



St. Jude Children's Research Hospital Proteomics Facility

<http://home.stjude.org/proteomics-mass-spectrometry/Pages/default.aspx>

Project name: Identification of proteins interacting with NS1
Service: Proteome profiling by spectral counting (SC)
PI: Dr. Linda Hendershot
User: Melissa Mann
Date submitted: 5/9/2019
Date reported: 5/14/2019
Facility staff (primary): Pagala, Vishwajeeth
Facility staff (secondary): Kavdia, Kanisha

Results (see other spreadsheets by clicking the tabs at the bottom left corner on this page)

Table 1. Summary of the MS analysis

Samples	Total Identified Proteins	Total Spectral Counts
NegControl	13	42
-MG132	28	332
+MG132	36	347

Note: the sequences of identified peptides are available upon request.

[NegCntrl vs -MG132- Spectral count comparison of proteins identified from the NegCntrl and -MG132 samples](#)

[NegCntrl vs +MG132- Spectral count comparison of proteins identified from the NegCntrl and +MG132 samples](#)

[NegMG132 vs +MG132- Spectral count comparison of proteins identified from the NegMG132 and +MG132 samples](#)

[Figure 1. Stained SDS Gel image of submitted samples](#)

Discussion

1. Spectral count, a semi-quantitative index, is the total number of MS/MS spectra matched to an assigned protein.
2. For the immunoprecipitation (IP) analysis, the bait protein needs to be among the top ten abundant proteins to improve the possibility of detecting its interacting proteins.

Attention: this table may include multiple pages.

NegCntrl vs -MG132- Spectral count comparison of proteins identified from the NegCntrl and -MG132 samples

SC: the summed number of spectral counts (i.e. MS/MS scans) assigned to one identified protein; TP: total number of peptides identified for a protein; Group: Identified proteins that share one or more peptides are grouped together (e.g. 01). The group is represented by the protein with maximal spectra count (e.g. 01.1). If other proteins in the same group are assigned with at least one uniquely identified peptides, these proteins are also counted as unique proteins (e.g. 01.2); Abundance: SC x 50 (KD) / protein size (KD). p value less than 0.05 generally indicates significant change. The p value is derived by G-test (Zhou JY, Afjeji-Sadat L, Asress S, et al. J Proteome Res. 2010, 9:5133-41). The summed SC of the control samples was compared with that of the Test samples.

Group	Reference	Description	SC NegCntrl	SC -MG123	TP NegCntrl	TP -MG123	Mass (KD)	Abundance	p-value
109198.1 sp P20029 GRP78_MOUSE		78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	2	151	2	39	72	180.99	2.14806E-43
100001.1 cu NS1_Cus NS1_Cus Light		chain Custom sequence	0.1	51	0	11	27	171.16	8.06923E-17
109199.1 sp P63017 HSP7C_MOUSE		Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=	3	26	2	11	71	51.53	4.80855E-06
109195.1 sp P17156 HSP72_MOUSE		Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV	0.1	15	0	5	70	22.99	8.91784E-06
105429.1 sp P17182 ENOA_MOUSE		Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	0.1	13	0	6	47	21.23	3.76529E-05
114887.1 sp P52480 KPYM_MOUSE		Pyruvate kinase PKM OS=Mus musculus GN=Pkm PE=1 SV=4	0.1	12	0	7	58	17.3	7.76021E-05
109192.1 sp Q61696 HS71A_MOUSE		Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	0.1	11	0	4	70	13.56	0.000160328
109194.1 sp P16627 HS71L_MOUSE		Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4	0.1	10	0	4	71	12.75	0.000332193
119792.1 sp P17751 TPIS_MOUSE		Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4	0.1	9	0	5	32	13.99	0.000690662
105211.1 sp P10126 EF1A1_MOUSE		Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	0.1	8	0	5	50	14.98	0.001441968
110677.1 sp P06151 LDHA_MOUSE		L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	0.1	7	0	4	36	13.71	0.003026258
117247.1 sp Q070456 1433S_MOUSE		14-3-3 protein sigma OS=Mus musculus GN=Sfn PE=1 SV=2	7	0.1	2	0	28	12.64	0.003026258
105507.1 sp Q8CGC7 SYEP_MOUSE		Bifunctional glutamate/proline--tRNA ligase OS=Mus musculus GN=Eprs PE	0.1	6	0	2	170	3.82	0.006393648
109186.1 sp P11499 HS90B_MOUSE		Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=	0.1	6	0	5	83	6.01	0.006393648
102600.1 sp P35564 CALX_MOUSE		Calnexin OS=Mus musculus GN=Canx PE=1 SV=1	0.1	5	0	4	67	3.72	0.01362796
109187.1 sp P08113 ENPL_MOUSE		Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	0.1	5	0	4	92	3.79	0.01362796
120283.1 sp P99024 TBB5_MOUSE		Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	0.1	5	0	2	50	11.08	0.01362796
120124.1 tr Q9ROT7 Q9ROT7_MOUSE		MCG15085 OS=Mus musculus GN=Try4 PE=2 SV=1	5	0.1	1	0	26	9.52	0.01362796
108974.1 sp P62806 H4_MOUSE		Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	4	0.1	2	0	11	17.6	0.0294083
109978.1 sp Q02257 PLAK_MOUSE		Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	4	0.1	3	0	82	2.45	0.0294083
117019.1 sp Q8K2B3 SDHA_MOUSE		Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondria	4	12	3	6	73	13.1	0.040759517
109258.2 sp P03975 IGEB_MOUSE		IgE-binding protein OS=Mus musculus GN=Iap PE=2 SV=1	0.1	3	0	1	63	5.58	0.064646504
109719.1 sp P24547 IMDH2_MOUSE		Inosine-5'-monophosphate dehydrogenase 2 OS=Mus musculus GN=Impdh	0.1	3	0	1	56	6.27	0.064646504
116659.1 sp P62908 RS3_MOUSE		40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	0.1	3	0	2	27	11.25	0.064646504
120282.1 sp P68372 TBB4B_MOUSE		Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1	0.1	3	0	1	50	5.02	0.064646504
105969.1 sp Q14BJ1 FA89A_MOUSE		Protein FAM89A OS=Mus musculus GN=Fam89a PE=2 SV=2	3	0.1	1	0	19	8.03	0.064646504
100058.1 tr Q14AA6 Q14AA6_MOUSE		MCG49183 OS=Mus musculus GN=1700009N14Rik PE=2 SV=1	0.1	2	0	2	24	4.11	0.146611857
101875.1 sp Q03265 ATPA_MOUSE		ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 I	0.1	2	0	2	60	4.19	0.146611857
105555.1 sp Q91X78 ERLN1_MOUSE		Erlin-1 OS=Mus musculus GN=Erlin1 PE=1 SV=1	0.1	2	0	1	39	2.57	0.146611857
106570.1 sp P16858 G3P_MOUSE		Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh	0.1	2	0	2	36	6.99	0.146611857
109185.1 sp P07901 HS90A_MOUSE		Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV	0.1	2	0	2	85	2.36	0.146611857
114565.1 sp Q922R8 PDIA6_MOUSE		Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=3	0.1	2	0	2	48	2.08	0.146611857
118320.1 sp Q64337 SQSTM_MOUSE		Sequestosome-1 OS=Mus musculus GN=Sqstm1 PE=1 SV=1	0.1	2	0	2	48	5.19	0.146611857
105319.1 sp P60843 IF4A1_MOUSE		Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=1 SV=1	2	0.1	1	0	46	2.17	0.146611857
108023.1 tr B2RXM2 B2RXM2_MOUSE		EG627828 protein OS=Mus musculus GN=Gm6793 PE=2 SV=1	2	0.1	1	0	37	5.47	0.146611857
110477.1 sp Q99M73 KRT84_MOUSE		Keratin, type II cuticular Hb4 OS=Mus musculus GN=Krt84 PE=2 SV=2	2	0.1	1	0	65	1.54	0.146611857
114894.1 sp P97350 PKP1_MOUSE		Plakophilin-1 OS=Mus musculus GN=Pkp1 PE=2 SV=1	2	0.1	1	0	81	1.24	0.146611857
120278.1 sp Q7TMM9 TBB2A_MOUSE		Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	2	3	2	1	50	7.02	0.653629236

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NegCntrl vs +MG132- Spectral count comparison of proteins identified from the NegCntrl and +MG132 samples

SC: the summed number of spectral counts (i.e. MS/MS scans) assigned to one identified protein; TP: total number of peptides identified for a protein; Group: Identified proteins that share one or more peptides are grouped together (e.g. 01). The group is represented by the protein with maximal spectra count (e.g. 01.1). If other proteins in the same group are assigned with at least one uniquely identified peptides, these proteins are also counted as unique proteins (e.g. 01.2); Abundance: SC x 50 (KD) / protein size (KD). p value less than 0.05 generally indicates significant change. The p value is derived by G-test (Zhou JY, Afjeji-Sadat L, Asress S, et al. J Proteome Res. 2010, 9:5133-41). The summed SC of the control samples was compared with that of the Test samples.

Group	Reference	Description	SC NegCntrl	SC +MG123	TP NegCntrl	TP +MG123	Mass (KD)	Abundance	p-value
109198.1 sp	P20029 GRP78_MOUSE	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	2	109	2	36	72	180.99	5.89411E-31
108080.1 tr	J3QK04 J3QK04_MOUSE	MCG67952 OS=Mus musculus GN=Gm7808 PE=4 SV=1	0.1	53	0	2	15	180.79	1.98692E-17
107863.1 tr	D3YYZ2 D3YYZ2_MOUSE	MCG1031578 OS=Mus musculus GN=Gm5239 PE=4 SV=1	0.1	51	0	2	14	181.31	8.06923E-17
100001.1 cu	NS1_Cus NS1_Cus Light	chain Custom sequence	0.1	41	0	9	27	171.16	9.00418E-14
109199.1 sp	P63017 HSP7C_MOUSE	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=	3	44	2	16	71	51.53	5.93345E-11
102095.1 sp	Q9Z1R2 BAG6_MOUSE	Large proline-rich protein BAG6 OS=Mus musculus GN=Bag6 PE=1 SV=1	0.1	21	0	12	121	8.68	1.22518E-07
109195.1 sp	P17156 HSP72_MOUSE	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV	0.1	17	0	6	70	22.99	2.12577E-06
109192.1 sp	Q61696 HS71A_MOUSE	Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	0.1	8	0	4	70	13.56	0.001441968
109194.1 sp	P16627 HS71L_MOUSE	Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4	0.1	8	0	4	71	12.75	0.001441968
114887.1 sp	P52480 KPYM_MOUSE	Pyruvate kinase PKM OS=Mus musculus GN=Pkm PE=1 SV=4	0.1	8	0	3	58	17.3	0.001441968
105211.1 sp	P10126 EF1A1_MOUSE	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	0.1	7	0	5	50	14.98	0.003026258
105429.1 sp	P17182 ENOA_MOUSE	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	0.1	7	0	2	47	21.23	0.003026258
105507.1 sp	Q8CGG7 SYEP_MOUSE	Bifunctional glutamate/proline--trNA ligase OS=Mus musculus GN=Eprs PE	0.1	7	0	2	170	3.82	0.003026258
117247.1 sp	O70456 1433S_MOUSE	14-3-3 protein sigma OS=Mus musculus GN=Sfn PE=1 SV=2	7	0.1	2	0	28	12.64	0.003026258
120283.1 sp	P99024 TBB5_MOUSE	Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	0.1	5	0	3	50	11.08	0.01362796
120124.1 tr	Q9R0T7 Q9R0T7_MOUSE	MCG15085 OS=Mus musculus GN=Try4 PE=2 SV=1	5	0.1	1	0	26	9.52	0.01362796
109186.1 sp	P11499 HS90B_MOUSE	Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=	0.1	4	0	4	83	6.01	0.0294083
109258.2 sp	P03975 IGEB_MOUSE	IgE-binding protein OS=Mus musculus GN=Iap PE=2 SV=1	0.1	4	0	2	63	5.58	0.0294083
109719.1 sp	P24547 IMDH2_MOUSE	Inosine-5'-monophosphate dehydrogenase 2 OS=Mus musculus GN=Impdh	0.1	4	0	1	56	6.27	0.0294083
108974.1 sp	P62806 H4_MOUSE	Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	4	0.1	2	0	11	17.6	0.0294083
109978.1 sp	Q02257 PLAK_MOUSE	Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	4	0.1	3	0	82	2.45	0.0294083
101875.1 sp	Q03265 ATPA_MOUSE	ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 I	0.1	3	0	2	60	4.19	0.064646504
106570.1 sp	P16858 G3P_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh	0.1	3	0	3	36	6.99	0.064646504
110677.1 sp	P06151 LDHA_MOUSE	L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	0.1	3	0	2	36	13.71	0.064646504
116659.1 sp	P62908 RS3_MOUSE	40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	0.1	3	0	3	27	11.25	0.064646504
118320.1 sp	Q64337 SQSTM_MOUSE	Sequestosome-1 OS=Mus musculus GN=Sqstm1 PE=1 SV=1	0.1	3	0	2	48	5.19	0.064646504
105969.1 sp	Q14BJ1 FA89A_MOUSE	Protein FAM89A OS=Mus musculus GN=Fam89a PE=2 SV=2	3	0.1	1	0	19	8.03	0.064646504
100183.1 tr	Q9CPN9 Q9CPN9_MOUSE	Protein 2210010C04Rik OS=Mus musculus GN=2210010C04Rik PE=2 SV=1	0.1	2	0	1	26	3.79	0.146611857
104172.1 sp	Q80TT8 CUL9_MOUSE	Cullin-9 OS=Mus musculus GN=Cul9 PE=1 SV=2	0.1	2	0	1	209	0.48	0.146611857
109185.1 sp	P07901 HS90A_MOUSE	Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 Sv	0.1	2	0	2	85	2.36	0.146611857
109187.1 sp	P08113 ENPL_MOUSE	Endoplasmic reticulum protein OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	0.1	2	0	1	92	3.79	0.146611857
110468.1 sp	Q3UV17 K22O_MOUSE	Keratin, type II cytoskeletal 2 oral OS=Mus musculus GN=Krt76 PE=2 SV=1	0.1	2	0	1	63	1.59	0.146611857
114886.1 sp	P53657 KPYP_MOUSE	Pyruvate kinase PKLR OS=Mus musculus GN=Pklr PE=2 SV=1	0.1	2	0	1	62	2.41	0.146611857
115629.1 sp	Q9QUM9 PSA6_MOUSE	Proteasome subunit alpha type-6 OS=Mus musculus GN=Pasma6 PE=1 SV=1	0.1	2	0	1	27	3.66	0.146611857
115630.1 sp	Q9Z2U0 PSA7_MOUSE	Proteasome subunit alpha type-7 OS=Mus musculus GN=Pasma7 PE=1 SV=1	0.1	2	0	2	28	3.59	0.146611857
115643.1 sp	P62192 PRS4_MOUSE	26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1	0.1	2	0	1	49	2.03	0.146611857
115644.1 sp	P46471 PRS7_MOUSE	26S protease regulatory subunit 7 OS=Mus musculus GN=Psmc2 PE=1 SV=5	0.1	2	0	1	49	2.06	0.146611857
120282.1 sp	P68372 TBB4B_MOUSE	Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1	0.1	2	0	2	50	5.02	0.146611857
105319.1 sp	P60843 IF4A1_MOUSE	Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=1 SV=1	2	0.1	1	0	46	2.17	0.146611857
110477.1 sp	Q99M73 KRT84_MOUSE	Keratin, type II cuticular Hb4 OS=Mus musculus GN=Krt84 PE=2 SV=2	2	0.1	1	0	65	1.54	0.146611857
114894.1 sp	P97350 PKP1_MOUSE	Plakophilin-1 OS=Mus musculus GN=Pkp1 PE=2 SV=1	2	0.1	1	0	81	1.24	0.146611857
117019.1 sp	Q8K2B3 SDHA_MOUSE	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondria	4	3	3	2	73	13.1	0.704975995
108023.1 tr	B2RXM2 B2RXM2_MOUSE	EG627828 protein OS=Mus musculus GN=Gm6793 PE=2 SV=1	2	2	1	1	37	5.47	1
120278.1 sp	Q7TMM9 TBB2A_MOUSE	Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	2	2	2	2	50	7.02	1

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NegMG132 vs +MG132- Spectral count comparison of proteins identified from the NegMG132 and +MG132 samples

SC: the summed number of spectral counts (i.e. MS/MS scans) assigned to one identified protein; TP: total number of peptides identified for a protein; Group: Identified proteins that share one or more peptides are grouped together (e.g. 01). The group is represented by the protein with maximal spectra count (e.g. 01.1). If other proteins in the same group are assigned with at least one uniquely identified peptides, these proteins are also counted as unique proteins (e.g. 01.2); Abundance: SC x 50 (KD) / protein size (KD). p value less than 0.05 generally indicates significant change. The p value is derived by G-test (Zhou JY, Afjeji-Sadat L, Asress S, et al. J Proteome Res. 2010, 9:5133-41). The summed SC of the control samples was compared with that of the Test samples.

Group	Reference	Description	SC -MG123	SC +MG123	TP -MG123	TP +MG123	Mass (KD)	Abundance	p-value
108080.1 tr J3QK04 J3QK04_MOUSE		MCG67952 OS=Mus musculus GN=Gm7808 PE=4 SV=1	0.1	53	0	2	15	180.79	1.98692E-17
107863.1 tr D3YYZ2 D3YYZ2_MOUSE		MCG1031578 OS=Mus musculus GN=Gm5239 PE=4 SV=1	0.1	51	0	2	14	181.31	8.06923E-17
102095.1 sp Q9Z1R2 BAG6_MOUSE		Large proline-rich protein BAG6 OS=Mus musculus GN=Bag6 PE=1 SV=1	0.1	21	0	12	121	8.68	1.22518E-07
119792.1 sp P17751 TPIS_MOUSE		Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4	9	0.1	5	0	32	13.99	0.000690662
109198.1 sp P20029 GRP78_MOUSE		78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	151	109	39	36	72	180.99	0.009042392
102600.1 sp P35564 CALX_MOUSE		Calnexin OS=Mus musculus GN=Canx PE=1 SV=1	5	0.1	4	0	67	3.72	0.01362796
117019.1 sp Q8K2B3 SDHA_MOUSE		Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondria	12	3	6	2	73	13.1	0.016187951
109199.1 sp P63017 HSP7C_MOUSE		Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=	26	44	11	16	71	51.53	0.03049836
100183.1 tr Q9CPN9 Q9CPN9_MOUSE		Protein 2210010C04Rik OS=Mus musculus GN=2210010C04Rik PE=2 SV=1	0.1	2	0	1	26	3.79	0.146611857
104172.1 sp Q80TT8 CUL9_MOUSE		Cullin-9 OS=Mus musculus GN=Cul9 PE=1 SV=2	0.1	2	0	1	209	0.48	0.146611857
108023.1 tr B2RXM2 B2RXM2_MOUSE		EG627828 protein OS=Mus musculus GN=Gm6793 PE=2 SV=1	0.1	2	0	1	37	5.47	0.146611857
110468.1 sp Q3UV17 K22O_MOUSE		Keratin, type II cytoskeletal 2 oral OS=Mus musculus GN=Krt76 PE=2 SV=1	0.1	2	0	1	63	1.59	0.146611857
114886.1 sp P53657 KPYR_MOUSE		Pyruvate kinase PKLR OS=Mus musculus GN=Pklr PE=2 SV=1	0.1	2	0	1	62	2.41	0.146611857
115629.1 sp Q9QUM9 PSA6_MOUSE		Proteasome subunit alpha type-6 OS=Mus musculus GN=PsmA6 PE=1 SV=1	0.1	2	0	1	27	3.66	0.146611857
115630.1 sp Q9Z2U0 PSA7_MOUSE		Proteasome subunit alpha type-7 OS=Mus musculus GN=PsmA7 PE=1 SV=1	0.1	2	0	2	28	3.59	0.146611857
115643.1 sp P62192 PRS4_MOUSE		26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1	0.1	2	0	1	49	2.03	0.146611857
115644.1 sp P46471 PRS7_MOUSE		26S protease regulatory subunit 7 OS=Mus musculus GN=Psmc2 PE=1 SV=5	0.1	2	0	1	49	2.06	0.146611857
100058.1 tr Q14AA6 Q14AA6_MOUSE		MCG49183 OS=Mus musculus GN=1700009N14Rik PE=2 SV=1	2	0.1	2	0	24	4.11	0.146611857
105555.1 sp Q91X78 ERL1_MOUSE		Erlin-1 OS=Mus musculus GN=Erlin1 PE=1 SV=1	2	0.1	1	0	39	2.57	0.146611857
114565.1 sp Q922R8 PDIA6_MOUSE		Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=3	2	0.1	2	0	48	2.08	0.146611857
105429.1 sp P17182 ENOA_MOUSE		Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	13	7	6	2	47	21.23	0.176361396
110677.1 sp P06151 LDHA_MOUSE		L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	7	3	4	2	36	13.71	0.199550991
109187.1 sp P08113 ENPL_MOUSE		Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	5	2	4	1	92	3.79	0.249110318
100001.1 cu NS1_Cus NS1_Cus Light		chain Custom sequence	51	41	11	9	27	171.16	0.296669142
114887.1 sp P52480 KPYM_MOUSE		Pyruvate kinase PKM OS=Mus musculus GN=Pkm PE=1 SV=4	12	8	7	3	58	17.3	0.369477642
109192.1 sp Q61696 HS71A_MOUSE		Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	11	8	4	4	70	13.56	0.490389144
109186.1 sp P11499 HS90B_MOUSE		Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=	6	4	5	4	83	6.01	0.525692869
109194.1 sp P16627 HS71L_MOUSE		Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4	10	8	4	4	71	12.75	0.637004118
101875.1 sp Q03265 ATPA_MOUSE		ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 I	2	3	2	2	60	4.19	0.653629236
106570.1 sp P16858 G3P_MOUSE		Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh	2	3	2	3	36	6.99	0.653629236
118320.1 sp Q64337 SQSTM_MOUSE		Sequestosome-1 OS=Mus musculus GN=Sqstm1 PE=1 SV=1	2	3	2	2	48	5.19	0.653629236
120278.1 sp Q7TMM9 TBB2A_MOUSE		Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	3	2	1	2	50	7.02	0.653629236
120282.1 sp P68372 TBB4B_MOUSE		Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1	3	2	1	2	50	5.02	0.653629236
109258.2 sp P03975 IGEB_MOUSE		IgE-binding protein OS=Mus musculus GN=Igap PE=2 SV=1	3	4	1	2	63	5.58	0.704975995
109719.1 sp P24547 IMDH2_MOUSE		Inosine-5'-monophosphate dehydrogenase 2 OS=Mus musculus GN=Impdh	3	4	1	1	56	6.27	0.704975995
109195.1 sp P17156 HSP72_MOUSE		Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV	15	17	5	6	70	22.99	0.723587226
105507.1 sp Q8CGC7 SEYP_MOUSE		Bifunctional glutamate/proline--tRNA ligase OS=Mus musculus GN=Eprs PE	6	7	2	2	170	3.82	0.781406072
105211.1 sp P10126 EF1A1_MOUSE		Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	8	7	5	5	50	14.98	0.796179498
109185.1 sp P07901 HS90A_MOUSE		Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV	2	2	2	2	85	2.36	1
116659.1 sp P62908 RS3_MOUSE		40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	3	3	2	3	27	11.25	1
120283.1 sp P99024 TBB5_MOUSE		Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	5	5	2	3	50	11.08	1