAGIR VIMITGDNKG TAIATCRRIG
641    IFSNEEVAD RAYTGREFDD LPLaEQREAC RRACCFARVE PSHKSkiveY LQSYDEITAM TGDGVNDAPA LKKAEIGIAM
721    GSGTAVAKTA SEMVLADDNF STIVAAVEEG RAIYNNMKQF IRYLISSNVG EVVCIFLTA LGLPEALIPV QLLWVNLVTD
801    GLPATALGFN PPDLDIMDRP PRSPKEPLIS GWLFFRYMAI GGYVGAATVG AAaWwFLYAE DGHVSYHQL THFMQCTEHN
881    PEFDGLDCEV FEaPEPMTMA LSVLVTIEMC NaLNSLSENO SLLRMPpWVN IWLlGSICLS MSLHFLILYV DPLPMIFKLR
961    ALDFTQWLMV LKISLPVIGL DELlKFIARN YLEG
  
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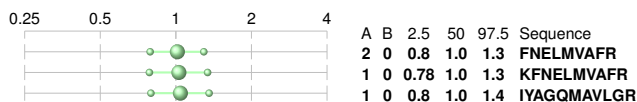


5.800 demethyl-Q 7 [Rattus norvegicus]

Protein Accession	gi 25453396
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.81, 1.27)
Associated Peptides	3
Associated Spectra	4
Coverage	0.117
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.13
Avg..iTRAQ.Ratio....116.114.	1.10
Avg..iTRAQ.Ratio....117.114.	1.05

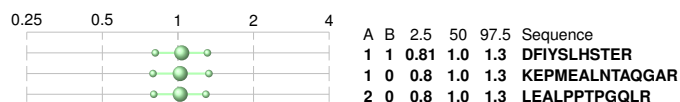
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1      MTLDNINRAA VDRIIRVDHA GEYGANR IYA GOMAVLGR TS VGPVIQKMWD QEKnhLkKfN ELMVAFVRP TVLMPLWNVA
81     GFALGAGTAL LGKEGGMACT VAveESIAHH YNNQIRLMME EDaEKYEELL QVIKQFRDEE LEHHDtGLEH DaELAPAYTL
161    LKRLIQAGCS AAIYLSERF
  
```



5.801 PREDICTED: similar to C33H5.19 [Rattus norvegicus]

Protein Accession	gj 109482276	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.826, 1.27)	
Associated Peptides	3	
Associated Spectra	5	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.93	0.863
Avg..iTRAQ.Ratio....116.114.	1.13	1.05
Avg..iTRAQ.Ratio....117.114.	1.10	1.07



5.802 "PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) [Rattus norvegicus]"

Protein Accession	gj 109481717	
Mean Expression Ratio	0.974	
Median Expression Ratio	0.976	
Credible Interval	(0.749, 1.27)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	NA	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.03	
Avg..iTRAQ.Ratio....116.114.	0.811	
Avg..iTRAQ.Ratio....117.114.	1.07	



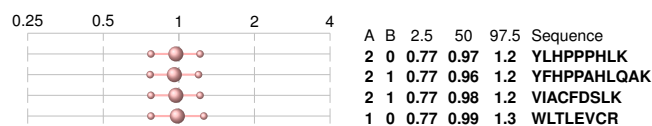


5.803 PREDICTED: similar to muscleblind-like 1 [Rattus norvegicus]

Protein Accession	gij109464914
Mean Expression Ratio	0.977
Median Expression Ratio	0.976
Credible Interval	(0.806, 1.18)
Associated Peptides	4
Associated Spectra	9
Coverage	0.0885
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.912
Avg..iTRAQ.Ratio....116.114.	1.1
Avg..iTRAQ.Ratio....117.114.	1.08

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1      MAVSVTPIRD TKWLTLEVCR EFQFGTCSR P DTECKFAHPS KSCQVENGRV IACFDSLKGR CSRENCKYLH PPPHLKTQLE
81     INGRNNLIQQ KNMAMLAQQM QLANAMMPGA PLQPVNLMQQ SFQKRGDCI SRWEGSPYYT GSDTNYQYCT VEPMFSVAPS
161    LATNASAAFN FYLGPVSPSL VPAEILPTAP MLVTGNPGVP VPAAAAAAQ KLMRTDRLEV CREYQRGNCN RGENDCRFAH
241    PADSTMIDTN DNTVTVCMDY IKGRCSREKC KYFHPPAHLQ AKIKAAQYQV NQAAAAQAAA TAAAMGIPQA VLPPLPKRPA
321    LEKTNGATAV FNTGIFQYQQ ALANMQLQQH TAFLEPPGSIL CMTFATSVVP MVHGATPATV SAATTSATSV PFAATATANQ
401    IPIISAEHLT SHKYVTQM
    
```



5.804 "PREDICTED: similar to eukaryotic translation initiation factor 1A, Y-linked [Rattus norvegicus]"

Protein Accession	gij109511789
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.763, 1.37)
Associated Peptides	1
Associated Spectra	1

Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	0.958
Avg..iTRAQ.Ratio....117.114.	1.32

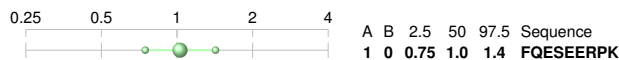


5.805 heat shock protein 4 [Rattus norvegicus]

Protein Accession	gi 24025637
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.761, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0107
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.3
Avg..iTRAQ.Ratio....116.114.	0.726
Avg..iTRAQ.Ratio....117.114.	1.38

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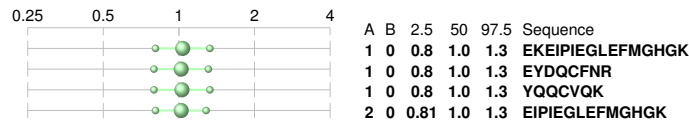
1      MSVVGIDLGF QSCYAVARA GGIETIANEY SDRCTPACVS FGPKNRSVGA AAKSQVISNA KNTVQGFKRF HGRAFSDFPV
81     EAEKSNLAYD IVQLPTGLTG IKVTYMEEER NPTTEQVTAM LLSKLNKETA SVLKKPVVDC VVSVPFSFYTD AERRSVMDAT
161    QIAGLNCLRL MNETTAVALA YGIYKQDLPA LEEKPRNVVF VDMGHSAYQV SVCAFNRGKL KVLATAFDTT LGGRKFDEVL
241    VNHFCSEFGK KYKLDIKSKV RALLRLSQEC EKLKLLMSAN ASDLPLSIEC FMNDIDVSGT MNRGKFLEMC DDLLARVEFP
321    LRSILDQSKL KKEDIYAVEI VGGATRIPAV KEKISKFFGK ELSTTLNADE AVTRGCALQC AILSPAFKVR EFSITDVVPY
401    PISLRWNSPA EEGSSDCEVF PKNHAAPFSK VLTFRYRKEPF TLEAYYSSPQ DLPYPDPAIA QFSVQKVTPQ SDGSSSKVKV
481    KVRVNVHGIF SVSSAALVEV HKSESESEPM ETDQNAKEE KMQVDQEEPH TEEQQPQTPA ENKAESEEME TSQAGSKDKK
561    MDQPPQAKKA KVKSTSTVDLP IESQLLWQLD REMLGLYTEN EGKMIMQDKL EKERNDAKNA VEYVYEMRD KLSGEYKFFV
641    SEDDRNNFTL KLEDTENWLY EDGEDQPKQV YVDKLAELRT LGQPIKTR Q FSEERPKLFE ELGKQIQQYM KVISSEFNKE
721    DQYEHDAAD MTKVEKSTNE AMEWMNSKLN LQNKQSLTAD PVVKTKEIEA KIKELTNICS PIISKPKPKV EPPKEEPKHA
801    EQNGPVDGQG DNPQTQAAEH GADTAVPSDG DKKLPAMDID
    
```



5.806 PREDICTED: similar to p53-inducible cell-survival factor [Rattus norvegicus]

Protein Accession	gij109496069
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.83, 1.27)
Associated Peptides	4
Associated Spectra	5
Coverage	0.408
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.10
Avg..iTRAQ.Ratio....117.114.	1.09

1 MNSVGEACTD MKR**EYDQCFN** **R**WFAEKFLKG DGSQDPCTDL FKR**YQQCVQK** AI**KEKEIPIE** GLEFMGHGKE KPENSS



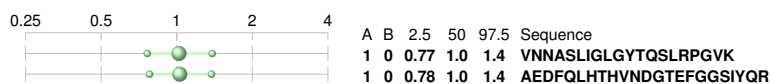
5.807 voltage-dependent anion channel 3 [Rattus norvegicus]

Protein Accession	gij13786204
Mean Expression Ratio	1.03
Median Expression Ratio	1.02
Credible Interval	(0.793, 1.33)
Associated Peptides	2
Associated Spectra	2
Coverage	0.152
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	1.15
Avg..iTRAQ.Ratio....117.114.	1.08

NHLBI Zile/Grant, Aged Rat

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1      MCSTPTYCDL GAAAKDVFNK GYFGFMVKID LKTKSCSGVE FSTSGHAYTD TKGASGNLET KYKVCNYGLI FTQKWNTDNT
81     LGTEISWENK LAEGLKLTVD TIFVPNTGKK SGKLNKASYRR DCFVSGSRVD IDFSGPTIYG WAVLAFEGWL AGYQMSFDTA
161    KSKLCQNNFA LGYKAEDFQL HTHVNDGTEF GGSIIYQVNE KIETSINLAW TAGSNNTRFG IAAKYRLDCR TSLSAKVNNA
241    SLIGLGYTQS LRPGVKLTLS ALVDGKNFNA GGHKVGLGFE LEA
  
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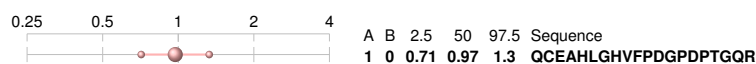


5.808 methionine sulfoxide reductase B [Rattus norvegicus]

Protein Accession	gij7225541
Mean Expression Ratio	0.977
Median Expression Ratio	0.976
Credible Interval	(0.719, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.115
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.09
Avg..iTRAQ.Ratio....116.114.	0.857
Avg..iTRAQ.Ratio....117.114.	0.903

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1      MARLLRALRG LPWLEAPGRA RGCAGSGRGD TGS LIKSKLS LSKADWQKKL TPEQFYVTR E KGTEAPFSGM YLKNKETGMY
81     HCVCCDSPLF SSEKKYCSGT GWPSFSEAHG TKGSDESHTG ILRRLDTSLG CPRMEVVCKQ CEAHLGHVFP DGPDP TGGQRF
161    CINSVALKFK PSKP
  
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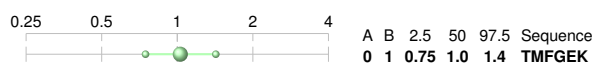
5.809 PREDICTED: similar to Gastric triacylglycerol lipase precursor (Gastric lipase) (GL) (Lingual lipas

Protein Accession	gij109463789
Mean Expression Ratio	1.03
Median Expression Ratio	1.02
Credible Interval	(0.756, 1.38)
Associated Peptides	1

Associated Spectra	1
Coverage	0.00845
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.852
Avg..iTRAQ.Ratio....116.114.	0.858
Avg..iTRAQ.Ratio....117.114.	1.1

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1      MTEDGYILLI FRIPHGKNE KSSHNTRRPV VYLHHGLTVS ADYWILDPPS NCLAFLLADA GFEVWLGNSR GTNNARKHVR
81     LDPDSKEFWD FSFNEQIEYD LPAIIFYFILN ETRQTQIYYI GHSQGVYLLAY AAFATNPQLA QKIKINFALG PVVITKYLTVG
161    VFRTIAYIHP TVIK TMFGEK DIFSksNAND ILRFLCHREQ IATACTSLLI VLFGYNPGNL NESRIDVYSE HIPAGTSVRS
241    ILHFSQSTPP IYNIEDMKVR TAMWSGERDL LGDPKDVKNL AAKTPNLIYH KKIPIYHNHMD FILGKDAVVQ VFKMWWLLRT
321    MCLIHVFGKI FCLLEPNKNP ESHMNVSEII KYWNYPSLEY EVVTDGGYIL PINRIPHGKN NANSSAPKMV VFCQHGLFST
401    PGVWVANPPD NSLAFILAEA GYDVWLGNSR GSTWAKKHVT LSPDSEEFWA FSPDQMIAYD LPATINFILN TTGQEQIYYI
481    GHSLGTLIAL GAFSTNQEIA EKIKLNILIA PVRTVKYVKG FGRLLAYFSP EAFKLVFGKK EFLPTVVFSE YSKYVCNIKL
561    VDAGCAGVLG SLTGFSEDL NTSRIDVYIT HSLAGTSTQI LIHAGQAIRS GEFQAYDWGS PSLNMQHYNQ TTPPLYSVEN
641    MKVPTVMFTG LKDFLADPKD VANLVPKIFN LIYHKTIPEF SHLDFIVGLN AKTEVSDEIL TILGEYDSSV
  
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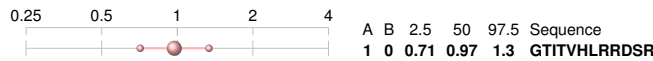


5.810 PREDICTED: similar to inositol hexaphosphate kinase 3 [Rattus norvegicus]

Protein Accession	gij109509163
Mean Expression Ratio	0.978
Median Expression Ratio	0.977
Credible Interval	(0.73, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0264
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.943
Avg..iTRAQ.Ratio....116.114.	1.17
Avg..iTRAQ.Ratio....117.114.	0.952

```

1      MELVKPLKES CWPSLGPAIG DGFQKTMEKA SYWHLLFTGS RRLVAQNHQG DMVVRHGSDK GKAGVGVPLE PFLHQVGGHL
81     SVLRYDAYTV CKPLIFQEQQ FYESLPLAMR RFTFPQYKGTI TVHLKRDSFG HGLGLVANPLK ENLEPFQVSP ESKRAVALWQT
161    LQQTTSSEGS PCPLAQMAHS LKESAAKALL RSDCHLSTQA SPLVESAVGS QIERKGFNPW GLHCHQAHLS RLCSQYPEDK
241    RHRFQAWVLL ISEPKTARSQ DLNHDLEVDG GNSRERRSRP QSGALRVTS A GEGSLGLDLC QPKVYQTDKK SFLCKDKYYG
321    RKLSVEGFRQ ALSQFLHDGI RLRTLELEPI LRRLQALLTV IRSQSSYRFY SSSLLI IYDG EPPQTAPAPQ TTQGSTSGST
401    SGDPAKV DVR MIDFAHTTYK GSWNERTTYE GPDPGYIFGL ENLIGILRDI QEGE
  
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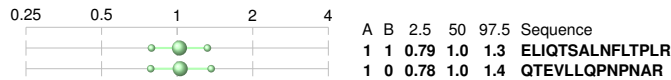



5.811 SH3-domain GRB2-like B1 [Rattus norvegicus]

Protein Accession	gi 58865428	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.804, 1.30)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	0.0767	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.17	1.13
Avg..iTRAQ.Ratio....116.114.	1.11	0.765
Avg..iTRAQ.Ratio....117.114.	1.04	1.16

```

1      MNIMDFNVKK LAADAGTFLS RAVQFTBEKL GQAEKTELDA HLENLLSKAE CTKVWTEKIM KQTEVLLQPN PNAE IEEFVY
81     EKLD RKAPSR INNPELLGQY MIDAGTEFGP GTAYGNALIK CGETQKRIGT ADRELIQ TSA LNFLTPLRNF IEGDYKTI AK
161    ERKLLQNKRL DLDAKTRLK KAKAAETKSS SEQELRITQS EFDRQAEITR LLEGISSTH AHHLRCLNDF VEAQMTYYAQ
241    CYQYMLDLQK QLG SFPSNYV SNNNQTS GTP VPYT LSN TIG PS AVASTGSL VITCPPNLSD LK DSSSTRKA RVL YDYDAAN
321    STELSLLADE VITVFSVVG M DSDWLMGERG NQKGKVPITY LELLN
    
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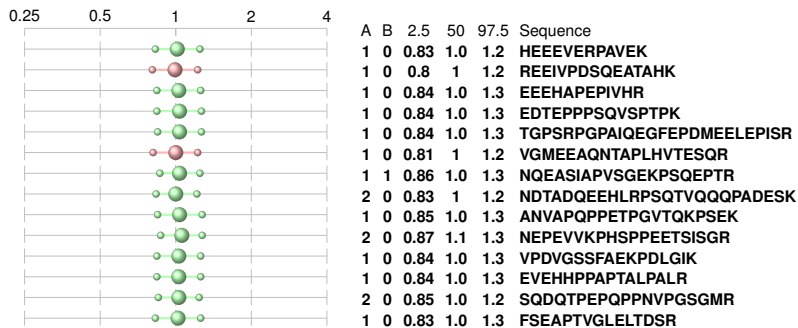


5.812 PREDICTED: similar to cardiomyopathy associated 5 [Rattus norvegicus]

Protein Accession	gi 109465895	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.9, 1.17)	
Associated Peptides	14	
Associated Spectra	18	
Coverage	0.0682	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.00	0.639
Avg..iTRAQ.Ratio....116.114.	1.08	1.39

Avg.iTRAQ.Ratio....117.114. 1.20 1.20

1	MASDSDGLAA	QGLLGWGAEE	EEPETEESSE	GEGETAAES	EEEPDARLSD	EDEEGKIKQE	CIISDPFSFM	VAVQREDSGI
81	TWETNSSRSS	TPWASEESQT	SGICSLGESA	LTSPPGVSF	IMDEVKTRTK	RTQKSKRGSP	SLRRKGSKRR	NSLESQDVL
161	NQEDGPLISE	KPVLNTEKEK	SSIGTYDKTR	RKKTESNTTP	ITGAIYKEHK	PLVLKPVYIG	TVQYKIKMFN	SVKEELIPLQ
241	FGTLPKGYV	IKEIHYRRGK	ESSISLEPDL	SNGGSNIASQ	RKLAQSPEED	RARELAPPWR	GALSKGSMTS	LFSHEEQKKT
321	YTDSSLNATS	STEHTLPSYS	RNDTADQEEH	LRPSQTVQQQ	PADESKTYRT	EPPSTPATMV	PERAKELEQ	NSQGMESSED
401	ASGLSGLAND	VQEQGMVSVN	HSMSWAAEKE	SLKTGSPRPG	PAIQEGFEPD	MEELEPISSE	KMPEVSEPV	SSEPIDHREE
481	EHAPEPIDHR	EEHHAPEPLV	HREEHAPPEL	LVRHEEHAP	EPVHREEEH	APEPIVHREE	EHAPEPIVHR	EEHHAPEPID
561	HREEHAPPEL	VHREEHAPPE	PLVHREEEHA	PEPIVHREQE	HAPEPIVHRE	KHAPEPIVHR	EEHHAPEPIV	RREEHAPPEP
641	IVHREEEHAP	EPLVHREKHA	PEPIVHREEE	HAPPEPIVHRE	BEHAPEPLLS	LASQEVESGA	ETSLPITDTI	EPEDSSLEEE
721	IIELDYPESP	LVSEKDSPLP	LSPVEVHRKE	PILPFSQMTFT	PEHITLSEEE	REESVSTVD	SAFVSEYSVL	QDLNRKSEKL
801	EVEAVSVSDV	KSSEPAVFSSE	DEEERESYSP	AVTSVSEHSL	SPSTTEKTSS	TQSPLFSTVS	PDLNLVLSGDE	ASETEASDSL
881	SATEYSGPAH	VQELLVRAGD	PKLPLKSHV	SEP I IQTEDE	KEDIGLLSSA	VVRHAALSED	EGLESQSFVS	DSKLPFKPSV
961	PQSATQEPPE	KTGDDTPOFK	PKGLAEPTIL	LEEEKEAIEL	SSSEVPAAE	RTLPPQTTEL	LSSEQAPPSW	PTSSEQEGLS
1041	EERSGEGQQR	SFSSTPELVH	TSPLLKKGAS	SPSALSEFPG	BEDSIGPLSP	DSAFASEFSF	SPYPTQLER	RELGRDSPLC
1121	LTSFSEHTVL	SDETEEAEL	FSPDSASQVS	IPRYIAETE	RNKVEADELL	PMSVPDFPY	FSGADEEETG	SSVATPVPEH
1201	SAPSKERKEE	FFPSIPVFDL	LSLPPSAVMT	TTQAEATKPD	VPTVSTVSSE	YLILAQRQKT	QASLEPEAED	VVPPPLTSGW
1281	EEEDAKSSST	ASTIAASASA	VSSVVEKETA	SILSTSGFSV	SPESARVPKT	EREPKASLTL	TSAEQEMALP	KVREIEIVPD
1361	SQEATAHKSQ	DQTEPQPPN	VPGSGMRYSV	LSDMGDEPKA	DVKPDLAPAV	TSELEQRMLS	KNEPEVVKPH	SPPEETSISG
1441	RKVL SAVQKE	VKQESKITRE	LPAASSGIER	FVEHHPPAPT	ALPALREETE	RETKASVSAT	PVPVTKLDSN	SAALGRDIEL
1521	TDSSLAGPAE	HPGFKGVGER	GLSGSEPSLT	MSAADPTVLR	PEPKLPIDLW	SEVERHDETP	PBSQVSPPTK	HTVPDDKPEE
1601	MTRSPDSENL	VSDDLAPTLL	ALRDEMNGQA	EEETSSPVLGS	FLSGKEELVK	LPPEPKKPKR	FSEAPTVGLE	LTDSDRDRGS
1681	LGIEIVKPSV	LEKGPTELRS	AGKEQEEHRG	LPVPATSPLE	TASSDLPIKQ	KELKKTLPGE	QAVKVPDVG	SFAEKPDLDGI
1761	KQLAQRKENL	EQPKPFMTAE	PADVIGTEVK	ETLISPDKNT	RMLDKPDGLV	SQHEDRKPGP	RQLESSESKD	LMPEKLGAA
1841	LDSDHPTGIR	NQEASIAPVY	GEKPSQEPTR	VQSKAVGDAA	EGRKLAPDVQ	VPAVKANVAP	QPPETPGVTO	KPSEKSLVAE
1921	QCPLPAEKGG	GISSFKSWM	SLLFGSSTPD	NKVADNKDLE	TQSPSLEKA	LTAVEPKGAV	PAEVTVAEKP	GVHSLPEVTV
2001	KLGEPEPRGGE	KLTFPLNTDV	LKQPASNSEN	YGKKGLPFGS	EGMGENLATS	AGDEHPGIHP	RSPMGEK	VGM EEAQNTAPLH
2081	VTESQRHQKP	EIAPPSMWSI	SVLKEEPPSSG	HKEAQLLSSD	VVDRTPQRPE	STLSAFARM	SEKQAPVSLP	VESEDSLIDL
2161	GEDRLRQEMP	KPTSLERHEE	EVERPAVEKD	GWTRSFSLA	GEKGLAEKQE	IMAPLEVGEN	KAVGKLQMP	ESRPFKSEGS
2241	KAERLEQRI	SPREELMEKP	SKTLASERRE	KEAQERVFPE	GEKEGGLSSS	PAAAMPVPGA	SAISWDKAQP	PSPVKPPVI
2321	EKPEHIFTEV	YPEI GERKAA	ETKPHQPEEG	KTLVEKTKAS	RVEPPHGEV	DGHSFTQGGN	LELEKSRER	VDLKERRFQ
2401	VMPELS LAAS	VAAEDGHAQP	RPLSRAAERT	AGHITDETNN	LGPPTLETSL	EQTAKKQETR	SDRPTVHTIQ	TSKHPEEMP
2481	KQSVLISKRR	LEAMEDVHRN	EPLSSAASSY	TQFMLSASAV	SADGAPPVGG	TFQEPGTS	KGEFVSVTSK	PAGLSEEQKS
2561	AFSIISEGCE	ILNHAPAFI	PSVDQBESE	MQDNLQYLEE	KSSFKISVVC	DERKAVASHK	TQKSELEVDP	RKITSPPTENE
2641	PKESYQTKEE	TATGSRSGDF	TSIQPGVSGE	EDYFEKTYLI	DYNLSPGSE	QKSTVEGSSE	EATETLTSFP	ESSAEQTLDH
2721	EYDLVKLDES	FYGPKEKNGS	SSHAEMPKSL	VIQKPSENA	PKGVGVVDSD	RSPGMLFDV	EEGVLSRRQI	FPTTPKAVNP
2801	ELLEPPALS	FFYKDLYEGA	LGEKNEGETA	SEGGSVDEST	SFRRHSDTD	DGTGMFEKY	VLKDDILHDE	SVNQEDQGS
2881	LEEKPVGENG	SQQLRIAASE	IGRKPSTFSW	ERNLEEQHKV	IDREGEPVSH	TETLNEVATQ	QKAPVTEQVT	AITQEMS YAV
2961	PFQDTHRVRT	SEPPSQGHEA	GNASPEVNLN	VPVQVSFPEE	ESTAGATYAP	EVSQEEVPC	VSRERLHNI	PVQDEYDFVD
3041	SLNQEIYSQG	ILPGEPYSEA	PKPEVLPPQT	ESLSHAGERE	LMSEGEPRKS	ASQEEWDRGG	EDQSARESVL	TKTQEKQKA
3121	QVDSYCYTCK	SLVSEMDKVL	DIHKKHEVSA	LDTAISAVKV	QLGEFLENLQ	EKSLRTEAFV	SEIESFFNTI	EKCKSKNEKR
3201	LEMQNEEMMK	KVLAQYDEKA	QSFEEVKKKK	MEFLHDQMVH	FLQSMDTAKD	TLETIVREAE	ELDETVFAS	FEEINERLS
3281	AMESTASLEN	MPAARSLFEH	YDSSARGDQ	MLQVAVPQP	PRLEPQEPNS	ATSTTIAVYV	SVNKEDVDS	FQVYCVPEPQ
3361	DDQEINELVE	EYRLTVKESC	CIFEDLEPDR	CYQVWMAVN	FTGCSLPSE	AIFRTAPFTP	VIHVEDCTVC	WNTATVRRWP
3441	ANTEATETYT	LEYCRQHSPE	GEGRLSFSGI	KGLQLKVNLS	PNDNYFFVYR	ATNASGTSEQ	SEAALISTRG	TRFLLLRETA
3521	HPALQISSNG	TVISFSERRR	LTEIPSVLGE	ELPACGQHYW	ETTVDTSPAY	RLGICSSSAV	RAGALGQGES	SWYMHCSFPQ
3601	RYTFFYSIGV	SEVHATERPA	RVGILLDYTN	QRLLFVNAES	GQLLFTVRHR	FNEGVPFAFA	LEKPGKCTLH	LGLEPPDSVR
3681	HK							

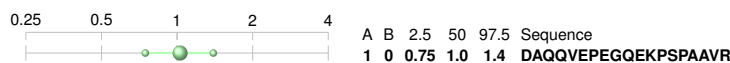


5.813 PREDICTED: similar to HBxAg transactivated protein 2 [Rattus norvegicus]

Protein Accession	gij 109475800
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.757, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0247
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.10
Avg..iTRAQ.Ratio....116.114.	1.24
Avg..iTRAQ.Ratio....117.114.	1.23

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1      MIATFQENQS  TWLQDPKPLG  TNYLPETRTH  PHVVPVLSEK  PTDKVPEPKE  QRQKQPWAGP  IKAQKLPDLS  LVENKEHKPG
81     FIGKERSLKN  RKVRDAQQVE  PEGQEKPSPA  AVI  STDPGTA  KETKAVSEMS  AEIGAMISVS  SPEYGTDAKE  SVTDYTTTSS
161    SLPNTVATNN  AKMEDTLVNN  VPLPSSLPLP  KREAMQQSSS  LTSVPPPTFS  LTFKMESARK  AWENSPNLRE  KGSPVTSTAP
241    PIVSGVSSSA  SGPSTANYNS  FSSASMPQIP  VASVTPTASL  SGACTYTTSS  LSTKSTTTSD  PPNICKVKPQ  QLQTSSSLPSA
321    SHFSQLSCMP  SLIAQQQQSP  QVYVSQSAAA  QIPAFYMDTS  HLFNTQHARL  APPSLAQQQG  FQPGLSQPTS  FQQIPIPIYA
401    PLQGQHQAQL  SLGAGPAVSQ  AQELFSSSIQ  PYRSQPAFMQ  SSSSQPSVVL  SGTALHNFFA  VQHQLAKAQ  SGLAFQQTSN
481    TQPIPILYEH  QLGGASGLGS  SQLIDTHLLQ  ARANLTQASN  LYSGVQQQPG  QTNFYNTAQS  PSALQQVTVP  LPASQLSLTN
561    FGSTGQPLIA  LPQTLQPQLQ  HTPQAQAQS  LSRPAQVSQP  FRGLIPAGTQ  HGMMATGKM  SEMELKAFGS  GIDIKPGTTP
641    IGGRTTPTPS  SFFRATSTSP  NSQSSKMNSI  VYQKQFSAP  ATVLAKQRAE  VLQSTQRFFS  EQQSKQIGG  KAQKVDSDTS
721    KPETLSDPPG  TCQEKVEEKP  PLAPTITTKP  VRTGPIKPA  IKTEETKS
  
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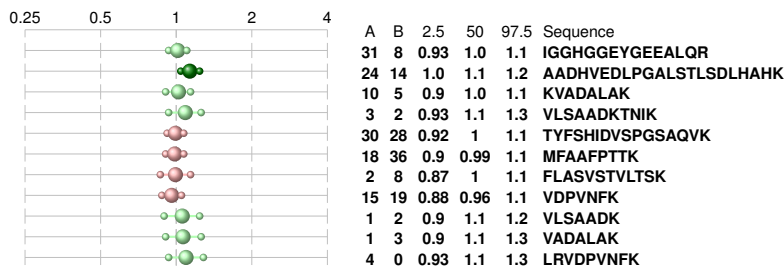


5.814 hemoglobin alpha 2 chain [Rattus norvegicus]

Protein Accession	gij 60678292	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.951, 1.10)	
Associated Peptides	11	
Associated Spectra	264	
Coverage	0.718	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.28	1.6
Avg..iTRAQ.Ratio....116.114.	1.15	1.09

Avg..iTRAQ.Ratio....117.114. 0.847 0.701

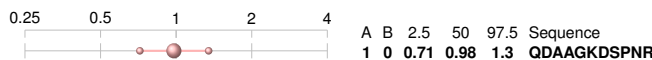
1 MVLSAADKTN IKNCWKGKIGG HGGEYGEEAL QRMFAAFPTT KTYFSHIDVS PGSAQVKAHG KKVADALAKA ADHVEDLPGA
 81 LSTLSDLHAH KLRVDPVNFK FLSHCLLVTL ACHHPGDFTP AMHASLDKFL ASVSTVLTSK YR



5.815 signal-induced proliferation-associated 1 like 3 [Rattus norvegicus]

Protein Accession	gij61556847
Mean Expression Ratio	0.98
Median Expression Ratio	0.977
Credible Interval	(0.727, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0188
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.09
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	0.816

1 MSSGDSSSGG LTSQESTMER PKPEPLWHVP AQARLSAMTG SMGSKHPSRQ DAAGKDSPNR HSKGEPQYSS HSSNTLSSN
 81 ASSSHSDDRWF DPLDPLEPE PDPFSKGGSS DSGIDTTLTYT SSPSCMSLAK TPRPTKPHKP PGSIGLCGGG RESAGRPHPA
 161 DRRREVSPAP AVAAQNKGYR PKMYSSGSST PPGLVGGSRD PPRQASDMGS RTGYPTQVYK TTSJETPRPS QLSQCSPFQL
 241 STSVPKSFFS KQPAHNKHSY GWKRADEPPP RPLPFTESSK QVDTNAKNVF GQPRLRASLR DLRSRPNYK STIEDDLKLL
 321 IIMDNLGPEQ DRDTGPPQKS LQRTLSDESL CSGRREPSYA SPTSLEPGLP SDVLFSTSTCT FPSSTLPARR QHQSHPPSPG
 401 APNTIPATGN GFPEKKSAYS ASELSLADGR DRPLRRLDPG MMPLPDTAAG LEWSSLVNAK KAYEVQRAVS LFSLNDPALS
 481 PDIPPAHSPV HSHLSLGERP QTPRTTPTMS EESPLDLTGK VYQLEVMLKQ LHTDLQKEKQ DRVVVLQSEVA SLRQNNQRLQ
 561 EESQAASEQL RKFALFSRE KKEL



5.816 "PREDICTED: similar to C-type lectin domain family 3, member a [Rattus norvegicus]"

Protein Accession	gij109508186	
Mean Expression Ratio	0.977	
Median Expression Ratio	0.977	
Credible Interval	(0.766, 1.25)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.97	0.823
Avg..iTRAQ.Ratio....116.114.	0.843	0.799
Avg..iTRAQ.Ratio....117.114.	1.42	0.648



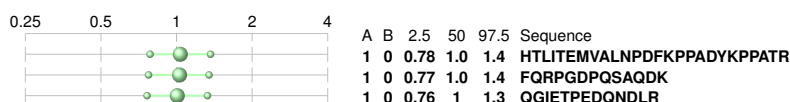
5.817 zinc finger protein 162 [Rattus norvegicus]

Protein Accession	gij61097924	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.803, 1.31)	
Associated Peptides	3	
Associated Spectra	3	
Coverage	0.104	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.16	
Avg..iTRAQ.Ratio....116.114.	1.13	
Avg..iTRAQ.Ratio....117.114.	1.02	

NHLBI Zile/Grant, Aged Rat

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1      MEPRHNGTED SDSRHAYGYP PWPDSGTRKS LYRSPSPPEI YNSEGKRLNT REFRTTRKLE EERHTLITEM VALNPDFKPP
81     ADYKPPATRV SDKVMIPQDE YPEINFVGLL IGPRGNTLKN IEKECNAKIM IRGKGSVKEG KVGRKDGQML PGEDEPLHAL
161    VTANTMENVK KAVEQIRNIL KQGIETPEDQ NDLRKMQLRE LARLNGTLRE DDNRILRPWQ SSETRSITNT TVCTKCGGAG
241    HIASDCKQQR FGDPQSAODK ARMDKEYLSL MAELGEAPVP ASVGSTSGPA TTPLASAPRP AAPASNPPPP SLMSTTQSRP
321    FWMNSGSPEN RPYHGMHGGG PGGPGGGPHS FPHPLPSLTG HGGHPPMQHN PNGPPPPWMQ PPPPPMNQGP HPPGHHGPPP
401    MDQYLGSTPV GSGVYRLHQQ KGMMPPPPMG MPPPPPPPS GQPPPPPSGP LPPWQQQQQQ PPPPPPPSSS MASSTPLPWQ
481    QRSLPAAAMA RAMRVTRFRA HW
  
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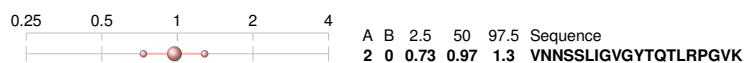


5.818 voltage-dependent anion channel 2 [Rattus norvegicus]

Protein Accession	gi 13786202
Mean Expression Ratio	0.975
Median Expression Ratio	0.977
Credible Interval	(0.741, 1.27)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0678
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.971
Avg..iTRAQ.Ratio....116.114.	1.18
Avg..iTRAQ.Ratio....117.114.	0.864

```

1      MAECCVPVCQ RPICIPPPYA DLGKAARDIF NKGFGFGLVK LDVTKKSCSG VEFSTSGSSN TDTGKVSRTL ETKYKWCYEG
81     LTFTEKWNTE NTLGTEIAIE DQICQGLKLT FDTTFSPTG KKSGKIKSAY KRECINLGCD VDFDFAGPAI HGSVFFGYEG
161    WLAGYQMTFD SAKSKLTRSN FAVGYRTGDF QLHTNVNNGT EFGGSIYQKV CEDFDTSVNL AWTSGTNCTR FGIAAKYQLD
241    PTASISAKVN NSSLIGVGYT QTLRPGVKLT LSALVDGKSF NAGGHKLGLA LELEA
  
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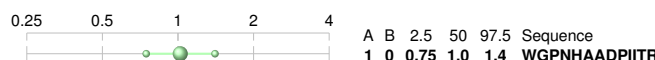
5.819 nudix -type motif 9 [Rattus norvegicus]

Protein Accession	gi 55741431
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.754, 1.38)

Associated Peptides	1
Associated Spectra	1
Coverage	0.0371
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	1.10
Avg..iTRAQ.Ratio....117.114.	1.07

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1      MAGRSLGKAV ATVSLSVALA SVTVRSSGCR AIPAPRNFFP SCGFHLKANI MSGSNGVKDN SHNKARTSPY PGSKVERSKV
81     PNEKVGWLVE WQDYNPVEYT AVSVLAGPQW ADPQISESSF SPRFNEKDGH VERKSQNGLY EIENGRPRNP AGRTGLVGRG
161    LLGRWGP115NHA ADP116LI117RWKR DESGNKITHP VSGKCILQFV AIKRRDCGEW AIPGGMVDPG EKISATLKRE FGEEALNSLQ
241    KSSAEKREIE EKLHALFSQE HLVIIYKGYVD DPRNTDNAWM ETEAVNYHDE TGETMDNLT115L EAGDDAGKVK WVDISDQLKL
321    YASHSQFIKL VAEKRD116AHWS EDCAADSHGL
  
```



5.820 "glucose regulated protein, 58 kDa [Rattus norvegicus]"

Protein Accession	gi 8393322
Mean Expression Ratio	0.976
Median Expression Ratio	0.977
Credible Interval	(0.723, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0277
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	0.688
Avg..iTRAQ.Ratio....117.114.	1.19

```

1      MRFSC115LALLP G116VALLLASAL L117SASADVLEL T115DENFESRVS D116TGSAGLMLV E117FFAPWCGHC K115RLAPEY116EAA A117TRLKGI115VPL
81     AKVDCTANTN TCNKYGVSGY PTLKIFRDGE EAGAYDGPRT ADGIVSHLKK QAGPASVPLR TEDEFKKFIS DKDASVVGFF
161    RDLFSDGHSE FLKAASNLRD NYRFAHTNVE SLVKEYDDNG EGITIFRPLH LANKFEDKIV AYTEKKMTSG KIKKFIQESI
241    FGLCPHMTED NKDLIQGKDL LTAYYDV115DYE K116NTKGSNYWR N117RVMMVAKTF LDAGHKL115NFA V116ASRKTFSHE L117SDFGLESTT
321    GEIPVVAIRT AKGEK115FVMQE E116FSRDGKALE R117FLQEYFDGN L115KRYLKSEPI P116ETNEGPVKV V117VAESFDDIV N115AEDKDLVLE
401    FYAPWCGHCK NLEPKYKELG EKLSKDPNIV IAKMDATAND VPSPEYVKG116F PTIYFSPANK K117LTPKKYEGG R115ELNDLISYL
481    QR115EATN116PP117II Q115E116E117KPK115KKK A116QEDL
  
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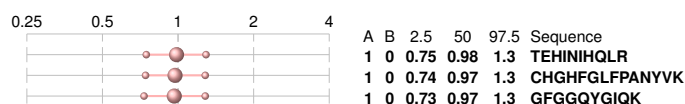


5.821 hematopoietic cell specific Lyn substrate 1 [Rattus norvegicus]

Protein Accession	gij58865374
Mean Expression Ratio	0.978
Median Expression Ratio	0.977
Credible Interval	(0.764, 1.24)
Associated Peptides	3
Associated Spectra	3
Coverage	0.0714
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.05
Avg..iTRAQ.Ratio....116.114.	1.07
Avg..iTRAQ.Ratio....117.114.	1.00

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1      MWKSVVGHNV SVSVETQGDD WDTDPDFVND ISEKEQRWGA KTIEGSGRTE HINIHQLRNK VSEEHDLK K RELESGPKAS
81     HGYGGRFGVE RDRMDKSAVG HEYVAEVEKH SSQTDAAKGF GKKYGVVERDR ADKSAVGFDY KGEVEKHASQ KDYSHGFGGR
161    YGVEKDKRDK AALGYDYKGE TEKHESQRDY AKGFGGQYGI QKDRVDKSAV GFNEMEAPT AYKKTPIEA ASSGARGLKA
241    KFESMAEEKR KREEEKAQQ MARQQQRKA MVKMSREAQQ PSVPVDEPAA PAPLPKKISS EVWPPAESHL PPQSEPVGGR
321    REYFVPSLPT RQPPPQNPLE DNEEPPALPP RTPEGLQVVE EPVYEAPEP EPEPEPDYED VGELDRPDEE AEGDYEDVLE
401    PEDTPSLSYQ AGHSAGAGGA GISAVALYDY QGEGSDELSF DPDDVITDIE MVDEGWWRGR CHGHFGLFPA NYVELL
  
```



5.822 PREDICTED: similar to plakophilin 2 [Rattus norvegicus]

Protein Accession	gij109494803
Mean Expression Ratio	0.976
Median Expression Ratio	0.977
Credible Interval	(0.724, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0138
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.859
Avg..iTRAQ.Ratio....116.114.	0.984
Avg..iTRAQ.Ratio....117.114.	1.08


```

1      MAIPGSLGEC GYIRTVLGQQ ILGHLDSSSL ALPSEARLRL AGSSGRGDPV ARSQR IQEQY QQTLLARGRS SVVGGNLHRT
81     SSVPEYVYKL HLVENDFVGR QSPAARDYDM LKAGVTATYG SRWGRGTAQY SSQKSVEERS WRQPLRRLEI SPDSSPERAH
161    YGHSEYQYAW RSHVVPGGRL TLPYARSEI LGLRQTGTAR RAPGCGSVSD AVFDNGPLNP TIPTHPPGTS HSAGSLEET
241    TVRVSQARFQ GLQSRAGRSS WPRSSVHSTL RESGRMLPTA GQAAVGSQDA HRDRSAFADS QLGNADLEMT LERAVNMLDA
321    DHVPLSKISA AATFIQHESE QKSEARKRVN QLQGIPKLLQ LLKVQNEDEVQ RAVCGALRNL VFEDNDNKLE VAEVNGVPRRL
401    LQVLKQTRDL ETKKQITGLL WNLSSSDKLK HLMITEALLT LTESVIIPFS GWPEGDYPKA NGLLDFDIFY NVTGCLRNM
481    SAGPDGRKVM RRCDGLIDSL VHYVRGTIAD YQPDDKATEN CVCILHNLSY QLEAELPEKY SQSIYMQNRN IQTNSNKSIG
561    CFGSRSRKVK EQYQDTPMPE ERSSPRGIEW LWSIVIRMY LSLIAKSSRN YTQEASLGAL QNLTAGSGPI PTVARMVVQ
641    KENGLQHTRK MLHVGDPSVK KTAVSLRNL SRNLSLQNEI AKETLPDLVS IIPDTPVSTD LLIETTASAC YTLNLMQNS
721    YQNARDLLNT GGLQKIMTIS IGEYAPNKA SKAASVLLYS LWAHTEHNA YKKAQFKKTD FVNSRTAKAS HSLKD
  
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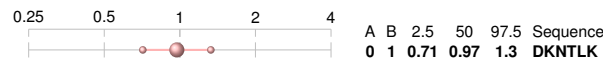


5.823 PREDICTED: similar to zinc finger protein 277 isoform 2 [Rattus norvegicus]

Protein Accession	gij109479322
Mean Expression Ratio	0.977
Median Expression Ratio	0.978
Credible Interval	(0.728, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0124
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.772
Avg..iTRAQ.Ratio....116.114.	0.821
Avg..iTRAQ.Ratio....117.114.	0.813

```

1      MRPQARFYWL SPRFAPPAAR PFQLVQVMAA PEAQGLGVDP REDRVRGVVG GIGHIDHEDS KDWILESLSL PERPGGTAAL
81     EGPSPVPCIF CEEHFPMTAQ DKLLKHMIIE HKIVIADVKL VADFQRYILY WRKRFTEQPI TDFCSVIRN STAFFEEDQN
161    YFLLCDVLPE DRILREELQK QKLKEILDQQ QREKNDTNFH GVCMFCENEEF RGNRSVLLNH MAREHAFNIG LPDNIVNCTE
241    FLCTLQKKLD NLQCLYCEKT FRDKNTLKDH MRKKQHRRIN PKNREYDRFY VINYLELGKS WEEVQLEDDR ELLDLQEDDW
321    SDWQEPVSA VCLFCEKQEE TIDKLYVHMK DTHEFDLLRI KSELGLNFYQ QVKLVNFIRR QVHQCKCYSC QAKFKSKAEL
401    RTHMENAKHT SLLPDSKTWD QLEYFYFPTYE NDTLLCTLSD SESDLTAQEQ TENVPIISED TSRLCALRQS SVLNQLLQEQ
481    CLEN
  
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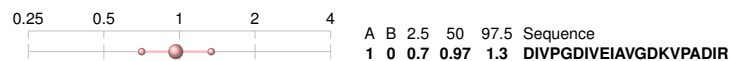


5.824 "ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Rattus norvegicus]"

Protein Accession	gij 8392935
Mean Expression Ratio	0.976
Median Expression Ratio	0.978
Credible Interval	(0.719, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0201
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.928
Avg..iTRAQ.Ratio....116.114.	0.889
Avg..iTRAQ.Ratio....117.114.	1.04

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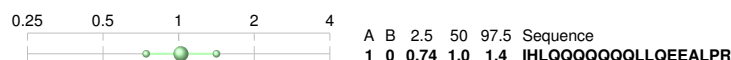
1  MENAHTKTVE  EVLGHFGVNE  STGLSLEQVK  KLERWGSNE  LPAEEGKTL  ELVIEQFEDL  LVRILLLAAC  ISFVLAWFEE
81  GEETITAFVE  PFVILLILVA  NAIVGWQER  NAENAIEALK  EYEPENMGVY  RQDRKSVQRI  KAKDIVPGDI  VEIAVGDKVP
161  ADIRLTSIKS  TTLRVDQSIL  TGESVSVIKH  TDPVPDPRAV  NQDKKNMLFS  GTNIAAGKAM  GVVVATGVNT  EIGKIRDEM
241  ATEQERTPLQ  QKLDFEGEQL  SKVISLICIA  VWIINIGHFN  DPVHGGSWIR  GAIYYFKIAV  ALAVAAIPEG  LPAVITTC
321  LGTRRMAKKN  AIVRSLPSVE  TLGCTSVICS  DKGTGLTTN  MSVCRMFLD  KVEGDTCSLN  EFTITGSTYA  FIGEVQKDD
401  PVKCHQYDGL  VELATICALC  NDSALDYNEA  KGVYKVGGEA  TETALTCLVE  KMNVPDTELK  GLSKIERANA  CNSVIKQLM
481  KEFTLEFSRD  RKSM SVYCTP  NKPSRTSMSK  MFVKGAPGEG  IDRCTHIRVG  STKVPMTPGV  KQKIMSVIRE  WSGSDTLR
561  LALATHDNPL  RREEMHLED  ANFIKYETNL  TFVGCVGMLD  PPRIEVASSV  KLCRQAGIRV  IMITGDNKGT  AVAICRRIG
641  FGQDEDVTSK  AFTGREFDEL  SPSAQRDA  CL  NARCFARVEP  SHKSKIVEFL  QSFDEITAMT  GDGVNDAPAL  KKSEIGIAM
721  SGTAVAKTAS  EMVLADDNFS  TIVAAVEEGR  AIYNNMKQFI  RYLISSNVGE  VVCIFLTAAL  GFPEALIPVQ  LLWVNLVTD
801  LPATALGFNP  PDLDIMNKPP  RNPKEPLISG  WLFERYLAIG  CYVGAATVGA  AAWWFIAADG  GPRVSFYQLS  HFLQCKEDNP
881  DFEQVDAIF  ESPYPMTMAL  SVLVTIEMCN  ALNSLSENQS  LLRMPPWENI  WLVGSICLSM  SLHFLILYVE  PLPLIFQITP
961  LNLTQWLML  KISLPVILMD  ETLKFFARNY  LEPGKECAQP  ATKPSCSLSA  CTDGISWPFV  LLIMPLVVVW  YSTD TNFSDM
1041  FWS
    
```



5.825 PREDICTED: similar to LIM domains-containing protein 1 [Rattus norvegicus]

Protein Accession	gij 109485581
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.755, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	NA

Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.22
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	1.22

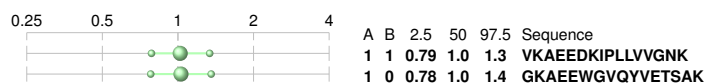


5.826 v-ral simian leukemia viral oncogene homolog B [Rattus norvegicus]

Protein Accession	gi 16758670	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.798, 1.3)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	0.155	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.10
Avg..iTRAQ.Ratio....116.114.	1.06	0.812
Avg..iTRAQ.Ratio....117.114.	1.24	1.35

```

1      MAANKGKSQG SLVLHKVIMV GSGGVGKSAL TLQFMYDEFV EDYEPTKADS YRKKVLDGE EVQIDILDTA GQEDYAAIRD
81     NYFRSGEGFL LVFSITEHES FTATAEFREQ ILRVKAEEDK IPLLVVGNKS DLEERRQVPV EEARGKAEW GVQYVETSAK
161    TRANVDKVFV DLMREIRAKK MSENKDKNGR KSGKSKKSFK ERCCLL
  
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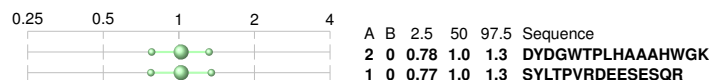


5.827 "protein phosphatase 1, regulatory (inhibitor) subunit 12A [Rattus norvegicus]"

Protein Accession	gij 25742846
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.796, 1.30)
Associated Peptides	2
Associated Spectra	3
Coverage	0.0318
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.09
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	1.19

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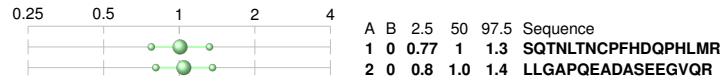
1      MKMADAKQKR NEQLKRWIGS ETDLEPPVVK RQKTKVKFDD GAVFLAACSS GDTDEVLKLL HRGADINYAN VDGLTALHQA
81     CIDDNVDMVK FLVENGANIN QPDNEGWIPL HAAASCGYLD IAEFLIGQGA HVGAVNSEGD TPLDIAEEEA MEELLQNEVN
161    RQGVDEI AAR KEEERIMLRD ARQWLNSGHI SDVRHAKSGG TALHVAAAKG YTEVLKLLIQ AGYDVNIKDY DGWTPHAAA
241    HWGHEEACRI LVDNLCDMET VNKVGQTAFD VADEDILGYL EELQKKQNLL HSEKRDKKSPL IESTANMEN NQPQKTFKKN
321    ETLIEPEKN ASRIESLEQE KADEEEEGKK DESSCSSEED EEDDSESEAE TDKTKPMASV TNAHTASTQA APAAVTPTPL
401    SSNQGTPSP VKKFPTSTTK ISPKEEERKD ESPASWRLGL RKTGSYGALA EITASKEAQK EKDTAGVIRS ASSPRLSSSL
481    DNKEKEKDNK GTRLAYVAPT IPRRLGSTSD IEEKENRESS NLRTSSSYTR RKWEDDLKKN SSINEGSTYH RSTSNRLWAE
561    DSTEKEKDSA PTAATILVAP TVVSAASST TALTTTTAGT LSSTSEVRER RRSYLTPVRD ESESQEKAR SRQARQSRRS
641    TQGVTLTDLQ EAERTIGRSR STRTREQENE EKDKKEEKQ DKEKQEEKKE SEVSREDEYK QKYSRTYDET YARYRPVSTS
721    SSSTPSSSSL STLGSSLYAS SQLNRPNSLV GITSAYSRLG TKDNEREGEK KEEKEGEDK SQPKSIRERR RPREKRRSTG
801    VSFWTQDSDE NEQERQSDTE DGSSKRDTQT DSVSRDYDSS TSSSDRYDSL LGRSASYSYL EERKPYGSRL EKDDSTDFKK
881    LYEQILAENE KLKQLHDTN MELTDLKLQL EKATQRQERF ADRSLEMEK RRRALERRI SEMEELKML PDLKADNQR
961    KDENGALIRV ISKLSK
  
```



5.828 cystatin C [Rattus norvegicus]

Protein Accession	gij 54234046
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.802, 1.31)
Associated Peptides	2
Associated Spectra	3
Coverage	0.25
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.06
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	1.17

1 MASPLRSLML LLAVLAVAWA GTSRPPRLL **GAPQEADASE** **EGVQFALDFA** VSEYNKGSND AYHSRAIQVV RARKQLVAGI
 81 NYYLDVEMGR TTCT**SQTNL** **TNCPFHDQPH** **LMK**KALCSFQ IYSVPWKGTH TLTKSSCKNA



5.829 rapostlin [Rattus norvegicus]

Protein Accession	gij 20302117
Mean Expression Ratio	0.98
Median Expression Ratio	0.978
Credible Interval	(0.729, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0242
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.16
Avg..iTRAQ.Ratio....116.114.	0.892
Avg..iTRAQ.Ratio....117.114.	1.03

1 MSWGT**ELWDQ** FDNLEKHTQW GIDILEKYIK FVKERTEIEL SYAKQLRNLS KKYQPKNSK EEEYKYTAC KAF**LSTL**NEL
 81 NDYAGQHEVI SENM**TSQITV** DLVRYVQELK QERKSNFHDG RKAQQHIETC WKQLESSKRR FERDC**KEADR** AQQVFEKMDA
 161 DINVT**KADVE** KARQQAQMRQ QMAEDSKADY SLILQRFNQE QWEYHHTHIP NIFQKIQEME ERRIVRIGES MK**TYAEVDRQ**
 241 **VIP**IGKCLD GIVKAAESID QKND**SQ**LVVE AYKSGFEPFG D**IE**FEDYTQP MKR**TVSD**NSL SSSKEGKPEL KFGGKSRGKL
 321 WPF**IK**KNKLM TLLTSPHQPP P**PP**PASASPS AVPNGPQSPK Q**Q**KEPLSHRF NEFMTSKPKI HCFRSLK**RGL** SLKLG**VP**ED
 401 FSNFP**PE**QRR KKLQ**Q**KVDDL NKEIQ**K**ETDQ RDAIT**K**MKD**V** YLKNP**Q**MGDP ASLDH**K**LAEV TQ**NI**EKL**R**LE AHK**F**EAWLAE
 481 VEGRL**P**ARSE QARR**S**GLYD GQ**T**HQ**T**VTNC A**Q**DRE**S**PDGS Y**T**EE**S**Q**S**ESE HKV**L**AT**D**FD**D** E**F**DDE**E**LP**A** I**G**T**C**KALY**T**F
 561 EGQ**NE**GTISV VE**G**ETLSVIE EDKGD**G**W**T**RI RR**NE**DEEGYV P**T**SYVEVYLD K**NA**K**G**AKTYI



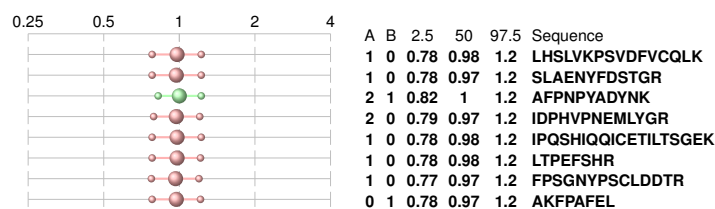
5.830 LanC-like 1 [Rattus norvegicus]

Protein Accession	gij 39930499
Mean Expression Ratio	0.978

Median Expression Ratio	0.978	
Credible Interval	(0.833, 1.15)	
Associated Peptides	8	
Associated Spectra	11	
Coverage	0.253	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1	1.03
Avg..iTRAQ.Ratio....116.114.	1.16	1.03
Avg..iTRAQ.Ratio....117.114.	0.888	0.741

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1   MAQRAFPNPY ADYNSLAEN YFDSTGRLTP EFSHRLTNKI RELLQQMERG LKSADPQDGT GYTGWAGIAY LYLHLHNVFG
81  DPAYLQMAHS YVKHSLNCLS RRSITFLCGD AGPLAVA AVL YHKMNSGKQA EDCITRLIHL NKIDPHVPNE MLYGRIGYIF
161 ALLFVNKNFG EEKIPQSHIQ QICEIILTSG ELSRKRNFT TKSPLMYEWY QEYVVGAAHG LAGIYYLMQ PSLHVSQGKL
241 HSLVKPSVDF VCQLKPPSGN YPSCLDLTR LLVHWCHGAP GVIYMLIQAY KVFKEEHYLC DAQQCADVIW QYGLLKKGYG
321 LCHGAAGNAY AFLALYNLTQ DAKYLYRACK FAEWCLDYGE HGCRTPDTPF SLFEGMAGTI YFLADLLVPT KAKFPAPEL
    
```



5.831 cathepsin H [Rattus norvegicus]

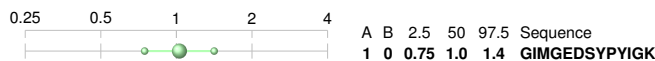
Protein Accession	gij 6978721
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.758, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0390
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.22
Avg..iTRAQ.Ratio....116.114.	0.966
Avg..iTRAQ.Ratio....117.114.	1.15

NHLBI Zile/Grant, Aged Rat

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1      MWTALPLLCA GAWLLSAGAT AELTVNAIEK FHFTSWMKQH QKTYSSREYS HRLQVFANNW RKIQAHNQRN HTFKMGLNQF
81     SDMSFAEIKH KYLWSEPQNC SATKSNYLRG TGPYPSSMDW RKKGNVVSFV KNQGACGSCW TFSTTGALES AVAIASGKMM
161    TLAEQQLVDC AQNFNNHGCQ GGLPSQAFEY ILYNKGIMGE DSYPIYIGNG QCKFNPEKAV AFVKNVNVIT LNDEAAMVEA
241    VALYNPVSFA FEVTEDFMMY KSGVYSSNSC HKTDPKVNHA VLAVGYGQN GLLYWIVKNS WGSNWNNGY FLIERGKNMC
321    GLAACASYPI PQV

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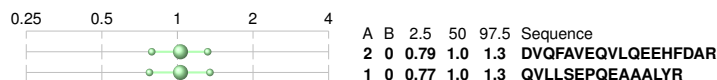
5.832 n-acylaminoacyl-peptide hydrolase [Rattus norvegicus]

Protein Accession	gij 6978513
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.8, 1.30)
Associated Peptides	2
Associated Spectra	3
Coverage	0.0451
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.17
Avg..iTRAQ.Ratio....116.114.	1.18
Avg..iTRAQ.Ratio....117.114.	0.953

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1      MERQVLLSEP QEAAALYRGL SRQPSLSAAC LGPEVTTQYG GLYRTVHTEW TQRDLERMEN IRFCRQYLVF HDGDSVVFAG
81     PAGNSVETRG ELLSRESPSG TMKAVLRKAG GTVSGEEKQF LEVWEKNRKL KSFNLSALEK HGPVYEDDCF GCLSWSHSET
161    HLLYVAEKRR PKAESFFQTK ALDISASDDE MARPKKPDQA IKGDQFVFYE DWGETMVSXS IPVLCVLDID SGNISVLEGV
241    PENVSPGQAF WAPGDTGVVF VGVVHPEPRL GIRYCTNRRS ALYYVDLGG KCELLSDGSL AICSPRLSPD QCRIVYLQYP
321    CLAPHHQCSQ LCLYDWTYKV TSVVVDIVPR QLGESFSGIY CSLLPLGCWS ADSQRVVFDS AQRSRQDLFA VDTQTGSITS
401    LTAAGSAGSW KLLTIDKDLM VAQFSTPSLP PSLKVGFLPP PGKEQSVSWV SLEEAEP IPIG IHWGVRLHP PPDQENVQYA
481    DLDFEAILLQ PSNPFDKTQV PMVVMFHGGP HSSFVTAWML FPAMLCKMGF AVLLVNYRGS TGFQDLSILS LPGNVGHQDV
561    KDVQFAVEQV LOEBHFDAFR VALMGGSHGG FLSCHLIGQY PETYSACIAR NPVINIASMM GSTDIPDPCM VETGFPYSNS
641    CLPDLNWEE MLDKSPIKIYI PQVKTPVLLM LGQEDRRVVF KQGMYYRAL KARNVPVRL LYPKSNHALS EVEAESDSFM
721    NAVLWLHHTL GS

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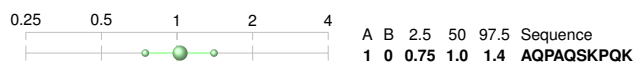
5.833 PDZ and LIM domain 7 [Rattus norvegicus]

Protein Accession	gij 27465579
Mean Expression Ratio	1.02

Median Expression Ratio	1.02
Credible Interval	(0.759, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0219
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.29
Avg..iTRAQ.Ratio....116.114.	0.816
Avg..iTRAQ.Ratio....117.114.	1.56

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1      MDSFKVILEG PWPWFRLQG GKDFNVPLSI SRLTPGGKAA QAGVAVGDWV LSIDGENAGS LTHIEAQNKI RACGERLSLG
81     LSRAQPAQSK PQKALTTPAD PPRYTFAPSA SLNKTARFFG APPPTDSALS QNGQLLRQLV PDASKQRLME NTEDWRPRPG
161    TGQSRFRIL AHLTGTEFMQ DPDEEFMKKS SQVPRTEAPA PASTIPQESW PGPTTPSPPTS RPPWAVDPAF AERYAPDKTS
241    TVLTRHSQPA TPTPLQNRIS IVQAAAGGGT GGGSNNGKTP VCHQCHKIIR GRYLVALGHA YHPEEFVCSQ CGKVLLEGGF
321    FEEKGAIFCP SCYDVRYAPS CAKCKKITG EIMHALKMTW HVPCFTCAAC KTFIRNRAFV MEEGAPY CER DYKMFQGTGK
401    RGCDFKIDAG DRFLEALGFS WHDTCFVCAI CQINLEKTF YSKKDKPLCK SHAFSHV
  
```



5.834 PREDICTED: similar to LIM domain only protein 7 [Rattus norvegicus]

Protein Accession	gij109500591
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.752, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0122
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.26
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	1.20

NHLBI Zile/Grant, Aged Rat

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1      MDVTCPNHQP KLECAEGPSE LDPSVVVMVM VGNLIQASGL GKKISYCTSA DAKQELKCTA GVGECLWTKL GEGTERRARA
81     TLAEVATVSS GSARRCPQGP ALGGGGEDGW RARRAGRGE RAPAEDAVLI PAAERFSTRR ASQMACPALG LEVLQPLQPE
161    PPPEPAFAEA QKWIEQVTGR SFGDKDFRTG LENGILLCEL LNAIKPGLVK KINRLFTPIA GLDNTILFLR GCKELGLKES
241    QLFDPDLQD TSNRVTVKNF DYSRKLNVL VTIYWLKAA NSCTSYSGTT LNLKEFEGLL AQMRKETDDI ESPKRSIRDS
321    GYIDCWDSESR SDSLSPRRHG RDDSFDSLDS FGSRSRQTPS PDVVLRGSSD GRGSDSESDL PHRKLDPVKK DDMARRTSH
401    GEPKSAVFPN QYLPNKSQNT AYVPAPLRKK KAEREERYKS WSTATSPLOG ERPFYRGPRT PVSDDAESTS MFDMRCEEEA
481    AVLPHSRARQ EQLQLINNQL REEDDKWQDD LARWKSRRRS ASQDLIKKEE ERKKMEKLMs GEDGTSERRK SIKTYREIVQ
561    EKERRERELH EAYKNARSGE EAEGILQQYI ERF TISEAVL ERLEMPKILE RSHSTEPNVs SFPNDPSPMK YLRQQSLPPP
641    KFTATVETTI ARTSVPESSV AAGTGSFSKT STPNTVPMLT PRPYSQPKNS QEVLKTFFKVD GKVSMNGETA RGDVEGKEKE
721    DPTAVAPGPS LTKSQMFEGV ATVHGSPVQV KQGSNSIEIN IKKPNSPQQE LTAASEETES NGRDDENGEE SSGARDVELD
801    SAE PQHFTTT VTRCSPTVAL VEFSSSPQLR NEVPEEQDQK KPENEMSGKV ELVLSQKVAK PKSPEPEATL TFPFLDKMPE
881    TDQLHLPLNL SQADSPSSEK SPASTPFKFW AWDPEEERRR QEKWQQEQER LLQERYQKEQ DKLKEEWEKA QKEVEEEERR
961    YEEERKIEE DTVPFTISS SSADQLSTSS SVTEGSGTRN KMDLENCQDR DKERRQNTPL QENDSDSSLK ARESGLPEEH
1041   SSSLTQPSAN SENSVSKGIS QDQQPETEAE ASHCGTNPQS AQDPPWNQOI SNPPTSXSSED VKPKTLALEK SINHQIESPG
1121   ERRKKSREN FRAGLSPSCS PTFPGQSPNR SISGKKLCSS CGLALGKGA MIIETLNLYF HIQCFCRCIC KGQLGDAVSG
1201   TDVIRINGLL NCTDCYMRSR SAGQPTTL

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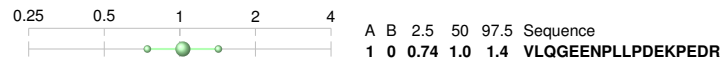
5.835 ADP-ribosyltransferase 3 [Rattus norvegicus]

Protein Accession	gi 58865636
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.754, 1.39)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0481
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.21
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.24

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1      MKMGHFELVT TLLAAMVLM DVFQVQAEVLD MAENVFDEY LKCN SRMEMK YIPRMHGEEL ANDELLQSVW DKAGIQWEAQ
81     KAQLSLPKNF KDAYGIALTA YVTEAQDQSP FYHTFNRAVK IAGLSRRRYI YNFPFKAFHF YLVRALQLLR RPCEESYKNV
161    VYSTSPNISF AFGEQNQARL GNFTLAYS AKPQTANEQRLL TIQTCFGVAV GKLLNKESEG IVLIPLSEVF QVSRKGTDDD
241    LILHSINSTC SYECSFLGG LKAGSCTTNP ENPDPGYLN NPDLD SQKLED SGRKSLDSVK MPEIKVLQGE ENPLLPDEKP
321    EDNRGRKANV PTPGLVVPFG PKSHPSSSSG HRLLPSTAS TILLIAAAVD FIAL

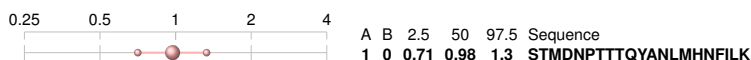
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5.836 "dynein, cytoplasmic, light chain 2A [Rattus norvegicus]"

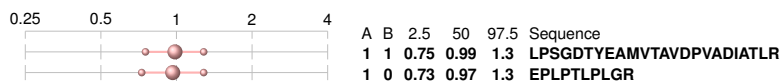
Protein Accession	gij18777767
Mean Expression Ratio	0.98
Median Expression Ratio	0.978
Credible Interval	(0.735, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.219
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.899
Avg..iTRAQ.Ratio....116.114.	0.973
Avg..iTRAQ.Ratio....117.114.	1.22

1 MAEVEETLKR LQSQKGVQGI IVVNTTEGIPI KSTMDNPTTT QYANLMHNF I LKARSTVREI DPQNDLTFLR IRSKKNEIMV
 81 APDKDYFLIV IQNPTE



5.837 "PREDICTED: similar to Serine protease HTRA2, mitochondrial precursor (High temperature requirement "

Protein Accession	gij109473705	
Mean Expression Ratio	0.978	
Median Expression Ratio	0.979	
Credible Interval	(0.765, 1.26)	
Associated Peptides	2	
Associated Spectra	3	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.872	1.96
Avg..iTRAQ.Ratio....116.114.	0.995	0.635
Avg..iTRAQ.Ratio....117.114.	0.927	1.12



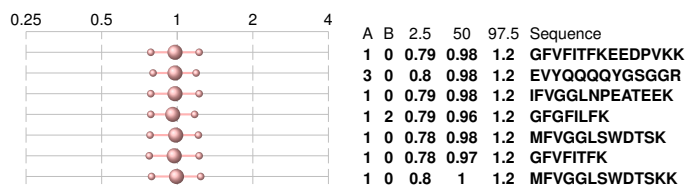
5.838 PREDICTED: similar to Delta-sarcoglycan (SG-delta) (35 kDa dystrophin-associated glycoprotein) (35D)

Protein Accession	gij109490601
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.75, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.04
Avg..iTRAQ.Ratio....116.114.	1.14
Avg..iTRAQ.Ratio....117.114.	1.30



5.839 heterogeneous nuclear ribonucleoprotein A/B [Rattus norvegicus]

Protein Accession	gij13786156	
Mean Expression Ratio	0.978	
Median Expression Ratio	0.979	
Credible Interval	(0.826, 1.15)	
Associated Peptides	7	
Associated Spectra	11	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.984	0.84
Avg..iTRAQ.Ratio....116.114.	1.04	0.957
Avg..iTRAQ.Ratio....117.114.	1.00	0.817

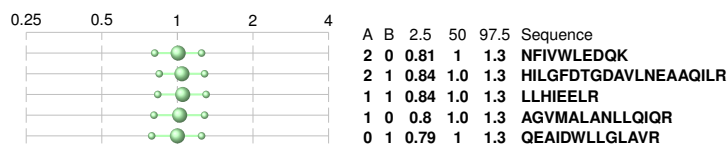


5.840 hypothetical protein LOC302247 [Rattus norvegicus]

Protein Accession	gi 114145722	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.858, 1.22)	
Associated Peptides	5	
Associated Spectra	9	
Coverage	0.220	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.995	1.17
Avg..iTRAQ.Ratio....116.114.	0.987	1.23
Avg..iTRAQ.Ratio....117.114.	0.979	1.01

```

1      MFRRKLTALD YHNPTGFNCK ARLNQDPNTA AAARRRSARF PARRRLSGHL LGQQDETEFR NFIVWLEDQK IRHYKIEDRG
81     NLRNIHSSDW PKFFEKYLDR VNCPPFKIQDR QEAI DWLLGL AVRL EYGDNA IDVLLLESEAF EFGARGKAEK YKDSVPDNRK
161    NADNAAKNSE PLINLDVNNP DFKAGVMALA NLLQIQI HDD YLVMLKAI RI LVQERLTQDA VAKANQMKEG LPVALDK HIL
241    GFDTGDAVLN EAAQILRL LH IEEL ELQTK INEAI VAVQA IIADEKTDHR LGKVGR
    
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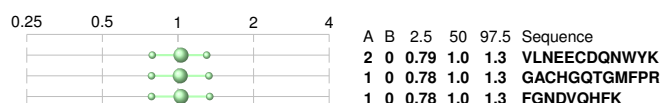
5.841 growth factor receptor bound protein 2 [Rattus norvegicus]

Protein Accession	gi 77539774	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.807, 1.28)	

Associated Peptides	3
Associated Spectra	4
Coverage	0.152
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	1.08

```

1      MEAIAKYDFK ATADDELSFK RGDILKVLNE ECDONWYKAE LNGKDGFIK NYIEMKPHPW FFGKIPRAKA EEMLSKQRHD
81     GAFLIRESES APGDFSLSVK FGNDVQHFV LRDGAGKYFL WVKFNSLNE LVDYHRSTSV SRNQQIFLRD IEQVPQQPTY
161    VQALFDFDPQ EDGELGFRRG DFIVMDNSD PNWWKGACHG QTGMFFRNYV TPNVNRNV
  
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5.842 peroxisome biogenesis factor 7 [Rattus norvegicus]

Protein Accession	gi 77628037
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.764, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.044
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.15
Avg..iTRAQ.Ratio....116.114.	1.18
Avg..iTRAQ.Ratio....117.114.	0.985

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1      MSAARTLRVP GRHGYAVEFS PYLPGFLACA AAQHYGIAGC GTLLVLDQNE SGLQIFRSFD WNDGLFDVTW SENNEHVLVT
81     CSGDGSLQLW DTAKATGPLQ VYKEHTQEVY SVDWSQTRDE QLVVSGSWDQ TVKVVDPTVG NSLCTFRGHE SVIYSTIWS
161    HIPGCFASAS GDQTLRIWDV KTTGVRIVIP AHQAEILSCD WCKYNENLLV TGAVDCSLRG WDLRNVRQPV FELLGHTYAI
241    RRVKFSFPHA SVLASCSYDF TVRFWNFSKP DPLETVEHH TEFTCGLDLS LQSPTEVADC SWDET VKIYN PVCLAVPG
  
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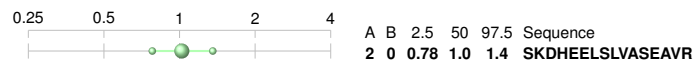


5.843 carboxypeptidase B2 (plasma) [Rattus norvegicus]

Protein Accession	gi 16758414
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.784, 1.34)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0379
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	1.10
Avg..iTRAQ.Ratio....117.114.	1.15

```

1      MKLYGLGLV  AIILYEKHGL  AFQSGHVLSA  LPRTSRQVQL  LQNLTTTYEV  VLWQPVTAEF  IEKKKEVHFF  VNASDVNSVK
81     AYLNASRIPF  NVLMNVEDL  IQQQTSDNTV  SPRASSSYE  QYHSLNEIYS  WIEVITEQHP  DMLQKIYIGS  SYEKYPLYVL
161    KVSGKEHRVK  NAIWIDCGIH  AREWISPAFC  LWFIGYVTF  HGKENTYTRL  LRHVDFYIMP  VMNVDGYDYT  WKKNRMWRKN
241    RSVHMNNRCV  GTDLNRFAS  KHWCEKGASS  FSCSETYCGL  YPESEPEVKA  VADFLRRNIN  HIKAYISMHS  YSQQILFPYS
321    YNRSKSKDHE  ELSLVASEAV  AIESINKNT  RYTHGSGSES  LYLAPGGSD  WIYDLGIKYS  FTIELRDTGR  YGFLPERFI
401    KPTCAEALAA  VSKIAHWVIR  NS
  
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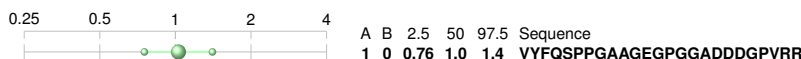


5.844 "protein phosphatase 1, regulatory (inhibitor) subunit 14B [Rattus norvegicus]"

Protein Accession	gi 25282423
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.764, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	0.17
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.44
Avg..iTRAQ.Ratio....116.114.	1.01
Avg..iTRAQ.Ratio....117.114.	1.22

NHLBI Zile/Grant, Aged Rat

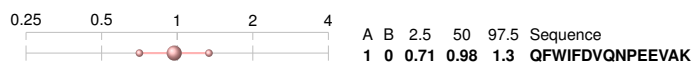
1 MADSGPAGGA ALAAPAPGPG SGSTGPRVYF QSPFGAAGEG PGGADDDGPV RFQGGKVTVKY DRKELRKRLN LEEWILEQLT
 81 RLYDCQEIII PELEIDVDEL LDMESDDTRA ARVKELLVDC YKPTEAFISG LLDKIRGMQK LSTPQKK



5.845 CD36 antigen [Rattus norvegicus]

Protein Accession	gij48675379
Mean Expression Ratio	0.98
Median Expression Ratio	0.98
Credible Interval	(0.73, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0318
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.973
Avg..iTRAQ.Ratio....116.114.	0.976
Avg..iTRAQ.Ratio....117.114.	0.895

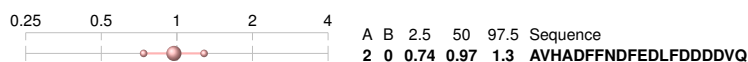
1 MGCDRNCGLI TGAVIGAVLA VFGGILMPVG DLLIEKTIKR EVVLEEGTIA FKNWVKTGTT VYRQFWIFDV QNPEEVAIENS
 81 SKIKVKQRGP YTYRVRYLAK ENITQDPKDS TVSFVQPNGA IFEPSLSVGT ENDNFTVLNL AVAAAPHIYT NSFVQGVLSN
 161 LIKRSKSSMF QTRSLKELLW GYKDPFLSLV PYPISITTVGV FYPYNTVDG VYKVFNGKDN ISKVAIIDTY KGRNLSYWE
 241 SYCDMINGTD AASFPPFVEK SRTLRFSSD ICRSIYAVFG SEVNLKGIPV YRFVLPANAF ASPLQNPDNH CFCTEKVISN
 321 NCTSYGVLDI GKCKEGKPVY ISLPHFLHAS PDVSEPIEGL NPNEDEHRTY LDVEPIGTFT LQFAKRLQVN ILVKPARKIE
 401 ALNLRKRPYI VPILWLNETG TIGDEKAEMF RNQVTGRIKL LGLVEMVLLG VGVVMEVAFM ISYCACRSKN GK



5.846 PREDICTED: similar to CG17059-PA [Rattus norvegicus]

Protein Accession	gij109486386
Mean Expression Ratio	0.978
Median Expression Ratio	0.98
Credible Interval	(0.745, 1.28)
Associated Peptides	1
Associated Spectra	2

Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.92
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	1.05

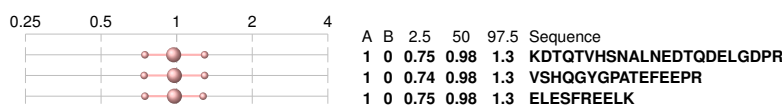


5.847 PREDICTED: similar to Alpha-2-macroglobulin receptor-associated protein precursor (Alpha-2-MRAP) (L

Protein Accession	gij109499860
Mean Expression Ratio	0.98
Median Expression Ratio	0.98
Credible Interval	(0.771, 1.24)
Associated Peptides	3
Associated Spectra	3
Coverage	0.136
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.924
Avg..iTRAQ.Ratio....116.114.	0.992
Avg..iTRAQ.Ratio....117.114.	1.13

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1   MAPLRDRVST LPRLQLLVLL LPPLLLVPPQ IAGHGGKYSR EKNEPEMAAK RESGEEFRME KLNQLWEKAK RLHLSPVRLA
81  ELHSDLKIQE RDELNWKLLK VEGLDGDGK EAKLVHNLNV ILARYGLDGR KDTQTVHSNA LNEDTQDELG DPRLEKLWHK
161 AKTSGKFSSE ELDKLWREFL HYKEKIH EYN VLLDTL SRAE EGYENLLSPS DMTHIKSDTL ASKHSELKDR LRSINQGLDR
241 LRKVSHQGYG PATEFEEPEV IDLWDLA QSA NFTEK ELESF REELKHFEAK IEKHNHYQKQ LEISHQK LKH VESIGDPEHI
321 SRNKEKYVLL EEKTKELGYK VKKHLQDLSS RVSRRARHNEL
  
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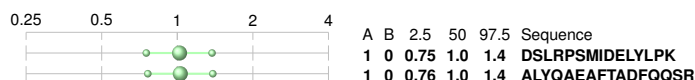


5.848 serine protease inhibitor 2c [Rattus norvegicus]

Protein Accession	gi 13928716
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.783, 1.34)
Associated Peptides	2
Associated Spectra	2
Coverage	0.076
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.12
Avg..iTRAQ.Ratio....116.114.	0.922
Avg..iTRAQ.Ratio....117.114.	1.22

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1   MDGIGSALLS  FPDCILGEDT  LFHEDQDKGT  QLDSLTLASI  NTDFAFSLYK  KLALRNPHKN  VVFSPLSISA  ALAVVSLGAK
81  GSSMEEILEG  LKFNLTTETPE  TEIHRGFGHL  LQRLSQPRDE  IQISTGNALF  IEKRLQVLAE  FQEKAKALYQ  ABAPTADFQQ
161 SEAKKLIND  YVSKQTQGKI  QGLITNLAKK  TSMVLVNYIY  FKGKWKVPFD  PRDTFQSEFY  SGKRRSVKVP  MMKLEDLTFP
241 YVRDEELNCT  VVELKYTGNA  SALFILPDQG  KMQQVEASLQ  PETLRRWKDS  LRPSMIDELY  LPKFSISADY  NLEDVLPPLG
321 IKEVFSTQAD  LSGITGDKDL  MVFQVVHKAV  LDVAETGTEA  AAATGVKFFV  MSAKLDPLII  AFDRPFLMII  SDTETAIAPF
401 LAKIFNPK
    
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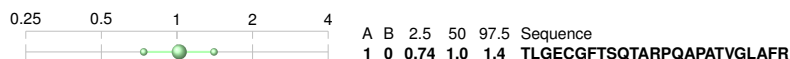


5.849 "transcription elongation factor B (SIII), polypeptide 2 [Rattus norvegicus]"

Protein Accession	gi 13592105
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.754, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.212
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.33
Avg..iTRAQ.Ratio....116.114.	1.08
Avg..iTRAQ.Ratio....117.114.	1.17

NHLBI Zile/Grant, Aged Rat

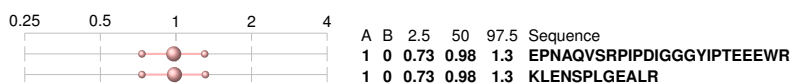
1 MDVFLMIRRH KTTIFDAKE SSTVFELKRI VEGILKRPE EQRLYKDDQL LDDGK¹LGEC GFTSQ²TAR³PQ⁴ APATVGLA⁵FR
 81 ADDTFEALRI E⁶FFSSPE⁷LP⁸ DVMKPQDSGG SANEQAVQ



5.850 OCIA domain containing 1 [Rattus norvegicus]

Protein Accession	gi 62078483
Mean Expression Ratio	0.981
Median Expression Ratio	0.98
Credible Interval	(0.751, 1.27)
Associated Peptides	2
Associated Spectra	2
Coverage	0.150
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.923
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	1.03

1 MNGRADFR¹EP² NAQVSR³PI⁴P⁵D⁶ IGGGYI⁷P⁸TEE⁹ E¹⁰W¹¹L¹²FAE¹³CHE¹⁴ ECFW¹⁵FRSV¹⁶PL¹⁷ AAT¹⁸SMLIT¹⁹Q²⁰ LISK²¹GILSSH²² PKYGSIP²³KLI²⁴
 81 FACIVGYFAG KLSYVKTCQE KFK¹LE²NS³PL⁴ GEAL⁵RS⁶GELR⁷ RSLPPGHYTQ KPKYDSNVSG QSSF⁸GTSPAA⁹ DNIEK¹⁰ETL¹¹PR¹²
 161 YEPI¹FFS²ASM³ NESTPTG⁴ITD⁵ HIAQ⁶GPDP⁷NL⁸ EDS⁹PKR¹⁰RS¹¹VT¹² YEEL¹³R¹⁴N¹⁵KN¹⁶RE¹⁷ SYG¹⁸VTLS¹⁹H²⁰KT²¹ DPS²²VR²³PM²⁴QER²⁵ GPQ²⁶RE²⁷V²⁸K²⁹V³⁰NK³¹
 241 YGDTWDE



5.851 PREDICTED: similar to ubiquinol-cytochrome c reductase complex 7.2kDa protein isoform a [Rattus nor]

Protein Accession	gi 109500943
Mean Expression Ratio	0.98
Median Expression Ratio	0.98
Credible Interval	(0.729, 1.31)
Associated Peptides	1
Associated Spectra	1

Coverage	0.266
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.986
Avg..iTRAQ.Ratio....116.114.	0.972
Avg..iTRAQ.Ratio....117.114.	0.851

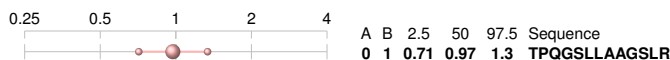
1 MASPTVTSRL YSLLFRRTST FALTIASVAL FFERAFDQGA DAVYDYINEG K LWKHIKHKY EKQE



5.852 PREDICTED: similar to DDHD domain containing 2 [Rattus norvegicus]

Protein Accession	gij109503511
Mean Expression Ratio	0.98
Median Expression Ratio	0.98
Credible Interval	(0.73, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0153
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.05
Avg..iTRAQ.Ratio....116.114.	0.99
Avg..iTRAQ.Ratio....117.114.	0.579

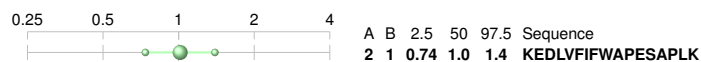
1 MVQLILSDRP FSHPSPAHRV LTGPTRGQDV RLPSRKHRFL VGPDTSSSQL LPQSLSPPTA TRVLPTPPAR ARRVPGGRRLL
 81 PAGGATSRAS PPHISRHFGR SSCASGPEPG ERTPQGSLLA AGSLRSPWCG IGARPQAPPV CPFRPAWESE MSSGESYQEQ
 161 LSQSDPSPSP NSSSSFELLD MDVGSSYEPV SPHWFYCKVI DSKELEWIPFN SEDSQLEEA HGSKDCNER VVPTDGGRYD
 241 VHLGERMRYA VYWDELPSV RRCTWFYKGD KDNKYVPYSE SFSQVLEDY MLAVTLDEWK KKLESPNREI IVLHNPKLMV
 321 HYQPITGSDE WGSTSTEQGR PRSVKRGVES IPVDIHCGEF LQIDHLVFFV HGIGPACDLR FRSIVQCVND FRVSLNLLQ
 401 THFKKAQENQ QIGRVEFLPV NWHSPHSTG VDIDLQRITL PSINLRHFT NDTILDVFFY NSPTYCQTV DTVASEMNRI
 481 YTLFLQRNPD FKGGVSIAGH SLGSLILFDI LTNQKDSIGD IDSEKGSLSL AEDLDGVSTL EEELKKLQLS EFVTVFEKEK
 561 VDREALALCT DRDLQEMGIP LGPRKKILNH FSATKSSVGI NRPTMSASEV NIPKEKGDYL DVGIGQVSVK YPRLNYPKEI
 641 FFAFGSPIGM FLTVRGLRRI DPNYKFPTCK GFFNIYHFFD PVAYRIEPMV VPGVEFEPML IPHHKGRSSL FTHISELREG
 721 LTRMSMDLKN NLLGSLRMAW KSFTRAPYPA LQASEMAEDT EAASEPSSSEK PSDANTEPP VEVKEEAPIN VGMLNGGQRI
 801 DYVLQEKPIE SFNEYLFALQ SHLCYWESED TVLLVLKEIY QTQGIPLDQP LQ



5.853 cofilin 1 [Rattus norvegicus]

Protein Accession	gi 8393101
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.755, 1.37)
Associated Peptides	1
Associated Spectra	3
Coverage	0.102
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.99
Avg..iTRAQ.Ratio....116.114.	1.88
Avg..iTRAQ.Ratio....117.114.	0.613

1 MASGVAVSDG VIKVFNDMKV RKSSTPEEVK KRKKAVLFCL SEDKKNILE EGKEILVGDV GQTVDDPYTT FVKMLPDKDC
 81 RYALYDATYE TKESK**KEDLV FIFWAPESAP** LKSKMIYASS KDAIKKKLTG IKHELQANCY EEVKDRCTLA EKLGGSAVIS
 161 LEGKPL



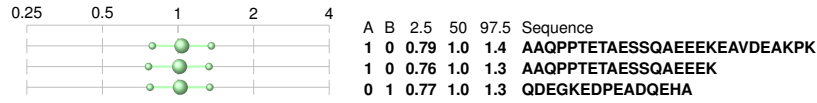
5.854 growth associated protein 43 [Rattus norvegicus]

Protein Accession	gi 8393415	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.805, 1.3)	
Associated Peptides	3	
Associated Spectra	3	
Coverage	0.186	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.46	0.84
Avg..iTRAQ.Ratio....116.114.	1.01	0.709
Avg..iTRAQ.Ratio....117.114.	1	1.11

NHLBI Zile/Grant, Aged Rat

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1      MLCCMRRTKQ VEKNDDEDQKI EQDGVKPEDK AHKAATKIQA SFRGHITRKK LKDEKKGDAP AAEAEAKEKD DAPVADGVEK
81     KEGDGSATTD AAPATSPKAE EPSKAGDAPS EEKKGEGDAA PSEKAGSAE TESAAKATTD NSPSSKAEDG PAKEEPKQAD
161    VPAAVTDAAA TTPAEDAAB AAQPPTETA E SSQAEEEEKA VDEAKPKESA RQDEGKEDPE ADQEHA
  
```



5.855 lipoiic acid synthetase [Rattus norvegicus]

Protein Accession	gi 58865650
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.783, 1.33)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0402
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.17
Avg..iTRAQ.Ratio....116.114.	1.27
Avg..iTRAQ.Ratio....117.114.	1.00

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1      MALRCWDAAR SLGSRIFGRY ACSVRALSSL PDEKKKFLHN GPDLQDFVSG DLADKSTWDD YKGNLKRQKG ERLRLPPWLK
81     TKIPMGKNYN KLKNTLRNLN LHTVCEEARC PNIGECWGGG EYATATATIM LMGDTCTRGC RFCVKTARN PPPLDPSEPD
161    NTAFAIAEWG LDYVVLTSVD RDDVVDGGAE HIAKTVSCLK ERNPKILVEC LTPDFRGDLR AVEKVALSGL DVYAHNVETV
241    FELQRKVRDP RANFDQSLRV LKHAKEVQPD VVSKTSMIG LGETDEQVYA TMKALRAADV DCLTLGQYMQ PTKRHLKVEE
321    YVTPEKFKYW EEVGNELGFH YTASGPLVRS SYKAGEFFLK NLVAKRRTKV SKV
  
```



5.856 "PREDICTED: similar to coronin, actin binding protein, 2B [Rattus norvegicus]"

Protein Accession	gi 109483534
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.753, 1.38)

Associated Peptides	1
Associated Spectra	1
Coverage	0.0208
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.18
Avg..iTRAQ.Ratio....116.114.	0.864
Avg..iTRAQ.Ratio....117.114.	1.37

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1      MTVTKMSWRP QYRSSKFRNV YGKVANREHC FDGIPITKNV HDNHFCAVNA RFLAIVTESA GGGSFVLIPL EQTGRIEPNY
81     PKVCGHQGNV LDIKWNPFID NIIASCSEDV SVRIWEIPEG GLLRNMTEAL LELHGHSRRV GLVEWHPTTN NILFSAGYDY
161    KVLINWLDIG EPVKMIDCHT DVILCMSFNT DGSLLTTTCK DKKLRVIEPR SGRVLQEANC KNHRVNRVVF LGNMKRLTTT
241    GVSRWNTRQI ALWDQEDLSM PMIEEEDGL SGLLFFPYDA DTHMLYLAGK GDGNIRYYEI STEKPYLSYL MEFRRSPAPQK
321    GLGVMPKHGL DVSACEVFRF YKLVTLKGLI EPISMIVPRR SDSYQEDIYP MTPGTEPALT PDEWLGGVNR DPVLMSLKEG
401    YKSSKVVFK APIREKKSUV VNGIDLLENV PPRTENELLR MFFRQQDEIR RLKEELAQKD IRLRQLQLEL KNLRNNPKNC
  
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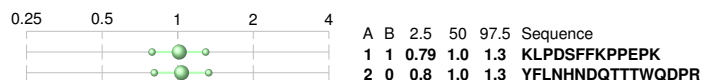


5.857 yes-associated protein [Rattus norvegicus]

Protein Accession	gj 85540438	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.815, 1.29)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.0792	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.07	0.811
Avg..iTRAQ.Ratio....116.114.	1.04	1.07
Avg..iTRAQ.Ratio....117.114.	1.10	1.39

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1      MEPAQQPPPO PAPAQGPAPPS VSPAGTPAAP PAPPAGHQVV HVRGDSETDL EALFNAVMPN KTANVPQTVP MRLRKLPDSF
81     FKPPEPK SHS RQASTDAGTA GALTPQHVR HSSPASLQLG AGTLTASGVV SGPAATPAAQ HLRQSSFEIP DDVPLPAGWE
161    MAKTSSGQRY FLNHNDQTTT WQDPPKAMLS QLNVPYSASP AVPQTLMNVA SGPLPDGWEQ AMTQDGEVYY INHKNKTTSW
241    LDPRLDPRFA MNQRITQSAP VKQPPPLAPQ SPQGGVVGSG SSNQQQIQL QQLQMEKERL RLKQQLFRQ AIRNINPSTA
321    NAPKCQTVRA GISSPPQVAL TGAGWRDSEC SVFSRDDSGI EDNDNQ
  
```



5.858 PREDICTED: similar to desmoglein 2 [Rattus norvegicus]

Protein Accession	gij109506355
Mean Expression Ratio	0.98
Median Expression Ratio	0.98
Credible Interval	(0.73, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0118
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	0.965
Avg..iTRAQ.Ratio....117.114.	0.874

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1      MKQPEKLQTG RIGPQRPVSR KLCKGGDPGG GGDTSGRGQP PKVPCGGRHR PQVRRAGTAS HLLAERALSP PPSRLRPGSR
81     LPFLTRPHLE PHPGPGGGGE GRPRERPGPE DRRDSGKARR QGRGEARRWR GARAAGAPYC CCCSCWRWCS QGSKAVQQVC
161    LDFGDGLHLE VFSTRGEDRL FTKRTHLVRQ KRAWITAPVA LREGEDLSKK NPIAKIHSDL AEERGIKITY KYTGKGITEP
241    PFGIFVFDNR TGDNLNITSIL DREETPFLLL TGYALDSRGN NLEKPLELRI KVLNDINDNEP VFTQEVFVGS IEELSAAHTL
321    VMKITATDAD DPQTLNSKIS YRIVSQEPAN TPVFYLNKDT GEIYTTSFAL DREEHSSYSL TVEARDGNGQ ITDKPVQQAQ
401    VQIRILDVND NIPVVEYGTY EGVVEENQVN VEVMRIKVTD ADEVGSDNWL ANFTFASGNE GGYFHIEDTD QTNEGIVTLV
481    KELDYEMMKK LDLSILVTNK AAFHKSVVSK YKATPIPIV KVKNVVEGHI FKSSVTTFRA SEAMDRSSLS RSIKGFQVFD
561    EDTGKAADVY YVKVQDNDNW VSDVSETSEI KLVKIPDFES RHVQNGTYTV KVVVASKGHP QKTVTGTILI NVEDVNDNCP
641    VLVDSVRSVC ADAPVNVVTA EDLDGPRNSG PFTFSIIDQP PGTAQKWKIT HQESTSVLLQ PSEKRLGRSE IPFLISDSQG
721    FSCLERQVLQ LTVCECLEGG GCVAALYDNY VGLGPAALAL MILALLLLL VPLLLLMCHC GEGAKGFAPI PGTIEMLHPW
801    NNEGAPPEDK VVPSLLVTDH VENSQVRRGG GGGGGVGGV KLKEGVSSSA SITKGQHELI EVDGRWEEHR SLLTSGLTHH
881    VATAGSIAAN DTTIRTRAT GASRDMSGAR GAVAMNEELL RSYFTEKAAS YAGEDDFHLA KDCLLVYSQE DTDSLRGSVG
961    CCSFIEGELD DLFLDDLGPK FKTLAEVCLG RKIDMDVDIE QRQKPVRETS VNAAPGSHYT QVTASSESTY SSNSGFQAPK
1041   PLHGAHTEKV TQEVVTESSV SSRQSQKVVV PPNPVASGNI IVTETSAAAG SAVPPSTVIL APRQPQSLIV TERYVAPAST
1121   LVDQHYANEE NVLVTERVIQ PNGGIPKPLE VTQHLNDAQY VMVRERESIL APSSGVQPTL AMPPSVAAGQ NVTVTERVLT
1201   PASTLQSSYQ IPSEASIKAR KTVLSSVGGM GPLPNLDLEE SGPPNSTVTT SSTRVTKHST VQHSYS
    
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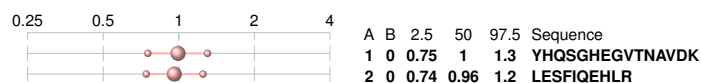
5.859 CD151 antigen [Rattus norvegicus]

Protein Accession	gij11968106
Mean Expression Ratio	0.98
Median Expression Ratio	0.98
Credible Interval	(0.766, 1.25)
Associated Peptides	2
Associated Spectra	3

Coverage	0.0988
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.868
Avg..iTRAQ.Ratio....116.114.	1.37
Avg..iTRAQ.Ratio....117.114.	0.868

```

1      MGEFNEKKAT CGTVCLKYLL FTYNCCFWLA GLAVMAVGIW TLALKSDYIS LLASSTYLAT AYILVVAGVV VMVTGVLGCC
81     ATPKERRNLL RLYFILLILLI FLLEIIAGIL AYVYYQQLNT ELKENLKDTM IKRYHQSGHE GVTNAVDKLO QEFHCCGSNN
161    SRDWRDSEWI RSGEADSRVV PDSCKTVVT GCGKREHASN IYKVEGGCIT KLESFIQEHL RVIGAVGIGI ACVQVFGMIF
241    TCCLYRSLKL EHY
  
```



5.860 reticulon 3 isoform A1 [Rattus norvegicus]

Protein Accession	gij 57977317
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.759, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	1.26

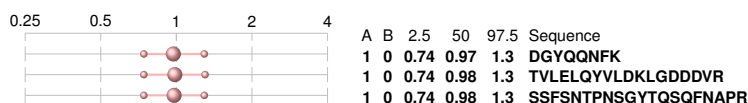


5.861 GPI-anchored membrane protein 1 [Rattus norvegicus]

Protein Accession	gi 87239978
Mean Expression Ratio	0.98
Median Expression Ratio	0.98
Credible Interval	(0.775, 1.25)
Associated Peptides	3
Associated Spectra	3
Coverage	0.065
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.93
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	1.02

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1      MPSATSHSGS  GSKSSGPPPP  SGSSGSEAAA  GAAAPASQHP  ATGTGAVQTE  AMKQILGVID  KKLRNLEKKK  GKLDYQERM
81     NKGERLNQDQ  LDAVSKYQEV  TNNLEFAKEL  QRSFMALSQD  IQKTIKKTAR  REQLMREEAE  QKRLKTVLEL  QYVLDKLGDD
161    DVR  TDLKQGL  SGVPIlseEE  LSLlDEFYKL  VdPERDMSLR  LNEQYEHASI  HLWDLLEGKE  KPVCgTTYKA  LKEIveRVFQ
241    SNYFDSTHhH  QNGLCEEEEA  ASAPIVEDQV  AEAEPEPTEE  YTEQSEVEST  EYVNRQFMAE  TQFSSGEKEQ  VDEWAVETVE
321    VVNSLQQPQ  AASPSVPEPH  SLTPVAQSDP  LVRRQRVQDL  MAQMGGPYNF  IQDSMLDFEN  QTLDPaIVSA  QPMNPTQNMd
401    MPQLVCPQVH  SESRLAQSNQ  VPVQPEATQV  PLVSSSTSEGY  TASQPLYQPS  HAAEQRPQKE  PIDQIQATIS  LNTeQTTASS
481    SLPAAASQPQV  FQAGASKPLH  SSGINVNAAP  FQSMQTVFNM  NAPVPPVNEP  ETLKQSQSYQ  ASYNQSFSSQ  PHQVEQTElQ
561    QDQLQTVVGT  YHGSQDQPHQ  VPGNHQQPPQ  QSTGFPRSSQ  PYYNSRGSVR  GGSRGARGLM  NGYRGPANGF  RGGYDGYRSS
641    FSNTPNSGYT  QSQFNAPRDY  SGYQRDGYQQ  NFRGSGQSG  PRGAPRGRGG  PFRPNRGMPQ  MNTQQVn
  
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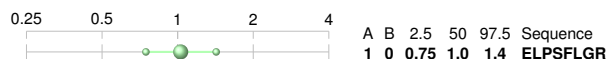


5.862 S100 calcium-binding protein A4 [Rattus norvegicus]

Protein Accession	gi 6981326
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.758, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0792
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.917
Avg..iTRAQ.Ratio....116.114.	1.12
Avg..iTRAQ.Ratio....117.114.	1.36

NHLBI Zile/Grant, Aged Rat

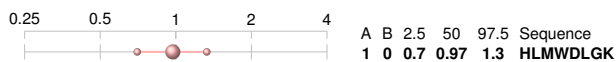
1 MARPLEEALD VIVSTFKYS GNEGDKFKN KTELKELLTR **ELPSFLGR** DEAAFQKLMN NLDSNRDNEV DFQEYCVFLS
 81 CIAMMCNEFF EGCPDKEPRK K



5.863 "succinate dehydrogenase complex, subunit C [Rattus norvegicus]"

Protein Accession	gi 53850596
Mean Expression Ratio	0.978
Median Expression Ratio	0.981
Credible Interval	(0.725, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0473
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.79
Avg..iTRAQ.Ratio....116.114.	1.28
Avg..iTRAQ.Ratio....117.114.	0.918

1 MAALLLRHIG RHCLRAHLSS QLCIRNAAPL GTTAKEEMAR FWNKNTSSNR PVSPHLTIYR WSLPMAMSV C HRGSGIAMSG
 81 GVSFLGLSAL LLPGNFESYL MLVKS LCLGP ALIHAARFVL VFPLMYHSLN GVR**HLMWDLG** KGLSISQVQL SGVTVLVLAV
 161 LSSAGLAAI



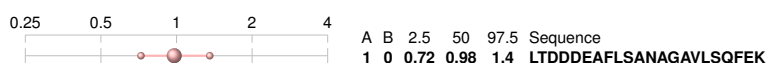
5.864 leucine zipper and CTNNBIP1 domain containing [Rattus norvegicus]

Protein Accession	gi 61557405
Mean Expression Ratio	0.982
Median Expression Ratio	0.981
Credible Interval	(0.729, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.116

Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.05
Avg..iTRAQ.Ratio....116.114.	0.998
Avg..iTRAQ.Ratio....117.114.	0.874

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1      MASRGKTETS KLKQNL EEQL DRLMQQLQDL EECREELDGD EYEETK KETL EQLSEFNDSL KKIMSGNMTL VDELSGMQLA
81     IQAAISQAFK TPEVIRLFAK KQPGQLRTRL AEMDRDLMVG KLERDLHTQQ RVEILTALRK LGEKLTDDDE AFLSANAGAV
161    LSQFEKVS TE LGSGDKVLAL AGFEVEKAKK
    
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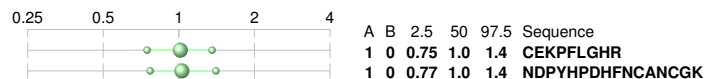


5.865 PREDICTED: similar to LIM and senescent cell antigen-like domains 1 [Rattus norvegicus]

Protein Accession	gi 62666039
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.784, 1.34)
Associated Peptides	2
Associated Spectra	2
Coverage	0.069
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.16
Avg..iTRAQ.Ratio....116.114.	1.08
Avg..iTRAQ.Ratio....117.114.	1.25

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1      MTALQLKELS QSGLYRRRE RPDLSRVNGL PEEELSNMAN ALASATCERC KGGFDPAEKI VNSNGELYHE QCFVCAQCFO
81     QFPEGLFYEF EGRKYCEHDF QMLFAPCCHQ CGEFIIGRVI KAMNNSWHPE CFRCDLCQEV LADIGFVKNA GRHLCRPCHN
161    REKARGLGKY ICQKCHAIID EQPLIFKNDP YHPDHFNCAN CGKELTADAR ELKGELYCLP CHDKMGVVIC GACRRPIEGR
241    VVNAMGKQWH VEHFVCAKCE KPFLGHRHYE RKGLAYCETH YNQLFGDVCF HCNRVIEGDV VSALNKAWCV SCFACSTCNT
321    KLTLLKNKFVE FDMKPVCKKC YEKFPLELKK RLKKLSETLG RK
    
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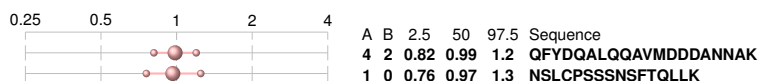


5.866 CD 81 antigen [Rattus norvegicus]

Protein Accession	gj 6978639	
Mean Expression Ratio	0.98	
Median Expression Ratio	0.981	
Credible Interval	(0.798, 1.20)	
Associated Peptides	2	
Associated Spectra	7	
Coverage	0.153	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.955	1.17
Avg..iTRAQ.Ratio....116.114.	0.967	0.858
Avg..iTRAQ.Ratio....117.114.	0.991	1.07

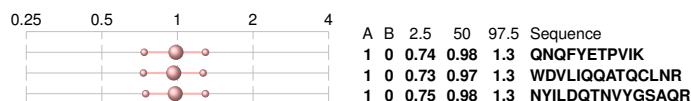
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1   MGVEGCTKCI KYLLFVFNFV FWLAGGVILG VALWLRHDPQ TTTLLYLELG DKPAPSTFYV GIYILIAVGA VMMFVGFLLGC
81  YGAIQESQCL LGTFFTCLVI LFACEVAAGI WGFVNKDQIA KDVRQFYDQA LQQAVMDDDA NNAKAVVKTF HETLNCCGSN
161 TLTTLTAVL RNSLCPSSSN SFTQLLKEDC HQRIDELFSG KLYLIGIAAI VVAVIMIFEM ILSMVLCCGI RNSSVY
    
```



5.867 PREDICTED: similar to EIB-55kDa associated protein 5 isoform 1 isoform 4 [Rattus norvegicus]

Protein Accession	gj 109461436	
Mean Expression Ratio	0.978	
Median Expression Ratio	0.981	
Credible Interval	(0.764, 1.25)	
Associated Peptides	3	
Associated Spectra	3	
Coverage	NA	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.987	
Avg..iTRAQ.Ratio....116.114.	0.983	
Avg..iTRAQ.Ratio....117.114.	1.03	

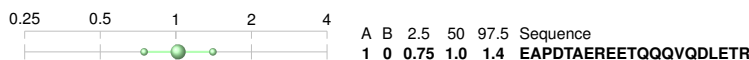


5.868 homer homolog 3 [Rattus norvegicus]

Protein Accession	gi 16758964
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.758, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0587
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.19
Avg..iTRAQ.Ratio....116.114.	1.3
Avg..iTRAQ.Ratio....117.114.	1.22

```

1      MSTAREQPIF STRAHVFQID PATKRNWIPA GKHALTVSYF YDATRNVYRI ISIGGAKAII NSTVTPNMTF TKTSQKFGQW
81     ADSRANTVYG LGFGSEQQLT QFAEKFQEVK EAARLAREKS QDGGELTSTA LAMASHQVPP SPLVSTNGPE EKLFRSQSAD
161    APGPTERERL KKMLSEGSVG EVQWEAEFFA LQDSNQRLAG ALREANAAT QWRQQLEVQR AEAHLRQRV AEALEAQVAE
241    PVRAGEKEAT SQSVEQLEAR VQTKDQEIQT LKNQSTGPRE APDTAEREET QQQVQDLETR NAELEQLRA MESNLEEARA
321    ERERARAEEV RAAQLLDVRL FELSELREGL ARLAEAAP
    
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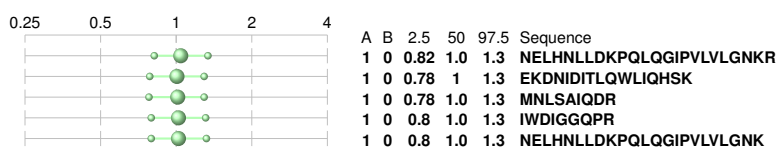
5.869 hypothetical protein LOC500282 [Rattus norvegicus]

Protein Accession	gi 66730258
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.829, 1.26)
Associated Peptides	5
Associated Spectra	5
Coverage	0.317

Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.04
Avg..iTRAQ.Ratio....116.114.	0.981
Avg..iTRAQ.Ratio....117.114.	1.18

```

1      MLALISRLLD WFRSLFWKEE MELTLVGLQY SGKTTFVNVI ASGQFSEDMI PTVGFNMRKV TKGNTIKIW DIGGQPRFRS
81     MWERYCRGVN AIVYMIDAAD REKIEASRNE LHNLLDKPQL QGIPVVLGN KFDLPNALDE KQLIEKMNLS AIQDREICCY
161    SISCKEKDNI DITLQWLIQH SF SRRS
    
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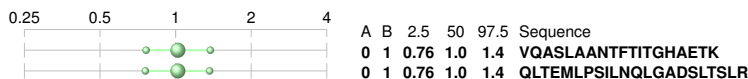


5.870 PREDICTED: similar to basic transcription factor 3 [Rattus norvegicus]

Protein Accession	gij109499130
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.783, 1.32)
Associated Peptides	2
Associated Spectra	2
Coverage	0.253
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.04
Avg..iTRAQ.Ratio....116.114.	0.735
Avg..iTRAQ.Ratio....117.114.	1.18

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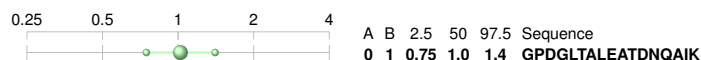
1      MKETIMNQEK LAKLQAQVRI GGKGTARRKK KVVHRTATAD DKKLQFSLKK LGVNSISGIE EVNMFTNQGT VIHFNPKVQ
81     ASLAANTFTI TGHAEKQLT EMLPSILNQL GADSLTSLRR LAEALPKQSV DGKAPLAAGE EEDEVPDLV ENFDEASKNE
161    AN
    
```



5.871 myotrophin [Rattus norvegicus]

Protein Accession	gi 13242275
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.756, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.144
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.893
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	0.977

1 MCDKEFMWAL KNGDLDEVKD YVAKGEDVNR TLEGGRKPLH YAADCGQLEI LEFLLKGD INAPDKHHIT PLLSAVYEGH
 81 VSCVKLLLSK GADKTVK**GP**D **GLTALEATDN** **QA**IKALLQ



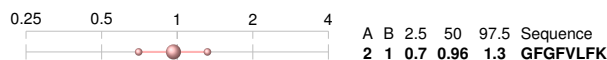
5.872 PREDICTED: similar to Stromal cell-derived factor 2 precursor (SDF-2) [Rattus norvegicus]

Protein Accession	gi 109491418
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.765, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.23



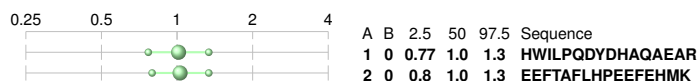
5.873 heterogeneous nuclear ribonucleoprotein D isoform a [Rattus norvegicus]

Protein Accession	gij 127138710
Mean Expression Ratio	0.981
Median Expression Ratio	0.982
Credible Interval	(0.726, 1.32)
Associated Peptides	1
Associated Spectra	3
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.938
Avg..iTRAQ.Ratio....116.114.	0.855
Avg..iTRAQ.Ratio....117.114.	0.729



5.874 PREDICTED: similar to Reticulocalbin-1 precursor [Rattus norvegicus]

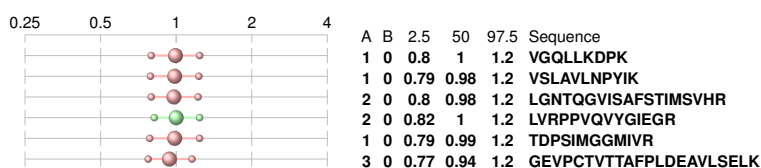
Protein Accession	gij 34856626
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.796, 1.31)
Associated Peptides	2
Associated Spectra	3
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.15
Avg..iTRAQ.Ratio....116.114.	1.01
Avg..iTRAQ.Ratio....117.114.	1.22



5.875 "mitochondrial ATP synthase, O subunit [Rattus norvegicus]"

Protein Accession	gij20302061
Mean Expression Ratio	0.983
Median Expression Ratio	0.982
Credible Interval	(0.832, 1.17)
Associated Peptides	6
Associated Spectra	10
Coverage	0.408
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.09
Avg..iTRAQ.Ratio....116.114.	0.897
Avg..iTRAQ.Ratio....117.114.	1.09

1 M A A P A T S V L S R Q V R S F S T S V V R P F S K L V R P P V Q V Y G I E G R Y A T A L Y S A A S K Q K R L D Q V E K E L L R V G Q L L K D P K V S L A V L N
81 P Y I R S I K V K S L K D I T T K E K F S P L T A N L M N L L A E N G R L G N T Q G V I S A F S T I M S V H R G E V P C T V T T A F P L D E A V L S E L K T V
161 L N S F L S K G Q I L N L E V K T D P S I M G G M I V R I G E K Y V D M S A K S K I Q K L S K A M R D L L



5.876 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gij109491432
Mean Expression Ratio	1.02
Median Expression Ratio	1.02

Credible Interval	(0.795, 1.32)	
Associated Peptides	1	
Associated Spectra	3	
Coverage	0.179	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.06	0.873
Avg..iTRAQ.Ratio....116.114.	1.02	1.04
Avg..iTRAQ.Ratio....117.114.	0.988	1.30

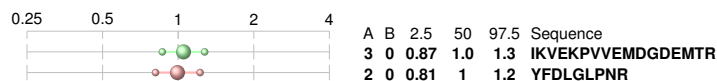
1 MAPLRGAELV QTPLQLYRYL LRCCRQLPTK GIQEBYKHAV RQSFQVHSDE DNPERIQQII RRAIEDADWI MNKYKKQN

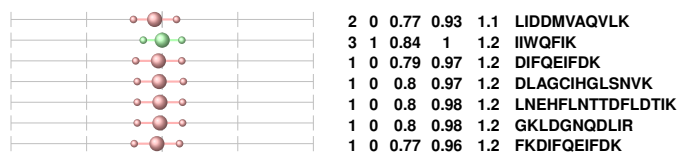


5.877 hypothetical protein LOC361596 [Rattus norvegicus]

Protein Accession	gij62079055	
Mean Expression Ratio	0.982	
Median Expression Ratio	0.982	
Credible Interval	(0.852, 1.13)	
Associated Peptides	9	
Associated Spectra	16	
Coverage	0.21	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	0.81
Avg..iTRAQ.Ratio....116.114.	0.886	0.76
Avg..iTRAQ.Ratio....117.114.	1.24	0.791

1 MAGYLRAVSS LCRASGSTR T WAPAALNVPS WPEQPRRHYA EKRIKVEKPV VEMDGDDEMTR IIWQFIEEKL ILPHVDVQLK
 81 YFDLGLPNRD QTNDQVTIDS ALATQKYSVA VKCATITPDE ARVEEFKLLK MWKSPNGTIR NILGGTVFRE PIICKNIPRL
 161 VPGWTKPITI GRHAHGQYK ATDFVVDRA G MFKLVFTPKD GSGAKEWEVY NFPAGGVGMG MYNTDESISG FAHSCFQYSI
 241 QKRWPLYLST KNTIMKAYDG R^FKDIFQEIF D^HYKTFDK NKIWEHRLI DDMVAQVLK SGGFVWACKN YGDVQSDIL
 321 AQQFGSLGLM TSVLVCPPDGK TIEEAAHGT VTRHYREHQK GRPTSTNPIA SIFAWTRGLE HRGKLDGNQD LIRFAQTLEK
 401 VCVQTVESGA MTKDLAGCIH GLSNVKLNEH FLNTDFLDT IKSNDLRALG KQ





5.878 PREDICTED: similar to 40S ribosomal protein S19 [Rattus norvegicus]

Protein Accession	gij109483232
Mean Expression Ratio	0.984
Median Expression Ratio	0.982
Credible Interval	(0.732, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0687
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.947
Avg..iTRAQ.Ratio....116.114.	1.01
Avg..iTRAQ.Ratio....117.114.	0.984

1 M P G V T V K **D V N** Q Q E F V R A L A A F L K K S P N G W T Q S S W P N V K S L P H T H E L L P Q H S N C T S V V V R G K G V G M L V P R P R S T E D R G R Q R
 81 N G V R P S H F N R G S K T V A R R V L Q A L E G L K N G G K G P R W E P Q A N T S G T E R S E Q D C

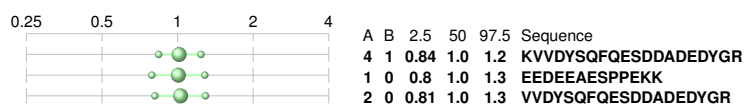


5.879 nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate [Rattus norvegicus]

Protein Accession	gij12248185
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.837, 1.23)
Associated Peptides	3
Associated Spectra	8
Coverage	0

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.913	0.837
Avg..iTRAQ.Ratio....116.114.	1.14	1.88
Avg..iTRAQ.Ratio....117.114.	1.12	0.972

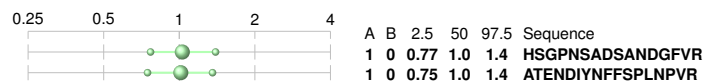
1 MLEFISRMLG KEPASKNVAK ERLRLVLVHD RATISPHMLN QLKEDLIKVI SNYMEIDEGA LEVNLNQDDR EVALIANIPV
 81 IKMKRDYSVK G



5.880 heterogeneous nuclear ribonucleoprotein F [Rattus norvegicus]

Protein Accession	gij 82546815
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.776, 1.33)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0795
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.1
Avg..iTRAQ.Ratio....116.114.	1.08
Avg..iTRAQ.Ratio....117.114.	1.02

1 MMLGPEGGEG YVVKLRGLPW SCSIEDVQNF LSDCTIHDGV AGVHFIYTR E GRQSGEAFVE LESEDDVKLA LKKDRESMGH
 81 RYIEVFKSHR TEMDWVLKHS GPN SADSAND GFVRLRGLPF GCTKEEIVQF FSGLEIVPNG ITPVDPPEGK ITGEAFVQFA
 161 SQELA EKALG KHKERIGHRY IEVFKSSQEE VRSYSDPPLK FMSVQRPGPY DRPGTARRYI GIVKQAGLDR MRSGAYSAGY
 241 GGYEEYSGLS DGYGFTTDLF GRDLSYCLSG MYDHRYGDSE FTVQSTTGHC VHMRLPYKA TENDIYNFFS PLNPFVRVHIE
 321 IGPDGRVTGE ADVEFATHEE AVAAMSKDRA NMQHRYIELF LNSTTGASNG AYSSQVMQGM GVSAAQATYS GLEQS SVSGC
 401 YGAGYSGQNS MGGYD

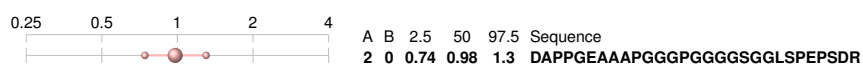


5.881 genethonin 1 [Rattus norvegicus]

Protein Accession	gi 62078705
Mean Expression Ratio	0.983
Median Expression Ratio	0.982
Credible Interval	(0.751, 1.29)
Associated Peptides	1
Associated Spectra	2
Coverage	0.087
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.928
Avg..iTRAQ.Ratio....116.114.	1.19
Avg..iTRAQ.Ratio....117.114.	1.04

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1   MGAVWSALLV GGGLAGALIL WLLRGDSGAP GKDGGAEPLK DAPPGEAAP GGGPGGGGSG GLSPEPSDRE LVSKAEHLRE
81  SNGHLISESK DLGNLTEAQR LQNVGNAREY VPVGKVPDTH SRANSETSRN QSPESRVGEW RLPKGHETAV KVAGSVAEKL
161 PSSSPLMDRA EAASLAQSAG HEDWEVVSRR SSWGSVGLGG SLEASRLSLN QGMDESRNSL VGGGWEVDGK VVSVKPRQVS
241 IQFKVHYSTS TDVQFIAVTG DHESLGGWNT YIPLHYCKDG LWSHSVFLPA DTVVEWKFVL VENKEVTRWE ECSNRRLQTG
321 HEDKVVHGWV GIH
  
```



5.882 hypothetical protein LOC309478 [Rattus norvegicus]

Protein Accession	gi 71795660
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.75, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0088
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.17

NHLBI Zile/Grant, Aged Rat

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1      MPFEQTQLFC DEKQTIKKI DTRNEIPDTI KSIPIPKISE AGFHYEPKNV NICLPKINIP NEILMKHEVE KYRKLQSKP
81     QTARKSVSVR TVSCAKGCAQ RCESERAEDE AGMKCAKILN FTCSKCQDRT QYSPNDLQKH FEMWHHGELP SFPCEMCSFS
161    ASDFQIFKQH RKTHRNTFVK CDICNSERSY TLLDLTKHFT SKHCVNGNFQ CEECRFFFTQD VGTFFVQHIHR HKEVHYKCGK
241    CHHLCFTKGE LQKHLRVHSG TLPFTCHYCS YGAIHKDQLV RHVITLHKEH LYAKEKLERD QYDKRVAKTT TGLKLILKRY
321    KIGPTKTFWK RKTIASGNDE SIGKNAQAFN IVSKTQTKSE DQSQEQLNEE KGGRQHCEDEG DKPIESGSEK ATVLSTGQCEN
401    KADEGASAPS SVLSAVQGPT VLLVRNKKIT IPANYSAKFM GFKMVDGRQH IVIKLLPANK QILPSPALQP NTEKESTANL
481    PPQAMDNTGF ATGLTAMNDT DFKAAAPLSC SSPELPRKVI SEKETAFAISE KNNMLQMVDV SKSVTSLPTP SESVTSVRLT
561    TKVEARDNVD LWENPSTQSH PDLIGTSINS PDKVNLITRP NAYSCGDMHN YCINYNVNSL PAESSNCFEF SNQGSPLFHN
641    YSKVNNKRRR FSRGAVCENL QRESSNKTVT QOSTSDSDTT SPLRKESNS DSSLASISPL SGTLLKIKTEI EEPDLEETQ
721    NFNESQSLFTN ENQNLLNMT EPKWDDIPCA GSPMPRITS VFSLQSEQAS EFLPPEVNQL LQDTLKRSD IKEDSNNIPS
801    KNLPDQCDQT LKKSKEEVK SSKDFQMQDI ISVPSASVGV NVPANDLNLK CNGQEKQALS VLQDVRDPGV TTKIPSIITL
881    LKTQSDAIIT QQLVKDKLRT TTQHSQPVYV QNPLLTSEQK NPVAVQTPKG FIIPHLVANK PGLHVFSGRP VPLVNTQSV
961    AALLVNKKPG VVLTVNNKGP EGVPTVKTEN VHSYGTVKE PCRTFFLKAH HNRYCLTPGL CSSIGSCVNM KTCSENTLPL
1041   KGSYIIKTSV SSSVKAVPFA NVLPEQQGPN VNVLDVAVKQO NESLFPKASLY TLMPPDGKQAV FFKCMMPNNT KLLKPLVQN
1121   STYQRIQPKR PAGAPQKILL KIFNPVLSMS AVNNLSVGN ASSFQKEIVP SKPTVHGEQK VPQSSRDALP VSVQDMLPAN
1201   EAVLSSTAAC PGSSEEPVHI SERSETRVSR SKANCTIERN FNKRKTCKNK FAKIKTRISQ DSETAFVSRN RSKRKYIDN
1281   YQEPFRKKA THRCKKERAN AEDVQETFGF SRPRLPKDSC RTLRLFPFNS EQLVKCPRRN QPVVVLNHPD ADAPEVERVM
1361   KKITKFNQGRV LKVSLSKATI NALLKPVVIT SETTYSDFSK RHKMLKPVNS VKERFVLLKT LKTKSKNNYQ IVKTTSEDVL
1441   KSKFNCWFCG RVFDNQDVWA GHGQRHLVEA TKDWNMLE

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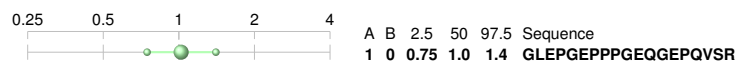
5.883 hypothetical protein LOC499331 [Rattus norvegicus]

Protein Accession	gi 66730339
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.758, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	0.114
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.41
Avg..iTRAQ.Ratio....116.114.	1.27
Avg..iTRAQ.Ratio....117.114.	0.886

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1      MAKRRAAEPL TFRVPWKRL L SDFPEEPPL WVPPSGAARP LKRQGDAGTM AEPASAPRKR RGGGDDEPEL QGRGLEPGE
81     PPGEGGEPQV SRAAGGGDRV ESAGSPQGD EVHSQHNEDF WQYNTFYWR NPLPPIDLAA LEDVANSNLT ETLEDKNEGV
161    EIDMES

```



5.884 "RAB4A, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gi 77404180
Mean Expression Ratio	0.98
Median Expression Ratio	0.983
Credible Interval	(0.732, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0734
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.982
Avg..iTRAQ.Ratio....116.114.	0.962
Avg..iTRAQ.Ratio....117.114.	1.16

```

1   MAQTAMSEY DFLFKFLVIG NAGTGKSCLL HQFIEKKFKD DSNHTIGVEF GSKIINVGGK YVKLQIWDTA GQERFRSVTR
81  SYRGAAGAL LVDITSRET YNALTNWLT D ARMLASQNI V IILCGNKKDL DADREVTFL E ASRFAQENEL MFLETSALTG
161 ENVEEAFMQC ARKILNKIES GELDPERMGS GIQYGDAALR QLRSPRR TQA PSAQECGC
    
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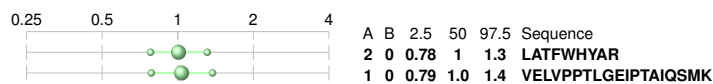


5.885 "ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit G [Rattus norvegicus]"

Protein Accession	gi 47058994
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.799, 1.31)
Associated Peptides	2
Associated Spectra	3
Coverage	0.272
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.05
Avg..iTRAQ.Ratio....116.114.	1.48
Avg..iTRAQ.Ratio....117.114.	0.87

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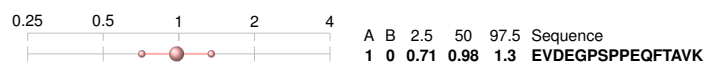
1   MAKFIRNLAD KAPSMVAAA V TYSKPRLATF WHYARVELVP PTLGEIPTAI QSMKNIHSA QTGNFKHLTV KEAVLNLVA
81  TEVMMWFYIG EIIGKRGIVG YDV
    
```



5.886 PREDICTED: similar to FRG1 protein (FSHD region gene 1 protein) [Rattus norvegicus]

Protein Accession	gij109503423
Mean Expression Ratio	0.983
Median Expression Ratio	0.983
Credible Interval	(0.732, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.104
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	0.967
Avg..iTRAQ.Ratio....117.114.	0.965

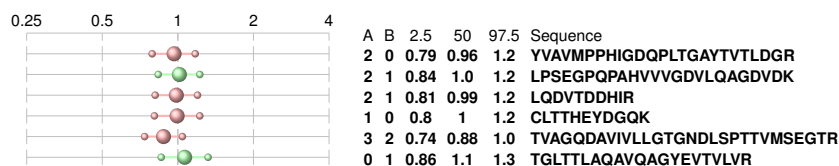
1 MAEYSYVKST KLVKGTAK SKKKSKDKK RKREDEEAQ LDIVGIWTV SNFGEISGTI AIEMDKGAYI HALDNGLFTL
81 GAPHREVDG PSPPEQFTAV KLSDSRIALK SGYGKYLGIN SDGLVVGRSD AIGPREQWEP VFQDXNIASL KTNS



5.887 PREDICTED: similar to biliverdin reductase B (flavin reductase (NADPH)) [Rattus norvegicus]

Protein Accession	gij34855391
Mean Expression Ratio	0.982
Median Expression Ratio	0.983
Credible Interval	(0.845, 1.14)
Associated Peptides	6
Associated Spectra	15
Coverage	NA

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.887	0.874
Avg..iTRAQ.Ratio....116.114.	0.847	1.52
Avg..iTRAQ.Ratio....117.114.	0.815	1.48

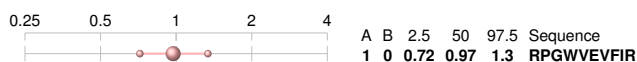


5.888 hypothetical protein LOC311430 [Rattus norvegicus]

Protein Accession	gij53850640
Mean Expression Ratio	0.98
Median Expression Ratio	0.983
Credible Interval	(0.732, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0197
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.09
Avg..iTRAQ.Ratio....116.114.	0.864
Avg..iTRAQ.Ratio....117.114.	0.871

```

1      MTFAEERTYK YIRYNHSEFC CVDVLEILPY LSCLTTSDD RLRASYKQLG NQGTWLWELFN TLQRRPGWVE VFIFALRICE
81     LPGLAEQVTR VYQSYLPPGA SLHSLDPLQS PRIPTTVSEP SAFAAGHTIP DSGFQDKPGY PKPVQDTQPP KSPVENSEEP
161    PQANFGAIPR MSGDSLSSP NPPALSPQPS REHPEQEP LGGPSTANVDS VPIATYGPVS PTVSFQPLPR IAPRTNLSFG
241    VTVSALSAKT TLSSSSTGSA FAKGAGDQAK AATCVSTKEG VPTNSVTTSS VPSIKPVPVN TMSGKLPIST KSTAATPSTV
321    PTNIAPSKLP INSVYTGIVP SKVTASVAKA SASTMPPER NQAKETLEA PATVVTTGSS LTRPDISSRS LHSGPELSKP
401    GVLVSQVDNE PFSACSMDLA ISPSTSLGSE PNHGPEENEY SSFRIQVDKS PSVDLLGSPE PLATQQSPPEE EEP CASSVSW
481    AKWLGATSAL LAAF LAVMLY RSRH LAQ
    
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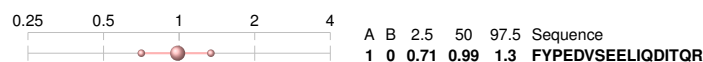


5.889 moesin [Rattus norvegicus]

Protein Accession	gi 13540689
Mean Expression Ratio	0.986
Median Expression Ratio	0.983
Credible Interval	(0.731, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0295
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.883
Avg..iTRAQ.Ratio....116.114.	0.783
Avg..iTRAQ.Ratio....117.114.	0.776

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1      MPKTISVRVT  TMDAELEFAI  QPNTTGKQLF  DQVVKTIGLR  EVWFFGLQYQ  DTKAFSTWLK  LNKKVTAQDV  RKESPLLFKF
81     RAKFYPEDVS  EELIQDITQR  LFFLQVKEGI  LNDDIYCPEE  TAVLLASYAV  QSKYGDFNKE  VHKSGYLAGD  KLLPQRVLEQ
161    HKLNKDQWEE  RIQVWHEEHR  GMLREDAVLE  YLKIAQDLEM  YGVNYFSIKN  KKGSELWLGV  DALGLNIYEQ  NDRLTPKIGF
241    PWSEIRNISF  NDKKFVIKPI  DKKAPDFVfy  APRLRINKRI  LALCMGNHEL  YMRRRKPDIT  EVQQMKAQAR  EEKHQKQMER
321    ALLENEKKKR  ELAEKEKEKI  EREKEELMEK  LKQIEEQTKK  AQQELEEQTR  RALELEQERK  RAQSEAEKLA  KERQEAEK
401    EALLQASRDQ  KKTQEQQLASE  MAELTARVSQ  LEMARKKES  EAEECHQKAQ  MVQEDLEKTR  AELKTAMSTP  HVAEPAENEH
481    DEQDENGAEA  SAELRADAMA  KDRSEERTT  EAEKNERVQK  HLKALTSELA  NARDESKKTT  NDMIHAENMR  LGRDKYKTLR
561    QIRQGNTKQR  IDEFESM
  
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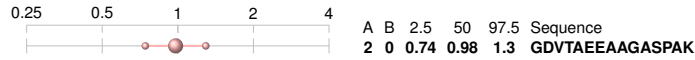
5.890 MARCKS-like protein [Rattus norvegicus]

Protein Accession	gi 13540687
Mean Expression Ratio	0.984
Median Expression Ratio	0.983
Credible Interval	(0.751, 1.29)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0754
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	0.898
Avg..iTRAQ.Ratio....117.114.	1.10

NHLBI Zile/Grant, Aged Rat

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1      MGSQSSKAPR  GDVTAEAAAG  ASPAKANGQE  NGHVKNSGDL  TPKGEGESPP  VNGADEAAGA  TGDAlEPAPP  SQEABAKGEV
81     APKETPKKKK  KFSPKPPFKL  SGLSFKRNRK  EGGDSSASS  PTEEEQEQQE  ISACSDGTA  QEGKAAATPE  SQEPQAKGAE
161    ASAVSKGGDA  EEEAGPQAAE  PSTPSGPESG  PASASAENE
  
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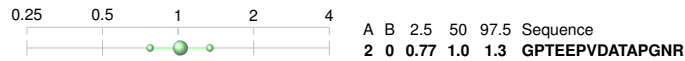


5.891 PREDICTED: similar to Feline leukemia virus subgroup C receptor-related protein 2 (Calcium-chelate)

Protein Accession	gij109458504
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.774, 1.34)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0129
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	1.07

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1      MPSVSLRHSG  SVTLPLPLPT  PASRWFLQFV  FPDHWSTKGR  AVLGTAPVAA  TARWPQQEEQ  AKRTDTSAVV  YPSALVYPSA
81     LVYPSALVYP  SALVYPSALV  YPSALVYPSA  LVYPSALVYP  SALVYPSALV  YPSALVYPSA  LVYPSALVYP  SAVVYPSAVV
161    YPSALVYPSA  LVYPSALVYP  SALVYPSALV  YPSALVYPSA  VVYPSALVYP  SALVYPSALV  YPSALVYPSA  LVYPSALVYP
241    SALVYPSALV  YPSALVYPSA  LVYPSALVYP  SALVYPSALV  YASVLVYPSV  LVYPSVLVYT  SLCPPFRIFVL  FMVYPSALVY
321    PSVLVYPSAV  VYPSALVYPS  ALVYPSVLVY  PSALVYPSAL  VYPSALVYPS  AVVYPSALVY  PSVLVYPSVL  VYPSALVYPS
401    ALVYPSALVY  PSAVVYPSAL  VYPSALVYPS  VLVYPSALVY  PSALVYPSAL  VYPSAVVYPS  ALVYPSVLVY  PSALVYPSAV
481    VYPSALVYPS  VLVYPSAVVY  PSALVYPSAL  VYPSALVYPS  ALVYPSAVVY  PSALVYPSAL  VYPSALVYPS  ALVYPSALVY
561    PSALVYPSAL  VYPSALVYPS  ALVYPSALVY  PSAVVYPSAL  VYPSVLVYPS  AVVYPSALVY  PSALVYPSVL  VYPSALVYPS
641    ALVYPSALVY  PSAVVYPSAL  VYPSVLVYPS  VLVYPSALVY  PSALVYPSAL  VYPSAVVYPS  ALVYPSALVY  PSATGVPICA
721    VVYPSALVYP  SVLVYPSVLV  YPSALVYPSA  LVYPSALVYP  SAVVYPSALV  YPSALVYPSV  LVYPSALVYP  SALVYPSALV
801    YPSAVVYPSA  LVYPSVLVYP  SALVYPSAVV  YPSALVYPSV  LVYPSAVVYP  SALVYPSALV  YPSALVYPSA  LVYPSAVVYP
881    SALVYPSALV  YPSALVYPSA  LVYPSALVYP  SALVYPPALV  YPSVLMYPPV  LVYPPVLVYP  SVLVYPPVLV  YPPVLVYPPV
961    LVYPPVLVYP  SALVYPSVLV  YPPVLVYPSV  LVYPSVLVYP  SVLVYASVLV  YPSVLVYPSV  LLLSTVCRGG  PSGRVRATDR
1041   DAAVMSRLSR  LQRQVLSLYR  ELLRAGRKPK  GAEARVRAEF  RQHASLPRSD  VLRIEYLIRR  GRRQLQLLRS  GHATAMGTFF
1121   RPRGPTEEPV  DATAPGNRLD  DSDALKNPCE  GTGARETRSD  GR
  
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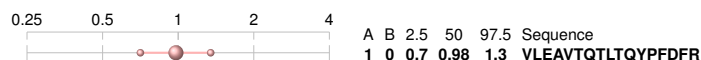
5.892 testicular ecto-ATPase [Rattus norvegicus]

Protein Accession	gij 25282445
Mean Expression Ratio	0.982
Median Expression Ratio	0.983
Credible Interval	(0.726, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0343
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.95
Avg..iTRAQ.Ratio....116.114.	0.97
Avg..iTRAQ.Ratio....117.114.	1.09

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1   MAGKLVSLVP  PLLLLAAAGLA  GLLLLCVPTQ  DVREPPALKY  GIVLDAGSSH  TSMFVYKWPA  DKENDTGIVG  QHSSCDVQGG
81  GISSYANDPS  KAGQSLVRCL  EQALRDVPRD  RHASTPLYLG  ATAGMRLNL  TSPEATARVL  EAVTQTLTQY  PFDPRGARIL
161 SQQDEGVFGW  VTANYLLENF  IKYGWVGRWI  RPRKGTLGAM  DLGGASTQIT  FETTSPSEDP  GNEVHLRLYG  QHYRVYTHSF
241 LCYGRDQILL  RLLASALQIH  RFHPCWPKGY  STQVLLQEVY  QSPCTMGQRP  RAFNGSAIVS  LSGTSNATLC  RDLVSRLFNI
321 SSCPFSQCSF  NGVFQPPVTG  NFIAFSAFY  TVDFLTTVMG  LPVGTLKQLE  EATEITCNQT  WTELQARVPG  QKTRLADYCA
401 VAMFIHQLLS  RGYHFDERSF  REVVFQKKA  DTAVGWALGY  MLNFTNLIPA  DLPGLRKGTH  FSSWVALLLL  FTVLILAALV
481 LLLRQVRSK  SPGAL

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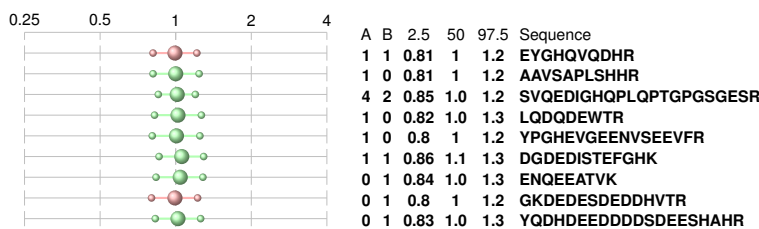
5.893 histidine rich calcium binding protein [Rattus norvegicus]

Protein Accession	gij 31077132	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.02	
Credible Interval	(0.874, 1.17)	
Associated Peptides	9	
Associated Spectra	16	
Coverage	0.167	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.978	1.16
Avg..iTRAQ.Ratio....116.114.	1.11	1.05
Avg..iTRAQ.Ratio....117.114.	0.874	0.957

NHLBI Zile/Grant, Aged Rat

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1      MGFQEPWLYS  CLLWATVAIL  LVPPVVTQEL  RGTGLGLGNW  NNNAGIPGSS  EDLSTEYGH  IHSYGAYQGE  KDRHHREDE
81     DFSREYGHQV  QDHRYPGHEV  GEENVSEEVF  RGHVRLHGH  HKPNSDLDG  SAESHFPRQ  SHNREEEDGV  VSGEDHRHIP
161    RHDHGNNEE   DDDGEEERV   GVMENSDDKH  QAHGHHSHK  ERDGLHHAH  HRHQGHDED  DDDDEDGVST  GEHQAHRYQD
241    HDEEDDDSD  EESHARLQG  QEDENDDDG  DSSENGHTQ  DHQGHKEQD  DDDEEEEEE  EEEEEEEEE  EEEEEEDDD
321    DSTEHRHRHQ  TQGHRKGD  DESDEDDHVT  RHGRRGHEDE  DDDDDDDDD  DDDNDGGSTE  NVHQAHRRG  HEHEDDGD
401    EEDYHHVPSH  GHQSHQNEE  EDEAVSTEHW  HQSPRHAHD  LGRNQEEAT  VKYSRHHV  RPQGHSAEED  SLEDSTNEVP
481    GHHHRVSRD  GDEDISTEFG  HFAPRRLQD  QDEWTRQGH  KSVQEDIGH  PLQPTGPG  ESFKEDDHSS  QEGEDLKQR
561    QEAHSEEEEE  EEEGHGLPM  LEDEEEEEK  KKEKSGDRA  VSAPLSHHK  HDDDDDDG  DDDDDNDDD  EILEENLLPF
641    TIIPNPLAGR  EVAREGSSE  ESREVTQQD  AQEYENYQP  SLCGYCSFC  RCSECESCH  DEENMGEHC  QCQHCQFCYL
721    CPLVCDTLCT  FGSYVDYFS  SVYQAVADML  ETQEP
  
```



5.894 "peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase [Rattus norvegicus]"

Protein Accession	gi 55741520
Mean Expression Ratio	0.984
Median Expression Ratio	0.983
Credible Interval	(0.735, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0307
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	0.817
Avg..iTRAQ.Ratio....117.114.	1.09

```

1      MAAVTWSRAR  CWCPSLLQVL  RLPVTKLHLG  RPAMRATQQD  FENAMNQVKL  LKKDPGNEVK  LRLYALYQQA  TEGPCTMPKP
81     GVFDVFNKAK  WDAWNALGSL  PFETARQNYV  DLVSSLSSSS  EASSQGKGG  DGKAQESKGI  LVTSEGGITK  ITFNRPSKKN
161    AITFQMYQDI  ILALKNASTD  DTVITVFTGA  GDYSSGNDL  TNFTSASGM  EEAANKGAI  V LREFVNTFID  FPKPLVAVVN
241    GPAVGISVTL  LGLFDVAVAS  DRATFHTPFS  HLGQSPEACS  SYTFKMMGS  AKAAEMLLFG  KKLTAAREAW  A QGLVTEVFPE
321    STFETEVTWR  LKTYAKLPPN  SMRISKELIR  KNEKEKLHAV  NEEECTTLRA  RWLSEECINA  IMSFVTRKPK  L
  
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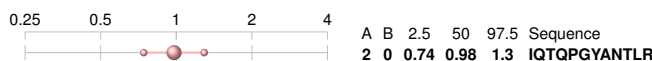


5.895 "solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 [Rattus norvegicus]"

Protein Accession	gi 20806141
Mean Expression Ratio	0.987
Median Expression Ratio	0.984
Credible Interval	(0.757, 1.30)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0337
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.948
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	0.938

```

1      MFSSVAHLAR ANPFNAPHLQ LVHDVSGPRS PPGPPRRSRH LAAAAVEGYS CEFGSMKYA LCGFGGVLSC GLTHTAVVPL
81     DLVKCRMQVD PQKYKGFNG FSITLKEDGV RGLAKGWAPT LIGYSMQGLC KFGFYEVFKA LYSNILGEEN TYLWRTSLYL
161    AASASAEFFA DIALAPMEAA KVRIQTOPGY ANTLREAVPK MYKEEGLNAF YKGVAPVWMR QIPYTMKFA CFERTVEALY
241    KFVVPKPRSE CTKAEQLVVT FVAGYIAGVF CAIVSHPADS VVSVLNKERG STASQVLQRL GFRGVWKGFL ARIIMIGTLT
321    ALQWFIYDSV KVFYFRLPRFP PPEMPESLKK KLGLTE
  
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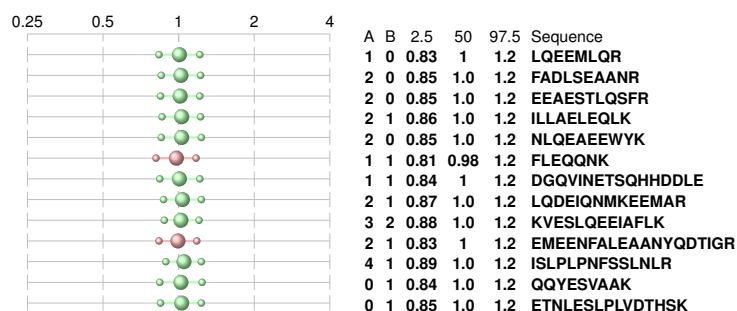
5.896 vimentin [Rattus norvegicus]

Protein Accession	gi 14389299	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.91, 1.14)	
Associated Peptides	13	
Associated Spectra	32	
Coverage	0.335	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.98	1.02
Avg..iTRAQ.Ratio....116.114.	0.824	0.845
Avg..iTRAQ.Ratio....117.114.	1.19	1.13

NHLBI Zile/Grant, Aged Rat

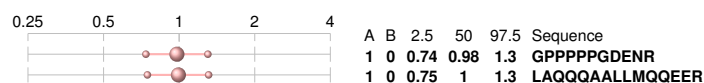
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1      MSTRSVSSSS YRRMFGGSGT SSRPSSNRSY VTTSTRYSL GSALRPSTSR SLYSSSPGGA YVTRSSAVRL RSSMPGVRL
81     QDSVDFSLAD AINTEFKNTR TNEKVELQEL NDRFANYIDK VRFLQQNKI LLAELEQLK GQKSRLGDLY EEMRELRRQ
161    VDQLTNDKAR VEVERDNLAE DIMRLREKLO EEMLQREEAE STLQSFRRQDV DNASLARLDL ERKVESLQEE IAFLLKHLDE
241    EIQLQAQIQ EQHVQIDVDV SKPDLTAALR DVRQQYESVA AKNLQEAEEW YRSKPADLSE AANRRNDALR QAKQESNEYR
321    RQVQSLTCEV DALKGTNESL ERQMREMEEN FALEAANYQD TIGRLQDEIQ NMKEEMARHL REYQDLLNVK MALDIEIATY
401    RKLLEGEESR ISLPLPNFSS LNLRETNLES LPLVDTHSKR TLLIKTVETR DGQVINETSQ HHDDLE
  
```



5.897 "PREDICTED: similar to splicing factor 3b, subunit 2 [Rattus norvegicus]"

Protein Accession	gij109459731
Mean Expression Ratio	0.986
Median Expression Ratio	0.984
Credible Interval	(0.76, 1.28)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	0.928
Avg..iTRAQ.Ratio....117.114.	1.21

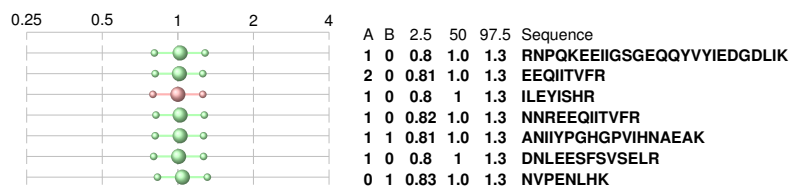


5.898 "lactamase, beta 2 [Rattus norvegicus]"

Protein Accession	gj 66730449	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.853, 1.21)	
Associated Peptides	7	
Associated Spectra	9	
Coverage	0.295	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.05	1.02
Avg..iTRAQ.Ratio....116.114.	1.05	0.973
Avg..iTRAQ.Ratio....117.114.	0.958	1.30

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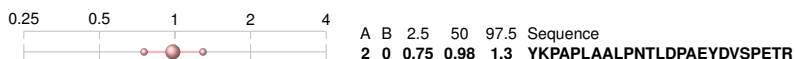
1   MAAALQRIEQ LSSRVVRLG CNPQPMTLQG TNTYLVGTGS RRILIDTGEP SVPEYISCLK QALAEFDTAI QEILVTHWHR
81  DHSGGIVDIC KNISNDATYC IKKLR RNPQK EEIIGSGEQQ YVYIEDGDLI KTEGATLRVL YTPGHTDDHM ALLLEENAI
161 FSGDCILGEG TTFEDLSDY MNSLKDLLKV KANIYYPGHG PVIHNAEAKI LEYISHRNNR EEQIITVFRD NLEESFSVSE
241 LRKMIYK NVP ENLHFMAEHN LLLHLRKLK DGKIFSIASP AKKWRASL
  
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5.899 "NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa [Rattus norvegicus]"

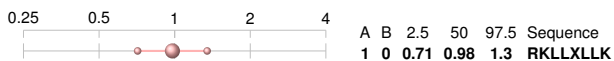
Protein Accession	gj 82617686	
Mean Expression Ratio	0.986	
Median Expression Ratio	0.984	
Credible Interval	(0.756, 1.29)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.194	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.921	
Avg..iTRAQ.Ratio....116.114.	1.05	
Avg..iTRAQ.Ratio....117.114.	1.11	

1 MSFSKYK**PAP** LAALPNTLDP AEYDVSP**ETR** KAQVERMSIR ARLKREYLLQ YNDPKRQTHI EDPALIRWTY ARSANVYPNF
 81 RPTPKNSLLG AVAGLGPLIF WYYVIKTRDRD KKERLIQEGK LDRKFSISY



5.900 PREDICTED: similar to nucleoporin 160 [Rattus norvegicus]

Protein Accession	gij109470295
Mean Expression Ratio	0.982
Median Expression Ratio	0.984
Credible Interval	(0.724, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.782
Avg..iTRAQ.Ratio....116.114.	0.818
Avg..iTRAQ.Ratio....117.114.	0.788



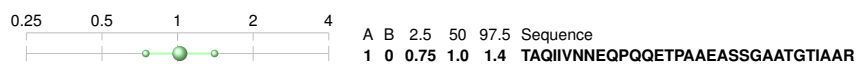
5.901 epidermal growth factor-containing fibulin-like extracellular matrix protein 1 [Rattus norvegicus]

Protein Accession	gij58865654
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.756, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0649

Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.938
Avg..iTRAQ.Ratio....116.114.	1.10
Avg..iTRAQ.Ratio....117.114.	1.79

```

1      MLQTVFLTML TLALVKSQVT EETITYTQCT DGYEWDVPRQ QCKDIDECDI VPDACKGGMK CVNHYGGYLC LPKTAQIIVN
81     NEQPQGETPA AEASSGAATG TIAARSMATS GVIPGGGFIA SATAVAGPEV QTGRNNFVIR RNPADPQRIP SNPSHRIQCA
161    AGYEQSEHNV CQDIDECTSG THNCRLDQVC INLRGSFTCH CLPGYQKRGE QCVDIDECVS PPYCHQGCVN TPGSFYQCQN
241    PFGQLAANNY TCVDINECDA SNQCAQQCYN ILGSFICQCN QGYELSSDRL NCEDIDECRT SSYLCQYQCV NEPGKFSCMC
321    PQGYQVRSR TCQDINECET TNECREDEM WNYHGGFRCY PQNPCQDPYV LTSENRCVCP VSNMTCRDVP QSIVYKYMNI
401    RSDRSVPSDI FQIQATTIYA NTINTFRIKS GNENGEFYLR QTSPVSAMLV LVKSLTGPRE HIVDLEMLTV SSIGTFRFTSS
481    VLRLTIIVGP FSF
    
```



5.902 gap junction membrane channel protein alpha 1 [Rattus norvegicus]

Protein Accession	gi 6978896
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.786, 1.33)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0942
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.21
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	1.06

```

1      MGDWSALGKL LDKVQAYSTA GQKVLVSVLF IFRILLGTA VESAWGDEQS AFRCNTQQPG CENVCYDKSF PISHVRFVWL
81     QIIFVSVPTL LYLAVFYVYM RKEEKLNKE EELKVAQTDG VNVMHLKQI EIKKFKYIE EHGKVMRGG LLRTYIISIL
161    FKSVEVAFL LIQWYIYGFS LSAVYTCKRD PCPHQVDCFL SRPTEKTIFI IFMLVSVLS LALNIIELFY VFFKGVKDRV
241    KGRSDPYHAT TGPLSPSKDC GSPKYAYFNG CSSPTAPLSP MSPPGYKLV GDRNNSSCRN YNKQASEQNW ANYSAEQNRM
321    GQAGSTISNS HAQPFDFPDD NQNARKVAAG HELQPLAIVD QRPSSRASSR ASSRPRPDDL EI
    
```



5.903 complement component factor h-like 1 [Rattus norvegicus]

Protein Accession	gij112984278
Mean Expression Ratio	1.02
Median Expression Ratio	1.02
Credible Interval	(0.777, 1.33)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0438
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.15
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.46

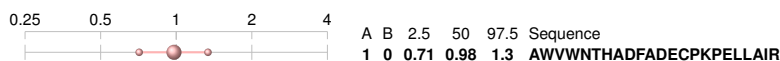
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1   MGFCRLLEFLV NVLLTSWFSS AKGEGIHCDF PKIRHGIVYD EKKYEPFSPV PGGKILYISC EYNFASPSS FWNPIICTEA
81  GWSPVVKCLR ICFPPSVENG HSTSSGQTHK EGDIVQIVCN QGYSLQNNQS TITCGEEGWS IPPKCISPNS AGKCGPPPSI
161 DNGDITSLSL PEYAPLSSVE YQCQNYFLK GNKIITCRNG KWSDPPTCLH ACVIPEDILE KHNIVLRWRE NGRIYSQSGE
241 NIEFMCKPGY RKLRGSPFFR SKCIDGHINY PTCL
    
```



5.904 PREDICTED: similar to Ran-specific GTPase-activating protein (Ran-binding protein 1) (RANBP1) (HpaI)

Protein Accession	gij62658198
Mean Expression Ratio	0.985
Median Expression Ratio	0.985
Credible Interval	(0.74, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.987
Avg..iTRAQ.Ratio....116.114.	0.875
Avg..iTRAQ.Ratio....117.114.	1.07

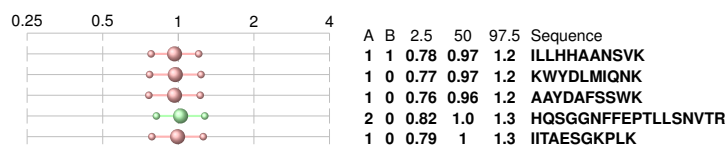


5.905 PREDICTED: similar to Succinate semialdehyde dehydrogenase (NAD(+)-dependent succinic semialdehyde

Protein Accession	gij109505749	
Mean Expression Ratio	0.985	
Median Expression Ratio	0.985	
Credible Interval	(0.818, 1.19)	
Associated Peptides	5	
Associated Spectra	7	
Coverage	0.115	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	0.766
Avg..iTRAQ.Ratio....116.114.	1.17	0.802
Avg..iTRAQ.Ratio....117.114.	0.88	1.1

```

1   MATCFLLRNF CAARPALRPP GRLLRPAGA QRRSYVGGPA DLHADLLRGD SFVGGRWLPT PATFPVYDPA SGAKLGTVAD
81  CGVPEARAAV R AAYDAFSSW EISVKERS LLR KWDLM I QNKDELAK I I TAESGKPLK AQGEILYSF FLEWFSEAR
161 RYVDIIYTS AKDKRGLVLK QPVGASIIIT PWNFPSSAMIT RKVGAALAAG CTVVVKPAED TPYSALALAQ LANQAGIPFG
241 VYNVIPCSRT KAKEVGEVLC TDPLVSKISF TGSTATGK I L LHHAANSVFR VSMELGGLAP FIVFDSANVD QAVAGAMASK
321 FRNAGQTCVC SNRFLVQRGI HDSFVTKFAE AMKSLRVGN GFEEGTTQGP LINEKAVEKV EKHVNDAVAK GATVVTGGKR
401 HQSGGNFFEP TLLSNVTR DM LCITEETFGP LAPVIKFDKE EEAVAIAAAA DVGLAGYFYS QDPAQIWRVA EQLEVGMVGV
481 NEGLISSVEC PFGGVKQSGL GREGSKYGID EYLEVKYVCY GGL
  
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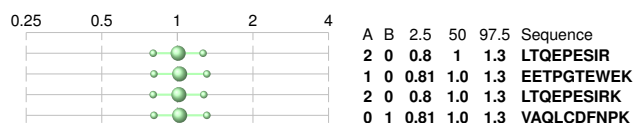
5.906 "clathrin, light polypeptide (Lcb) [Rattus norvegicus]"

Protein Accession	gij16758690	
Mean Expression Ratio	1.02	
Median Expression Ratio	1.02	
Credible Interval	(0.835, 1.24)	
Associated Peptides	4	

Associated Spectra	6	
Coverage	0.131	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.983	0.985
Avg..iTRAQ.Ratio....116.114.	1.05	1.08
Avg..iTRAQ.Ratio....117.114.	1.14	0.804

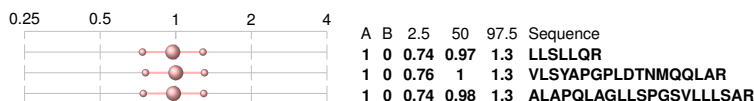
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1      MAEDFGFFSS  SESGAPEAAE  EDPAAAFDAQ  QESEIAGIEN  DSGFGAPAAS  QVASAQPLA  SGGGSEDMGT  TVNGDVFQEA
81     NGPADGYAAI  AQADRLTQEP  ESIRKWREEQ  KKRLQELDAA  SKVTEQEWRE  KAKKDLEWN  QRQSEQVEKN  KINNRIADKA
161    FYQQPDADTI  GYVASEEAFV  KESKEETPGT  EWEKVAQLCD  FNPKSSKQCK  DVSRLRSVLM  SLKQTPLSR
    
```



5.907 PREDICTED: similar to Sepiapterin reductase (SPR) [Rattus norvegicus]

Protein Accession	gij 34856334
Mean Expression Ratio	0.984
Median Expression Ratio	0.985
Credible Interval	(0.772, 1.25)
Associated Peptides	3
Associated Spectra	3
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.18
Avg..iTRAQ.Ratio....116.114.	1.04
Avg..iTRAQ.Ratio....117.114.	0.882



5.908 PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]

Protein Accession	gij109475178
Mean Expression Ratio	0.984
Median Expression Ratio	0.985
Credible Interval	(0.737, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	0.172
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.964
Avg..iTRAQ.Ratio....116.114.	0.818
Avg..iTRAQ.Ratio....117.114.	1.02

1 MFQYDSTHGK FNGTVKAENE KLVINRRPIT IFQERDPANI LWGDAGDEYV VESTGHSR



5.909 cytochrome b [Rattus norvegicus]

Protein Accession	gij110189675
Mean Expression Ratio	0.985
Median Expression Ratio	0.985
Credible Interval	(0.736, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0237
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.979
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	0.918

NHLBI Zile/Grant, Aged Rat

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1      MTNIRKSHPL FKIINHSEFD LPAPSNISSW WNFSGLLGVC LMVQILTGLF LAMHYTSDTM TAFSSVTHIC RDVNYGWLIR
81     YLQANGASMF FICLFLHVGR GLYYGSYTFE ETWNIGIILL FAVMATAFMG YVLPWQMSF WGATVITNLL SAIPYIGTTL
161    VEWIWWGGSV DKATLRFFA FHFILPFIIA ALAIVHLLFL HETGSNNPTG LNSDADKIPF HPYYTIKDLL GVFMLLLFLM
241    TLVLFPPDLL GDDNYTPAN PLNTPPHIKP EWYFLFAYAI LRSIPNKLGG VVALILSILI LAFPLFLHTS KQRSLTFRPI
321    TQILYWILVA NLLVLTWIGG QPVEHPFIII GQLASISYFS IILILMPISG IVEDKMLKWN
  
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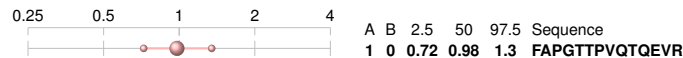


5.910 "proteasome (prosome, macropain) subunit, beta type 10 [Rattus norvegicus]"

Protein Accession	gi 71043724
Mean Expression Ratio	0.985
Median Expression Ratio	0.985
Credible Interval	(0.731, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0513
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.992
Avg..iTRAQ.Ratio....116.114.	0.994
Avg..iTRAQ.Ratio....117.114.	0.975

```

1      MLKQAVEHRG GFSFENCQRN ASLEHVLPGL RVPLARKTGT TIAGLVFRDG VILGADTRAT NDSVVADKSC EKIHFIAPKI
81     YCCGAGVAAD TEMTTRMAAS KMELHALSTG REPRVATVTR ILRQTLFRYQ GHVGASLIVG GVDLNGPQLY SVHPHGSYSR
161    LPFTALGSGQ DAAVALLEDR FQPNMTLEAA QELLVEAITA GILGDLGSGG SVDACVITAG GARLQRALSS PIEPVQRAGQ
241    YRFAPGTPV QTQEVRALTL ELLEETVQAM EVE
  
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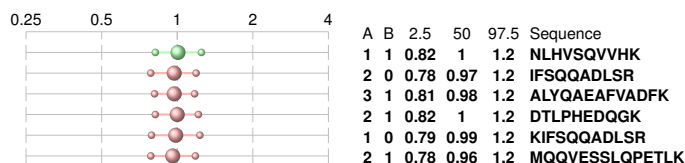
5.911 serine protease inhibitor 2b [Rattus norvegicus]

Protein Accession	gi 6981576
Mean Expression Ratio	0.985
Median Expression Ratio	0.985
Credible Interval	(0.843, 1.15)
Associated Peptides	6

Associated Spectra	15	
Coverage	0.143	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.987	0.777
Avg..iTRAQ.Ratio....116.114.	0.94	0.817
Avg..iTRAQ.Ratio....117.114.	1.03	0.968

```

1      MAGICPAVLC  DGILGRDTLP  HEDQGNGRQL  HSLTLASINT  DFTLSLYKKL  ALRNPDKNVV  FSPLSSISAAL  AILSLGAKDS
81     TMEEILEVLK  FNLTEITEEE  IHQGFGHLLQ  RLSQPEDQAE  INTGSALFID  KEQPILSEFQ  EKTRALYQAE  AFVADFKQCN
161    EAKKFINDYV  SNQTQGGIAE  LFSELDERTS  MVLVNYLLFK  GKWKVPPFNP  DTFESEFYLD  EKRSVKVPM  KIKDLTTPYI
241    RDEELSCSVL  ELKYTGNASA  LFILPDQGK  QQVESSLQPE  TLKKWKDSL  PRIISELRMP  KFSISTDYNL  EEVLPDLGIR
321    KIFSQQADLS  FITGTKNLHV  SQVVHAVLD  VDETGTEGAA  ATAVTAALKS  LPQTIPLLN  NRPFMLVITD  NNGQSVVFMG
401    KVTNPM
  
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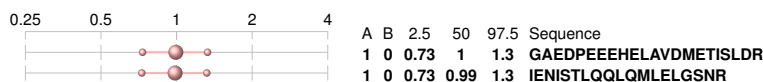


5.912 "protein phosphatase 1, regulatory (inhibitor) subunit 7 [Rattus norvegicus]"

Protein Accession	gi 57634526
Mean Expression Ratio	0.989
Median Expression Ratio	0.985
Credible Interval	(0.756, 1.30)
Associated Peptides	2
Associated Spectra	2
Coverage	0.114
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.04
Avg..iTRAQ.Ratio....116.114.	1.10
Avg..iTRAQ.Ratio....117.114.	0.938

```

1      MAAERGAGQQ  QSQEMMEVDR  RVESEESGDE  EGKKGGGIV  ADLSQQSLKD  GVERGAEDPE  EEHELAVDME  TISLDRDAED
81     VDLNHYRIGK  IEGFEVLKKV  KSLCLRQNLI  KCIENLDELQ  SLRELDLYDN  QIKKIENLEA  LTELEVLDIS  FNLLRNIEGI
161    DKLTQLKKLF  LVNNKINKIE  NISTLQQLQM  LELGSNIRA  IENIDTLTNL  ESFLGKNKI  TKLQNLDALS  NLTVLSMQSN
241    RLTKIEGLQN  LVNLRELYLS  HNGIEVIEGL  ENNNKLTMLD  IASNRIKKIE  NISHLTELQE  FWMNDNLLES  WSDLDELKGA
321    RSLETVYLER  NPLQKDPQYR  RKVMLALPSV  RQIDATFVRF
  
```

5.913 mannose phosphate isomerase [Rattus norvegicus]

Protein Accession	gij51854221
Mean Expression Ratio	0.986
Median Expression Ratio	0.986
Credible Interval	(0.734, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0378
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.993
Avg..iTRAQ.Ratio....116.114.	0.982
Avg..iTRAQ.Ratio....117.114.	0.943

```

1   MANPRVFPLS  CVVQQYAWGK  VGSKSEVACL  LACSDPLTQI  SEDKPYAELW  MGAHPRGDAK  ILDNRISQKT  LGQWIAENQN
81  SLGQKVKDTF  NGKLPFLFKV  LSVETALSIQ  AHPNKELEAK  LHLQAPHEYP  DANHKPEMAI  ALTPFQGLCG  FRPVVEIVTF
161 LKKVPEFQSL  IGEDATAQLK  KSMNEGSAM  ASALKNCFSH  LMKSEKKVVV  EQLNLLVKRI  SQQISNGNSM  DDICGELLQ
241 LHQQYPGDIG  CFAYILLNLI  TLKPGEAMFL  EANVPHAYLK  GDCVECMACS  DNTVRAGLTP  KFDIVSTLCE  MLDYTPSPSK
321 DRLFAPTLSQ  DDPYLSIYDF  PVPDFTVMKI  EVPGSVTEYK  VLTLDASAIL  LLVQGTVTAI  IPSVQGEIPL  SRGGVLFIGA
401 NETVLLKLTV  PKNLLIFRAC  CLL
    
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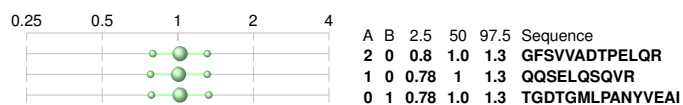
5.914 LIM and SH3 protein 1 [Rattus norvegicus]

Protein Accession	gij14249130	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.809, 1.28)	
Associated Peptides	3	
Associated Spectra	4	
Coverage	0.144	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.01	0.906

Avg..iTRAQ.Ratio....116.114.	0.949	0.866
Avg..iTRAQ.Ratio....117.114.	1.22	1.24

```

1      MNPNCARCGK IVYPTKVNK LDKFWHKACF HCETCKMTLN MKNYKGYEKK PYCNAHYPKQ SFTMVADTPE NLRLKQOSEL
81     QSQVRYKEEF EKNKGGGFSV VADTPELQRI KKTQDQISNI KYHEEFKSR MGPSGGEGIE PERREAQDSS SYRRPTEQQQ
161    PQQPHIPTSA PVYQQPQQQQ VTPSYGGYKE PAAPVSIQRS APGGGGKRYR AVYDYSADE DEVSFQDGDG IVNVQQIDDG
241    WMYGTVERTG DTGMLPANYV EAI
    
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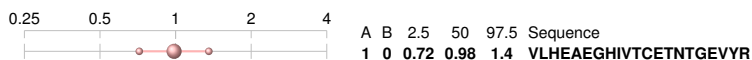


5.915 PREDICTED: similar to small nuclear ribonucleoprotein D3 [Rattus norvegicus]

Protein Accession	gij109509970
Mean Expression Ratio	0.987
Median Expression Ratio	0.986
Credible Interval	(0.73, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	0.167
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.985
Avg..iTRAQ.Ratio....116.114.	0.84
Avg..iTRAQ.Ratio....117.114.	1.13

```

1      MSIGVPIKVL HEAEGHIVTC ETNTGEVYRG KLIEAEDNMN CQMSNITVTY RDGRVAQLEQ VYIRGSKIRF LILPDMLKNA
81     PMLKSMKKNK QGSGAGRGKA AILKAQVAAR GRGRGMGRGN IFQKRR
    
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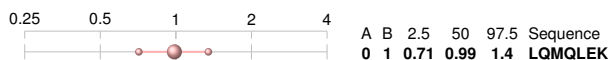


5.916 "PREDICTED: similar to myosin, heavy polypeptide 9, non-muscle [Rattus norvegicus]"

Protein Accession	gj 109492331
Mean Expression Ratio	0.986
Median Expression Ratio	0.986
Credible Interval	(0.732, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00556
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.556
Avg..iTRAQ.Ratio....116.114.	0.907
Avg..iTRAQ.Ratio....117.114.	1.30

```

1    MAEPEDQADG SNLEGEQ TSA EEETEQQYTE GHEVSPQLEN SGQKTAEGRE PTQDPERGIT TDSEGRLEGE MVDAERVSTE
81   GEAISEGEVG SIGEAPPETE VEFIGEAPPD TVVEFIGEAP PGTEVEFIGE TTPETQAEPT GEATPGVAVK TIRKAEQVEVE
161  VIREVISETD VDSIVKAIQG VDLESIGATI POKKVKYTAK ARPQDEAEPT GEPAPEGDFD VSEQEKAGHP SELDELSDI I
241  SSPAFSYSDV SPWDMGEEEA KALTTQDISQ ESVYEPIELI QPTEPTEPPE DSVVSAFQCL PAYPSRQRF PMGARHRFRL
321  SIMGSLTPSD IDDLPLETEE ALQQESVQPP PRAHEETRIQ FLDQVQTL SL EDETQIERPM SEGSDAE EEE GAQLMVLDPD
401  HPLMVRFEA LKSYLNRQID KLKLDIQELD VATKQTRIQR QELGVNLYGV QQHLAR LQMQL EFSHDRHSL VACERRRKEE
481  ELQCNRALYN KTYATAKEER KKFAALQTEM ESLALHLFYM QNIDQDVRDD IQVMKQVVKK TETEKMNAEI EKKKQDLFVD
561  QLTERAHQLE ENIALYEAQY LSQAEDTRVL RKAVTEAITE IDTIIMEKKR ILQQWTTSLV GMKHRNEAYR TVMDALRECE
641  HQVKSIDSEI EAYKKSIMQE EKNEKLARL LNRAETEAL VQKMTQCLS KQETLQTEFN TYHLALQDTE EMLNKGVEH
721  SAVLSELQGT RQAVHQEQL RQKMDISIMD KLQEHGTSSK MTKYFHQLLR KLQKENTNLV THLSKIDGDI AQTLDITNT
801  NGKVMHKKT LLDLDKEVVR FNELITNSES EIVRRTILIE RKQSLINFFN KQLEQMVSVL GGEAGPLEL EIKRLSKLTE
881  EYNTGVTQAO MTWLR LQOEL VQISHEREER LESVDLQKKE VHIMEQKKLR IENKIEHEKR EQKMVSRHMR DLDNDLSKLN
961  MLLDKNRCSS ELLEQNNAVA ETEFVRTLKD AERETIQMQE KLSELCEEKA TLLNSLVEAE HQIMLWEKKI QLAKEMRSSV
1041 DSDTGQTEIR AMKAEIHRMR VKHGQLLKQQ EK MIRDME LA VARRETIVIQ AEGQSKIDKK IVTKSDFHFQ QSELRKKIRE
1121 VHKATEECSK TVLEEEAQK LSSSLQEKQ QSLSDMQSDT DVLEEEISHL SALKRKNLLE IVALQTRAKH LQAAVDGKYV
1201 FLHRNSKAQL MERKRLGMKL SQLSSVLSRV QEDYPQYQEM LQKIQEKIAT RLEAPEFS
    
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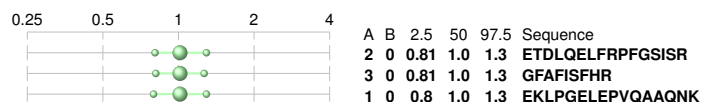
5.917 "eukaryotic translation initiation factor 3, subunit 4 (delta) [Rattus norvegicus]"

Protein Accession	gj 61556927
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.832, 1.25)
Associated Peptides	3
Associated Spectra	6
Coverage	0.128

Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	1.10
Avg..iTRAQ.Ratio....117.114.	0.994

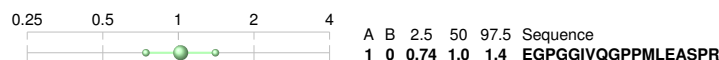
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1      MPTGDFDSKP SWADQVEEEG EDDKCVTSEL LKGIPLPTGD TSPEPELLPG DPLPPPKEVI NGNIKTVTEY KVEEDGKKFK
81     IVRTFRIETR KASKAVARRK NWKKFGNSEF DPPGPNVATT TVSDDVSMTF ITSKEDLNCQ EEEDPMNKLK GQKIVSCRIC
161    KGDHWTRCP  YKDTLGPMQK ELAEQLGLST GEKEKLPGEL EPVQAAQNT GKYVPPSLRD GASRRGESMQ PNRRADDNAT
241    IRVTNLS EDT RETDLQELFR PFGSISRIYL AKDKTTGQSK GFAFISFHR EDAARAIAGV SGFGYDHLIL NVEWAKPSTN
    
```



5.918 PREDICTED: similar to Cdc42 effector protein 4 (Binder of Rho GTPases 4) [Rattus norvegicus]

Protein Accession	gij 34875025
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.758, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.12
Avg..iTRAQ.Ratio....116.114.	1.17
Avg..iTRAQ.Ratio....117.114.	1.07

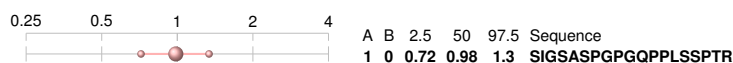


5.919 membrane-associated DHHC5 zinc finger protein [Rattus norvegicus]

Protein Accession	gi 86129562
Mean Expression Ratio	0.984
Median Expression Ratio	0.986
Credible Interval	(0.737, 1.31)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0266
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.27
Avg..iTRAQ.Ratio....116.114.	0.895
Avg..iTRAQ.Ratio....117.114.	1.02

```

1      MPAESGRKRF  PSKYVVPVSA  AIFLVGATTL  FFAFTCPGLS  LDVSPAVPIY  NAIMFLFVLA  NFSMATFMDP  GIFPRAEED
81     DKEDDFRAPL  YKTVEIKGIQ  VRMKWCATCR  FYRPPRCSHC  SVCDNCVEEF  DHHCPWVNNC  IGRNRYRYFF  LFLSLTAHI
161    MGVFGFGLLY  VLCHIEELSG  VRTAVTMAMV  CVAGLFFIPV  AGLTGFHVVL  VARGRTTNEQ  VTGKFRGGVN  PFTNGCCNV
241    SRVLCSSPAP  RYLGRPKKEK  TIVIRPPFLR  PEVSDGQITV  KIMDNIGIQE  LRRTKSKGSL  EITESQSADA  EPPPPKPD
321    SRYTGLRTHL  SLATNEDSSL  LGKDSPTTPT  MYKYRPGYSS  SSTSAMPHS  SSAKLSRGDS  LKEPTSIADS  SRHPSYRSE
401    SLEPESFRSP  TFGKSFHFD  LSSGSRSSSL  KSAQGTGFEL  GQLQSIRESG  TTSTSYKSLA  NQTRNGSLSY  DSSLTPSD
481    DFEVQAGPE  PDPPLGYTSP  FLSARLAQQR  EAERHRPRLP  TGPPHREPS  VRYDNLRSRI  VASLQEREKL  LRQSPPLA
561    EEEPGLGDSG  IQSTPGSGHA  PRTSSSSDD  KRSPLSKTPL  GRPAVPRFGK  PDGLRGRGLG  SPEPGTTAPY  LGRSMSYS
641    KAPSGVSETE  EVALQPLLTP  KDEVQLKTTY  SKSNGQPKSI  GSASPGGQP  PLSSPTRGGV  KKVSGVGGTT  YEISV
    
```



5.920 WW domain binding protein 2 [Rattus norvegicus]

Protein Accession	gi 20376818
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.755, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0382
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.02
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	1.13

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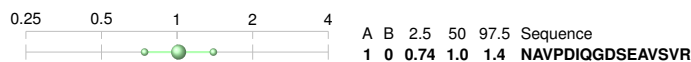
1      MALNKNHSEG  GGVIWNNTES  ILMSYDHVEL  TFNDMKNVPE  AFKGTKKGTV  YLTPYRVIFL  SKGKDAMRSF  MMPFYLMKDC
81     EVKQPVFGAN  FIGTVKAEA  GGGWEGSASY  KLTFTAGGAI  EFGQQLQVA  SQASRGEVFN  GAYGYPYMP  GAYVFPVVA
161    NGMYPCPPGY  PYPPEPEFY  PGPPMDGAM  GYVQPPPPY  PGPMEPPVVS  GPSAPPTPAA  EAKAAEAAAS  AYYNPGNPHN
241    VYMPTSQPPP  PYPYPPEDKK  TQ
    
```



5.921 cAMP-dependent protein kinase inhibitor gamma [Rattus norvegicus]

Protein Accession	gij 23618889
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.758, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	0.211
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	1.22

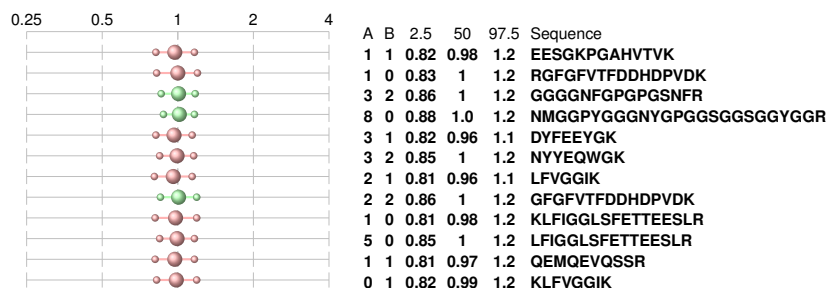
1 MMEVESSYSD FISCRTGRR NAVPDIQGDSEAVSVRKLKAG DMGELALEGA EGQAEGSTPD KEASSQPSS DANTSS



5.922 PREDICTED: similar to Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1) [Rattus

Protein Accession	gij 109473494	
Mean Expression Ratio	0.987	
Median Expression Ratio	0.986	
Credible Interval	(0.891, 1.09)	
Associated Peptides	12	
Associated Spectra	41	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.962	1.04
Avg..iTRAQ.Ratio....116.114.	1.06	0.955

Avg..iTRAQ.Ratio....117.114. 0.953 1.00



5.923 PREDICTED: similar to Integrin beta-1-binding protein 2 (Melusin) [Rattus norvegicus]

Protein Accession	gij 34881120
Mean Expression Ratio	0.987
Median Expression Ratio	0.986
Credible Interval	(0.728, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	0.948
Avg..iTRAQ.Ratio....117.114.	0.962

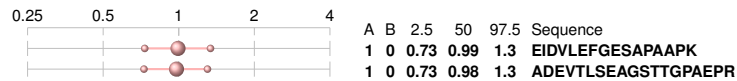


5.924 paralemmi [Rattus norvegicus]

Protein Accession	gi 18677765
Mean Expression Ratio	0.987
Median Expression Ratio	0.986
Credible Interval	(0.754, 1.28)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0914
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.02
Avg..iTRAQ.Ratio....116.114.	1.00
Avg..iTRAQ.Ratio....117.114.	1.06

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1      MEVLATDTVS QQERLQAIAE KRRKQAEIES KRRQLEDDRR QLQYLKSKAL RERWLLEGTP SSASEGDEDM RKQMQEDEQK
81     ARSLEESITR LEKEIDVLEF GESAPAAPKE NSAAPSPIRP HSTSPAKEEQ KSETMVNAQQ TPLGTPKENR KSTPVRSPGG
161    SMMKAAMYS VEITVEKDKV TGETRVLSSST TLLPRDPLPQ GVKVYEDETK VVHAVDGLSE NGIQPLSSE VDELIHK ADE
241    VTLSEAGSTT GPAEPRGLAE DVTRTTPSRR EITGVEAQPQ EATSGPPGIQ PGQEPVVTMV FMGYQNVDE AETKKVLGLQ
321    DTIKAELVVI EDSVTPREPA PLNGSAAELP ATKEENQTGP TTPSDTQDL DMKKPRCRC SV
    
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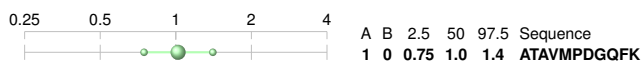


5.925 peroxiredoxin 1 [Rattus norvegicus]

Protein Accession	gi 16923958
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.757, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0553
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.1
Avg..iTRAQ.Ratio....116.114.	1.07
Avg..iTRAQ.Ratio....117.114.	1.07

```

1      MSSGNAKIGH PAPSFKATAV MPDGGQFKDIS LSDYKGYVY FFFYPLDFTF VCPTEIIAFS DRAEEFKLN CQVIGASVDS
81     HFCHLAWINT PPKQGGLGPM NIPLVSDPKR TIAQDYGVLK ADEGISFRGL FIIDDRGILR QITINDLPVG RSVDEILRLV
161    QAFQFTDKHG EVCAPAGWKP SDTIKPDVNK SKEYFSKQK
    
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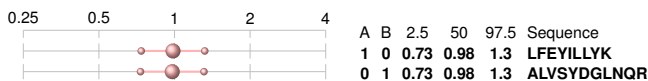



5.926 ependymin related protein 2 [Rattus norvegicus]

Protein Accession	gi 56090361	
Mean Expression Ratio	0.985	
Median Expression Ratio	0.987	
Credible Interval	(0.753, 1.28)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	0.0893	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.17	0.728
Avg..iTRAQ.Ratio....116.114.	1.08	0.844
Avg..iTRAQ.Ratio....117.114.	0.821	1.06

```

1      MLTRAPRRLV QGPRETWLLG GLWVWILCGL GMAGSPGTPQ PCQAPQQWEG RQVLYQQSSG HNSRALVSYD GINQVRVLD
81     ERKALIPCKR LFEYILLYK D GVMFQIEQAT KLCAKIPLAE PWDPLDIPQN STFEDQYSIG GPQEQIMVQE WSDRRTARSY
161    ETWIGVYTAK DCYPVQETFI RNYTVVLSTR FFDVQLGIKD PSVFTPPSTC QTAQPEKMKE NCSL
  
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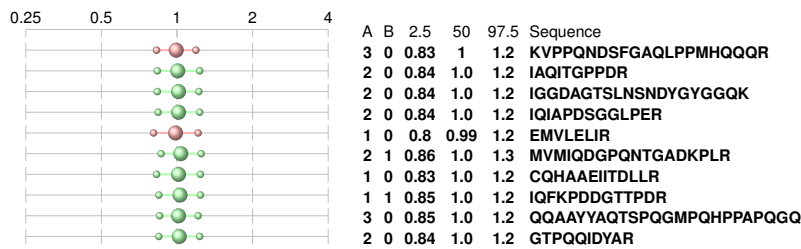
5.927 far upstream element (FUSE) binding protein 1 [Rattus norvegicus]

Protein Accession	gi 83320094	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.895, 1.15)	
Associated Peptides	10	
Associated Spectra	21	
Coverage	0.235	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.986	1.14
Avg..iTRAQ.Ratio....116.114.	1.14	0.935

Avg..iTRAQ.Ratio....117.114. 1.03 1.31

```

1      MADYSTVPPP SSGSAGGGGG GGVNDAFKDA LQRARQIAAK IGGDAGTSLN SNDYGYGGQK RPLEDGDQPD AKKVPPQND
81     FGAQLPPMHQ QRRSVMTEEY KVPDGMVGF IGRGGEQISR IQQESGCKIQ IAPDSGGLPE RSCMLTGTPE SVQSAKRLLD
161    QIVEKGRPAP GFHHGDGPGN AVQEIMIPAS KAGLVIGKGG ETIKQLQERA GVKMVMIQDG PQTGADRPL RITGDPYKVO
241    QAKEMVLELI FDQGGFREVR NEYGSRIGGN EGIDVPIPRF AVGIVIGRNG EMIKKIQNDA GVRIQFKPDD GTTPDRIAQI
321    TGPPDRCQHA AEIITDLES VQAGNPGGPG PGGRRGRGQ GNWNMGPPGG LQEFNFIVPT GKTGLIIGKG GETIKSISQQ
401    SGARIELQRN FPPNADPNMK LFTIRGTPQQ IDYARQLIEE KIGGFVNLPG PVPFHGPHGV PGPHGPPGPP GPGTTPMGPYN
481    PAPYNPFPFG PAPHGPPAPY APQGWGNAYP HWQQQAPPDP AKAGTDPNSA AWAAYYAHYY QQAQPPFAA PAGAPTTPQT
561    NGQGDQQNPA PAGQVDYTKA WEEYYKMGQ AVPAPAGAPP GGQPDYSAAW AEYYRQAAAY YAQTSPQGM P HPPAPQGG
    
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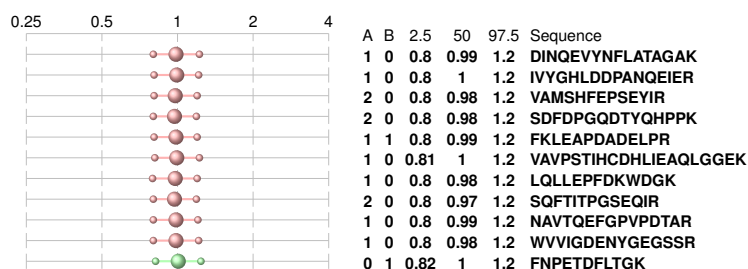


5.928 "aconitase 2, mitochondrial [Rattus norvegicus]"

Protein Accession	gij 40538860	
Mean Expression Ratio	0.987	
Median Expression Ratio	0.987	
Credible Interval	(0.858, 1.14)	
Associated Peptides	11	
Associated Spectra	15	
Coverage	0.206	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	0.996
Avg..iTRAQ.Ratio....116.114.	0.89	1.10
Avg..iTRAQ.Ratio....117.114.	1.03	1.07

```

1      MAPYSLLVTR LQKALGVRQY HVASALCQRA KVAMSHFEPS EYIRYDLLEK NINIVRKRNL RPLTLSEKIV YGHLDDPANQ
81     EIERGKTYLR LRPDRVAMQD ATAQMAMLQF ISSGLPKVAV PSTIHCDHLI EAQLGGEKDL RRAKDINQEV YNPLATAGAK
161    YGVGFWRPFG GIIHQIILEN YAYPGVLLIG TDSHTPNGGG LGGICIGVGG ADAVDVMAGI PWELKCPKVI GVKLTGTLSG
241    WTSFKDVILK VAGILTVKGG TGAIVEYHGP GVDSSISCTGM ATICNMGAEI GATTSVFPYN HRMKKYLST GRADIANLAE
321    EFKDHLVDPD GCQYDQVIEI NLNELKPHIN GPFTPDLAHP VADVGTVAEK EGWPLDIRVG LIGSCTNSSY EDMGRSAAVA
401    KQALAHGLKC KSFPTITPGS EQIRATIERD GYAQILRDVG GIVLANACGP CIGQWDRKDI KKGKNTIVT SYNRFNFTGRN
481    DANPETHAFV TSPEIVTALA IAGTLKNPE TDFLTGDPDGK KFKLEAPDAD ELPRSDFDDPG QDTYQHPPPKD SSGQRVDVSP
561    TSQRLQLLEP FDKWDGKDL DLQILIKVKG KCTTDHISAA GPWLKFRGHL DNISNLLIG AINIENKAN SVRNAVTQEF
641    GPVPDTAFYY KKHGIRWVVI GDENYGESS REHAALEPRH LGGRAITKS FARIHETNLK KQGLLPLTFA DPSYDNKIHP
721    VDKLTIQGLK DFAPGKPLNC IIKHPNGTQE TILLNHTFNE TQIEWFRAGS ALNRMKELQQ
    
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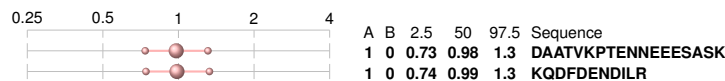


5.929 PREDICTED: similar to Eukaryotic translation initiation factor 5B (eIF-5B) (Translation initiation)

Protein Accession	gij109508037
Mean Expression Ratio	0.985
Median Expression Ratio	0.987
Credible Interval	(0.754, 1.29)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0247
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	0.847
Avg..iTRAQ.Ratio....117.114.	1.06

```

1      MGKKQKNKSE DSTKDDTDLG ALAAEIEGAG AAKEQEPQKG KGKKKKEKK QDFDENDILR ELEELSLEAQ GIGADRDAAT
81     VKPTENNEEE SASQDKKKK GQKGGKTSFD ENDSELEEDK DSKSKKPARP NSEVLLSGSE DADDPNKLKSK KGKKAQKSTK
161    KRDSSEEDD NSKRKRSR VNSSGESGGE SDEFLOSRKG QKKNQKNKSV PTIDSGNEDD DSSFKIKTVA QKKAKKERE
241    RKKREERKAK LRKVKKEEL EKGRKEQSKQ REPQKRDEE VLVLRGTPDA GAASEEKGDI AATLEDDNEG DKKKKDKKKK
321    KTEKDDKEKE KKGPSKSTV KAIQEALAKL REEERQKRE EEERIKRLEE LEAKRKEER LEQEKRRERK QKEKERKERL
401    KKEGKLLTKS QREARARAEV TLRHLQAQGV EVPSKDSLPK KRPVYEDKKK KPTPQQLLESK EALETVEVSA PEETPPSVDA
481    EDEETEDAG LDDWEAMASD EEREKGNMIE IEVEENPEEE EEEEEDEDEE DSEDEDEEGD SEDSEYDSD DRTKEERAYD
561    KAKRRIEKRR LEHGKVNTE KLRAPIICVL GHVDTGKTKI LDKLRHTHVQ DGEAGGITQQ IGATNVPLEA INEQTKMIK
641    FDRNVRIIPG MLIIDTPGHE SFSNLRNRGS SLCDIALLV DIMHGLEPQT IESINILKSK KCPFIVALNK IDRLYDWKKS
721    PDSDVAVTLK KQKNKTKDEF EERAKAIVE FAQQGLNTAL FYENKDPRTF VSLVPTSHT GDGMGSLIYL LVELTQTMLS
801    KRLAHCEELR AQVMEVKALP GMGTTIDVIL INGRKKEGDT IIVPGVEGPI VTQIRGLLLP PPMKELRVKN QYKHKVEEA
881    AQGVKILGKD LEKTLAGLPL LVAYKDDEIP VLKDELIHEL KQTLNAIKLE EKGVYVQAST LGSLEALLEF LKTSEVPYAG
961    INIGPVHKD VMKASVMLEH DPQYAVILAF DVRIERDAQE MADSLGVRIF SAEIIYHLFD AFTKYRQDYK KQKQEEFKHI
1041   AVFPCKMKIL PQYIFNSRDP VVIGVTVEAG QVKQGTPMC VPSKNFVDIGI VTSIEINHKKQ VDVAKKGQEV CVKIEPIPGE
1121   SPKMFGRHFE ATDILVSKIS RQSIDALKDW FRDEMQRSDW QLIVELKKVF EII
    
```



5.930 fractured callus expressed transcript 1 [Rattus norvegicus]

Protein Accession	gi 16758100
Mean Expression Ratio	0.987
Median Expression Ratio	0.987
Credible Interval	(0.77, 1.26)
Associated Peptides	2
Associated Spectra	3
Coverage	0.34
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.96
Avg..iTRAQ.Ratio....116.114.	1.10
Avg..iTRAQ.Ratio....117.114.	1.01

1 MEHQQQQLRN LRDFLLVYNR MTELCFQRCV PSLHHRALDA EEEACLHSCA GKLIHSNHR L MAAYVHLMPA LVQFRMADYE
 81 AASAVPGVPA EQPRDSPSGS



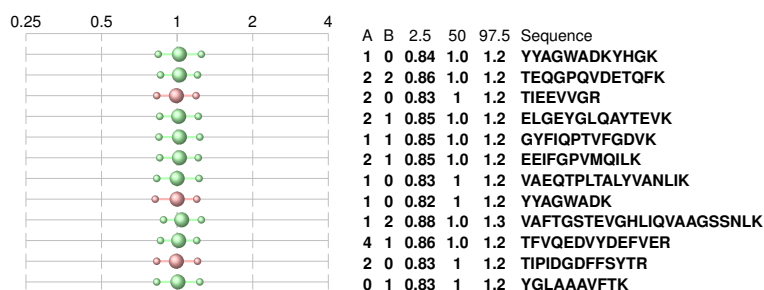
5.931 aldehyde dehydrogenase 2 [Rattus norvegicus]

Protein Accession	gi 14192933	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.903, 1.13)	
Associated Peptides	12	
Associated Spectra	28	
Coverage	0.287	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.99	1.02
Avg..iTRAQ.Ratio....116.114.	0.95	0.945
Avg..iTRAQ.Ratio....117.114.	0.848	1.86

NHLBI Zile/Grant, Aged Rat

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1      MLRAALSTAR RGPRLSRLLS AAATSAVPAP NQQPEVFCNQ IFINNEWHDA VSKKTFPTVN PSTGEVICQV AEGNKEDVDK
81     AVKAAQAAFQ LGSPWRRMDA SDRGRLLYRL ADLIERDRTY LAALETLDNG KPYVISYLVD LDMVLKCLRY YAGWADKYHG
161    KTIPIDGDFE SYTHHEPVGV CGQIIPWNFP LLMQAWKLGK ALATGNVVVM KVAEQTPLTA LYVANLIKEA GFPPGVVNI
241    PFGGPTAGAA IASHEDVDKV AFTGSTVEVGH LIQVAAGSSN LKRVTLLEGG KSPNIIMSDA DMDWAVEQAH FALFFNQGC
321    CCAGSRFFVQ EDVYDEFVER SVARAKSRV GNPFDSEEQ GPQVDETQFK KILGYIKSGQ QEGAKLLCGG GAAADRGYFI
401    QPTVFGDVKD GMTIAKEEIF GPVMQILKFK TIEEVVGRAN NSKYGLAAAV FTKDLKANY LSQALQAGTV WINCYDVFGA
481    QSPFGGYKMS GSGRELGEYG LQAYTEVKTV TVKVPQKNS
  
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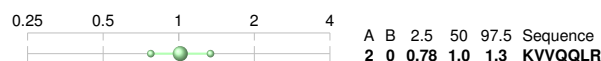


5.932 "guanine nucleotide binding protein (G protein), gamma 5 subunit [Rattus norvegicus]"

Protein Accession	gi 13242281
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.774, 1.32)
Associated Peptides	1
Associated Spectra	2
Coverage	0.103
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.921
Avg..iTRAQ.Ratio....116.114.	1.04
Avg..iTRAQ.Ratio....117.114.	1.21

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1      MSGSSSSVAAAM KKVQQLRLE AGLNRVKVSP AAADLKQFCL QNAQHDPPLT GVSSSTNPFPR PQKVCSEFL
  
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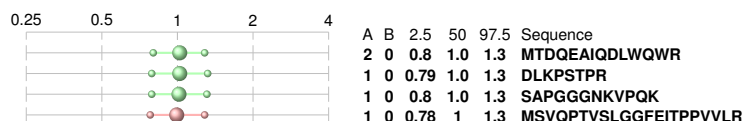


5.933 nucleophosmin 1 [Rattus norvegicus]

Protein Accession	gi 7242160
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.821, 1.25)
Associated Peptides	4
Associated Spectra	5
Coverage	0.188
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.02
Avg..iTRAQ.Ratio....116.114.	0.954
Avg..iTRAQ.Ratio....117.114.	1.25

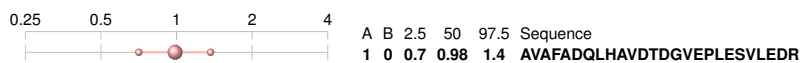
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1   MEDSMDMDMS PLRPQNYLFG CELKADKDYH FKVDNDENEH QLSLRTVSLG AGAKDELHIV EAEAMNYEGS PIKVTLATLK
81  MSVQPTVSLG GFEITPPVVL RLKCGSGPVH ISGQHLVAVE EDAESEDEDE EDVKLLGMSG KR SAPGGGNK VPQK KVKLDE
161 DDDDDDDDE DEDDDDDDF DEEETEKVP VKKSVRDTPA KNAQKSNQNG KDLKPSTPR S KGQESFKQE KTPKTPKGPS
241 SVEDIKAKMQ ASIEKGGSLP KVEAKFINYV KNCFRMTDQE AIQDLWQWFK SL
  
```



5.934 "PREDICTED: similar to CG33649-PA, isoform A [Rattus norvegicus]"

Protein Accession	gi 109497345
Mean Expression Ratio	0.987
Median Expression Ratio	0.988
Credible Interval	(0.719, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
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Avg..iTRAQ.Ratio....117.114.	1.26

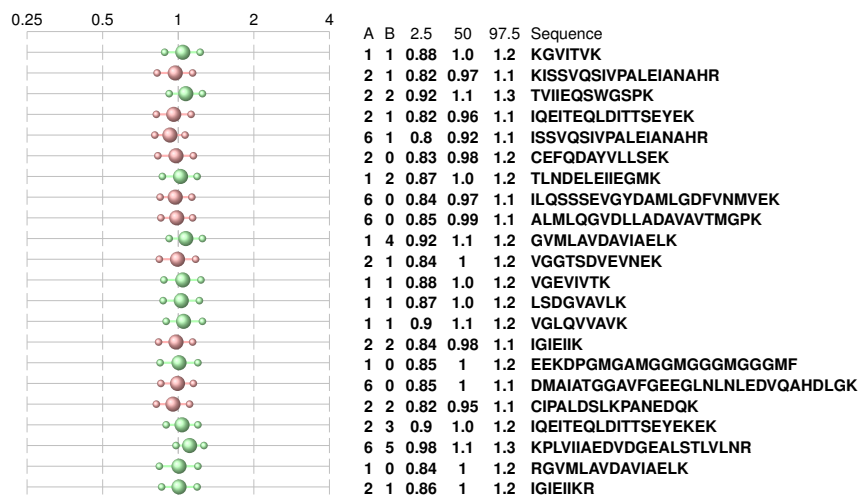


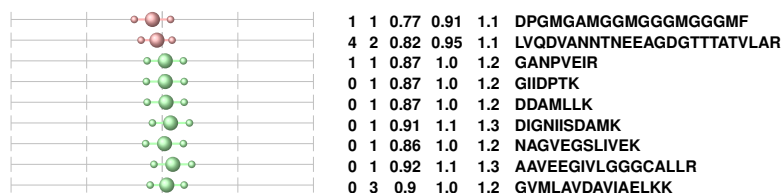
5.935 heat shock protein 1 (chaperonin) [Rattus norvegicus]

Protein Accession	gi 11560024	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.948, 1.08)	
Associated Peptides	31	
Associated Spectra	103	
Coverage	0.639	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.99	1.08
Avg..iTRAQ.Ratio....116.114.	0.876	1.02
Avg..iTRAQ.Ratio....117.114.	1.00	1.05

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1   MLRLPTVLRQ MRPVSRALAP HLTRAYAKDV KFGADARALM LQGVDLLADA VAVTMGPKGR TVIIEQSWGGS PKVTKDGVTV
81  AKSIDLKDXY KNIGAKLVQD VANNTNEEAG DGTTTATVLA RSIAKEGFEX ISKGANPVEI RRGVMLAVDA VIAELKXQSK
161 PVTTPPEEIAQ VATISANGDK DIGNIIISDAM KKVGRKGVIT VKDGKTLNDE LEIIEGMKFD RGYISPYFIN TSKGQKCEFQ
241 DAYVLLSEKK ISSVQSIVPA LEIANHRKP LVIIAEDVDG EALSTLVLNR LKVGQLQVVAV KAPFGDNRK NQLKDMAIAT
321 GGAVFGEGL NLNLEDVQAH DLGKVGIVV TKDDAMLLKG KGDKAHIEKR IQEITEQLDI TTSEYEKELK NERLAKLSBG
401 VAVLKVGGS DVEVNEKDR VTDALNATRA AVEEGIVLGG GCALLRCIPA LDSLKPANED QKIGIEIKR ALKIPAMTIA
481 KNAGVEGSLI VEKILQSSSE VGYDAMLGDF VNMVEKGIID PTKVVRTALL DAAGVAPLLT TAEAVVTEIP KEEKDPGMGA
561 MGGMGGGGMG GMF
    
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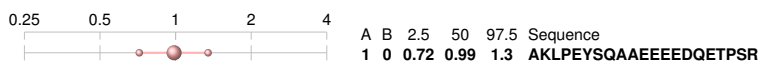


5.936 PREDICTED: similar to Apoptotic chromatin condensation inducer in the nucleus (Acinus) [Rattus norv

Protein Accession	gij109501606
Mean Expression Ratio	0.988
Median Expression Ratio	0.988
Credible Interval	(0.729, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0163
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.941
Avg..iTRAQ.Ratio....116.114.	1.16
Avg..iTRAQ.Ratio....117.114.	1.05

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1      MWRKRPNSS  GGTRGILSGN  RGVVDYGSGRG  QFGTFEGRWR  KLPKMPEAVG  TDPSTSRKMA  ELEEVTLDGK  PLQALRVTDL
81     KAALQQRGLA  KSGQKSALVK  RLKGALMLEN  LQKHSTPHAA  FQPNSQIGEE  MSQNSFIKQY  LEKQOELLRQ  RLEREAREAA
161    ELEGKSSSFS  EEKGESDDEK  PRKGERRSSR  VRQARAKLPE  YSQAAEEBED  QETPSNLRV  RADRNKLVVEE  EEEEEEEEDD
241    EEEEEEVDEG  QKSREAAEPI  LKQFEDEDGE  EMTRAKPEKV  VDEKPPPIRS  QEKDELEKGG  RVTRSQEEAR  RSHLARQQQE
321    KETQIVSLPQ  EENEVKSSQG  LEEKSQSPSL  PPLPEDLEKA  PVVLQPEQIV  SEETPPPLL  TKEASSPPTH  MQLQDEEVEE
401    PAEGPAPPVL  IQLSPPGTD  GTREPIVSPH  TVQLLRGLSP  LSSTADTKAE  SPAERVSEES  VLPLAQRSIL  PEHSAQKGAE
481    SEREKSAPLL  PLTREELAPA  KGITEESVKK  QSLEQEEGR  ASHTLFPDHS  LKPSADSSSS  RSSSPSSSSS  RSRSRSPDSS
561    ASRSQSSPRS  KQREVSQARV  HANPHDRAKM  GSRSTSESR  RSRSRSRAS  SGSRKSLSPG  VSRDGNTRYT  ETKDPSCGQE
641    AAAPSVPQLQ  VLEPKKAPT  CSASVRGRHM  SQPEPEQKHV  IQLQPEQES  PPKCEAEAE  PPAATQPQTS  EPQLSQLPEA
721    ERTPHAAEK  EDVTMDTSEN  RPENEVPEPP  VPIADQVSD  DRPEGSAAEE  ERKESMMPKS  FRKRISVST  KGVQAGNSDT
801    EGGQPGRKRR  WGASTAATQK  KPSISITTES  LKEAVVDLHA  DDSRISEDT  ERNGDDGTHD  KGLKICRTVT  QVVPAAEQEN
881    GQREEEEEKE  PEAEPPAPPQ  ASVEAALPPP  VEHEVKKVTL  GDTLTRRSIS  QQKSGVSITI  DDPVRTAQVP  SPPRGKISNI
961    VHSINLVRPF  TLGQLKELLG  RTGTLVEEAF  WIDKIKSHCF  VTYSTVEEAV  ATRTALHGVK  WPQSNPKFLC  ADYAEQDELD
1041  YHRGLLVDRP  SEAKTEEQGA  PRPLHPPPPP  PVQPPHPHRA  EPREQERAVR  EQWAEREREM  ERRERTSER  EWDRDKVREG
1121  PRSRSRSDR  RRKERAKSKE  KKSEKKEKAQ  EEPKAKLLDD  LFRKTKAAPC  IYWLPLTESQ  IVQKEAEQAE  RAKEREKRRK
1201  EREEEEQKER  EKEAERERNR  QLEREKRREH  SRERERDRER  ERDRGDRDRD  RERDRDRGRE  RDRRDTKRHS  RSRSRSTPVR
1281  DRGGRR
    
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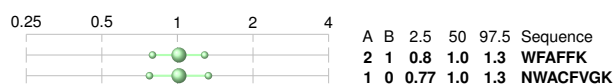


5.937 cathepsin C [Rattus norvegicus]

Protein Accession	gi 8393218	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.8, 1.28)	
Associated Peptides	2	
Associated Spectra	4	
Coverage	0.0303	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.04	1.03
Avg..iTRAQ.Ratio....116.114.	1.09	1.05
Avg..iTRAQ.Ratio....117.114.	0.878	1.24

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1      MGPWTHSLRA ALLLVLLGVC TVSSDTPANC TYPDLLGTWV FQVGPRHPRS HINCSVMEPT EEKVVHLKK LDTAYDEVGN
81     SGYFTLIYNQ GFEIVLNDYK WFAFFPYEVK GSRAISYCHE TMTGWVHDVL GRNWACFVGK KMANHSEKVV VNVVHLGGGLQ
161    EKYSERLYSH NNNFVKAINS VQKSWTATTY EEEKLSIRD LIRRSQHSGR ILRPKPAPIT DEIQQQILSL PESWDWRNVR
241    GINFVSPVRN QESCGSCYSF ASLGMLEARI RILTNSQTP ILSPQEVVSC SPYAQGCDDG FPYLIAGKYA QDFGVVEENC
321    FPYTATDAPC KPKENCLRY YSSEYYYVGGF YGGCNEALMK LELVKHGPMA VAFEVHDDFL HYHSGIYHHT GLSDPFNPFEE
401    LTNHAVLLVG YKDPVTGLD YWIVKNSWGS QWGESGYFRI RRGTDCAIE SIAMAAIPIP KL
  
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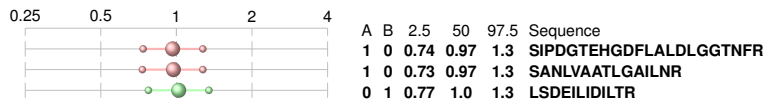
5.938 hexokinase 1 [Rattus norvegicus]

Protein Accession	gi 6981022	
Mean Expression Ratio	0.987	
Median Expression Ratio	0.988	
Credible Interval	(0.772, 1.26)	
Associated Peptides	3	
Associated Spectra	3	
Coverage	0.0534	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.922	0.947
Avg..iTRAQ.Ratio....116.114.	0.818	0.884
Avg..iTRAQ.Ratio....117.114.	0.726	3.49

NHLBI Zile/Grant, Aged Rat

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1      MIAAQLLAY FTELKDDQVK KIDKLYAMR LSDEILIDIL TRFKKEMKNG LSRDYNPTAS VKMLPTFVRS IPDGSEKGF
81     IALDLGSSSF RILRVQVNH KQNVSMESE IYDTPENIVH GSGTQLFDHV ADCLGDFMEK KIKDKKLPV GFTSFPCRQ
161    SKIDEAVLIT WTKRFKASGV EGADVVKLLN KAIKKRGDYG ANIVAVVNDT VGTMMTCGYD DQQCEVGLII GTGTNACYME
241    ELRHIDLVEG DEGRMCINTE WGAFGDDGSL EDIRTEFDRE LDRGSLNPGK QLFKEMVSGM YMGELVRLIL VKMAKEGLLF
321    EGRTTPELLT RGKFNSTDVY AIEKDKREGIQ NAREILTRLG VEPDSDVDCVS VQHICTIVSF RSANLVAATL GAILNRRLDN
401    KGTFRRLRTV GVDGSLYKMH PQYSRRFHKT LRRLVPSDV RFLLESSEGTG KGAAMVTAVA YRLAEQHRQI EETLAHFRLS
481    KQTLMEVKKR LRTEMEMGLR KETNSKATVK MLPSFVR SIP DGTGHEGDFLA LDGGTNFRV LLVKIRSGKK RTVMHNKIY
561    SIPLEIMQGT GDELFDHIVS CISDFLDYMG IKGPRMPLGF TFSFPCHQTN LDCGILISWT KGFKATDCEG HDVASLLRDA
641    VKRREEFDLD VVAVVNDTVG TMMTCAYEEP TCEIGLIVGT GTNACYMEEM KNVEMVEGNQ GQMCINMEWG AFGDNGCLDD
721    IRTDFDKVVD EYSLNSGKQR FEKMISSGMYL GEIVRNILID FTKKGFLFRG QISEPLKTRG IFETKFLSQI ESDRLALLQV
801    RAILQQLGLN STCDDSIKLV TVCGVVSKRA AQLCGAGMAA VVEKIRENRG LDHLNVTVGV DGTLYKLHPH FSRIMHQTVK
881    ELSPKCTVSF LLSEDGSGKG AALITAVGVR LRGDPSIA
  
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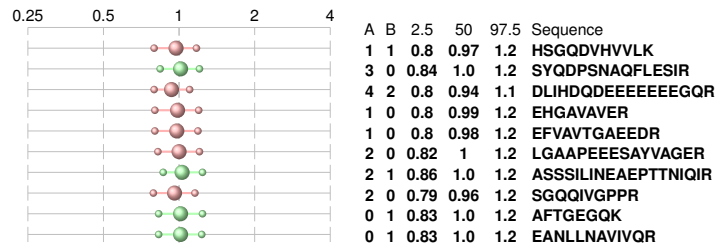


5.939 NSFL1 (p97) cofactor (p47) [Rattus norvegicus]

Protein Accession	gi 14010837	
Mean Expression Ratio	0.989	
Median Expression Ratio	0.988	
Credible Interval	(0.871, 1.12)	
Associated Peptides	10	
Associated Spectra	22	
Coverage	0.349	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.86	1.18
Avg..iTRAQ.Ratio....116.114.	0.974	1.51
Avg..iTRAQ.Ratio....117.114.	0.856	1.17

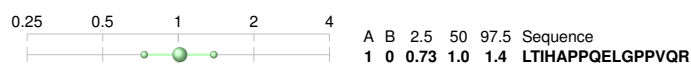
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1      MAEERQDALR EFVAVTGAEE DFARFFLESA GWDLQIALAS FYEDGGDEDI VTISQATPSS VSRGTAPSDN RVTSFRDLIH
81     DQDEEEEEEE GQRFYAGGSE RSGQQIVGPP RKKSPNELVD DLFKGAKEHG AVAVEFVTKS PGETSKPRPF AGGGYRLGAA
161    PEEESAYVAG ERRRHSGQDV HVVLELWKTG FSLDNGDLRS YQDPSNAQFL ESIRRGEVPA ELRRLAHGGQ VNLDMEDHRD
241    EDFVKPKGAF KAFTGEGQFL GSTAPQVLNT SSPAQQAENE AKASSSILIN EAEPPTNIQI RLADGGRLVQ KFNHSHRISD
321    IRLFIVDARP AMAATSFLVM TTFPNKELAD ENQTLK EANL LNAVIVQRLT
  
```



5.940 PREDICTED: similar to translocated promoter region protein [Rattus norvegicus]

Protein Accession	gij109498798
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.745, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	0.999
Avg..iTRAQ.Ratio....117.114.	1.03

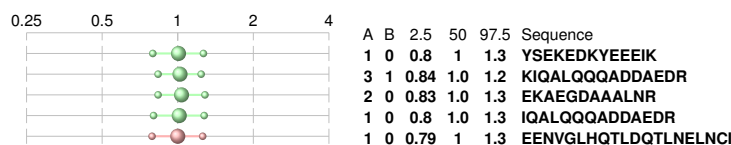


5.941 tropomyosin 4 [Rattus norvegicus]

Protein Accession	gij6981672	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.848, 1.21)	
Associated Peptides	5	
Associated Spectra	9	
Coverage	0.242	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.998	0.7
Avg..iTRAQ.Ratio....116.114.	0.917	0.954
Avg..iTRAQ.Ratio....117.114.	0.97	0.933

NHLBI Zile/Grant, Aged Rat

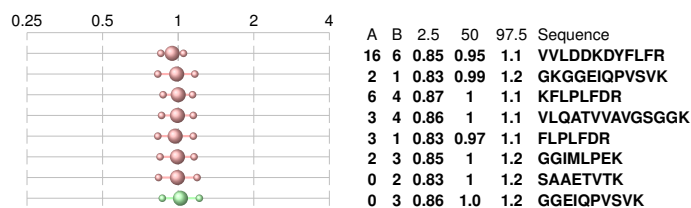
1 MAGLNSLEAV KRKIQALQQQ ADDAEDRAQG LQRELDGERE RREKAEGDAA ALNRRIQLVE EELDRAQERL ATALQKLEEA
 81 EKAADESERG MKVIENRAMK DEEKMEIQEM QLKEAKHIAE EADRKYEEVA RKLVIILEGEL ERAEERAEVS ELKSSDLEEE
 161 LKNVTNNLKS LEAASEKYSE KEDKYEEEIK LLSDKLKEAE TRAEFAERTV SKLEKTIDDL EEKLAQAKEE NVGLHQTLDQ
 241 TLNELNCI



5.942 heat shock 10 kDa protein 1 [Rattus norvegicus]

Protein Accession	gij6981052	
Mean Expression Ratio	0.989	
Median Expression Ratio	0.989	
Credible Interval	(0.894, 1.09)	
Associated Peptides	8	
Associated Spectra	56	
Coverage	0.608	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.816	0.983
Avg..iTRAQ.Ratio....116.114.	0.959	0.972
Avg..iTRAQ.Ratio....117.114.	0.998	0.967

1 MAGQAFR KFL PLFDF VLVER SAAETVTKGG IMLPEK SQGK VLQATVVAVG SGGKKGGEI QPVSXVGDG VLLPEHGGTK
 81 VVLDKDYFL FRDGDILGKY VD



5.943 nucleosome assembly protein 1-like 1 [Rattus norvegicus]

Protein Accession	gi 77404363
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.747, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0281
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.06
Avg..iTRAQ.Ratio....116.114.	0.983
Avg..iTRAQ.Ratio....117.114.	1.11

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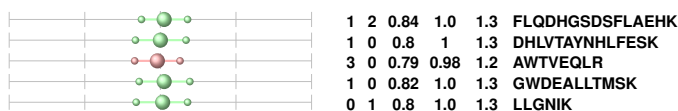
1   MADIDNKEQS ELDQDLEDVE EVEEEETGEE TKIKARQLTV QMMQNPQILA ALQERLDGLV DTPTGYIESL PKVVKRRVNA
81  LKNLQVKCAQ IEAKFYEEVH DLERKYAVLY QPLFDRRFEI INAIYEPTEE ECEWKPDEED EVSEELKEKA KIEDEKKDEE
161 KEDPKGIPGF WLTVEKQVNDL LSDMVQEHDE PILKHLKDIK VKFSDAGQPM SFILFHFHFP NEYFTNEVLT KTYRMRSEPD
241 DSDPFSFDGP EIMGCTGCQI DWKKGKNVTL KTIKKKQKHK GRGTVRTVTK TVSNDSFFNF FAPPEVPENG DLDDDAEAIL
321 AADFEIGHFL RERIIPRSVL YFTGEAIEDD DDDYDEEGEE ADEEGEEEGD EENDPDYDPK KDQNPACCKQ Q
    
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5.944 PREDICTED: similar to FK506-binding protein 3 (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotam)

Protein Accession	gi 27664664	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.846, 1.21)	
Associated Peptides	5	
Associated Spectra	9	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	1.13
Avg..iTRAQ.Ratio....116.114.	0.965	1.01
Avg..iTRAQ.Ratio....117.114.	0.92	1.06



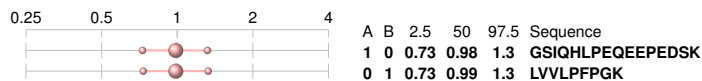


5.945 fetuin beta [Rattus norvegicus]

Protein Accession	gi 17865327	
Mean Expression Ratio	0.988	
Median Expression Ratio	0.989	
Credible Interval	(0.751, 1.3)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	0.0661	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.908	0.99
Avg..iTRAQ.Ratio....116.114.	1.00	0.733
Avg..iTRAQ.Ratio....117.114.	1.01	1.00

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1      MGVLRLLVLC TLAACCVARS PPAPPLPNAP FAPLRPLGCN DSEVLAVAGF ALQNINRVQK DGYMLTLNRV HDARVHRQED
81     MGSIFYLTLD VLETGCHVLS RKALKDCGPR IFYETVHGQC KAMFHVNKPR RVLVLPAYNC TLRPVSKRRI HSMCPDCPHP
161    VDL SAPSVLE AATESLAKFN SENPSKQYAL VKVTKATTQW VVGPSYFVEY LIKESPECTQS QDSCSLQASD SEPVGLCQGS
241    LKSPGVPPQ RFKKTVTVSC EFFESQDQVP GGENPADTQD AKKLPQKN TA PTSSPSITAP RGSIQHLPEQ EEPEDSKGKS
321    PEEFFPVQLD LTTNPQGD TL DVSFLYLEPE EKKLVVLPFP GKEQRSPECP GPEKQRT P
    
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5.946 "solute carrier family 38, member 1 [Rattus norvegicus]"

Protein Accession	gi 20301960	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.747, 1.34)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0186	

Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.817
Avg..iTRAQ.Ratio....116.114.	0.867
Avg..iTRAQ.Ratio....117.114.	0.897

```

1      MMHFKSGLEL TELQNMTVPE DDNVSNDSND FTEVENGQIN SKFISDRESR RSLTNSHLEK RKCDEYIPGT TSLGMSVFNL
81     SNAIMGSGIL GLAFALANTG ILLFLILLTS VTLLSIYSIN LLLICSKETG CMVYEKLGEG VFGTTGKLV I FGATSLQNTG
161    AMLSYLEFIVK NELPSAIKSL MGEEEFSAW YVDGRVLVVM VTFGIILPLC LKKNLGYLGY TSGFSLSCMV FFLIVVIYKK
241    FQIPCMNGEQ NSTVSANVTD ACTPKYVTFN SKTVYALPTI AFAFVCHPSV LPIYSELKDR SQKKMQMVSN ISFFAMFVMY
321    FLTAIFGYLT FYEKQSDLL HKYQSTGDIL ILTVRLAVIV AVILTVPVLF FTVRSSLFEL AKKTKFHLCR HVLVTIILLV
401    IINLLVIFIP SMKDFGVVG VTSANMLIFI LPSSLYLKIT NQDGDKNQOR IWAALFLALG VLFSLISLPL VIYDWACSSS
481    NGEHG
    
```



5.947 "PREDICTED: similar to lymphocyte antigen 6 complex, locus E ligand [Rattus norvegicus]"

Protein Accession	gij109513128
Mean Expression Ratio	0.988
Median Expression Ratio	0.989
Credible Interval	(0.73, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0542
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.901
Avg..iTRAQ.Ratio....116.114.	1.04
Avg..iTRAQ.Ratio....117.114.	1.01

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1      MAAPSSGFWT ALVLAALAAK LAAAVSEPTT VPFDVRPGGV VHSFSQDIGP G GKFTCTFTY ASQGGTNEQW QMSLGTSEDS
81     QHFTCTVWRA QGKSYLYFTQ FFAELQGAEI DAVLFQSKAA FERESDVPLK SEEFVTKTA VSHRPGAFKA ELSKLVIVAK
161    AAHSEL
    
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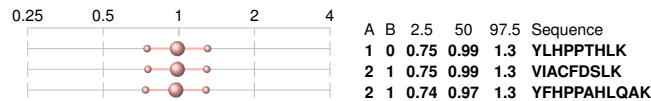


5.948 PREDICTED: similar to muscleblind-like 2 isoform 1 isoform 4 [Rattus norvegicus]

Protein Accession	gj 109502855	
Mean Expression Ratio	0.988	
Median Expression Ratio	0.989	
Credible Interval	(0.773, 1.26)	
Associated Peptides	3	
Associated Spectra	7	
Coverage	0.0777	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.923	0.975
Avg..iTRAQ.Ratio....116.114.	1.08	0.816
Avg..iTRAQ.Ratio....117.114.	1.13	0.781

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1      MALNVAPVRD TKWLTLEVCR QYQRGTCRSR DEECKFAHPP KSCQVENGRV IACFDSLKGR CSRENCKYLH PPTHLKTQLE
81     INGRNNLIQQ KTAAAMLAQQ MQFMFPGTPL HPVPTFFVGP TIGTNAAISF APYLAPVTPG VGLVPTEVLP TTPVIVPGSP
161    PVTVPGSTAT QKLLRTDKLE VCREFQRGNC ARGETDCRFA HPADSTMIDT NDNTVTVCMD YIKGRCMREK CKYFHPPAHL
241    QAKIKAAQHQ ANQAAVAAQA AAAAATVMTQ STAKALKRPL EATVDLAFPP GALHPLPKRQ ALEKSNGAST VFNPSVLHYQ
321    QALTSAQLQQ HTAFIPTVPM MHSATSATVS AATTPATSVP FAATATANQI ILK
  
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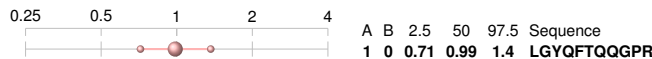
5.949 tropomodulin 3 [Rattus norvegicus]

Protein Accession	gj 58865562	
Mean Expression Ratio	0.988	
Median Expression Ratio	0.99	
Credible Interval	(0.729, 1.34)	
Associated Peptides	1	
Associated Spectra	1	
Coverage	0.0312	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	1.15	
Avg..iTRAQ.Ratio....116.114.	0.864	
Avg..iTRAQ.Ratio....117.114.	0.953	

NHLBI Zile/Grant, Aged Rat

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1      MALPFRKDLG DYKDLDEDEL LGKLTSESEL QLETVLDDLD PENALLPAGF RQKNQTSKSA TGFDRERLL SYLEKEALEY
81     KDREYVPT  GEKKGKIFIP KQKPVQTFTE ETISLDPELE EALTSASDTE LCDLAAILGM HSLIADTQFC DVLGSSNGDD
161    QEHFPNVVKG EKILPVFDEP PNPTNVEESL KRIRENACL VEVNLNNIKN IP IPTLKDFA KLETNTHVK HFSLAATRSN
241    DPVAAAFADM LKVNKTKLSL NMESNFTGT  GVLALIDALK DNETLSELKI DNQRQLGTS VELEMARMLE ENTNILK LGY
321    QFTQQGPRTR AANAITKND  LVRKRRIEGD  QQ
  
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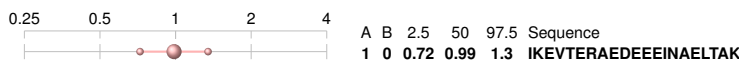


5.950 "PREDICTED: similar to Myosin-1 (Myosin heavy chain, skeletal muscle, adult 1) isoform 7 [Rattus nor"

Protein Accession	gij109488234
Mean Expression Ratio	0.99
Median Expression Ratio	0.99
Credible Interval	(0.736, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0110
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
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Avg..iTRAQ.Ratio....117.114.	1.87

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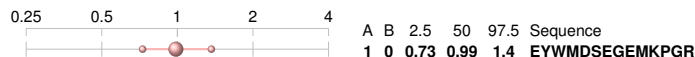
1      MSSDAEMAVF GEAAPYLRSK EKERIEAQNK PFDKSSVVF VDAKESFVKA TVQSREGGKV TAKTEGGATV TVKDDQVFPF
81     NPPKYDKIED MAMMTHLHEP AVLYNLKERY AAWMIYTYSG LFCVTVNPK WLPVYNAEVV AAYRGKRRQE APPHIFSISD
161    NAYQFMLTDR ENQSILITGE SGAGKTVNTK RVIQYFATIA VTGKKEKKEA PSGKMGGTLE DQIISANPLL EAFGNAKTVR
241    NDNSRRFGKF IRIHFGTTGK LASADIETYL LEKSRVTFQL KAERSYHIFY QIMSNKKPDL IEMLLITNP YDYAFVSQGE
321    ITVP SIDDQE ELMATDSAD ILGFTSDERV SIYKLTGAVM HYGNNKFKQK QREEQAE PDG TEVADKAAAYL QNLNSADLLK
401    ALCYPRVKVG NEYVTKGQTV QQVYNAVVAL AKAVYEKMLF WMVTRINQQL DTKQPRQYFI GVLDIAGFEI FDFNSLEQLC
481    INFPTNEKLQQ FFNHMHFVLE QEEYKKEGIE WEFIDFGMDL AACIELIEKP MGIFSI LEE C MFPKATDTS FKNKLYEQLH
561    GKSNNFQKPK PAKGKVEAHF SLVHYAGTVD YNIAGWLDKN KDPINETVVG LYQKSSMKTLL AYLFSGAAAA AEAESGGGGG
641    KKGAKKGGSS FQTVSALFRE NLNKLMTNLR STPHFVRCI IPNETKTPGA MEHELVLHQL RCNGVLEGR ICRKGFPSRI
721    LYADFQRYK VLNASAIPEG QFIDSKKASE KLLGSIDIDH TQYKFGHTKV FFKAGLLGLL EEMRDDKLAQ LITRTQAMCR
801    GYLARVEYQK MVERRESIFC IQYNVRAFMM VKHWPWKLY FKIKPLLSA ETEKEMANMK EEFKTKENL AKAEAKRKEL
881    EEKMNVALMQE KNDLQLQVQS EADSLADAE RCDQLIKTKI QLEAK I KEVT ERADEEEIN AELTAK RRKL EDCSELKDD
961    IDLELTLAK VEKKEHATEN KVKNLTEEMA GLDETIAKLT KEKALQEAH QQTLDLQAE EDKVNLTKA KIKLEQQVDD
1041   LEGSLEQEKK IRMDLERAKR KLEGDLKLAQ ESTMDVENDK QQLDEKLLKK EFEMSNLQSK IEDEQALGMQ LQKKIKELQA
1121   RIEELEEEIE AERASRAKAE KQRSLSREL EEISERLEEA GGATSAQIEM NKKREAEFQK MRRDLEATL QHEATAATLR
1201   KKHADSV AEL GEQIDNLQRV KQKLEKESK MKMEIDDLAS NMEVISKSKG NLEKMCRTLE DQVSELTKE EEQRLINEL
1281   TAQRGRQLTE SGEYSRQLDE KDSLVSQLSR GKQAFQTQIE ELKRQLEEEV KAEQRAMSK ANSEVAQWRT KYETDAIQR
1361   EELEEAKKKL AQLRQDAEEH VEAVNAKAS LEKTKQLQN EVELMIDVE RTNAACAALD KKQRNFDKIL AEWKQYEET
1441   HAELEASQKE SRSLSTELFK IKNAYEESLD QLETLLKREN NLQQEISDLT EQIAEGGKRI HELEKIKKQI EQKSELQAA
1521   LEEAEASLEH EEGKILRIQL ELNQVKSEID RKIAEKDEEI DQLKRNRHV VESMSTLDA EIRSRNDAIR IKKMEGDLN
1601   EMEIQLNHSN RMAAEALRNY RNTQGILKDT QLHLDLALRG QEDLKEQLAM VERRANLLQA EIEELRATLE QTERSRIAE
1681   QELLDASERV QLLHTQNTSL INTKKKLETD ISQIQGEMED IVQEARNAEE KAKKAITDAA MMAEELKKEQ DTSAHLERMK
1761   KNLEQTVKDL QHRLDAEQL ALKGGKKQIQ KLEARVRELE GEVENEQKRN VEAIKGLRKH ERVKELTYQ TEEDRKNVLR
1841   LQDLVDKLSQ KVKAYKRQAE EAEEQSNVNL AKFRKIQHEL EAEERADIA ESQVNKL RVK SREVHTR IIS EE
  
```



5.951 RNA polymerase II transcriptional coactivator [Rattus norvegicus]

Protein Accession	gi 57526804
Mean Expression Ratio	0.99
Median Expression Ratio	0.99
Credible Interval	(0.74, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.110
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.934
Avg..iTRAQ.Ratio....116.114.	1.01
Avg..iTRAQ.Ratio....117.114.	0.995

1 MPKSKELVSS SSSGSDSDSE VEKCLKRRKQ VVPEKPVKKQ KPGESSRALA SSKQSSSSRD DNMFQIGKMR YVSVRDFKGG
 81 ILIDIREYWM DSEGEKPKGR KGISLNMEQW SQLKEQISDI DDAVRKL



5.952 PREDICTED: similar to absent in melanoma 1 [Rattus norvegicus]

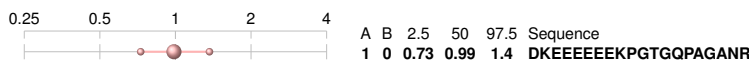
Protein Accession	gi 109494199
Mean Expression Ratio	0.992
Median Expression Ratio	0.99
Credible Interval	(0.74, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00658
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.986
Avg..iTRAQ.Ratio....116.114.	1.05
Avg..iTRAQ.Ratio....117.114.	1.25

NHLBI Zile/Grant, Aged Rat

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1      MSKDATYYTC YGRRGGRCW LPLGAGSSGR GQEEEPHGSA RAGQAGRAPP AARADSRCAQ RARAAATRAP ASGSSGPADG
81     PAARGEMSGG RRRGSAPWHS FSRFFAPRNP SRDKEEEEE KPGTGGPAGA NFSASAENE SMSTSQKKN APSSEAVKIP
161    QVEDRRNPAAE QPAILPMVDD PLKPKDLPDS TVDAKTGESD RQPKESFFQF LGNLFNISGK SSLGEVQKSS FKDDQDKPEK
241    DPQTPTGPPE EGSQREKEIT SCPVRRILP EDQRESNSSE LSDAFSLDIT QESEQETTDI LKTDTAGKPE KPSVTYATYR
321    GPTQIRKYLK QPGSETVNH LNREDGNSDS STQARTGSR S IPDVTVTVLS TASKDVTTKG HLLGGPLEVS GYSQTNTNIE
401    NDLESPPLEQ KIASSKYILN KNSLGDPFSS WASPSSVSNP SYVVGEPDSQ MERSLVCSSV FRGSKSSQGP CPEFQRKTAT
481    ENTLRVNSSA VSDGLPSVPA EERVQPQRPA VSDFFCSKSD GSDTTKMEST NLSSPNKSIR HEDVRLPEK CCDKPAVDNP
561    SRQDVNHRV TTLRHGAVTD SGLVNEGKKL PAQDKQKNVL SEVLRETECA SGSEPTTYSH VRAPEVRIES LPKTELEPCD
641    TETEKLVGEP HVQTPPQEMG ETQEDPGSVK SVSDSVGIAC TESETAHELK SESNRNPISD SPCLEPLLQQ GEVFSAEATP
721    LNLDCKTSDC SASPPTSASR TDRLGQLGFP GLKGERSTSS RTGQGNVCSH PNECREAVGA HSVAADREN P RAPRQLRQAS
801    AIVDSKDILR DGEKQFPSSG PETPGTHSAG LGLLNFEPGD LSENLSVPS HSPKKAALVS SSAKASRPV EKSDSLPLET
881    QTAKMLGNLE VCDQSSFLVE LSSGRGKTL S VPPVSAEPR DVSQC DISS QGTAAEKLSE TVLSELNLYG MEKDKDAQPV
961    DHRESKLLCC SGGFKENHQT GIPPAKSHQS VQTEINTLG TTASILRSRL PGINLAPEEE STRHMAQCK ASTSLLSPSF
1041   AVCGTKKSSS ISEMEELRLD NISPKFQETD NTQVYTSFLG SDGRLEKNVL APEVSSSLNV PSLPGLGED SSGHDNSYFQ
1121   SAGTGSTSPS CHSKGSTDVD NSHDLPSNFE SLKVNVLGT EGASVTDPLG HNSFYLALDI PNPKETDMS IQGGLGHTHR
1201   KASLDSPTLA YFDNPMKAET GTVAGAPVSV NRSQQCSEA SADQTEARRR AHDPLLRS LLAKADTLE EILSSIREEL
1281   KSKHTVGSQC EHLAQDDIMN PGTVKEAIPS EVVLAGIQLK ESLDEKVDN MSEVKEEQ T SVSSVVSETS LFLDLRVHS
1361   SYLLEEQAKE LVNEVYAVQ ENLLNDAFDE IENTWVSEPQ ADPSNIWNSN GGDEPHALVR ERLVAEQTVN QSTCEISENE
1441   VLSKFSSVSH LLSGTESVKG REIVPYQESV GFGSAGQSV SRKLQRSETV VQAEGMPPTS LEGKVRPRL VSEDYRKAEE
1521   TECVDNHKMA TEETRTLVLN FNLPLANDDI HAPGTSKSSF SDSLVCISEK SLPWHNKSM LVMSDLGKAY KIDNEVNVGK
1601   MVALPSMLET GKTNRDAEL NIRKHEAAPL MPHREKCKM DAELNIMKAE FEVNMFTRG VYQMDAQMHV EKPEDLPTVL
1681   GMEKAYKMS EGDIGKADV MVMSELKALH LKDAEGDIK TEVAPISIE M ESFYQKHAEG DVGKTVGASV MSDVDIFVQK
1761   DVVGISPKAE VTTVTLGMED TYQKEEESDV AKTDVTGMVP AELEMEDTYP KGSEGDTDST EGKPIRLEVI NIYQKYSDRV
1841   TGRMGRMSP LRDAEDVLGN SETVVPVLDV KETYQEVHS PLDILEKRVQ RDTEETNGTE PVPSEINMEV MAPEDSSGSI
1921   KNPEVGTVEVA IESTNRTTPE VITRMEAMG PVYESEMGPQ EYMEKSIGEL EELSSEVKEG LILHGDRLAS HFRGYESPTL
2001   SRDYEGYPAL AMPDFQEDT VVRLNKIMSV PAVDDKRRDM DYRGEKEESD LAFVSQDEQD SSSFTILYEE FLQEDKKIS
2081   AEVRLSTRSL FPDTSSSGMP GLACERSESR TDLVHHFEKE GKLAFAFDGD NSEMFLSVEA KRYKIYPLAL SPIYEDDSQ
2161   EDVLSNEVSP GHGHTKSR E SANQPSVLS LLQSVSERLQ RNFDGDDGDD RQVAEEEEEE AAVAASGKG LRTERRERTV
2241   FHLDPDSITF YPDDQESAG ISKSYVEFSE PTTSSLOHSL WPEKVPFLQK SDLTSKLHSS LKSAYHQYLO TSTRHSETG
2321   TRFGGTLQEP VSKHFRVQDH AGRLSAYMEN VDRLTLRCPN RPKMIIYDL HGSKYQEVY CNIPDATAWS FPNGALIRVY
2401   RGCWILYKPF HFQGGKCVLE EGEKVLNRDW LLQNRKHPER TFVLSIKRV LKDCSIP EIE LRPKSDPGWC PIYIHRSPN
2481   LEEELNIPKSS TFTVKSGVWL AYPDVNFKGQ ATVLEEDQGL FEISAAEMKS LQTLQMGGLK VEMPMNLKVI IYKPHFRGH
2561   AKEFSEHIES VPKFLKSDK FRGIGSIRVI GGVVVAEKE HFKGQFLE EGDFFESSAC GALSGPIMSF RYLQANFIES
2641   SITLFESDLE SGKFIDITNQ EISDLEEIGF GRETRSIVHK SGAWVAYHQK FFCGDQYILE KGKYKCFDWD GGSSNIILSI
2721   RPIQLEPLGI NEPPHLLKAF SKAGFQGECI DFKECADLT SFTPASFKVL RGCWLLYYQE DGFYHQCVLE EGLYTDLTSC
2801   GCPSARVRAL KPIDYFFEEP SISLFALEHC EGRELHLEDV VNSVLNKDLH FYTQSVWIKS GLWIAYESGN FLGRQILLVP
2881   NEIPNWTAFS GWKTIGSVRP MRQPAVYIRI RNRAQDEYLT VTGNPADART MSVCVSPYSG KDTQIWHYCR GLFRKASASDT
2961   CLDVIGGRDT PGAKVALWTE HGQFRQKWRM NRNGTISSYL SDELVLVVK GNYCDKTHVI VNQPLEGEET QKWDIEIL

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5.953 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gij109463613
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.753, 1.38)
Associated Peptides	1
Associated Spectra	1
Coverage	0.048
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.804
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	1.05

NHLBI Zile/Grant, Aged Rat

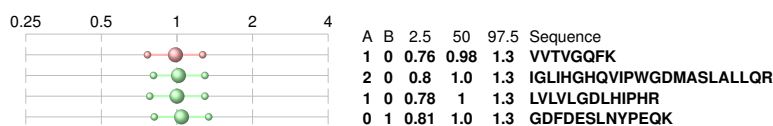
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1      MASPGLRRGA  GRLPGPAFCA  SSGAAASGSQ  PRPPARAPPL  REASAAAHGG  VFSRVGTRTR  TPGPPASDCA  PPGSAAAAAA
81     APRGPEASCK GPALRTRRPA  LQSHPGVRGP  SATLHPPRTS  CASGSAGARV  DRAARSRPPP  SLRTEQDGRG  GTAPPPCGSA
161    QWLQEGVAPP  GQSAKANSHP  RKRPWSPGAG  STRAIPAPEA  NAGTQLCSLL  KNGTVCLSVF  SAARAVSTS
  
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5.954 PREDICTED: similar to vacuolar protein sorting 29 isoform 2 [Rattus norvegicus]

Protein Accession	gij109497394	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.822, 1.25)	
Associated Peptides	4	
Associated Spectra	5	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.923	1.46
Avg..iTRAQ.Ratio....116.114.	1.09	1.24
Avg..iTRAQ.Ratio....117.114.	0.959	1.15



5.955 PREDICTED: similar to Protein C6orf203 [Rattus norvegicus]

Protein Accession	gij109510282	
Mean Expression Ratio	0.99	
Median Expression Ratio	0.99	
Credible Interval	(0.756, 1.29)	
Associated Peptides	1	
Associated Spectra	2	

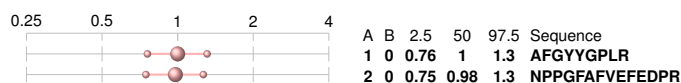
Coverage	NA	
	A	B
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.96	0.868
Avg..iTRAQ.Ratio....116.114.	0.915	0.957
Avg..iTRAQ.Ratio....117.114.	1.06	0.807



5.956 "PREDICTED: similar to Splicing factor, arginine/serine-rich 3 (Pre-mRNA splicing factor SRP20) (X16"

Protein Accession	gij109505347
Mean Expression Ratio	0.99
Median Expression Ratio	0.99
Credible Interval	(0.772, 1.26)
Associated Peptides	2
Associated Spectra	3
Coverage	0.156
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.893
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	0.958

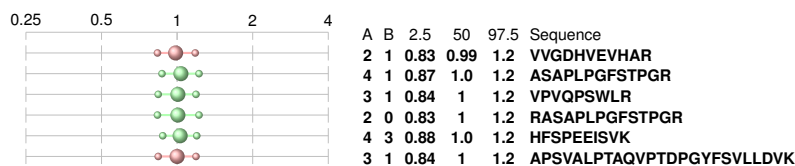
1 MHRDSCPLDC KVVYGNLGN GNKTELERAF GYYGPLLSVW VARNPPGFAP VEFEDPRDAA DAVRELDGRT LCGCRVRVEL
 81 SNGEKRSRNR GPPPSWGRPP RDDYRRRSPP PRRRSRPRSF SRSRSRSLSR DRRRERSLSR ERNHKPS



5.957 "heat shock protein, alpha-crystallin-related, B6 [Rattus norvegicus]"

Protein Accession	gij20302069	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.888, 1.15)	
Associated Peptides	6	
Associated Spectra	25	
Coverage	0.426	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.959	0.92
Avg..iTRAQ.Ratio....116.114.	1.06	1.21
Avg..iTRAQ.Ratio....117.114.	1.05	0.84

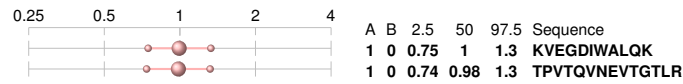
1 MEIRVPVQPS WRRASAPLP GFSTPGRLFD QRFGEGLLEA ELASLCPAAI APYYLRAPSV ALPTAQVPTD PGYFSVLLDV
 81 KHFSPEEISV KVVGDHVEVH AFHEERPDEH GFIAREFHRR YRLPPGVDPFA AVTSALSPEG VLSIQATPAS AQASLPSPPA
 161 AK



5.958 mitochondrial ribosomal protein L49 [Rattus norvegicus]

Protein Accession	gij114145567	
Mean Expression Ratio	0.99	
Median Expression Ratio	0.99	
Credible Interval	(0.766, 1.29)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	0.151	
Experiment	A	
Avg..iTRAQ.Ratio....115.114.	0.892	
Avg..iTRAQ.Ratio....116.114.	1.14	
Avg..iTRAQ.Ratio....117.114.	0.952	

1 MAANVFRVIL HDWKTCVRWS YGRRQLSQTQ GPPDNPSFVE SVDEYQFVER LLPPTKIPEP PKHKHYTPS GWQPPRDPLP
 81 SLPYFVRRSR MHNIPVYKEI THGNRQMTLI RKVEGDIWAL QKDVEEFLSP LLGKTPVTQV NEVTGTLRIK GYFDEQLKAW
 161 LLEKGF



5.959 ankyrin repeat and SOCS box-containing protein 12 [Rattus norvegicus]

Protein Accession	gij82654230
Mean Expression Ratio	0.988
Median Expression Ratio	0.99
Credible Interval	(0.73, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0357
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.94
Avg..iTRAQ.Ratio....116.114.	0.507
Avg..iTRAQ.Ratio....117.114.	1.47

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1      MNLMDIAKIF SLLQPEKEEE DADTGEKQAL NQAVYDNDSC TLDHLLHQER YKRFINSRSG WGIPGTPRLR AASYGHLDCV
81     KVLLEHGADV DSLDVKAQTP LFTAVSHGHL ECVRILLEAG ACPSGSIYNN CSPVLTASRD GAFAILQELL GHGAEANVKA
161    KLPVWASNIA SCSGPLYLAA VYGHLDLDFRL LLLYGADFDY NCIDQALLSR VPQPRTLLEI CLHHCNCEPEY IQLLIDFGAN
241    IYLPSPPLDP TSQDDKGIKL LLQARATPRS LLSQARLVIR RSLCRANQFQ AIDQLDIPPV LISYLNKHQ
    
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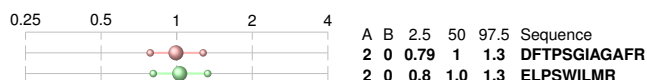


5.960 "PREDICTED: similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2"

Protein Accession	gij109495163
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.808, 1.27)
Associated Peptides	2
Associated Spectra	4
Coverage	0.239
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.97

Avg..iTRAQ.Ratio....116.114. 1.18
 Avg..iTRAQ.Ratio....117.114. 1.06

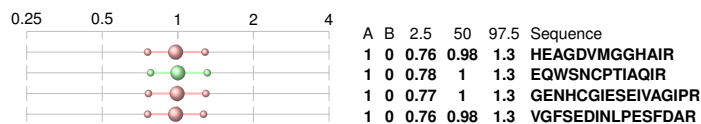
1 MASIVPLKEK KLMEVKLR EL PSWILMRDFT PSGIAGAFRR GYDRYINKYI NVRKGSISGI NMVLAAYVVF SYCISYKELK
 81 HERRRKYH



5.961 cathepsin B preproprotein [Rattus norvegicus]

Protein Accession	gi 82830420
Mean Expression Ratio	0.992
Median Expression Ratio	0.99
Credible Interval	(0.799, 1.24)
Associated Peptides	4
Associated Spectra	4
Coverage	0.174
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.13
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	0.919

1 MWWSLIPLSC LLALSAHDK PSFHPLSDDM INYINKQNTT WQAGRNFYNV DISYLKLCG TVLGGPKLPE RVGFSEDINL
 81 PESFDAREQW SNCPTIAQIR DQSGSGSCWA FGAVEAMSDR ICIHTNGRVN VEVSADLLT CCGIQCGDGC NNGYPSGAWN
 161 FWTRKGLVSG GVINSHIGCL PYTIPPCEHH VNGSRPPCTG EGDTPKCNKM CEAGYSTSYK EDKHYGYTSY SVSDSEKEIM
 241 AEIYKNGPVE GAFTVFSDFL TYKSGVYKHE AGDVMGGHAIR IILGWGIENG VPYWLVANWS NVDWGDNGFF KILRGENHCG
 321 IESEIVAGIP RTQQYWGRF



5.962 PREDICTED: similar to boIA-like 3 isoform 1 [Rattus norvegicus]

Protein Accession	gi 109472256
Mean Expression Ratio	0.992
Median Expression Ratio	0.99
Credible Interval	(0.747, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	0.865



5.963 pancreatic trypsin 1 [Rattus norvegicus]

Protein Accession	gi 6981420	
Mean Expression Ratio	0.99	
Median Expression Ratio	0.99	
Credible Interval	(0.78, 1.25)	
Associated Peptides	1	
Associated Spectra	4	
Coverage	0.0813	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.989	0.85
Avg..iTRAQ.Ratio....116.114.	0.882	1.20
Avg..iTRAQ.Ratio....117.114.	1.22	0.835

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1      MSALLLILALV GAAVAFPLED DDKIVGGYTC PEHSVPYQVS LNSGYHFCGG SLINDQWVVS AAHCYKSRIQ VRLGEHNINV
81     LEGDEQFINA AKIIKHPNYS SWTLNNDIML IKLSSPVKLN ARVAPVALPS ACAPAGTQCL ISGWGNTLSN GVNNPDLLQC
161    VDAPVLSQAD CEAAYPGEIT SSMICVGFLE GGRDSCQGDS GGPVVCNGQL QGIVSWGYGC ALPDNPGVYT KVCNFVGWIQ
241    DTIAAN
    
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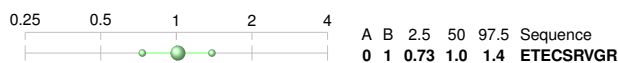


5.964 coactivator-associated arginine methyltransferase 1 isoform d [Rattus norvegicus]

Protein Accession	gi 77539446
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.741, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0154
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.847
Avg..iTRAQ.Ratio....116.114.	1.04
Avg..iTRAQ.Ratio....117.114.	0.895

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1      MAAAAATAVG PGAGSAGVAG PGGAGPCATV SVFPGARLLT IGDANGEIQR HAEQQALRLE VRAGPDAAGI ALYSHEDVCV
81     FKCSVSR ETE CSRVRQSF I TLGCNSVLI QFATPHDFCS FYNILKTCRG HTLERSVFSE RTEESSAVQY FQFYGYLSQQ
161    QNMMQDYVRT GTYQRAILQN HTDFKDKIVL DVGCGSGILS FFAAQAGARK IYAVEASTMA QHAEVLVXSN NLTDRIVVIP
241    GKVEEVS LPE QVDIIISEPM GYMLFNERML ESYLHAKKYL KPSGNMFPTI GDVHLAPFTD EQLYMEQFTK ANFWYQPSFH
321    GVDLSALRGA AVDEYFRQPV VDTFDIRILM AKSVKYTVNF LEAKEGDLHR IEIPFKFHML HSGLVHGLAF WFDVAFIGSI
401    MTVWLSTAPT EPLTHWYQVR CLFQSP LFAK AGDTLSGTCL LIANKRQSYD ISIVAQVDQT GSKSSNLLDL KNPFFRYTGT
481    TSPPPGSHY TSPSENMMNT GSTYNLSSGV AVAGMPTAYD LSSVIAGGSS VGHNNLIPLG SSGAQGGGGS SSAHYAVNNQ
561    FTMGGPAISM ASPMSIPTNT MHYGS
  
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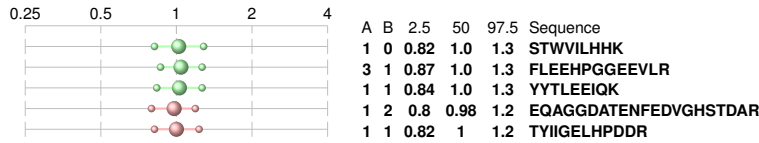


5.965 cytochrome b-5 [Rattus norvegicus]

Protein Accession	gi 11560046	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.865, 1.19)	
Associated Peptides	5	
Associated Spectra	12	
Coverage	0.478	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	0.785
Avg..iTRAQ.Ratio....116.114.	0.988	0.993

Avg..iTRAQ.Ratio....117.114. 1.10 1.17

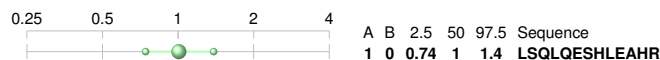
1 MAEQSDKDVK **YYTLEEIQ**H KDSK**STWVIL** **HHVYDLTKF** **LEEHPGGEEV** **LREQAGGDAT** ENFEDVGHST **DAR**ELSKTYI
 81 **IGELHPDDRS** KIAKPSETLI TVESNSSWW TNWVIPAISA LVVALMYRLY MAED



5.966 similar to Epidermal growth factor receptor substrate 15-like 1 (Eps15-related protein) (Eps15R) (E

Protein Accession	gi 71361633
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.747, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0148
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.04
Avg..iTRAQ.Ratio....116.114.	0.983
Avg..iTRAQ.Ratio....117.114.	1.18

1 MAAPLLPLSQ QIPSGNPLYE **SYKQVDPAY** TGRVGASEAA LFLKKSGLSD IVLGKIWDLA DPEGKGFIDK QGFYVALRLV
 81 ACAQSGHEVT LSNLGLTMPP PKFHDTS SPL MATQSSAEAH WAVRVEEKAK FDGIFESLLP VNGLLSGDVK KPVLMNSKLP
 161 LDVLRVWDL SDIDKDGHL RDEFVAVMHL VYRALEKEPV PVLPPPLIP PSKRKKTVFA GAVPVLPASP PPKDSLRSSTP
 241 SHGSVSSLNS TGSLSPKHSV KQTQPPVAWV VPVADKMRFD EIFLKTDLDL DGYVSGQEVK EIFMHSGLTQ NLLAHIWALA
 321 DTRQTGKLSK EQFALAMYFI QQKVSXGIDP PQVLSPPMVP PSEKGTPIPD SSSALGSGEF TGVKELDDIS QEIAQLQREK
 401 YSLEQDIRES EEAIRQKASE VQELQNDLDR ETSSLQELEA QKQDAQDRLD EMDQQKAKLR DMLSDVQRKC QDETQTISL
 481 KTQIQSRES LKSQEDDLNR AKSELNRLQQ EETQLEQSIQ AGRAQLETIL RSLKCTQDDI NQARSK **LSQLQESHLEA**RRS
 561 LEQYDQDDPF KNKALLFSNN SQELHPDPFQ AEDPFKSDPF KGADPFKGFDP FQSDPFSEQQ TAVTDPFPGD PFKESDPPFHS
 641 STSDDFFKKQ TKNDPFTSDP FTKNPSLPSK LDPFESSDPF SSSSISSKGS DPFGLDPPG SSSFSSEAEGF ADFSQMSKPP
 721 PSGPFSSSLG GTGFSDDPFK SKQDTPALPP KKPAPPRPKP PSGQSTPVSQ LGSSAFPESP DPFQPLEADS GDPFQNKKGF
 801 GDPFSGKDPF APSSSAKPPK ASSSGFADFT SFGNEEQQLA WAKRESEKAE QERLARLRRQ EQEDLELAIA LSKADMPA



5.967 clathrin light chain [Rattus norvegicus]

Protein Accession	gi 14010873
Mean Expression Ratio	0.993
Median Expression Ratio	0.99
Credible Interval	(0.735, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0323
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.916
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	1.07

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1      MAELDPFGAP AGAPGGPALG NGVAGAGEED PAAAFLAQQE SEIAGIENDE AFAILDGGAP GPQAHGEPFG GPDAVDGVMN
81     GEYYQESNGP TDSYAAISEV DRLQSEPESE RKWREEQTER LEALDANSRK QEAEWKEKAV KELEEWYARQ DEQLQKTKAS
161    NRVADEAFYK QPFADVIGYV TNINHPCYSL EQAAEEAFVN DIDESSPGTE WERVARLCDF NPKSSQAKD VSRMRSVLIS
241    LKQAPLVH
    
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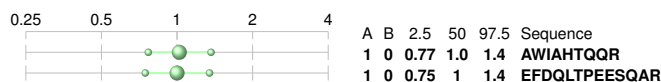


5.968 "reticulocalbin 3, EF-hand calcium binding domain [Rattus norvegicus]"

Protein Accession	gi 56744249
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.778, 1.32)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0671
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.988
Avg..iTRAQ.Ratio....116.114.	0.935
Avg..iTRAQ.Ratio....117.114.	1.27

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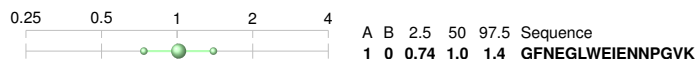
1      MMWRWTMLL LLLLHRWALG KPSPDAGPHG QDRVHHGTPL SEAPHDDAHG NFQYDHEAFL GRDVAK EFDQ LTPEESQARL
81     GRIVDRMDLA GDSDGWVSLA ELRAWIAHTQ QEHIRDSVSA AWHTYDTRD GRVGWEELRN ATYGHYEPGE EFHDVEDAET
161    YKKMLARDE RFRVADQDGD SMATREELTA FLHPPEEFPHM RDIVVAETLE DLDKNKDGIV QVEEYIADLY SAEPGEEPA
241    WVQTERQQFR DFRDLNKDGR LDGSEVGYWV LPPSQDQPLV EANHLLHESD TDKDGRLSKA EILSNWNMFV GSQATNYGED
321    LTRHHDEL
    
```



5.969 "hepatoma-derived growth factor, related protein 3 [Rattus norvegicus]"

Protein Accession	gi 21955178
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.752, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0792
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	1.14

1 MARPRPREYK AGDLVFAKMK GYPHWPARID ELPEGAVKPP ANKYPIFFFG THETAFLGPK DLFPYKEYKD KFGKSNKRK
 81 FNEGLWEIEN NPGVFTGYQ TIQQSSSET EGGGNTADA SSEEEDRVE DGKGRKNEK GSKRKSYSY SKKSSKQSRK
 161 SPGDEDDKDC KEEENKSSSE GGDAGNDRN TTSDLQKAGE GT

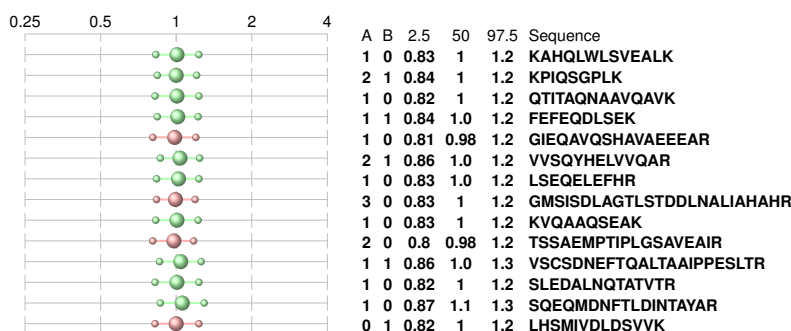


5.970 "inner membrane protein, mitochondrial [Rattus norvegicus]"

Protein Accession	gi 77917546	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.893, 1.14)	
Associated Peptides	14	
Associated Spectra	23	
Coverage	0.342	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.971	1.08
Avg..iTRAQ.Ratio....116.114.	1.01	0.827
Avg..iTRAQ.Ratio....117.114.	1.08	1.42

```

1      MLRACQLSGV TVAAQSCLCG K FVLRPLRPC RRYSTSSSSG VTAGKIAGAG L LFVGGGIGG TILYAKWDSH FRESVEKTIP
81     YSDKLFGMVL GSAPYTVPLP K KPIQSGPLK ISSVSEVMTD SELPMAQTQE TNGDTPASAA GDPAPEVEHE DTINTECPNT
161    DEGTSTFVTA ALAK SLEDAL NQTATVTRQT ITAQNAAVQA VKAHSSTLKT AMDNSEIAGE KKSQAQWRTVE GALKERRKAV
241    DEADALKA KEELEKMKTI IEDAKKREIA GATPYITAAE EK LHSMIVDL DSVVKKVQAA QSEAKVVSQY HELVVQAFDD
321    FRKELDSITP DITPGWK GMS ISDLAGTIST DDLNALTAAH HRRIDQLNRE LAQQKATEKQ HIELALERQK LEEKRAFDSA
401    VAKALEHHR S EIQA EQDRKV EEVRDAMENE MRTQLRRQAA AHTDHLRDVL KVQEQLKFE FEQDLSEKLS EQELEFHRS
481    QEQMDNFTLD INTAYARLR IEQAVQSHAV AEEEARKAHQ LWLSVEALKY SMK TSSAEMP TIPLGSAVEA IRVSCSDNEF
561    TQALTAATIPP ESLTFGVYSE ETLRARFYAV QKLAGRVAMI DETKNSLYQ
  
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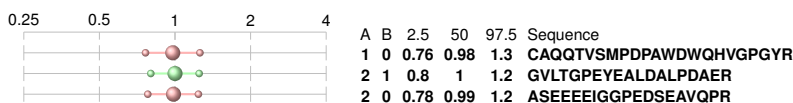


5.971 nucleolar protein 3 [Rattus norvegicus]

Protein Accession	gi 50582542	
Mean Expression Ratio	0.99	
Median Expression Ratio	0.99	
Credible Interval	(0.808, 1.21)	
Associated Peptides	3	
Associated Spectra	6	
Coverage	0.276	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.906	0.763
Avg..iTRAQ.Ratio....116.114.	1.15	0.723
Avg..iTRAQ.Ratio....117.114.	0.977	3.29

```

1      MGNMQERPSE TIDREKRRLV ETLQADSGLL LDALVAR GVL TGPEYEALDA LPDAER RVRR LLLLVQSKGE AACQELLRCA
81     QQTVSMPDPA WDWQHVGPY RDRSYDPPCP GHWTPEAPSS GTTCPLPRA S EEEEEIGGPE DSEAVQPRTP EEPLEAEAT
161    KGDEPDLEQE MEPEPEPEVE PEPEPEPEPE PEPEPEPEPE PEPEREPDFQ EGDESEGCEN T
  
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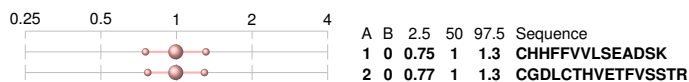


5.972 caseinolytic peptidase X [Rattus norvegicus]

Protein Accession	gi 56119122
Mean Expression Ratio	0.992
Median Expression Ratio	0.99
Credible Interval	(0.779, 1.28)
Associated Peptides	2
Associated Spectra	3
Coverage	0.0474
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.998
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.03

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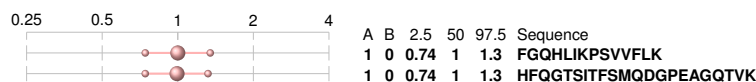
1      MSSCGACTCG AAAARLLTTS LTSAQRGISC GRIHVPVLR LGTLDTQILR RAPLRTFSET PAYFASKDGT NKDGSGDGNK
81     KSVTEGSSKK SSGNSGKGG NQLRCPKCGD LCTHVETFVS STRFVKCEKC HFFFVVLSEA DSFKSIIKEP ESAAEAVKLA
161    FQKPPPPPK KIYNYLDKYV VGQSFQKVL SVAVYNHYKR IYNNIPANLR QQAEVEKQTS LTPRELEIRR REDEYRFTKL
241    LQIAGISPHG NALGASMQQQ GSQQMPQEKR GGEVLDSPHD DIKLEKSNIL LLGPTGSGKT LLAQTLAKCL DVPFAICDCT
321    TLTQAGYVGE DIESVIAKLL QDANYNVEKA QQGIVFLDEV DKIGSVPGIH QLRDVGEGEV QQGLLKLLEG TIVNVPEKNS
401    RKLGETVQV DTTNILFVAS GAFNGLDRII SRRKNEYLG FGTPSNLGKG RRAAAAADLA NRSGESNTHQ DIEEKDRLLR
481    HVEARDLIEF GMIPEFVGR L PVVVPLHSLD EKTLVQILTE PRNAVIPQYQ ALFSMDKCEL NVTEDALKAI ARLALERKTG
561    ARGLRSIM EK LLEPFMFEVP NSDIVCVEVD KEVVEGKKEP GYIRAPSKES SEEDYDSGVE EDGWPRQADA ANS
  
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5.973 fragile histidine triad [Rattus norvegicus]

Protein Accession	gi 11120730
Mean Expression Ratio	0.994
Median Expression Ratio	0.99
Credible Interval	(0.76, 1.29)
Associated Peptides	2
Associated Spectra	2
Coverage	0.24
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.18
Avg..iTRAQ.Ratio....116.114.	0.98
Avg..iTRAQ.Ratio....117.114.	0.955

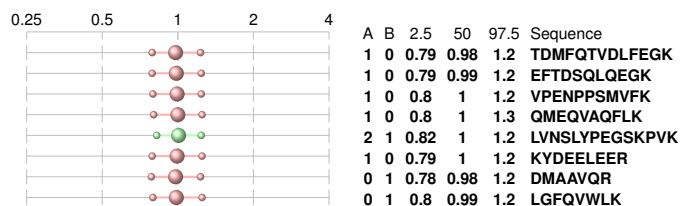
1 MSFKFGQHLLI KPSVVFLKTE LSFALVNRKP VVPGHVMCP LRPVERFRDL RPDEVADLFQ VTQRVGTVVE KHFQGTSTTF
 81 SMQDGPPEAGQ TVKHVHVHIL PRKSGDFRRN DNIYDELQKH DREEEDSPAF WRSEEMAAE AEVLRAYFQA



5.974 transgelin [Rattus norvegicus]

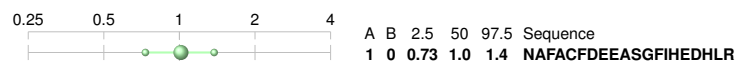
Protein Accession	gij13928744	
Mean Expression Ratio	0.992	
Median Expression Ratio	0.99	
Credible Interval	(0.844, 1.17)	
Associated Peptides	8	
Associated Spectra	10	
Coverage	0.413	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.94	0.752
Avg..iTRAQ.Ratio....116.114.	0.851	0.83
Avg..iTRAQ.Ratio....117.114.	1.30	1.11

1 MANKGPSYGM SREVQSKIEK KYDEELEERL VEWIVMQCGP DVGRPDRGRL GFQVWLKNGV ILSKLVNSLY PEGSKPVKVP
 81 ENPPSMVFKQ MEQVAQFLFA AEDYGVTKTD MFQTVDLFEG KDMAAVQR TV MALGSLAVTK NDGHYRGDPN WFMKKAQEHK
 161 REFTDSQLQE GKHVIGLQMG SNRGASQAGM TGYGRPRQII S



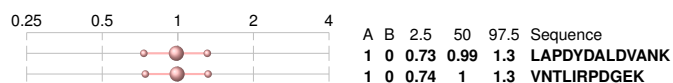
5.975 "PREDICTED: similar to Myosin regulatory light chain 2, smooth muscle isoform (Myosin RLC) [Rattus n"

Protein Accession	gij109469114
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.753, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.95
Avg..iTRAQ.Ratio....116.114.	0.84
Avg..iTRAQ.Ratio....117.114.	1.23



5.976 PREDICTED: similar to 60S ribosomal protein L23a isoform 1 [Rattus norvegicus]

Protein Accession	gij109488568
Mean Expression Ratio	0.99
Median Expression Ratio	0.99
Credible Interval	(0.76, 1.29)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	0.787
Avg..iTRAQ.Ratio....117.114.	1.16



5.977 PREDICTED: similar to THO complex subunit 4 (Tho4) (RNA and export factor binding protein 1) (REF1-

Protein Accession	gij109489472
Mean Expression Ratio	0.993
Median Expression Ratio	0.99
Credible Interval	(0.737, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.07



5.978 "capping protein (actin filament) muscle Z-line, alpha 2 [Rattus norvegicus]"

Protein Accession	gij57163991
Mean Expression Ratio	0.99
Median Expression Ratio	0.99
Credible Interval	(0.734, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	0.063
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.15
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	0.879

NHLBI Zile/Grant, Aged Rat

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1      MADLEEQLSD EEKVRIAAKF I IHAPPGEFN EVFNDVL LLL NNDNLLREGA AHAFAYQYNDL QFTVPKIEGY EDQVLITEHG
81     DLGNGKFLDP KNRICFKFDH LRKEATDPRP YEAEANAIESW RTSVETALRA YVKEHYPNGV CTVYGKKVDG QQTIIACIES
161    HQFQAKNFWN GRWRSEWKFT VTPSTTQVVG ILKIQVHYEY DGNVQLVSHK DIQDSLTVSN EVQTAKEFIK IVEAAENEYQ
241    TAISENYQTM SDTTFKALRR QLPVTRTKID WNKILSYKIG KEMQNA
  
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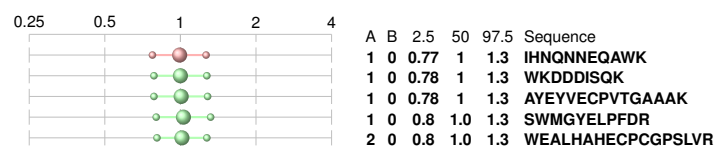


5.979 PREDICTED: similar to Cytochrome c-type heme lyase (CCHL) (Holocytochrome c-type synthase) [Rattus]

Protein Accession	gij109510612
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.824, 1.23)
Associated Peptides	5
Associated Spectra	6
Coverage	0.23
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	1.05

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1      MGSSASSPAT AVNTSNASDH QPASASPPSG CPMHEGQRKG CPVTAAASDL TSESKAHSVP AHQDRAYEYV ECPVTGAAAK
81     NKENLDPSNL MPPPNTSPS DQPFALSTSR EESSIPRADS EKKWVYPSEQ MFWNAMLRKG WKWKDDDISQ KDMYNIIRH
161    NQNNNEQAWKE ILKWEALHABH ECPCGPSLVR FGGKAREYSP RARIRSWMGYL ELPPFDHDWI INRCGTEVRY VIDYYDGGEV
241    NKDYQFTILD VRPAFDSFSA VWDRMKVAWV RWTS
  
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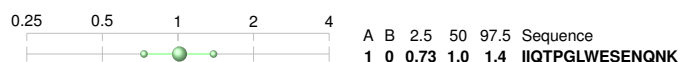


5.980 "RAB18, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gij60223069
Mean Expression Ratio	1.01
Median Expression Ratio	1.01

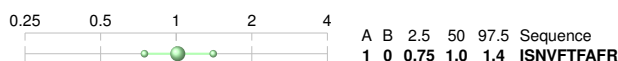
Credible Interval	(0.742, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0728
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.12
Avg..iTRAQ.Ratio....116.114.	0.984
Avg..iTRAQ.Ratio....117.114.	1.13

1 MDEDVLTTLK ILIIGESGVG KSSLLLRFTD DTFDPELAAT IGVDFKVKTI SVDGNKAKLA IWDTAGQERF RLLTPSYRGR
 81 A QGVILVYDV TRRDTFVKLD NWLNELETYC TRNDIVNMLV GNKIDKENRE VDRNEGLKFA RKHSMLFIEA SAKTCDGVQC
 161 AFEELVEK I I QTPGLWESEN QNKGVKLSPR EESHGGGACG GYCSVL



5.981 PREDICTED: similar to lactoperoxidase [Rattus norvegicus]

Protein Accession	gij109488749
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.757, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.04
Avg..iTRAQ.Ratio....116.114.	1.08
Avg..iTRAQ.Ratio....117.114.	1.07



5.982 "protein phosphatase 3, catalytic subunit, alpha isoform [Rattus norvegicus]"

Protein Accession	gij 8394030
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.749, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0192
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	1.07

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1      MSEPKAIDPK LSTDRVVKV VFPFPHRLT AKEVFDNDGK PRVDILKAHL MKEGRLEESV ALRIITEGAS ILRQEKNLDD
81     IDAPVTVCGL IHGQFFDLK LFEVGGSPAN TRYLFGLDYG DRGYFSIECV LYLWALKILY PKTLFLLRGN HECRHLTEYF
161    TFKQECKIKY SERVDACMD AFDCLPLAAL MNQQLFCVHG GLSPEINTLD DIRKLDRFKE PPAYGPMCDI LWSDFLEDFG
241    NEKTQEHFTH NTVRGCSYFY SYPAVCDFLQ HNNLLSILRA HEAQDAGYRM YRKSQTTGFP SLITIFSAPN YLDVYNNKAA
321    VLKYENNVMM IRQFNCSPPH YWLPNFMDVF TWSLPPFVGEK VTEMLVNVLN ICSDDDELGSE EDGFDGATAA ARKEVIRNKI
401    RAIGKMARVF SVLREESESV LTLKGLTPTG MLP SGVLSGG KQTLQSATVE AIEADEAIGK FSPQHKITSF EEARKGLDRIN
481    ERMFPRRDAM PSDANLNSIN KALASETNGT DSNNGSNSSNI Q
    
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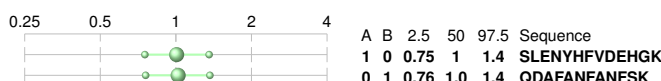


5.983 PREDICTED: similar to Epsin-4 (Epsin-related protein) (EpsinR) (Enthoprotin) isoform 2 [Rattus norv]

Protein Accession	gij 109490559	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.773, 1.32)	
Associated Peptides	2	
Associated Spectra	2	
Coverage	0.0404	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.18	0.888
Avg..iTRAQ.Ratio....116.114.	0.895	0.99
Avg..iTRAQ.Ratio....117.114.	0.915	0.95

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1      MHICAFFFLY STNVVMYSE IESKVREATN DDPWGPSGQL MGEIAKATFM YEQFPPELMNM LWSRMLKDNK KNWRRVYKSL
81     LLLAYLIRNG SERVVTARE HIYDLRLEN YHFVDEHGKD QGINIRQVKV ELVEFAQDDD RLREERKKAK KNKDKYVGVS
161    SDSVGGFRYN ERYDPEPKSK WDEEWDKNKS AFFFSDKLGE LSDKIGSTID DTISKFRRKD REDSPERCSD SDEEKKARRG
241    RSPKGEFKDE EETVTKHHI IQATETTTT RHKRTANPSK TIDLGAAAHY TGDKASPDQN ASTHTPQSSA KPSVPSSKSS
321    GDLVDLFDGS GQTTGGATDL FGGFADFQSA AASGSFSSQA TSGNGDFGDW SAFNQAPSGP VASGGELFGS APQPAVELIS
401    GSQPALGPPP AASNSDDLFD LMGSSQATMT SSQSMNFSLM STNTVGLGLP MSRSQPLQNV SAVLQKPNPL YNQADMVQK
481    SASKTLPSTW SDPSVNISLD NLLPDMQQPL NVMTQSFQAV NLSSPSNMLP VRPQTNPLMG GPMPMMPGV MTGTMGMAPL
561    GNTAGMSQGI VGMNMNMGMS ASGMGLTGTM GMGMPSMAMP SGTVQPKQDA FANFANFSK
    
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5.984 PREDICTED: similar to StAR-related lipid transfer protein 9 (StARD9) (START domain-containing prote

Protein Accession	gij109470690	
Mean Expression Ratio	0.989	
Median Expression Ratio	0.991	
Credible Interval	(0.78, 1.25)	
Associated Peptides	1	
Associated Spectra	4	
Coverage	0.00242	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.985	1.27
Avg..iTRAQ.Ratio....116.114.	0.928	1.13
Avg..iTRAQ.Ratio....117.114.	0.84	0.627

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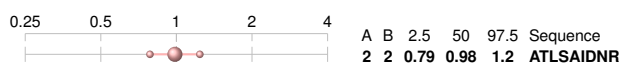
1      MSPFPVPLTQ QMPEKTLSTD TVPQATACPP RTGCLGRNSL HSSRWKRFSP ARGASVSSQK IESFGKQSCQ MSSQGQSTKK
81     QKPTDGSRIF TPAAQTKAKG LVASVNTQTV WQKEESCATY KAPKETTSHP TYLSGSEQVA GHRKVVKTSL AESKPPPPSR
161    ASKKHQVRLA ARARDIAKFF SRLSCGCPK KQPSAEDPTS FTDSRPIMDH VREEDKDLSL TESSYSVDSL SYIYAKVPKE
241    LLKPEELQGK WDLPPDPNSE SGNSQISEDS LAGKGHQSLP ENSAGEYSMK DYGHSRARPS ASVRGLPMYS DSSLCTHTDR
321    SFLSHSLIGP ENRQGEFFLG SADEMPTEF WHLQKATLSA IDNKQGATDR PSPINHRVGV RVNNILPKSN SFYHDLQYQP
401    RCEQLESEME TSYSEQINPL RGIQLARESP LLSVDSWFSC DSKVNPSSPS GVIHSLCPSP DIHETQPYSE KPQHWLSSEE
481    PNTCKLPQTS TEPPCCSDLY ATSASDTSKP SVCGSQRLLO PGVDGFFQGR EMPDMTNQGI SEESHNSDMS SVLATSATSF
561    THVRSINKKD WAALHQEYLL ELSDSIFEAI GEPRPAFFFL EESSSSLADA SDKVDSPLPT GPGLSRNLDF CSFPAHLSQI
641    RHLNAEKDHD SLSANVESAS DLFSTVERMS CNEYPTDIE SLTSGSINAQ ACTAGNAIPS SMTEAWEVNQ ASLEGCLQGG
721    RHSALKTSSG QYFFQKRTYH NHDTSASEVD YLPQDETLLR KNTPVQPGLL SHNSHQHPLL EEKAASQEC S EEVAGTHIDA
801    CCTFPGPEL VLHSDPWSF P SFLQSPSLE TFYVTKSRDA LTETALEIPA CREAWPSPSP PREAWGFGHS HQVPQKAHKK
881    NNLPKLSQSQ NSKIDSPHQ I TKRPTDTNI GEVTGELGKR PRNMKKEEPH DSAYCFVAQN RQHLPSTRLK ACECRNLGI
961    LNKYSLSVHE DGEASAWHH CSVAFNGSES KTLFLICDSK ASGEEQSPLL PETQSSGTHS QSPPGDRSDF IGKITNLDLE
1041  KVMPPEETA VS LKSRSLHCRS SPAIMAGGRS PTHRWEGRNE TVLLREVISK DIREEFSLPG TQYTCERCHL VMCSQERKPT
1121  ECKAHGQSQE IQCKEKPLGE KQNKRVNSTD EMARLIRSVI QLETGILEIE SKQNKQLHAS HTPSTELMLQ DLQDQKKTQD
1201  VPEPSSGKH LCFEGYPSFP IQIEDGIFED NKAREIEGNS AISNNAQVQK ITGSPFRSRD CKQTRGSERE HTYPPPGAHR
1281  LARDICGSLG KGEALRKPSN MSLHSRRMKA LARSLLQRS PERAEKDEL LKASAKFQEQ TWALESELEL ESVESFQESQ
1361  IIAVPSDEL EDVKTGPRVE EMTVDRGGNL KENENVEIST PSQHWKGTVF RQENVSPFHN QRFDSALPY GELSGIQPVH
1441  SPSFPRSCCH VSDTKGVSSF ENILEPTMLK TNRNSLATGV GDQDHSGETG SSSLQGSVSG DASTTHTPWG GSVMPMLMRA
1521  NGQSVTSDSI QLETEDWITV STSSQEDQEG DFRVTSSTGLT TQEGLGSEAE ATEQEETKTS SLDTVLRQTE RRVSFLLQED
1601  SDQGEERQK AEEKSEDQQL PNSACLPPVS VLKGPDPPEL LLPDSSVHAS ICLSILEEIR QAKAQRKQLN DFVAEGTVLP
1681  YETSQEAECF SEAAGRSQTQ TVTLGWDSTR NDAKTQGLHV ASPPPVFANL LADERRAQAS AGSLQHVLLNP ETRDRGPQHHL
    
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NHLBI Zile/Grant, Aged Rat

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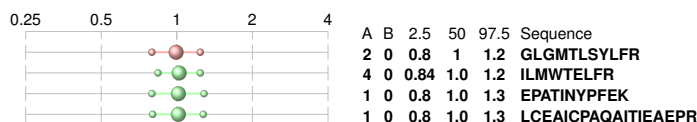
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1841 CDGPGRILHG QSQLAAWETA EDISFGGKDT VLGHQKPSLD STCGGDSGKI SVTTQKQKAV HSERQSVIRT VDNTVYLSQP
1921 KQDHWQCSDA SAGLEGMAS PKSCALQPGA PRKVEAEANI WHPVKWKNVD SGLAEACGSD SKNLRSTPFI DKRPSLHPSG
2001 VREEAPGLCP EECLVFKGNT GGSRLPLGLSY GEEENCPLHS GSQPAAAVHD CRSHSSTLPC YRDGVLRKGT LWAAPHPDHS
2081 LFIIVPSRVE VDGAGESFSK DSQVSLAHLG KHKCGPVDNS IPNPSTIALV SSPAQNCSCCL CTSEMKANCL THTVARGRSV
2161 DSGSEKTTGK KASTAPEDSY PSSPAGMSSE PRRTLKNNVS SENVQASQTT PEHPAVTQRP YSNEESVDSK LEIAAQFGHL
2241 ENTIRCCSKK MPPSTKVRGH SCLDSQAKFV DMLKHTCHPQ IETSWEEEEEQ QRDQVSGDGK VHAQVRNLVS SNIGSFDGCG
2321 TRDGERKEIV VAKSSASQTF FSDFEAQTEP SQPAAQTPSQ LCSRDREQLFP SHRHLPLVIA IFSGPKRARY SPRPQFTVVS
2401 SSRSGLQELNL SVKPPSPTEDE DAQGNCLWS PHLRGHSSQK FVSTSQKSD YSQKASCNLS NSHTDHRPLN FVIPPYPTSS
2481 TVSCMPTPEF MTTWMPGTLE QAHFGKTDKL SVQGMENWH SQVDKEMLHF DSSNLSPLYVL PWCPCQGPVHI GWKYVFGSA
2561 VDASGSQKSQ CLIQSKMAQC SSMDNVLEDK KSPFHFKPT DAQTQDLPLNI HSGIGNDQSS NELPLAGGST TAQVEIILL
2641 CPPETGCAGG EASMNTEFQG TRTLGSRLHS NCTDVSQPD ARTMSDSDLA SWTRMHNLSL HLSQLLHSTS ELLGSLSPS
2721 VIVKEQNGNS ESLDEAQQAL MMDGSTQTTV DEGIQTDLAL PPLAFQAPEV KSEEVSVILH VMDSGITVA QEKGDVPPVF
2801 QKKEAEEAAE FPDLHKGSTH VKLQSPVTS PHLRFQADF QQNFTFMNFP ASPDGSPLPS LQPEESCMVV NMSRISHHSR
2881 LTLGASEFTQ EPSTQNRGLS SSAYLVDRAS SPILTFASAI QELSNPLACL TSVPSAHPL EDFQKLDINP DPEVGDLRFP
2961 MGNSQATDKA GVSRRASVD REVKSPGLKS SERLFLYSS PCSPQSSSP QVSFSGKAPQ QLQLKSTTGD QSKSPSSPPR
3041 HRILDDSVVS ERVASTEHGF PSSGRPSQCQ GRAANEDGKS VFMVESQPNV DRPSSRRGLQ PLSPCQISAT TGLQSPAVDP
3121 PQVCQPVGLL CPGSQMYVAS GPQHNLRDL SVHNKFNWY GVQDGPCKSL HVGDSLVGRC DLSSVGTQRP LQPSDKYSQE
3201 PEYLRLEHIP LQAGVQKPSL SVELTEAKLH HGFGETDALL KVLQSGTGEV FAPPEFAMLS CEEFYTRQKK TFEFLRRRT
3281 ERLHNFRTR SLSPQKRLRF LP SKDLPTGE LDLPSSRQEQY LQRLRKHVVE TRIPEPAPR LARPPSDIEL MLQEQYRQARE
3361 EAKAEIAQAR DRLKERSEQE KRIRQIIS QLLKEEKLO ILANSSSLYT SNGSISSGV TSDYNSSPAF LGHLQSLEVL
3441 EDSQVPDQD TWIGDWRGRS TVRNSYLYLT GSSWKNLAHS CRASMGSGCC SPSSLSLGT CFSFPYQDLA KHI VNTSMAD
3521 VMAACSDNLH NLFIRQASAG WNYQGEQEV QLYYKFSST RHGFLGAGVV SQPLSQVWAA VSDPTLWPLY HKPIQTSRLH
3601 QRVNTNSISLV YLVCDDTLCA LKQLRDFCCV CVEAKEGHS IMATQSVYDA SMPRPSRKMV RGEILPSAWV LQPVLLGKGE
3681 ITRVIFLVQV ELGAPGFFPH LLNSFIKQFP LVAKLASFL RR

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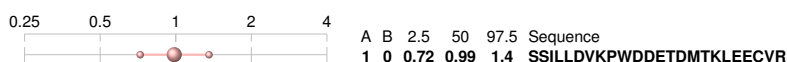
5.985 PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 8 [Rattus norvegicus]

Protein Accession	gi 27661165
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.836, 1.21)
Associated Peptides	4
Associated Spectra	8
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.92
Avg..iTRAQ.Ratio....116.114.	1.21
Avg..iTRAQ.Ratio....117.114.	1.07



5.986 PREDICTED: similar to eukaryotic translation elongation factor 1 beta 2 [Rattus norvegicus]

Protein Accession	gij109487231
Mean Expression Ratio	0.99
Median Expression Ratio	0.991
Credible Interval	(0.734, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.943
Avg..iTRAQ.Ratio....116.114.	0.846
Avg..iTRAQ.Ratio....117.114.	1.28

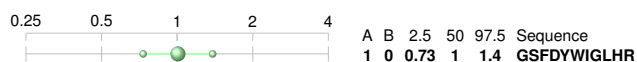


5.987 hypothetical protein LOC362447 [Rattus norvegicus]

Protein Accession	gij114326303
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.754, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0531
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.04
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.07

NHLBI Zile/Grant, Aged Rat

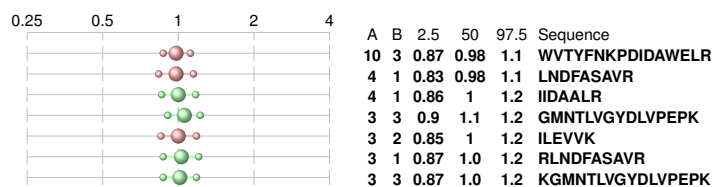
1 MSAKKASQPM LNTTGSLOEG EMGKMFHGKC LRIVSPESPA KLYCCYGVIM VLSVAVVALS VALSVKMTPQ ISTINTYAAC
 81 PRNWIGVGNK CFYFSEYASN WTFSQTFCKA QEAELARFDT EEELNFLSRY KGSFDYWIGL HRESSEHPWK WTDNTQYNYS
 161 LSIRGVERYA YLNDIGISSA RYADKRWSC SKLNSYSLQC KTPFSPM



5.988 "cytochrome c oxidase, subunit Va [Rattus norvegicus]"

Protein Accession	gi 24233541	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.906, 1.12)	
Associated Peptides	7	
Associated Spectra	44	
Coverage	0.377	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.891	1.12
Avg..iTRAQ.Ratio....116.114.	1.06	0.994
Avg..iTRAQ.Ratio....117.114.	1.03	0.912

1 MAAALRRC T AAAAARGLLH PVSAPSPAAA VCSIRCYSHG SHETDEEFDA R~~WV~~TYFNKPD IDAWELR~~KGM~~ NTLVG~~YDLV~~P
 81 EPKIIDAALR ACRR~~L~~NDFAS AVR~~I~~LEV~~V~~KD KAGPHKEIYP YVIQELRPTL NELGISTPEE LGLDKV



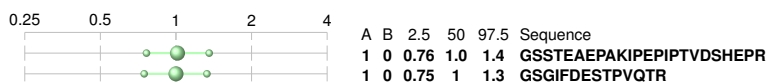
5.989 HN1-like protein [Rattus norvegicus]

Protein Accession	gi 61557209
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.77, 1.29)

Associated Peptides	2
Associated Spectra	2
Coverage	0.2
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.1
Avg..iTRAQ.Ratio....116.114.	0.969
Avg..iTRAQ.Ratio....117.114.	1.22

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1      MFRGADGQAS KSGFRSMKPP GGESNDIFGS PEEGVPSKPK HRMASNIFGP TEEPKNIPKR TNPPGGKGGG IFDESTPVQT
81     RQRLNPPGGK TSDIFGSPVT ATAPLAHPNK PKDHVLLCEG EDCKSDLKAA TNSTPRGEQG EKGSSTEAEAP AKIPEPIPTV
161    DSHPEPLGPR PRSHNKVLNP PGGKSSISFY
    
```



5.990 target of myb1 homolog [Rattus norvegicus]

Protein Accession	gij56605806	
Mean Expression Ratio	1.01	
Median Expression Ratio	1.01	
Credible Interval	(0.77, 1.32)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.0346	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.16	1.12
Avg..iTRAQ.Ratio....116.114.	0.878	0.86
Avg..iTRAQ.Ratio....117.114.	1.03	1.16

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1      MDFLLGNPFS SPVGQRIEKA TDGSLQSEDW ALNMEICDII NETEEGPKDA FRAVKKRIVG NKNFHEVMLA LTVLETVCVN
81     CGHRFHVLVA SQDFVENVLV RTILPKNNPP TIVHDKVLNL IQSWADAFRS SPDLTGVVAV YEDLRRKLE FPMTDLML
161    PIHTPQRTVF NSETPSRQNP VVSNSSHRGD LSQHATPLPT PAVLPGDSP I TPTPEQIGKL RSELEMVNGN VRVMSEMLTE
241    LVPTQVEPAD LELLQELNRT CRAMQQRILE LIPRISNEQL TEELLMINDN LNNVFLRHER FERFRTGQTA KASGEAELAA
321    DLIDMGPPDA ATSNLSSQLA GVDLGSSRVR AGLQSLEASG HLEDDFDMFA LTRGSSLADQ RKGVKYEAPO TTDGLAGALD
401    ARQQSTGAIP ATQARIMEDI EQWLS TDVGS SAEPPSGVTS EEFDFLEER AKAADRLPNL ASPSAEGPPR PCPGAAPRRK
481    TQEKDDVLF AL
    
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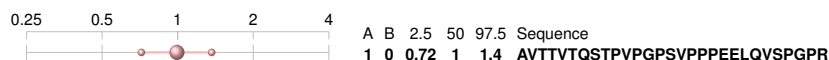


Protein Accession	gij109511332
Mean Expression Ratio	0.993
Median Expression Ratio	0.992
Credible Interval	(0.738, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0143
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.949
Avg..iTRAQ.Ratio....116.114.	0.957
Avg..iTRAQ.Ratio....117.114.	1.81

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1   MASAVSPANL PAVLLQPRWK RVVWGSQGPV RPRHGHRAVA IKELIVVFGG GNEGIVDELH VYNTATNQWF IPAVRGDIPP
81  GCAAYGFVCD GTRLLVFGGM VEYGYKSNL YELQASRWEW KRLKAKTPKN GPPPCPRLGH SFSLVGNKCY LFGGLANDSE
161 DPKNINIPRYL NDLYILELRP GSGVVAWDIP ITYGVLPFPR ESHTAVVYTE KDNKKSCLVI YGGMSGCRLG DLWTLDIETL
241 TWNKPSLSGV APLPRSLHSA TIGNKMYVF GGWVPLVMD VKVATHEKEW KCTNTLACLN LDTMAWETIL MDTLEDNIPR
321 ARAGHCVAI NTRLYIWSGR DGYRKAWNNO VCCKDLWYLE TEKPPPPARV QLVRRANTNSL EVSWGAVATA DSYLLQLQKY
401 DIPATAATAT SPTPNPVPV PANPPKSPAP AAAAPAVQPL TQVGITLVPQ AAAAPPSTTT IQVLPPTVPGS SISVPTAART
481 QGVPAVLKVT GPQATTGTPL VTMRPASQAG KAPVTVTSLP ASVRMVVPTQ SAQGTVIGSN PQMSGMAALA AAAAATQKIP
561 PSSAPTIVLSV PAGTIVKTV AVTPGTTTLP ATVKVASSPV MVSNPATRML KTAQAQVGTG VSSAANTSTR PIITVHKSQT
641 VTVAQQAQVV TTVVGGVTKT ITLVKSPISV PGGSALISNL GKVMSVVQTK PVQTSAVTQO ASTGPPVTQII QTKGPLPAGT
721 ILKLVTSADG KPTTIITTTQ ASGAGTKPTI LGISSVSPST TKPGTTTTIK TIPMSAIITQ AGATGVTSSP GIKSPITITIT
801 TKVMTSGTGA PAKIITAVFK IATGHGQQGV TQVVLKAGPG QPGTILRTPV MGGVRLVTPV TVSAVKPAVT TLVVKGTTGV
881 TTLGTVTGTV STSLAGAGAH STSASLATPI TTLGTIATLS SQVINPTAIT VSAAQTTLTA AGGLTTPITIT MQPVSQPTQV
961 TLITAPSGVE AQPVHDLVPS ILASPTTEQP TATVTIADSG QGDVQPGTVT LVCSNPPCET HETGTTNTAT TTVVANLGGH
1041 PQPTQVQFVC DRQEAASLV TSAVQQQNGN VVRVCSNPPC ETHETGTTNT ATTATSNMAG QHGCSNPPCE THETGTTSTA
1121 TTAMSSMGTG QQRDARRATN TP TVVRIITVA P GALERAQGT VKPPCQTQQT NMTSTMTMTVQ ATGAPCSAGP LLRPSVALET
1201 GSHSPAFAVQL ALPSVRVGLS GPSSKDVPTG RQPETYHTYT TNTPTTARSI MVAGELGTAR VVPTSQYDCL QASSPSSMT
1281 MTALEALCPC SATVTQVCSN PPCETHETGT TNTATTSNAG SAQRVCSNPP CETHETGTTT TATTATSNNGG AGQPEGGQQP
1361 ASGHPCETHQ TTSTGTTMSV SVGALIPDAT PSHGTLESGL EVVAVPTVTS QAGATLLASF STQRVCSNPP CETHETGTTT
1441 TATVTSNMS SNQDPPPAAS DQGEVASTQG DSTNITSASA ITTIVSSTLP RAVTTVTQST PVPGPSVPPP EELQVSPGPR
1521 QQLPFRQLLQ SASPTLMGES AEVLSASQTP ELQAAVDLSS TGDPSVVQEP TTSAVVATVV VQPPQPTQSE VDQLSLPQEL
1601 MAEAQAGTTT LMVTGLTPEE LAVTAAAEAA AQAAATEEAQ ALAIQAVLQA AQQAVMGTGE PMDTSEAAAA VTQAEELGHL
1681 AEGQEQGATT IPIVLTQQL AALVQQQQL QEAQAQQQQ HHLPTALAP ADSLNDPSIE SNCLNELASA VPSTVALLPS
1761 TATESLAPSN TFVAPQPVVV ASPAKMQAAA TLEVANGIE SLGVPKDLPP PPSKAP IKKE NQWFDVGVK GTSVMVTHYF
1841 LPPDDAVQSD DDSGTVPDYN QLKKQELQPG TAYKFRVAGI NACGRGPFSE ISAFKTCPLG FPGAPCAIKI SKSPDGAHLT
1921 WEPVSVTSGK IIEYSVYLAI QSSQASGEPK SSTPAQLAFM RVYCGPSPSC LVQSSSLSNA HIDYTTKPAI IFRIAARNEK
2001 GYGPATQVRW LQETSKDSSG TKPASKRPMSP SEM

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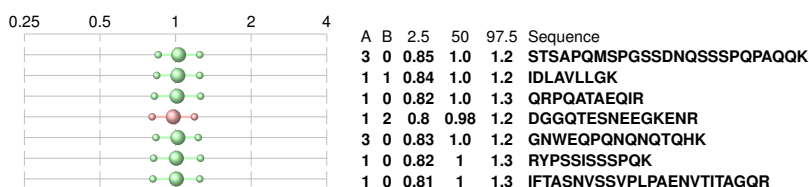
5.993 PREDICTED: similar to Nice-4 protein homolog isoform 1 [Rattus norvegicus]

Protein Accession	gij109467037
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.871, 1.18)

Associated Peptides	7	
Associated Spectra	14	
Coverage	0.100	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.979	0.872
Avg..iTRAQ.Ratio....116.114.	1.04	0.711
Avg..iTRAQ.Ratio....117.114.	1.23	1.16

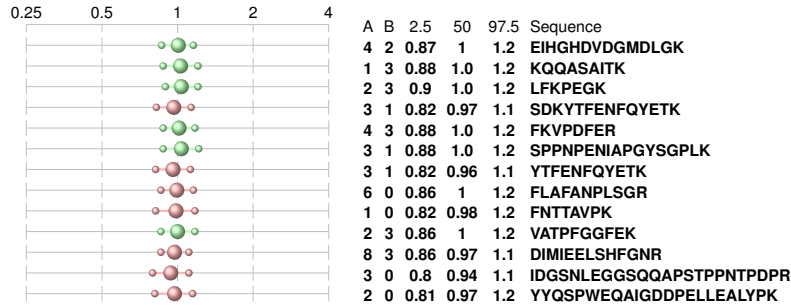
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81     RAINVLLEGN PDTHSWEMVG KKKGVSGQK GGGTESNEEG KENRDRDRDY SRRRGGPPRR GRGASRGREF RGQENGLDGT
161    KSGGPSGRGT DRGRRGRGRG RGSSGRRGGR FSAQGMGTFN PADYAEPANT DDNYGSSSGN TWNNTGHFEP DDGTRLDFIG
241    VEGSNYPRKF ETAPGAWRTA TEWGTEDWN EDLSETK IFT ASNVSSVPLP AENVTTITAGQ RIDLAVLLGK TPSSMENDSS
321    NLDPSQAPSL AQPLVFSNSK QNAISQPASG NTFSHHSMVS MLGKGFCDVG EAKGGSTTGS QFLEQFKTAQ ALAQLAAQHS
401    QSGSTTTSSW DMGSTTQSPS LVQYDLKSAN DSTVHSPFTK RQAFTPSSTM MEVFLQEKPP AVATSTAAPP PPSPLPSK
481    TSAPQMSPPG SDNQSSSPQF AQQKQKQKK KTSLTSKIPA LAVEMPGSAD ISGLNLQFGA LQFGSEPVLS DYESTPTTSA
561    SSSQAPSSLY TSTASESSST VSSNQSQESG YQSGPIQSTT YTSQNNAGQP LYEQRSTQTR RYPSSISSSP QKDLTQAKNG
641    FSSVQATQLQ TTQSVEGATG SAVKSESPST SSIPSLNETV PAASLLTTAS QHSSLSLGLS HSEIIPNTTT TQHSSALSTQ
721    QNTLSSSTSS GRTSTSTLLH TSVSEANLH SSSSTFTTS STVSAPPVV SVSSSLNSGS SLGLSLGNS TVTASTRSSV
801    ATTSKAPPN LPPGVPLLP NPYIMAPGLL HAYPPQVYGY DDLQMLQTRF PLDYYSIPFP TPTTPLTGRD GSLASNPYSG
881    DLTKFGRGDA SSPAPATTLA QPQQNQQTQH HTTQQTFLNP ALPPGYSYTS LPYYTGVPGL PSTFQYGPV FVPVPTSSKQ
961    HGVNVSVNAS ATPFQQPSGY GSHGYNTGVS VTSNTGVPD ISGSVYSKTQ QSEKQGFHS GTPAASFNLP SALGSGGPIN
1041   PATAAAYPPA PFMHILTPHQ QPHSQILHHH LQQDQGLPYL QMILCCQRQQ EEQDILTLVD DQLGE
  
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5.994 PREDICTED: similar to myozenin 2 [Rattus norvegicus]

Protein Accession	gi 27695760	
Mean Expression Ratio	0.992	
Median Expression Ratio	0.992	
Credible Interval	(0.909, 1.08)	
Associated Peptides	13	
Associated Spectra	62	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.03	0.96
Avg..iTRAQ.Ratio....116.114.	0.943	0.935
Avg..iTRAQ.Ratio....117.114.	1.08	0.906



5.995 PREDICTED: similar to shroom [Rattus norvegicus]

Protein Accession	gij6266648
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.753, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.00538
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.735
Avg..iTRAQ.Ratio....116.114.	1.21
Avg..iTRAQ.Ratio....117.114.	0.811

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1      MENRPGSFQY VPVQLQGGAP WGFTLKGGL ECEPLTVSKI EDGGKAALSQ KMRTGDELVN INGTPLYGSR QEALILIKGS
81     FRILKLIYVR RNTPVSRPHS WHVAKLLEGC PDVATTMHFP SEAFSLSWHS GCNTSDVSVQ WCPLSRHCST EKSSSIGSME
161    SLEQPQQATY EGHLLPIEQN MYPSQRDSAY SFSASSNAS DCALSLKPEE PPSTDCVMSG PGPTKVTDDQ ANVSETSGSS
241    HSTSGGHMTS TSHASSCSEE GHHSHPAKMV RGPPEPPVRR DSLQASRAQL LNGEQHRASE PVDLSLQKKEK PALETMLPFR
321    SSNQFCCISG QDQVTGEDHQ NCELSKPSSE SQDDCDHLLI EGSSKALDSP KAHDKGSNKE FGLLKEASAD LANTLSFGAI
401    PHLRGSIEHR HSAPEQLLAS HLQQMHLDSR GNKGMELEPTG QDGHQWTMSP LHNNPKGKKS PGLPTGGTQD QTSKERKIKP
481    TDDKLMVSAN QSQSDALLGE VDGHPSERTY LDSNRASRAS SDLTGQQPSA TCSVPVQTRD FFSANKVVGH TEATEEGDNE
561    PKEGGRLGGR RSGGPRGSI QNRRKSERFA TNLRNEIQRR KAQLQKSKGP LSQLCDTKED VEETQEPPEP PPLPASNSSL
641    LPSYKNVPSH GDQLFNKSMI LRARSSECLS QASESSKARV GLEGRMSPGQ RSGQSSLALN TWWKASDSST LDTEKANAAH
721    GVCRCGHRWS PEHNAQPQVA LSTEGPSNPD DNKELKIPTP QAGDEAILMP FADRRKFEE SSKSLSTSHL PGLTTHNKPF
801    IQRPKPIDQN FQSVSYREL R CHPMDQSYHS ADQPYHAADQ SYHSLSPLOS EAPTYPDCFA PKGVDNSLYC KPVHHGDCDY
881    HRTC SHPCS A QGTVMHDP CI CCSGEICPAL LKRNLKPKCH NCRCHHHQCI RCTGCCCHSPQ HGAHEDSSMA SGNAWKSRKA
961    AIQEFFVDKW KPITGNRKTS HSGREMAHSK ANLSLSAPFR PHIENSALDL SNYRAVSSLD LLGDFKHASN TPRESSVYED
1041   ESSVAMPRP LRSRAFSESH ISLEPQNTA WGKQQRSEFS KGSETQPD TL GARKKAFPPP RPPPPNWEKY RLFRAAQQQQ
1121   QQQQQQQQQQ QQQQQQCEKE EEEKEQEKEE GEKEEDLPPQ YFSSETTGSC APITEEQPQS LKMGHQEASR QSSQSLQEQE
1201   AYAVHPSNFV FAVRSYPVTQ PEKAQPPCY Y GAHGLWRTTE QEATVTPKQE FQHFSPPTGA SGIPTSY SAY YNISVAKAEL
1281   LNKLQQPEM AEAGLGECEV DYELAQKKIQ LIESISRKLS VLREAQRGLL DDINANAALG EEEVENVLKV CKSNELEKYH
1361   LFIGDLKVV NLLLSLSGRL ARVENALNSI DAESNQEKLV LREKKQQLTN QLADAKELKE HVRDRREKLVF SMVSRYPQD
1441   QLQDYQHVVK MXSALIEQR ELEEKIKLGE EQLKCLKESL HLGPSNF
    
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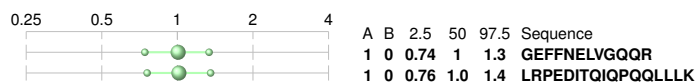
5.996 PREDICTED: similar to Protein diaphanous homolog 1 (Diaphanous-related formin-1) (DRF1) (mDIA1) (p1)

Protein Accession	gij109507224
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.749, 1.37)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.772
Avg..iTRAQ.Ratio....116.114.	0.844
Avg..iTRAQ.Ratio....117.114.	1.1



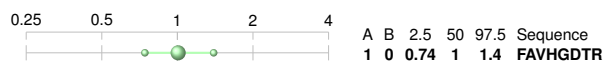
5.997 integrin beta 1 [Rattus norvegicus]

Protein Accession	gij8393636
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.77, 1.30)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	0.919
Avg..iTRAQ.Ratio....117.114.	1.27



5.998 PREDICTED: similar to tubulin polymerization-promoting protein [Rattus norvegicus]

Protein Accession	gij109460644
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.751, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.16
Avg..iTRAQ.Ratio....116.114.	0.985
Avg..iTRAQ.Ratio....117.114.	1.03



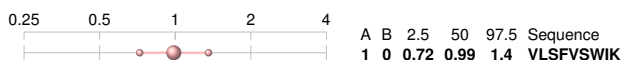
5.999 PREDICTED: similar to granzyme C [Rattus norvegicus]

Protein Accession	gij109501721
Mean Expression Ratio	0.994
Median Expression Ratio	0.993
Credible Interval	(0.737, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0321

Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.987
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	1.09

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1      MPVRSLSPHI VHLHPRAVSA RPSSNLNSLA GKMPVVLILL NLLLPLGVGA EEIIGSNEVS PHSRPMAYF EFLNDNEKKT
81     FCGGFLVREN FVLMAAHCRCG RSMTVTLGAH NIKAKERKQQ IIPVTNTTPH PAYNTDKRSN DIMLLKLVRS AKRTSAVRPL
161    NLPRRNALVK SGDVCYMAGW GKITPQGEFP NTLREGELIV QKDRVCESQF QSSYIKAIEI CVGDSKIKGD SFEEDSGGPL
241    VYKKAAGIV SYGKTDGSAP QVFTRVLSFV SWIKKTMKNS
    
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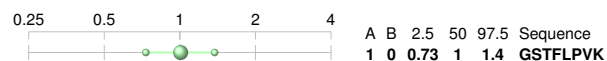
5.1000 PREDICTED: similar to Prickle-like protein 2 [Rattus norvegicus]

Protein Accession	gj 62647849
Mean Expression Ratio	1.00
Median Expression Ratio	1.01
Credible Interval	(0.744, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	0.988



5.1001 PREDICTED: similar to Alpha platelet-derived growth factor receptor precursor (PDGF-R-alpha) isoform

Protein Accession	gi 109500453
Mean Expression Ratio	1.00
Median Expression Ratio	1.01
Credible Interval	(0.74, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.991
Avg..iTRAQ.Ratio....116.114.	1.1
Avg..iTRAQ.Ratio....117.114.	1.06



5.1002 PREDICTED: similar to RNA binding motif protein 3 [Rattus norvegicus]

Protein Accession	gi 62666588
Mean Expression Ratio	0.993
Median Expression Ratio	0.993
Credible Interval	(0.766, 1.30)
Associated Peptides	1
Associated Spectra	2
Coverage	0.115
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.08
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	0.917

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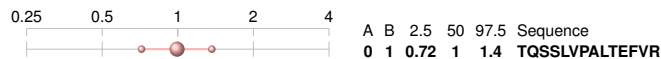
1      MSSEEGKLFV GGLNFNTDEQ ALEDHFSSFG PISEVVVVKD RETQSRGFG FITFTNPEHA SDAMRAMNGE SLDGRQIRVD
81     HAGKSARGTR GGAFGAHGRG RSYSRGGGDQ GYGSGRYDSR PGGYGYGYGR SRDYSGRSQG GYDRYSGGNY RDNYDN
  
```



5.1003 divalent cation tolerant protein CUTA [Rattus norvegicus]

Protein Accession	gij47059185
Mean Expression Ratio	0.991
Median Expression Ratio	0.993
Credible Interval	(0.727, 1.33)
Associated Peptides	1
Associated Spectra	1
Coverage	0.091
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.703
Avg..iTRAQ.Ratio....116.114.	1.17
Avg..iTRAQ.Ratio....117.114.	0.92

1 MPALLPVASR LLLLPRALLS MASGSPPSQP SPASGSGYVP GSVSAAFVTC PNEKVAKEIA RAVVEKRLAA CVNLIPQITS
 81 IYEWKGIIE DSEVLMMIKT **QSSSLVPALTE** FVFSVHPYEV AEVIALPVEQ GNPPYLHWVH QVTESVSGSG KALP



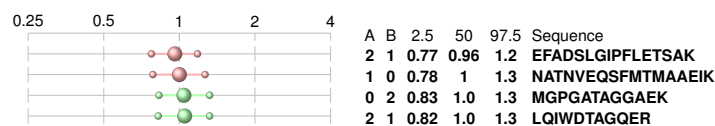
5.1004 "RAB1, member RAS oncogene family [Rattus norvegicus]"

Protein Accession	gij45433570	
Mean Expression Ratio	1.00	
Median Expression Ratio	1.01	
Credible Interval	(0.827, 1.22)	
Associated Peptides	4	
Associated Spectra	9	
Coverage	0.273	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.949	1.02
Avg..iTRAQ.Ratio....116.114.	0.918	0.672
Avg..iTRAQ.Ratio....117.114.	1.05	1.38

NHLBI Zile/Grant, Aged Rat

```

1      MSSMNPEYDY LFKLLIGDS GVGKSCLLLR FADDTYTESY ISTIGVDFKI RTIELDGKTI KLQIWDTAGQ ERFRITSSY
81     YRGAHGIIVV YDVTDQESFN NVKQWLQEID RYASENVNKL LVGNKCDLTT KKVVDYTTAK EFADSLGIPF LETSAKNATN
161    VEQSFMTMAA EIKKRMGPGA TAGGAEKSNV KIQSTPVKQS GGGCC
  
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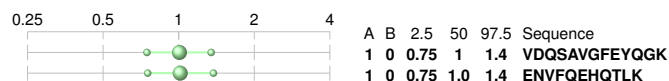


5.1005 cortactin isoform B [Rattus norvegicus]

Protein Accession	gi 76563930
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.766, 1.32)
Associated Peptides	2
Associated Spectra	2
Coverage	0.0472
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.953
Avg..iTRAQ.Ratio....116.114.	1.16
Avg..iTRAQ.Ratio....117.114.	1.08

```

1      MWKASAGHAV SITQDDGGAD DWETDPDFVN DVSEKEQRWG AKTVQGSQH QEHINIHKLR ENVFQEHQTLK EKELETGPKA
81     SHGYGGKFGV EQDRMDKSAV GHEYQSKLSK HCSQVDSVRG FGGKFGVQMD RVDQSAVGFE YQGGTEKHAS QKDYSSGFGG
161    KYGVQADRVD KSAVGFQYQG KTEKHESQKD YSKGFGGKYG IDKDKVDKSA VGFQYQGGKTE KHESQKDYVK GFGGKFGVQT
241    DRQDKCALGW DHQEKQLLHE SQKDYAKGFG GKYGVQKDRM DKNASTFEEV VQVPSAYQKT VPIEAVTSKT SNIRANFENL
321    AKEREQEDRR KAAEERAQRM AQERQEQEEA RRLLEEQARA KKQTPPASPS PQPAEDRPPS SPIYEDAAPL KAEP SYGSSE
401    PEPEYSTEAA GLPEASNQQG LAYTSEPVYE TTEVPVGHYQA EDDTYDGYES DLGITAIALY DYQAAGDDEI SFDPPDDVITN
481    IEMIDDGWWR GVCKGRYGLF PANYVELRQ
  
```



5.1006 DAMP-1 protein [Rattus norvegicus]

Protein Accession	gi 37693510
Mean Expression Ratio	1.01
Median Expression Ratio	1.01

Credible Interval	(0.754, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.064
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.954
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	1.17

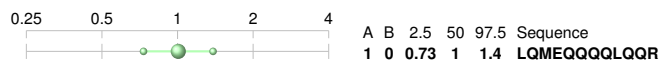
1 MAPSFYHYLP VAMDERWEPK GWSIRRWLV AAILVVLIGV VLVCLIVYFA NAAHSEACKN GLRLQDECRN TTHLLKHQLT
 81 RAQDSLLQTE MQANSCNQTV MDLRDSLKK **KVSQTQEQQAR** IKELENKIER LNQELENLRT QKEISTTVQV NSGGSVVVSS
 161 LLVLVAVLFL HF



5.1007 TOM22 protein [Rattus norvegicus]

Protein Accession	gij47058998
Mean Expression Ratio	1.00
Median Expression Ratio	1.01
Credible Interval	(0.742, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0845
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.941
Avg..iTRAQ.Ratio....116.114.	1.21
Avg..iTRAQ.Ratio....117.114.	0.97

1 MAAVAAAAGA GEPLSPEELV PKAAEKAEE DLEEDDDDEL DETLSERLWG LTEMFFERVR SAAGATFDLS LFVAQKMYRF
 81 SRAALWIGTT SFMILVLPV FETEK **LQMEQ** **QQQLQQI** QIL LGPNTGLSGG MPGALPPLPG KI



5.1008 "zinc binding alcohol dehydrogenase, domain containing 1 [Rattus norvegicus]"

Protein Accession	gij 62543513
Mean Expression Ratio	0.995
Median Expression Ratio	0.994
Credible Interval	(0.766, 1.30)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0569
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.23
Avg..iTRAQ.Ratio....116.114.	0.992
Avg..iTRAQ.Ratio....117.114.	1.02

```

1      MIIQRVVLD S  RPGKNGNPVA  ENFRVEEVSL  PDTINEGQVR  VRTLYLSVDP  YMRCKMNEET  GADYLAPWQL  AQVADGGGLG
81     VIEESKHQKL  AKGDFVTSFY  WPWQTKAILD  GNGLEKVDPO  LVDGHLSTYFL  GAIGMPGLTS  LIGVQEKGHV  SAGSNQTMVV
161    SGAAGACGSL  AGQIGHLLGC  SRVVGICGTH  EKCLFLTSEL  GFDAAVNYKT  GNVAEQLREA  CPDGVVDVYFD  NVGGDISNAV
241    ISQIKETVAN  GLENMGVAFQ  SMMTGGNIGK  QIVRISEDSS  P
  
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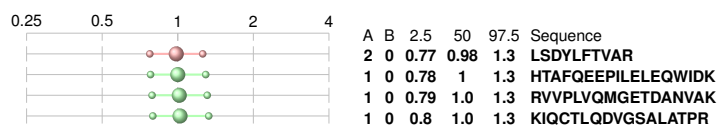


5.1009 PREDICTED: similar to methylmalonic aciduria (cobalamin deficiency) type B homolog [Rattus norvegicus]

Protein Accession	gij 109497496
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.821, 1.25)
Associated Peptides	4
Associated Spectra	5
Coverage	0.262
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	1.16
Avg..iTRAQ.Ratio....117.114.	0.973

```

1      MAVWTFGGRL GLRGRLLGGCR LLCPRFQSFQ PQGGEDGDRP QPSSKAAKVL KIYTKTGDKG LSSTFTGERR PKDDQVFEAL
81     GTTDELSSAI GFAMELITEK GHTFAEELR K IQCTLQDVGS ALATPRSSAR EAHLK HTAFQ EEPFILELEQW IDWYSSQLPP
161    LTAFILPSGG KSSSALHFCA AVCRRRAER RV VPLVQMGETD ANVAKFLNRL SDYLFVTVAR Y AAMKEGSQEK IYKKRDV
    
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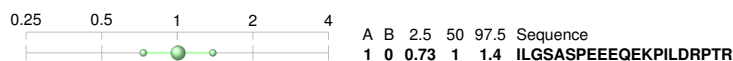


5.1010 "PREDICTED: similar to putative MAPK activating protein PM20,PM21 isoform 1 [Rattus norvegicus]"

Protein Accession	gij109477601
Mean Expression Ratio	1.00
Median Expression Ratio	1.01
Credible Interval	(0.741, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0894
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.993
Avg..iTRAQ.Ratio....116.114.	1.11
Avg..iTRAQ.Ratio....117.114.	1.12

```

1      MTTARPQARQ DPRPRRTQGP RRTRGAPGSP GIKRRRRRRL AAARHRERPH LGQPAPRSRF RVSARFKAQA RGGVGGGGKA
81     ASKMEDEEVA ESWEAAADSG EIDRRLEKKL KITQKESRKS KSPPKVPIVI QDDSLPTGPP PQIRILKRPT SNGVSSPNS
161    TSRPALPVKS LAQREAEYAE ARRRILGSAS PEEEQEKPIIL DRPTRISQPE DSRQPSNVIR QPLGPDGSQG FKQRR
    
```



5.1011 PREDICTED: hypothetical protein isoform 1 [Rattus norvegicus]

Protein Accession	gij109485833
Mean Expression Ratio	0.992
Median Expression Ratio	0.995
Credible Interval	(0.74, 1.33)

Associated Peptides	1
Associated Spectra	1
Coverage	0.124
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	1.01

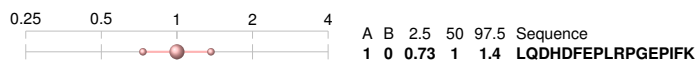
1 MRGRRRLRDR A GRGGCRSIRG AWRRRGRWFSR SARLLGSSLL NHSLRKKSSQ EGKPEPSKQA LKKSCLPVGR FDSLDDSPPEE
81 RXPTAEVSR



5.1012 aspartoacylase-3 [Rattus norvegicus]

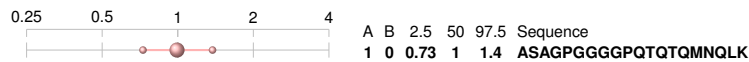
Protein Accession	gi 57526957
Mean Expression Ratio	1
Median Expression Ratio	0.995
Credible Interval	(0.745, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0533
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.04
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	1.21

1 MCSLPGSRKP LLRVAVTGGT HGNEMCGVYL ARYWLQNPGE LQRPSFSAMP VLANPAATAA CRRYIDRDLN RTFTLTFLGS
81 TATPDDPYEV KRAQELNQLL GPKGTCQAFD FILDHNTTA NTGACLISEV SQNPPNLHLC HYLQQLQNPGL PCRLFQFEPP
161 GTESYSMDSV SKNGISLELG PQQQGVLR AE LFSQMRAMVA SILDFIELFN QGMEFFAFEM EVYKNLGSVD FPRTDGHHT
241 GTVHSRLQDH DFEP LRPGEF IFKLFSGEDV L YEGDSVVYP L FVNEAAYYE KRVAF LKSEK IRISVPALPG LTPSSTQTF



5.1013 PREDICTED: similar to Probable ATP-dependent RNA helicase DDX6 (DEAD box protein 6) (ATP-dependent

Protein Accession	gij62653587
Mean Expression Ratio	0.995
Median Expression Ratio	0.995
Credible Interval	(0.741, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.77
Avg..iTRAQ.Ratio....116.114.	0.82
Avg..iTRAQ.Ratio....117.114.	0.808

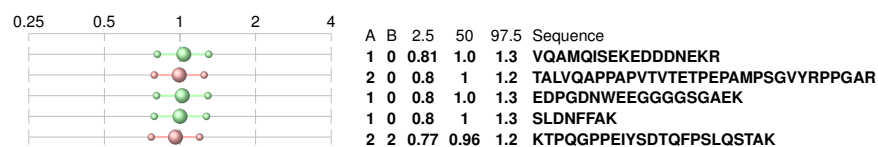


5.1014 hypothetical protein LOC315970 [Rattus norvegicus]

Protein Accession	gij62078927
Mean Expression Ratio	1.01
Median Expression Ratio	1.01
Credible Interval	(0.833, 1.22)
Associated Peptides	5
Associated Spectra	9
Coverage	0.415
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.92
Avg..iTRAQ.Ratio....116.114.	1.08
Avg..iTRAQ.Ratio....117.114.	1.22

```

1      MAETEERSLD NFFAARDKKK KKERSRAAN AASGAGGSSA AAGSRPGDGG SLGSGARSGD GGSSGSGARS GDGGS LGSGA
81     RSGDGGTSRS GDGGSAGPGG KAITKDENEW KEFEQKEVDY SGLRQAMQI SEKEDDDNEK REDFGDNWEE GGGSGAEKS
161    SGPWNKTALV QAPPAPVTVT ETPEPAMPSG VYRPPGARLT TTRKTPQGPP EIYSDTQFPS LQSTAKHVES RNRYLK
    
```



5.1015 ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) [Rattus norvegicus]

Protein Accession	gij16758810
Mean Expression Ratio	1.00
Median Expression Ratio	1.01
Credible Interval	(0.774, 1.32)
Associated Peptides	2
Associated Spectra	2
Coverage	0.197
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	1.00
Avg..iTRAQ.Ratio....117.114.	1.13

1 MAGLPRIIK ETQRLLAEPV PGIKAEPDES NAR YFHVVIA GPQDSPFEGG TPKLELFLPE EYPMAAPKVR FMTKIYHPNV
 81 DKLGRICLDI LKDKWSPALQ IRTVLLSIQA LLSAPNPDDP LANDVAEQWK SNEAQAIETA RAWTRLYAMN NI



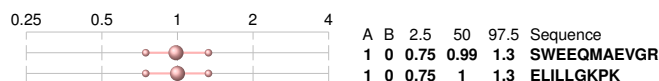
5.1016 "transcription factor A, mitochondrial [Rattus norvegicus]"

Protein Accession	gij13786148
Mean Expression Ratio	0.995
Median Expression Ratio	0.995
Credible Interval	(0.766, 1.29)
Associated Peptides	2
Associated Spectra	2
Coverage	0.082

Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.06
Avg..iTRAQ.Ratio....116.114.	0.99
Avg..iTRAQ.Ratio....117.114.	0.981

```

1      MALFRGMWGV LRTLGRGTVE MCAGCGGRIP SPVSLICIPK CFSSLGNYPK KPMSSYLRF S TEQLPKFKAK HPDAKVSELI
81     RKIAAMWREL PEAEKKVYEA DFKAENKVIK EAVSKYKEQL TPSQLMGLEK EARQKRLKKK AQIKRRELIL LGKPKRPRSA
161    YNIYVSESFQ GAKDESPQ GK LKLVNQAWKN LSHDEKQAYI QLAKDDRI RY DNEMKSWEEQ MAEVGRSDLI RRSVKRPPGD
241    ISEN
    
```



5.1017 PREDICTED: similar to Methionine aminopeptidase 2 (MetAP 2) (Peptidase M 2) (Initiation factor 2-as

Protein Accession	gij109506609
Mean Expression Ratio	1.01
Median Expression Ratio	1.00
Credible Interval	(0.75, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0378
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.977
Avg..iTRAQ.Ratio....116.114.	0.785
Avg..iTRAQ.Ratio....117.114.	0.775

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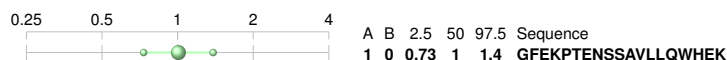
1      MAGVEEASSF GGHLNGDLDP DDREEGTSST AEEAAKKRRR KKKKGKGA VS AGQQELD KES GTSVDEVA KQ LERQALEE KE
81     KDDDDDEDG DG DGDGAAGKK KKKKRGPRVQ TDPSPV P ICD LYPNGVFP KG QECEYPP TQD GQTAAWRT TS EEK KALDQAS
161    EEIWNDFREA AEHRQVRKY VMSWIKPGMT MIEICEKLED CSRKPIKENG LNAGLAFPTG CSLNNCAAHY TPNAGDTTVL
241    QYDDICKIDF GTHISGRIID CAFTVTFNPK YDILLKAVKD ATNTGIK CAG IDIRLCDVGE AIQEVME SYE VEIDGKTYQV
321    KPIRNLNGHS IGPYRIHAGK TVPIVKGGEA TRMEEGEVYA IETFGSTGKG VVHDDMECSH YMKNFVDEHV PIRLPRTKHL
401    LNVINENFDT LAFCRRLDR LGESKYL MAL KNLCDLGIVD PYPPLCDIK SYTAQFEHTI LLRPTCF EVV SRGDDY
    
```



5.1018 "actin related protein 2/3 complex, subunit 5-like [Rattus norvegicus]"

Protein Accession	gi 83642824
Mean Expression Ratio	1.00
Median Expression Ratio	1.00
Credible Interval	(0.744, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.188
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.979
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	1.10

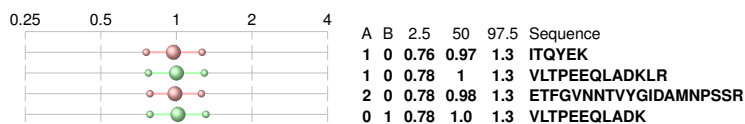
1 MLRAFHAALR NSPINTKNQA VKERAQGIVL KVLTNFKSSE IEQAVQSLDR NGIDLLMKYI YKGF¹FEKPTEN S²SAVLLQWHE
 81 KALAVGGLGS IIRVLTAR³KT V



5.1019 "eukaryotic translation initiation factor 3, subunit 1 alpha [Rattus norvegicus]"

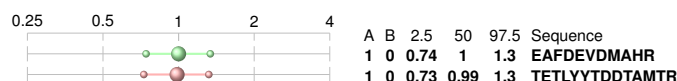
Protein Accession	gi 117940021	
Mean Expression Ratio	0.994	
Median Expression Ratio	0.995	
Credible Interval	(0.803, 1.23)	
Associated Peptides	4	
Associated Spectra	5	
Coverage	0.151	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.875	1.03
Avg..iTRAQ.Ratio....116.114.	0.987	0.99
Avg..iTRAQ.Ratio....117.114.	1.10	1.22

1 MAAAAAAAAAG DSDSWDADTF SMEDPVRKVA GGGTAGGDRW EGEDEDEDVK DNWDDDDDEN KEEAEVKPEV KISEKKKIAE
 81 KIKEKERQ¹QK KRQEEIKKRL EPEESK²VLT PEEQLADK³LR LKKLQEESDL ELAKET⁴FGVN NTVYGIDAMN PSS⁵DDFTEF
 161 GKLLKDK I⁶TO YEK⁷SLYYASF LEALVRDVCI SLEIDDLK⁸KI TNSLTVLCSE KQKQEKQSKA KKKKKG⁹VVPG GGLKATMKDD
 241 LADYGGYDGG YVQDYEDFM



5.1020 PREDICTED: similar to ecto ADP-ribosylhydrolase [Rattus norvegicus]

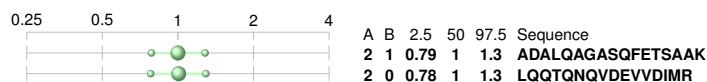
Protein Accession	gij109475505
Mean Expression Ratio	0.993
Median Expression Ratio	0.995
Credible Interval	(0.754, 1.30)
Associated Peptides	2
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.16
Avg..iTRAQ.Ratio....116.114.	1.1
Avg..iTRAQ.Ratio....117.114.	0.933



5.1021 vesicle-associated membrane protein 3 [Rattus norvegicus]

Protein Accession	gij16923936
Mean Expression Ratio	0.994
Median Expression Ratio	0.996
Credible Interval	(0.787, 1.25)
Associated Peptides	2
Associated Spectra	5
Coverage	0.320
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.99
Avg..iTRAQ.Ratio....116.114.	1.04
Avg..iTRAQ.Ratio....117.114.	1.12

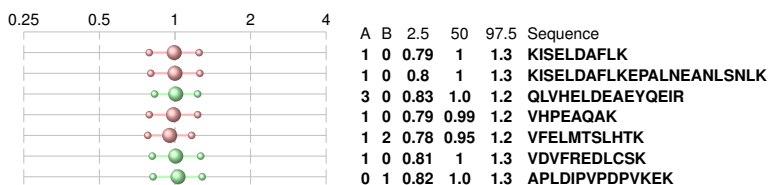
1 MSTGVPSGSS AATGSNRR LQ QTQNQVDEVV DIMRVNVDKV LERDQKLSL DDRADALQAG ASQFETSAAK LKRKYWKNC
 81 KMWAIGISVL VIIIVIIIIVW CVS



5.1022 "protease (prosome, macropain) 28 subunit, alpha [Rattus norvegicus]"

Protein Accession	gj 61098214	
Mean Expression Ratio	0.997	
Median Expression Ratio	0.996	
Credible Interval	(0.848, 1.18)	
Associated Peptides	7	
Associated Spectra	11	
Coverage	0.329	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.08	0.862
Avg..iTRAQ.Ratio....116.114.	1.03	0.951
Avg..iTRAQ.Ratio....117.114.	1.02	0.729

1 MATLRVHPEA QAKVDVFRD LCSKTENLLG SYFPKISEL DAFLKEPALN EANLSNLKAP LDIPVDPVK EKEKEERKKQ
 81 QEKEEKDEK KGDDEDDKGP CGPVNCKEIK VLLQLRLKPE IKDVIEQLNL VTTWLQLQIP RIEDGNNFGV AVQEKVPELM
 161 TSLHTKLEGF QTQISKYFSE RGDVAKAAK QPHVGDYRQL VHELDEAEYQ EIRLMVMEIR NAYAVLYDII LKNFEKLEKP
 241 RGETKGMIV

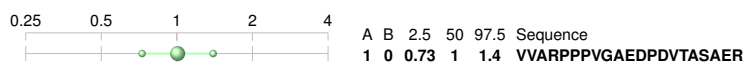


5.1023 myeloid cell leukemia sequence 1 [Rattus norvegicus]

Protein Accession	gi 51036650
Mean Expression Ratio	1.00
Median Expression Ratio	1.00
Credible Interval	(0.739, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0636
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.10
Avg..iTRAQ.Ratio....116.114.	1.18
Avg..iTRAQ.Ratio....117.114.	1.02

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1      MFGLRRNAVI  GLNLYCGGAS  LGAGGGSPAG  TRLAEEAKA  RREGGGEAAL  LPGARVVARP  PPVGAEDPDV  TASAERLLK
81     SPGLLAVPPE  EMAASAAAIM  SPEEELDGCE  PEVLKRPVAV  LPLLERVSEA  AKSSGADGSL  PSTPPPPPEE  DDELYRQSL
161    IISRYLREQA  TGSKDAKPLG  EAGAAGRRA  ETLRRVGDGV  QRNHETAFQG  MLRKLDIKNE  DDVKSFSRVM  THVFKDGV
241    WGRIVTLISF  GAFVAKHLKS  INQESCIPL  AESITDVLVR  TKRDWLKQR  GWDGFVEFFH  VQDLEGGIRN  VLLAFAGV
321    VGAGLAYLIR
  
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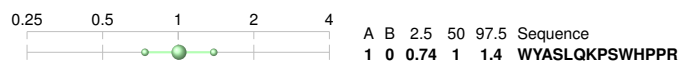


5.1024 benzodiazepin receptor [Rattus norvegicus]

Protein Accession	gi 6978575
Mean Expression Ratio	1.01
Median Expression Ratio	1.00
Credible Interval	(0.744, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0828
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.905
Avg..iTRAQ.Ratio....116.114.	1.19
Avg..iTRAQ.Ratio....117.114.	1.04

```

1      MSQSWVPAVG  LTLVPSLGGF  MGAYFVRGEG  LRNYASLQKP  SWHPPRWTLA  PIWGTLYSAM  GYGSYIIWKE  LGGFTEEAMV
81     PLGLYTGQLA  LNWAWPPIFF  GARQMGWALV  DLMLVSGVAT  ATTLAWHRVS  PPAARLLYPY  LAWLA FATML  NYVVRDMSG
161    RRGSRLTE
  
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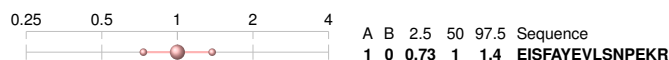


5.1025 "DnaJ (Hsp40) homolog, subfamily A, member 2 [Rattus norvegicus]"

Protein Accession	gi 56799412
Mean Expression Ratio	0.998
Median Expression Ratio	0.996
Credible Interval	(0.74, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0364
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	0.852
Avg..iTRAQ.Ratio....117.114.	1.17

```

1      MANVADTKLY  DILGVPPGAS  ENELKKAYRK  LAKEYHPDKN  PNAGDKFKKI  SFAYEVLSPN  EKFELYDRYG  EQGLREGSGG
81     GGGMDDIFSH  IFGGGLFGFM  GNQSRSRNGR  RRGEDMMHPL  KVSLEDLYNG  KTKKLQLSKN  VLCSACSGQG  GKSGAVQKCS
161    ACRGRGVRIM  IRQLAPGMVQ  QMQSVCSDCN  GEGEVINEKD  RCKKCEGKKV  IKEVKILEVH  VDKGMKHGQR  ITFTGEADQA
241    PGVEPGDIVL  LLQEKEHEVF  QRDGNDLHMT  YKIGLVEALC  GFQFTFKHLD  ARQIVVKYPP  GKVIEPGCVR  VVRGEGMPQY
321    RNPFEKGLDY  IKFDVQFFEN  NWINPDKLSE  LEDLLPSRPE  VPNVIGETEE  VELQEFDSTR  GSGGGQRREA  YNDSDEESS
401    SHHGGVQCA  HQ
  
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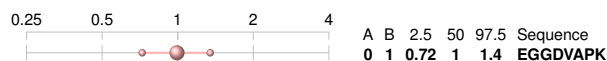
5.1026 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gi 109496074
Mean Expression Ratio	0.996
Median Expression Ratio	0.996
Credible Interval	(0.743, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0386
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.796
Avg..iTRAQ.Ratio....116.114.	1.06

Avg..iTRAQ.Ratio....117.114. 0.784

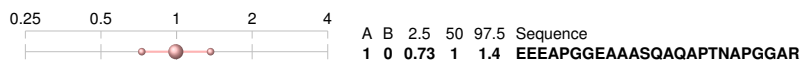
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1      MCTDRGTGAM SVEILQDTT SWSLSWYIQK YVSWILRIRK EGTETGCCVS DDDVPQKRKH FSHGTRIRLW PPSRVEPTYP
81     SDVSNRVIME VVPCVSSEEE DEESVGKVES ADKENIILEN LRDSFHPHRR SEESIKYPNW NVQRQWDWSS DEEDCEGHSI
161    SVTALVHAEA CLSDTEEEEK AEEAIKSQDE ASREGGDVAP KTEAAAL
    
```



5.1027 PREDICTED: similar to DNA polymerase epsilon subunit 4 [Rattus norvegicus]

Protein Accession	gi 34856269
Mean Expression Ratio	0.994
Median Expression Ratio	0.996
Credible Interval	(0.74, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	0.981
Avg..iTRAQ.Ratio....117.114.	0.999



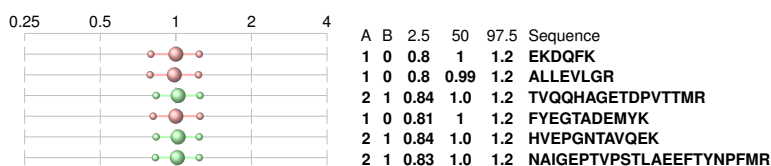
5.1028 hydroxyacyl glutathione hydrolase [Rattus norvegicus]

Protein Accession	gi 15375320
Mean Expression Ratio	1.00
Median Expression Ratio	1.00
Credible Interval	(0.856, 1.18)

Associated Peptides	6	
Associated Spectra	12	
Coverage	0.292	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.977	0.97
Avg..iTRAQ.Ratio....116.114.	0.977	1.28
Avg..iTRAQ.Ratio....117.114.	1	1.31

```

1      MKIELLPALT  DNYMYLIIDE  DTQEAADVDP  VQPQKVIETV  KKHRVKLTV  LTHHHWDHA  GGNEKLVKLE  PGLKVYGGDD
81     RIGALTHKVT  HLSTLEVGLS  SVKCLSTPCH  TSGHICYFVS  KPGSSEPSAV  FTGDTLFVAG  CGKFYEGTAD  EMYKALLEVL
161    GRLPPDTKVI  CGHEYTVNNL  KFARHVEPGN  TAVQEKLAWA  KEKNAIGEPT  VPSTLAEEFT  YNPFMRVKEK  TVQQHAGETD
241    PVTTMRAIRR  EKDQFKVPRD
  
```



5.1029 PREDICTED: similar to Nucleosome binding protein 1 (Nucleosome binding protein 45) (NBP-45) (GARP45)

Protein Accession	gij109512216
Mean Expression Ratio	1
Median Expression Ratio	0.996
Credible Interval	(0.742, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0365
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.12
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	1.03

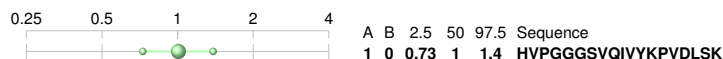
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1      MPKRKAAGDA  SQEPKRRSAR  LSAMPVFPTP  ELKPKRSTS  RKTKTNVVE  ESKDAGATTI  PETKPEVVKG  ECNMENAENG
81     EAKIIEAPIS  KMETEEVKEQ  INEDTEGDGG  EKKEAVVTKG  KNDELEANIQ  DVEKDEDEKE  HEDTGEEGED  GEREGGLKEK
161    PDVAEIEDAK  EAKDDEEKED  KEKEDDKGGD  GKKEEEKDDE  GEAETEEEVK  EQQKEETEGD  DGKCKVENK  EDGKEDLHEE
241    DGKEDLHEED  GKEDLHEEEG  KEDLHEEEGK  EDLHEEEGKE  DLHEEEGKED  LHEEEGKEDL  HEEEGKEDLH  EEEGKEDLHE
321    EDGKEGQHEE  EGKEDLHEEE  GKEDLHEEDG  KEGQHEEDGK  KKADGNEDRK  EEEEQEAAAE  GNDENKVEVE  EEADNKDFKE
401    DGEKGEPVST  V
  
```



5.1030 microtubule-associated protein tau [Rattus norvegicus]

Protein Accession	gij8393752
Mean Expression Ratio	1.00
Median Expression Ratio	1.00
Credible Interval	(0.745, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.993
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	1.07



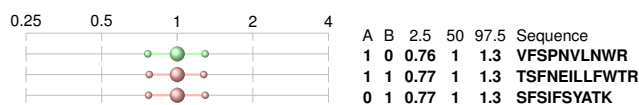
5.1031 "C-reactive protein, petaxin related [Rattus norvegicus]"

Protein Accession	gij8393197	
Mean Expression Ratio	0.998	
Median Expression Ratio	0.996	
Credible Interval	(0.795, 1.25)	
Associated Peptides	3	
Associated Spectra	4	
Coverage	0.139	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.02	1.22
Avg..iTRAQ.Ratio....116.114.	0.983	1.09
Avg..iTRAQ.Ratio....117.114.	0.901	0.75

NHLBI Zile/Grant, Aged Rat

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1      MEKLLWCLLI TISFSQAFGH EDMSKQAFVF PGVSATAYVS LEAESKKPLE AFTVCLYAHA DVSRSFSIFS YATKTSFNEI
81     LLFWTRGQGF SIAVGGPEIL FSASEIPEVP THICATWESA TGIVELWLDG KPRVRKSLQK GYIVGTNASI ILGQEQDSYG
161    GGFANQSLV GDIGDVMWD FVLSPEQINA VYVGRVFSPN VLNWRALKYE THGDVFIKPQ LWPLTDCCES
  
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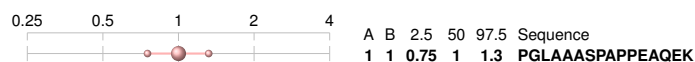


5.1032 "COX17 homolog, cytochrome c oxidase assembly protein [Rattus norvegicus]"

Protein Accession	gij16758308	
Mean Expression Ratio	0.998	
Median Expression Ratio	0.996	
Credible Interval	(0.763, 1.31)	
Associated Peptides	1	
Associated Spectra	2	
Coverage	0.254	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.812	1.20
Avg..iTRAQ.Ratio....116.114.	0.864	1.32
Avg..iTRAQ.Ratio....117.114.	0.729	0.932

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1      MPGLAAASPA PPEAQEKKPL KPCCACPETK KARDACIIEK GEEHCGHLIE AHKECMRALG FKI
  
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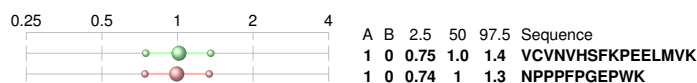
5.1033 heat shock 22kDa protein 8 [Rattus norvegicus]

Protein Accession	gij16758408	
Mean Expression Ratio	1.00	
Median Expression Ratio	1.00	
Credible Interval	(0.757, 1.3)	
Associated Peptides	2	

Associated Spectra	2
Coverage	0.138
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.973
Avg..iTRAQ.Ratio....116.114.	1.02
Avg..iTRAQ.Ratio....117.114.	1.10

```

1      MADGQLPFPC SYPSRLRRDP FRDSPLSSRL LDDGFGMDPF PDDLTPWPFE WALPRLSSAW PGTLRSGMVP RGPTATARFG
81     VPAEGRNPPF FFGEPNKVCY NVHSFKBEEL MVTTKDGYVE VSGKHEEKQQ EGGIVSKNFT KKIQLPAEVD PVTVFASLSP
161    EGLLIIEAPQ VPPYSPPGES SFNNELPQDN QEVTCs
    
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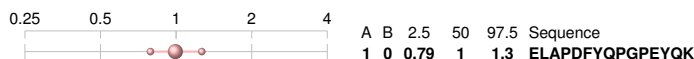


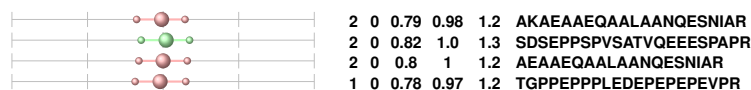
5.1034 junctophilin 2 [Rattus norvegicus]

Protein Accession	gi 83816931
Mean Expression Ratio	0.996
Median Expression Ratio	0.997
Credible Interval	(0.831, 1.19)
Associated Peptides	5
Associated Spectra	8
Coverage	0.114
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.11
Avg..iTRAQ.Ratio....116.114.	0.963
Avg..iTRAQ.Ratio....117.114.	1.12

```

1      MSGGRFDFDD GGAYCGGWEG GKAHGHGLCT GPKGQGEYSG SWNFGFEVAG VYTWPSTGNTF EGYWSQGRH GLGIETKGRW
81     LYKGEWTHGF KGRYGIRQST NSGAKYEGTW NNGLQDGYGT ETYADGGTYQ GQFTNGMRHG YGVRQSVPYG MAVVVRSLR
161    TSLSSLRSEH SNGTVAPDSP AADGPTLPLP PVPRGGFALS LLATAEAARP PGLFTRGALL GRLRRSESRT SLGSQRSRLS
241    FLKSELSSGA SDAASTGSLA EGAEGPDDAA APFDADIDAT TTETYMGWEK NDKRSGFGVS ERSGLRYEG EWLDNLRHGY
321    GRITLDPDHR EEGKYRHNVL VKGTKRRLVP LKSNKVRQKV EHGVEGAQRA AAIARQKAEI AASRTSHAKA KAEAAEQAAL
401    AANQESNIAR TLAKELAPDF YQPGPEYQKR RLLQEIENS ESLLPRERG PGTGLPERPR ESPQLHERET PQEGGPPSP
481    AGTFFPQKRP RFGSSKDGLL SPGAWNPEPG GEGSRPATPS DGAGRRSPAR PASEHMAIEA LQPPPAPSRE PEVALYRGYH
561    SYAVRTGPEE PPLEDEPEP EPEVPRSDSE PPSPVSATVQ EESPPAPSR VPAKPATLEP KPIVPKAEPK AKARKTEARG
641    LSKAGAKKKG RKEVAQEAEA EVEVEVPNT VLICMILLN IGLAILFVHL LT
    
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5.1035 PREDICTED: similar to Ataxin-2 (Spinocerebellar ataxia type 2 protein homolog) [Rattus norvegicus]

Protein Accession	gij109497407
Mean Expression Ratio	1.00
Median Expression Ratio	1.00
Credible Interval	(0.741, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.01
Avg..iTRAQ.Ratio....116.114.	1.12
Avg..iTRAQ.Ratio....117.114.	1.18



5.1036 "PREDICTED: similar to cytochrome P450, family 2, subfamily J, polypeptide 2, B [Rattus norvegicus]"

Protein Accession	gij109494685
Mean Expression Ratio	1.00
Median Expression Ratio	1.00
Credible Interval	(0.745, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0117
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.999
Avg..iTRAQ.Ratio....116.114.	0.94

Avg..iTRAQ.Ratio....117.114. 1.21

```

1      MDSVTLGWIQ  GVGRYSEDVR  QKLSTGCRKV  GSHTQRAIIA  KGAMGCLVSP  QLAQTHGNVF  TVWLGSTPIV  VLNGFRAVKE
81     ALVSNSEQFS  GRPLTPFFFR  LFGKGGVICS  NGLTWRQRR  FCLTTLRELG  LGKQALELQL  QHEAAELAEV  FHQEQGRAF
161    PQVPIIRSTT  RVIGALVFGH  HFLSEEPFIFL  ELIRAINLGL  AFASTTWRV  IGSWGGWHAG  SLSGPFSLQL  YDMFPWALRY
241    LSGPHQKIFQ  YHEAVRGFIH  HEIIRHKLRT  PEAPKDFISC  YLSQITKAMD  DPVSTFSEEN  LIQVVIDLFL  GGTDTTATL
321    HWAIYLVVHH  RAIQERVQQE  LDEVLGTAQA  VCYEDRERLP  YTRAVLHEVQ  RLSSVAVGA  VRQCVTPW  HGYYVSKGTI
401    ILPNLASVLC  DPECWETPHQ  FNPGFHLDKD  GDFVTNEAFL  PFSAGHRVCP  GEQLARMELE  LMFATLLRTF  RFQLPEGSQG
481    LRLEYVFGGT  LQPQPKICA  VPRLSLSLSPR  EP
    
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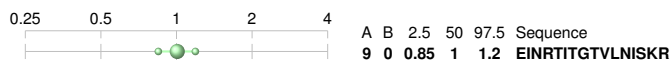


5.1037 Ac1158 [Rattus norvegicus]

Protein Accession	gi 57114334
Mean Expression Ratio	1.00
Median Expression Ratio	1.00
Credible Interval	(0.82, 1.23)
Associated Peptides	1
Associated Spectra	9
Coverage	0.0296
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.957
Avg..iTRAQ.Ratio....116.114.	1.3
Avg..iTRAQ.Ratio....117.114.	0.957

```

1      MEEDPQVIGI  NVAELRLRMV  VKLSCRSGVL  DNEYQQAFPA  AKQPLEELRA  ERSPLHSILS  ESSEVCLFTK  DECDSPQE
81     GFYKLLKKH  GVNTISQIIP  FKTLKTEYKA  YEAKLRLLS  FDFVIADERI  RRHLPHTHGR  HFYQRKKVPV  SVNLLAKNLS
161    KEINRRTITGT  VLNIKRGSC  STIRIGHTGM  EIQHIENIL  TVSEMLSEKL  PEEPKRRKH  EKQKLLKESK  MLKKSKKAT
241    SLLTQGGGLV  SAPARGPGAQ  KKRTSKASTQ  PKVTEEYEET  IPQLVPIGET  PDKENMKMQE  NITGKKSPPK  KSDPRTQAK
321    QDAQRKEAQQ  EEGPDPHCG  QETRGQKGGQ  SFEKRPKNFG  IEQDIQPKRD  LTRFVKWSCY  IRLQRQRAIL  YKGSKYLLSS
401    TSSPRPWTGR  QRLSCLSLPT  SIGQRQSRRR  SKGCWPVLR  KLLAKGTSQL  RDHLSSTKRP  PVLQAGVNTV  TTSVENQKAQ
481    LVVEDKGALA  KLVEAIRTNY  NDRYDEIRRH  WGNVNLGPKS  VARIAKLEKA  KAKELTTKLG
    
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5.1038 PREDICTED: similar to Prefoldin subunit 5 (C-myc-binding protein Mm-1) (Myc modulator 1) (EIG-1) [R]

Protein Accession	gij 27665420
Mean Expression Ratio	1
Median Expression Ratio	0.997
Credible Interval	(0.746, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.95
Avg..iTRAQ.Ratio....116.114.	1.03
Avg..iTRAQ.Ratio....117.114.	1.15



5.1039 PREDICTED: similar to DISCO Interacting Protein 2 CG7020-PA [Rattus norvegicus]

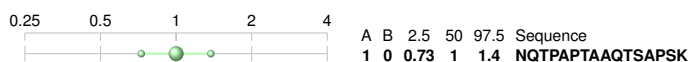
Protein Accession	gij 109482891
Mean Expression Ratio	1
Median Expression Ratio	0.997
Credible Interval	(0.75, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0102
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.20
Avg..iTRAQ.Ratio....116.114.	1.23
Avg..iTRAQ.Ratio....117.114.	0.883

NHLBI Zile/Grant, Aged Rat

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1    MAERGLEPSP AAVAALPPEV RAQLAELELE LSEGDITQKG YEKRRSKLLS PYSPOQTQETD STGQKERNQT PAPTAAQTSA
81   PSIYHRSRSG GARDERYRSD IHTEAVQAAL AKHKEQKMAL PMPTKRRSTF VQSPADACTP PDTSSASEDE GSLRRQAALS
161  AALQQSLQNA ESWINRSIQG SSTSSSASST LSHGEVKGTS GSLADVFANT RIENVSAAPPD VTATTSSSSS LLRSPANIDL
241  PSGIVKGMHK GSNRSSLMDT ADGVPVNSRV STKIQLLNT LKRPKRPLK EFFVDDSEEI VEVPPQDPNQ PKPEGRQMT
321  VKGEPLGVIC NWPPALESAL QRWGTQAKC PCLTGLDVTG KPVYTLTYGK LWSRSLKLAY TLLNKLGTKN EPVLKPGDRV
401  ALVYPNNDPV MFMVAFYGC LAEVIVPPIE VPLTRKDAGG QQIGFLLGSC GIALALTSEI CLKGLPKTON GEIVQFKGWP
481  RLRWVVTDK YLSKPPKDWQ PHISPAGTEP AYIEYKTSKE GSVMGVTVSR LAMLSHCQAL SQACSYSEGE TVVNVLDFFK
561  DAGLWHGMFA NVMNMHTIS VPYSVMKTCP LSWVQRVHAH KAKVALVKCR DLHWAMMAHR DQRDVSLSL RMLIVTDGAN
641  PWSVSSCDF LSLFQSHGLK PEAICPCATS AEAMTIAIRR PGVPGAPLPG RAILSMMNGLS YGVIRVNTED KNSALTVQDV
721  GHVMPGGMMC IVKPDGLPQL CKTDEIGEIC VSSRTGGMMY FGLAGVTKNT FEVIPVTSSG SPVGDVVFIR SGLLGFVGGP
801  SLVFVVGKMD GLLMVSRRH NADDIVATGL AVESIKTVYR GRIAVFSVSV FYDERIVVVA EQRPDASEED SFQWMSRVLQ
881  AIDTIHQGV YCLALVPANT LPKTPLGGIH ISQTKQLFLE GSLHPCNILM CPHTCVTNLP KPRKQKQGVG PASVMVGNLV
961  AGKRIAQAAG RDLGQIEEND LVRKHQFLAE ILQWRAQATP DHVLYVLLNA KGTTVCTASC LQLHKRAERI ASVLGDKGHL
1041 NAGDNVLLY PPGIELIAAF YGCLYAGCIP VTVRPPHAQN LTATLPTVRM VVDVSKAACV LTTQTLMRL KSREAAAADV
1121 VKTWPALIDT DDLPRKRLPQ LYKPPTEPML AYLDVSVST GMLTGVMKMSH SAVNALCRAI KLQCELYSSR QIAICLDPYC
1201 GLGFALWCLC SVYSGHQSVL IPPMELESNL SLNLATVNYQ KIRDTFCSYS VMELCTKGLG SQVEALKTRG INLSCIRTCV
1281 VVAERPRVT LQQSFSKLFK DIGLSPRAVS TTFGSRVVA ICLOGTSQPD PTTVYVDLKS LRHDRVRLVE RGAPQSLLS
1361 ESGKILPGVK VVIVNPETKG PVGDSHLGEI WVNSPHITASG YTYIYDSETL QADHFNTRLS FGDAAQTLWA RTGYLGFVRR
1441 TELTAATGER HDALYVVGAL DETLELRGLR YHPIDIETSV SRVHRISIAEC AVFTWTNLLV VVVELCGSEQ EALDLVPLVT
1521 NVVLEEHYLI VGVVVVVDPG VVPINSRGEK QRMHLRDSFL ADQLDPIYVA YNM

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5.1040 PREDICTED: similar to insulinoma-associated 2 [Rattus norvegicus]

Protein Accession	gij109478234
Mean Expression Ratio	1
Median Expression Ratio	1.00
Credible Interval	(0.762, 1.31)
Associated Peptides	1
Associated Spectra	2
Coverage	0.0227
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.911
Avg..iTRAQ.Ratio....116.114.	1.08
Avg..iTRAQ.Ratio....117.114.	0.966

```

1    MNSHSITEAR SPDRYWMADV LPPSSLTGR GTLTRSADS RPSRWPSLHC PPEAAEPFSA TSRRGPCRLP ASGRLVASGS
81   PARGPRRLCC APQAPSCPLV FPRLCRGARP VGGPAPGPAP TPDWPAQAEQ PGPTGPGVSA IKRAAACPAR SGPPSSGACP
161  GTRTIMPRGF LVKRTRKRS GS FYRTRPAEPL FPPPGPLAAP PSPEEPDPLG LGSPCLAPPQ DSTEWAGAGG DGPSPSPAR
241  AGPELRRRFL ERCLRSPVSA ESFPSATAFC SAAPAAATSG EQLVPPRVFV SVVPVVPVSV PAPHGLQRRG KGAPGCSAP
321  AAVRKPKA VR RLSFADEVTT SPVLGLKIKI EEPGAPARAL GGVTPLGEF ICQLCKQQYA DPFALAQHRC SRIVRVEYRC
401  PECDKVFS CP ANLASHRRWH KPRPTFACTA SKPPHAPLTP PDPSLAAGKE NGCLPRTEDQ HPQARDSGD GQHRDAAALP
481  GLQALVHPEA ARPQAPYSEV ILGRHGPRPS GASTGATSEV FVCPYCHKKF RRQAYLRKHL GTHETGSARA TTPFGGSERT
561  APLTFACPLC GAHFPSADIR EKHRLWHA VR EELLPLALVG APTEAGP GGA SEGSAQQIFS CRKYCPSTFFS SPGLTRHINK
641  CHPSESQRVL LLQMPLRPGC

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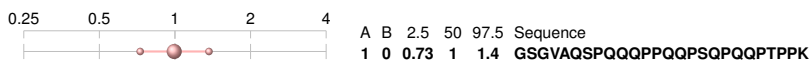


5.1041 phosphofurin acidic cluster sorting protein 1 [Rattus norvegicus]

Protein Accession	gij19705535
Mean Expression Ratio	0.996
Median Expression Ratio	0.998
Credible Interval	(0.744, 1.32)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0271
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	0.898
Avg..iTRAQ.Ratio....117.114.	1.31

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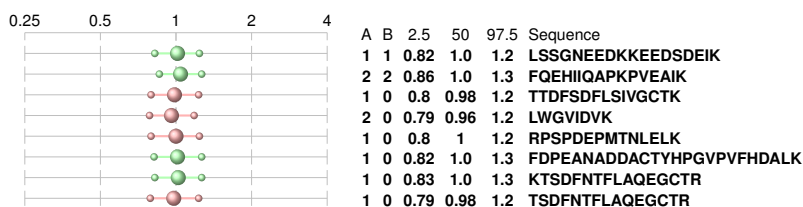
1   MAERGGAGGG PGGAGGSSQ R GSGVAQSPQ QQPPQQPSQP QQPTPPKLAQ ATSSSSSTSA AAASSSSSST STSMVAVAS
81  GSAPPPGGPGR GRTPAPVQMN LYATWEVDRS SSSCVPRLFS LTLKKLVMLK EMDKDLNSV IAVKLGSKR IILRSNEIILP
161 ASGLVETELQ LTFSLQYPHF LKRDKANKLQI MLQRRKRYKN RTILGYKTLA VGLINMAEVM QHPNEGALVL GLHSNVKDVS
241 VPVAEIKIYS LSSQPIDHEG IKSKLSDRSP DIDNYSEEEE ESFSSEQEGS DDPLHGQDLF YEDEDLKRKVK KTRRKLSTST
321 AITRQPNIKQ KFVALLKRFK VSDEVGFGL E HVSREQIREV EEDLDELIDS LEMYNPDSG PEMEETESIL STPKPKLPPF
401 FEGMSQSSSQ TEIGSLNSKG SLGKDTTSPM ELAALERVKS TWIRNQDDSL TETDTLEITD QDMFGDASTS LVVPEKVKTP
481 MKSSKADLQG SASPSKVEGT HTPRQKRSTP LKERQLSKPL SERTNSSDSE RSPDLGHSTQ IPRKVVVDQL NQILVSDAAL
561 PENVILVNTT DWQGGQYVAEL LQDQRKPVVC TCSTVEVQAV LSALLTRIQR YCNCNSSMPR PVKVAAVGSO SYLSILRFF
641 VKSLASKTPD WLGHRMFLIV PLGSHPVAKY LGSVDSRYSS TFLDSAWRDL FSRSEPPVSE PLDVVGRVMQ YVNGATTTHQ
721 LPVAEAMLTC RHKFPDEDSY QKFIFFIGVV KVGLEDSPS TAGDGDDSPV VSLTVPSTSP PSSSGLSRDA TATFPSSPSM
801 SSALAIIVGSP NSPYGDVIGL QVDYWLGHGP ERRREGDKRD ASSKNTLKS V FRSVQVSRLP HAGEAQLSGT MAMTVVTKEK
881 NKRVPITIFLS KKPPEKEVDS KSQVIEGISR LICSAKQQQT MLRVSIDGVE WSDIKFFQLA AQWPTHVKHF PVGLFSGSKP
961 T
  
```



5.1042 "PREDICTED: similar to cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1"

Protein Accession	gij34860374
Mean Expression Ratio	1.00
Median Expression Ratio	1.00
Credible Interval	(0.856, 1.17)
Associated Peptides	8
Associated Spectra	13

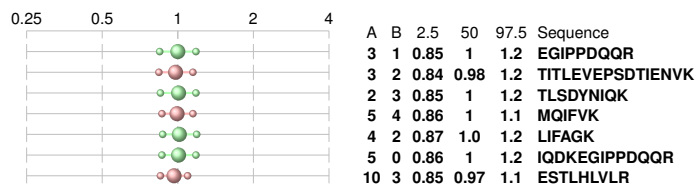
Coverage	NA	
	A	B
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.928	1.60
Avg..iTRAQ.Ratio....116.114.	0.955	1.15
Avg..iTRAQ.Ratio....117.114.	0.913	1.54



5.1043 ribosomal protein S27a [Rattus norvegicus]

Protein Accession	gi 13592077	
Mean Expression Ratio	0.997	
Median Expression Ratio	0.998	
Credible Interval	(0.898, 1.10)	
Associated Peptides	7	
Associated Spectra	47	
Coverage	0.378	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.965	1.04
Avg..iTRAQ.Ratio....116.114.	0.998	1.13
Avg..iTRAQ.Ratio....117.114.	0.811	1.25

1 MQIFVKTLTG KTITLEVEPS DTIENVKAKI QDKEGIPPDO QRLIFAGKQL EDGR~~TLSDYN~~ IQKESTLHLV LRLRGGAKKR
 81 KKS~~SY~~TPPK NKHKRKKVKL AVLKYYK~~VDE~~ NGKISRLRRE CPSDECGAGV FMGSHFDRHY CGKCCLYCF NKPEDK



5.1044 "protein phosphatase 5, catalytic subunit [Rattus norvegicus]"

Protein Accession	gij13929024
Mean Expression Ratio	0.999
Median Expression Ratio	0.998
Credible Interval	(0.74, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0361
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.961
Avg..iTRAQ.Ratio....116.114.	1.06
Avg..iTRAQ.Ratio....117.114.	1.17

```

1      MAMAEGERT E CAEPPRDEPP AEGTLFRAEE LKTQANDYFK AKDYENAIKF YSQAIELNPS NAIYYGNRSL AYLRTCEYGY
81     ALGDATRAIE LDKKYIKGY Y RRAASNMALG KFRAALRDYE TVVKVKPNDK DAKMKYQEC S KIVKQKA FER AIAGDEHRRS
161    VVDSLDI ESM TIEDEYSGPK LEDGKVTITF MKDLMQWYKD QKKLHRKCA Y QILVQVKEVL CKLSTLVETT LKETEKITVC
241    GDTHGQFYDL LNIFELNGLP SETNPYIFNG DFVDRGFSFV EVILTLFGFK LLYPDHFHLL RGNHETDNMN QIYGFEGEVK
321    AKYTAQMYEL FSEVFEWLPL AQCINGKVL I MHGGLFSEDG VTLDDIRKIE RNRQPPDSGP MCDLLWSDPQ PQNGRSVSKR
401    GVSCQFGPDV TKAFLEENQL DYIIRSHEVK AEGYEVAHGG RCVTVFSAFN YCDQMGNKAS YIHLQGSDLR PQFHQFTAVP
481    HPNVKPMAYA NTLLQLGMM
  
```



5.1045 PREDICTED: similar to kinesin family member 23 [Rattus norvegicus]

Protein Accession	gij62653782
Mean Expression Ratio	0.997
Median Expression Ratio	0.998
Credible Interval	(0.736, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.17
Avg..iTRAQ.Ratio....116.114.	1.08
Avg..iTRAQ.Ratio....117.114.	0.945

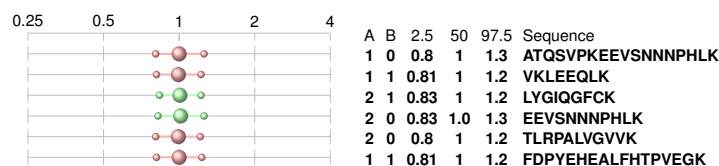


5.1046 "GrpE-like 1, mitochondrial [Rattus norvegicus]"

Protein Accession	gj 13324704	
Mean Expression Ratio	1.00	
Median Expression Ratio	1.00	
Credible Interval	(0.852, 1.17)	
Associated Peptides	6	
Associated Spectra	12	
Coverage	0.290	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.967	1.13
Avg..iTRAQ.Ratio....116.114.	1.04	0.947
Avg..iTRAQ.Ratio....117.114.	1.03	0.81

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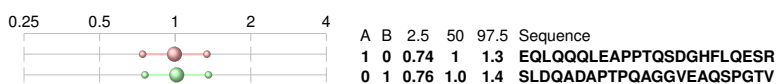
1   MAARCVRLAR RSLPALALSF RPSRLLCTA TKQKNNGQNL EEDLGHCEPK TDPSSADKTL LEEKVKLEEQ LKETMEKYKR
81  ALADTENLRQ RSQKLVEEAK LYGIQGFCKD LLEVADILEK ATQSVPKKEEV SNNNPFLKSL YEGLVMTEVQ IQKVFTKHGL
161 LRLDPIGAKF DPYEHEALFH TPVEGFEPGT VALVSKVGYK LHGR1TLRPAL VGVV1DA
    
```



5.1047 PREDICTED: similar to syncoilin [Rattus norvegicus]

Protein Accession	gj 109475536	
Mean Expression Ratio	1.00	
Median Expression Ratio	1.00	
Credible Interval	(0.774, 1.30)	

Associated Peptides	2	
Associated Spectra	2	
Coverage	NA	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.913	0.527
Avg..iTRAQ.Ratio....116.114.	1.05	1.24
Avg..iTRAQ.Ratio....117.114.	0.901	2.24

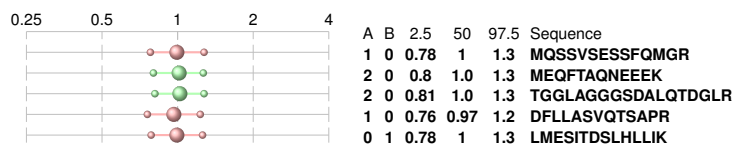


5.1048 PREDICTED: similar to Synaptopodin-2 (Myopodin) [Rattus norvegicus]

Protein Accession	gij109467523	
Mean Expression Ratio	0.998	
Median Expression Ratio	0.998	
Credible Interval	(0.821, 1.22)	
Associated Peptides	5	
Associated Spectra	7	
Coverage	0.065	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.06	0.754
Avg..iTRAQ.Ratio....116.114.	0.94	1.15
Avg..iTRAQ.Ratio....117.114.	1.23	0.74

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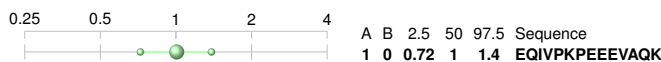
1      MGTGDFICIS MTGGAPWGFR LQGGKEEKQP LQVAKIRSQS KASDSGLCVG DEVVSINGNP CADLTYPEVI KIMESITDSL
81     HLLIKRPTSG TSEALDSETE NTNHQHLPHG GPMESTTLQI QHAAKTQGKD FLLASVQ TSA PR TEDQGN AW GYAECTTEDQ
161    VSQMPGSQEG HLVEEVILRK KPEAGQPGHV VELQLSLSKE RQRCTSDPIV TLLGNEKFKS PDPDWGTQHG RTVHINSIPA
241    PEKADTSLTS GTTVQTSSGR ELTVIQGRDP GGTGLPQVEV ILDCSDRLKA EECRLQAGRG CVASPVGGR SEAPPSLVSF
321    AVSSEGTEQG EDQRSKGDQG RPHKHRARHA RLRRSELSSE KQVKEAKSKC KSIALLLTD A PNPNSKGVLM FKKRRRRARK
401    YTLVSYGTGE LEREEEEEDQ EAGDKDEISD LAFLGTSESE VDELLSDVD DNTQVNFVDW DSGLV DIEKR LNRGDKMEML
481    PDTTGKGALM FAKRRRMEQ FTAQNEE EKT GGLAGGGS DA LQTDGLR TMT SYQRKEESVR MQSSVSESSF QMGR SLGSVP
561    QQNGFSGVSE TAGPQRMIPM NRTAKPFLGS VNQTAAPFSP TQSVTSPIDP FPAPPPYS AV SPPPEAFSRG ISSPVAGPAQ
641    PPPWPQPAPW SQPAFYDSE QIASRDERIA VPAKRTGILQ EAKRRGTTKP MFTFKETKVS PNP ELLSLLQ NAEGKRGTGA
721    GGD SGPEEDY LSLGAEACNF MQSSARQKTP PPVAPKPAVK TSSSSQP VAP VSPVWSPGVA PAQGPAPFST NPPNPPQVTA
801    VSSIKIAQPT CPPARPASAL NLAGPFKGPQ AAVVSHNYTP KPSAPTPLVN AAPAGAGGPS NELPGMSGKG AQLFAKRQSR
881    MEKYVVDSDT VQAHTVRAQS PTFSLPASWK YSSNVRAPPP VAYNFIHSPS YPLAAIKSQP PGAQASKTSK KKGKFLNNTL
961    DVMKHQPYQL NASLFTFQPP DSKDGLPQKS TVKVSSVAPA MKQALPPRQA DIGSPTNAKA SSVYSVPAYT SQPNFFAEAT
1041   SPVSASPVV SVPTSPKQET TSTSYFVAPR PKFSAKKSGV TVQVWKPSVV EE
    
```



5.1049 PREDICTED: similar to 60S ribosomal protein L17 (L23) (Amino acid starvation-induced protein) (ASI)

Protein Accession	gij 109461025
Mean Expression Ratio	1.01
Median Expression Ratio	1.00
Credible Interval	(0.743, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0761
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.14
Avg..iTRAQ.Ratio....116.114.	0.94
Avg..iTRAQ.Ratio....117.114.	1.01

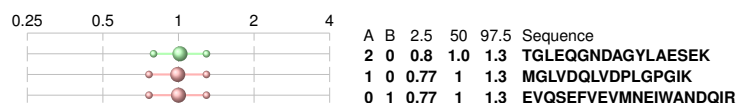
1 MVRYSLDPEN PTKSCKSRGS NLRVHFKNTR ETAQAIKGMH IRKATKYLKD VTLKKQCVPL RRYNGGVDR C AQAQKQGWTO
 81 GRWPKKSAEF LLHMLKNAES NAELKGLDVD SLVIEHIQVN KAPKMRRRTY RAHSRINPYM SSPCHIEMIL TEK **EQIVPKP**
 161 **EEEVAQ**KKI SQKKLKRQKL MARE



5.1050 "mitochondrial trifunctional protein, alpha subunit [Rattus norvegicus]"

Protein Accession	gij 18677763
Mean Expression Ratio	1.00
Median Expression Ratio	0.999
Credible Interval	(0.803, 1.26)
Associated Peptides	3
Associated Spectra	4
Coverage	NA

Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	1.12	0.563
Avg..iTRAQ.Ratio....116.114.	0.927	0.866
Avg..iTRAQ.Ratio....117.114.	1.19	1.85



5.1051 phospholemmann precursor [Rattus norvegicus]

Protein Accession	gi 13928896
Mean Expression Ratio	1.00
Median Expression Ratio	1.00
Credible Interval	(0.749, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	0.130
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.884
Avg..iTRAQ.Ratio....116.114.	1.18
Avg..iTRAQ.Ratio....117.114.	1.01

1 MAPLHHILIV CVCLLSMASA EAPQEPDPFT YDYHTLRIGG LTAGILLFIL GILIILSKRC RCKFNQQQR T **GEPDEEEGTF**
 81 **RSSIRRLSTR** RR



5.1052 PREDICTED: similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase) (Cyclophilin A) (Cy

Protein Accession	gij109481830
Mean Expression Ratio	1
Median Expression Ratio	1.00
Credible Interval	(0.743, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	0.022
Experiment	B
Avg..iTRAQ.Ratio....115.114.	1.03
Avg..iTRAQ.Ratio....116.114.	1.12
Avg..iTRAQ.Ratio....117.114.	1.14

```

1      MFLNQETFRN PEVSQGAGSG SPSRPDSPAR ASRTVGGEGS HPGSRAAQAG QRIGESGRLS AAPLDGEPPA RRVHALGSHG
81     AGQSGGACPV SPPRSGEVQE PRLGVRRRGR GERARSGGPP AGTQARRSRE EGGGPWDPAG ADIAVCCFSP LAELVNPTV
161    YFNITADGEP LGHVSELFPA DNVPKTAENF HALSTGEKGF GYKASSFHRI IPGFMCQGGN VTCHNGAGGR SIYREKFEGE
241    DVILKHTGPG ILSMANDEPN TSGSQFFICT AKTEWLGGKG VVFEKAKDGM NIVEAMERFG SRNGKTSKQI TISGCGQC
  
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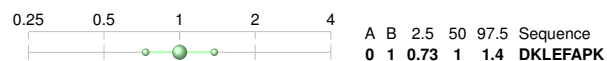


5.1053 PREDICTED: hypothetical protein [Rattus norvegicus]

Protein Accession	gij109475521
Mean Expression Ratio	1.00
Median Expression Ratio	1.00
Credible Interval	(0.745, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0412
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.897
Avg..iTRAQ.Ratio....116.114.	0.92
Avg..iTRAQ.Ratio....117.114.	0.829

```

1      MTLRKDTANL REYSSLAGAQ PITVPRESLD ASRRGLGRRP AGYWEPRRSC CSRLAGAARG RSGLFGLGRR VFRGPNCTK
81     HSGCLLLCGV AAQLLGARLP DVMWPVLWTV VRTYAPVTF PVAFVVGAVG YHLEWFIRGK DPQPVEEEKS ILERREDRKL
161    DEMLGKDHTQ VVSLKQKLEF APKAVLNNRR PEKN
  
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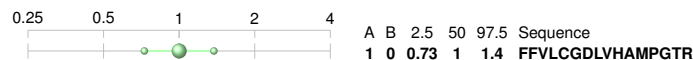


5.1054 hypothetical protein LOC302890 [Rattus norvegicus]

Protein Accession	gi 62078655
Mean Expression Ratio	1.00
Median Expression Ratio	1.00
Credible Interval	(0.739, 1.35)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0513
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.952
Avg..iTRAQ.Ratio....116.114.	1.04
Avg..iTRAQ.Ratio....117.114.	1.22

```

1      MSAAGAADV F HRARGRTLDA FSSEKEREW T GPFYFVQ GAD PQFGLMKAW S TGNCNDNGGDE WGQEIRLTEQ AVEAINKLNP
81     KPK FVLCGD LVHAMPGTW RKEQTRDLQR VLKVVDDIP LVLVSGNHD L GNAPTAETVE EFCQTWGGDY FSWVGGALF
161    LVLNSQFLYD ASKCPALKQA QDHWLDQQLS IAEQQQCQHA IVFQHIPLFL KSIDEDDDYF NLTKTVRQEL ADKFTRAGIR
241    AVFSGHYHRN AGGT YQNLD M VVSSAIGCQL GKDTHGLRVV VVTAEKIVHR YVSLDELSKR GLDDDLRELL KE
    
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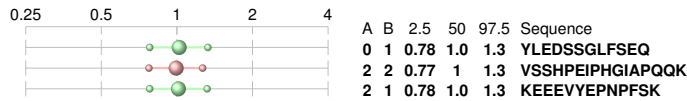


5.1055 PREDICTED: similar to Protein C6orf142 homolog [Rattus norvegicus]

Protein Accession	gi 109485017
Mean Expression Ratio	1
Median Expression Ratio	1
Credible Interval	(0.794, 1.25)
Associated Peptides	3
Associated Spectra	8
Coverage	0.0511
Experiment	B
Avg..iTRAQ.Ratio....115.114.	0.841
Avg..iTRAQ.Ratio....116.114.	0.875
Avg..iTRAQ.Ratio....117.114.	1.04

```

1      MCFSDITAVI GLLSEQLLS DCRNNYFQMT SCVLGSIET TPKFEYSDHM TFSCEskeer DQRILDYPSE VSGKNSQRKE
81     FNTKEPQGMQ KGDLFKAeyV FIVDSDGEDE ATCRQGEQGP PGATGNIATR PKSLAISSSL ASDVVRPKVR GVDVKVSSH
161    EIPHGIApQQ KHGQKTPPV AKVSGTtVLE EFHIRRldVH GASEEETATY FHTTAHDsPL PAWKGASTLV FSPSAQLPgs
241    SLCGSNVADH TRGLAPEAQK KVSTSSALNP REDVRTSPSP ASGASLRSPS ASYIPVRIVM HSLSPSPKPL TSSSHGSLST
321    VCSQTSSSGN LSKSGLKSPV PSRSLSLTAI LKSNPshQRP LSPASCPtFS LNSLASSTLT LDQKIKQTPS TPkKSLSSCS
401    LTTGStEQEQ ASAESHQpCH LSFFSKtTPL SQAQPPSPPA LASSSYAATD TEKIPGStLR SSTTPPQsQT DLfSLADVfS
481    VTPGLSPSS SKGRKDGDLR APEKRNrNIC RPSTLSfIPP INESTALSS GKCFHPSPAL SDLIDRSKRT CSQRHSDQRp
561    NPSALPTPPV SRAGSASHpH LGYSILpPES SLTQALQRSP SALHPSCGSA TCPSRTGMPD STASNRSSRV STPSLPVSLT
641    RTKELISPCA LMSAGPENK KPKQYKtKSS YKAFAAIPTN TLLLEQKALD EPARTESNSK ASVSDLPVEH SSSPSRPSQ
721    TMLGSETIKT PTHPRAAGR ETkYANLSSS SstTSESqLT KPGVIRPVPI KSKLFLKKEE EVYEPNPFsk YLEDSSGLfS
801    EQ
    
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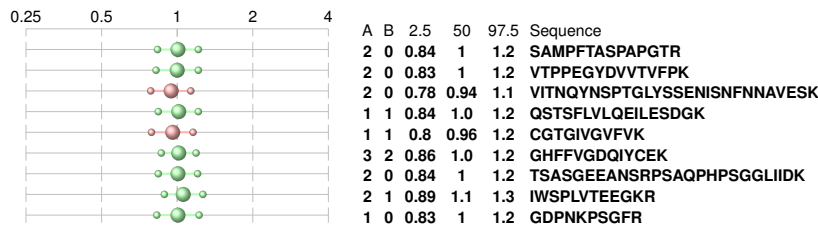


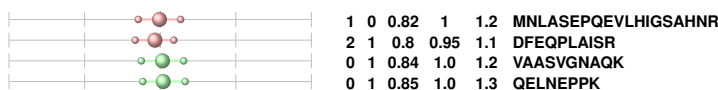
5.1056 LIM protein [Rattus norvegicus]

Protein Accession	gij8393153	
Mean Expression Ratio	1	
Median Expression Ratio	1	
Credible Interval	(0.89, 1.12)	
Associated Peptides	13	
Associated Spectra	27	
Coverage	0.59	
Experiment	A	B
Avg..iTRAQ.Ratio....115.114.	0.944	0.933
Avg..iTRAQ.Ratio....116.114.	1.02	1.07
Avg..iTRAQ.Ratio....117.114.	1.11	0.828

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1      MTTQQIvLQg PGpWGFRLVg GKDFEQPLAI SRVTPGSKAA IANLCIGDLI TAIDGEDTSS MTHLEAQNKI KGCVDNMtLT
81     VSRSEQK WS PLVTEEGRH PYKMNLASEP QEVLHIGSAH NRSAMPFTAS PAPGTRVITN QYNSPTGLYS SENISNFNNA
161    VESKTSASGE EANSRPSAQp HPSGGLIIDK ESEVYKMLQE KQELNEPPKQ STSFLVLQEI LESDgKGDPN KPSGFRsvKA
241    PVTkVAASVg NAQKLPICDK CGTgIVGVfV KLRDHHHPPE CyVCTDCGIN LKQKghffVg DQIYCEH HAR ERVTPPEgYD
321    VVTEVfPK
    
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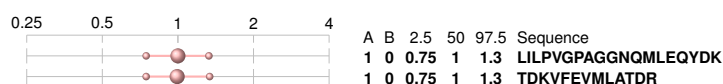




5.1057 protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 [Rattus norvegicus]

Protein Accession	gij 56961640
Mean Expression Ratio	0.998
Median Expression Ratio	1
Credible Interval	(0.769, 1.30)
Associated Peptides	2
Associated Spectra	2
Coverage	0.141
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.02
Avg..iTRAQ.Ratio....116.114.	0.946
Avg..iTRAQ.Ratio....117.114.	1.07

1 MAWKSGGASH SELIHNLRKN GIIK**TDKVF**E VML**ATDR**SHY AKSNPYMDSP QSIGFQATIS APHMAYALE LLFDQLHEGA
 81 KALDVGSGSG ILTACFARMV GHSGKVIID HIKELVDDSI TNVKKDDPML LSSGRVRLV GDGRMGFAEE APYDAIHVGA
 161 AAPVVPQALI DQLKPGGR**LI** LPVGPAGGNQ MLEQYDK**L**QD GSVKMKPLMG VIYVPLTDKE KQWSRWK



5.1058 PREDICTED: similar to prefoldin 1 [Rattus norvegicus]

Protein Accession	gij 109507152
Mean Expression Ratio	1
Median Expression Ratio	1
Credible Interval	(0.765, 1.31)
Associated Peptides	1
Associated Spectra	2
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.99

Avg..iTRAQ.Ratio....116.114. 1.05
 Avg..iTRAQ.Ratio....117.114. 1.11

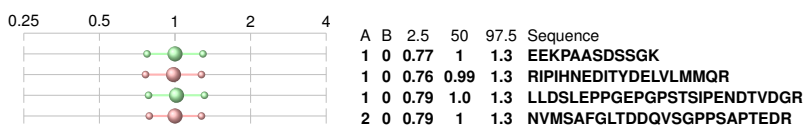


5.1059 Trk-fused [Rattus norvegicus]

Protein Accession	gj 58865858
Mean Expression Ratio	1
Median Expression Ratio	1
Credible Interval	(0.808, 1.25)
Associated Peptides	4
Associated Spectra	5
Coverage	0.206
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.05
Avg..iTRAQ.Ratio....116.114.	1.09
Avg..iTRAQ.Ratio....117.114.	1.11

```

1      MNGQLDLSGK LIIKAQLGED IRRIPIHNE D ITYDELVLMM QRVFRGKLLS NDEVTIKYKD EDGDLITIFD SSDLSFAIQC
81     SRILKLTFLV NGQPRPLESS QVKYLRRELI ELRNKVNRL L DSLEPPGEGP PSTSIPENDT VDGREEKPA A SDSSGKQSTQ
161    VMAASMSAFD FLKNQDEINK NVMSAFGLTD DQVSGPPSAP TEDRSGT PDS IASSSSAAHP AAGQPQPPY AGAQTQAGQI
241    EGQMYQQYQQ QAGYSAQQPQ APPQQYGIQY SASYSQQTGP QQPQQFQGYG QQP T SQAPAP AFSGQPQLP AQPFPQQYQAS
321    TYPPTQYTTQ TSQPANYTVP PGSQPGMAPS QPGAYQPRPG FTSPASTMA PPSTGANPYA RNRPPFGQGY TQPGPGYR
    
```



5.1060 PREDICTED: similar to ribosomal protein L31 [Rattus norvegicus]

Protein Accession [gj|109468817](#)

Mean Expression Ratio	1
Median Expression Ratio	1
Credible Interval	(0.74, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.07
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.40
Avg..iTRAQ.Ratio....116.114.	0.847
Avg..iTRAQ.Ratio....117.114.	1.30

1 MTKSEDTKE ELFKADIFLA PAKKGGKKK DCSAVNEVVT RECTINIHKC IHGVGFKKRA PRALKEIWKF AMKEMGTPDV
 81 CIDIRLNKAI WAKRIRNVFY CIRVLSRKR NEDESPNKL YTLVTYMPVT TFKNLQTVNV DEN



5.1061 PREDICTED: similar to Microfibrillar-associated protein 5 precursor (MFAP-5) (Microfibril-associate

Protein Accession	gij109474158
Mean Expression Ratio	1
Median Expression Ratio	1
Credible Interval	(0.744, 1.34)
Associated Peptides	1
Associated Spectra	1
Coverage	NA
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.955
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	1.03

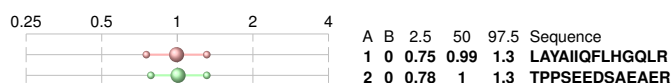


5.1062 "small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha [Rattus norvegicus]"

Protein Accession	gij12083667
Mean Expression Ratio	1
Median Expression Ratio	1
Credible Interval	(0.786, 1.27)
Associated Peptides	2
Associated Spectra	3
Coverage	0.086
Experiment	A
Avg..iTRAQ.Ratio....115.114.	1.07
Avg..iTRAQ.Ratio....116.114.	1.13
Avg..iTRAQ.Ratio....117.114.	0.982

```

1      MDNRKRLAYA I IQFLHGQLR HGGLSSDAQE SLEVAIQCLE TAFGVTLEDS DLALPQTLPE IFEAATASKE MPQDPRGPDR
81     TPPSEEDSAE AERLKTEGNE QMKLENFEAA VHLYGKAIEL NPANAVYFCN RAAAVYSKIGN YVGAVQDCER AIGIDPGYSK
161    AYGRMGLALS SLNKHAAEAVA YKKALELDP DNDTYKSNLK IAELKLRAP SPTGGVGS LD IAGLLNPHF ITMASSLMNS
241    PQLQQLMSGM ISGGHNPLGT PGSSPQHSDL ASLIQAGQQF AQQMQQQNPE FVEQIRSQVV RSRTPSASHE EQQE
    
```



5.1063 "tumor protein, translationally-controlled 1 [Rattus norvegicus]"

Protein Accession	gij16758734
Mean Expression Ratio	1.00
Median Expression Ratio	1
Credible Interval	(0.742, 1.36)
Associated Peptides	1
Associated Spectra	1
Coverage	0.0756
Experiment	A
Avg..iTRAQ.Ratio....115.114.	0.902
Avg..iTRAQ.Ratio....116.114.	0.991
Avg..iTRAQ.Ratio....117.114.	1.16

NHLBI Zile/Grant, Aged Rat

1 MIIYRDLISH DELFSDIYKI REIADGLCLE VEGKMVSRTE GAIDDSLIGG NASAEGPEGE GTESTVVTGV DIVMNHHLQE
81 TSFTKEAYKK YIKDYMKSLK GKLEEQKPER **VKPFMTGAAE** **QIK**HILANFN NYQFFIGENM NPDGMVALLD YREDGVTFPM
161 IFFKDGLEME KC

