Supplemental Table SI. SEQUEST Results for Proteins Identified in Tables I - IV.

SEQUEST search
Database.uniprot_sprot_090305.fasta.hdr (3/5/2009); ipi.MOUSE_090305.fasta
data were searched using both databases to confirm protein identifications and final ID's were cross-correlated with Swissprot accesion numbers
Filter(s)... deltacn>=0.100 ; xc (± 1,2,3,4)=1.50,2.00,2.50,3.00 ; peptide probability<=5e-002 ; # distinct peptides>=2
Mods: (M* +15.99492) C=160.03068
parent tolerance - 10 ppm; fragment tolerance - 0.5 amu

Reference					P	Sf	Score	Coverage	
Scan(s)	Swiss Prot No.	Sequence	MH+	z	P	Sf	XC	DeltaCn	Sp
Fructose-bisphosphate aldolase A	P05064				2e-008	2.5	30.2	0.0	0
6		K.GILAADESTGSIAK.R	1332.70	2	3e-008	0.89	3.783	0.150	893.2
16		K.GILAADESTGSIAK.R	1332.70	2	1e-007	0.94	4.052	0.105	1351.2
18		K.IGEHTPSALAIM*ENANVLAR.Y	2123.09	3	3e-006	0.89	4.231	0.341	858.7
24		K.GILAADESTGSIAK.R	1332.70	2	1e-007	0.94	4.133	0.177	1317.5
33		K.GILAADESTGSIAK.R	1332.70	2	2e-008	0.94	4.049	0.139	1361.4
36		K.IGEHTPSALAIM*ENANVLAR.Y	2123.09	3	6e-005	0.83	3.995	0.275	684.1
42		K.GILAADESTGSIAK.R	1332.70	2	3e-008	0.95	4.204	0.202	1341.5
45		K.IGEHTPSALAIM*ENANVLAR.Y	2123.09	3	0.001	0.90	4.074	0.379	949.8
49		K.FSNEEIAM*ATVTALR.R	1668.83	2	4e-006	0.65	2.526	0.370	492.7
60		K.FSNEEIAM*ATVTALR.R	1668.83	2	9e-005	0.68	2.593	0.503	376.4
65		K.IGEHTPSALAIM*ENANVLAR.Y	2123.09	3	0.002	0.84	3.876	0.356	645.5
71		K.FSNEEIAM*ATVTALR.R	1668.83	2	4e-005	0.62	2.315	0.444	369.4
78		K.FSNEEIAM*ATVTALR.R	1668.83	2	5e-006	0.82	2.749	0.542	580.9
83		K.IGEHTPSALAIM*ENANVLAR.Y	2123.09	3	0.0005	0.87	4.172	0.327	759.6
104		K.FSNEEIAM*ATVTALR.R	1668.83	3	0.001	0.89	3.040	0.601	667.1
Superoxide dismutase 2	P09671				1e-006	1.6	20.2	0.0	0
5		K.GDVTTQVALQPALK.F	1440.81	2	1e-006	0.89	3.482	0.419	695.8
15		K.GDVTTQVALQPALK.F	1440.81	2	1e-005	0.89	3.586	0.452	640.8
24		K.GDVTTQVALQPALK.F	1440.81	2	6e-006	0.80	3.164	0.353	572.2
33		K.GDVTTQVALQPALK.F	1440.81	2	2e-006	0.84	3.197	0.351	660.3
41		K.GDVTTQVALQPALK.F	1440.81	2	3e-006	0.91	3.474	0.441	784.9
96		K.HHAAYVNNLNATEEK.Y	1710.82	3	0.03	0.75	2.739	0.393	586.4
173		K.GDVTTQVALQPALK.F	1440.81	3	0.03	0.83	2.837	0.559	774.9
Aconitate hydratase, mitochondrial	Q99KI0				8e-007	4.5	60.2	0.0	0
5		K.SQFTITPGSEQIR.A	1463.75	2	0.03	0.30	2.006	0.352	228.5
6		R.NAVTQEFGPVPDTAR.Y	1601.79	2	0.001	0.71	2.821	0.559	246.1
7		K.IVYGHLDDPANQEIER.G	1868.91	3	0.02	0.72	3.035	0.523	268.6
8		R.DGYAQILR.D	935.49	2	0.001	0.84	2.478	0.269	694.6

14		K.SQFTITPGSEQIR.A	1463.75	2	0.02	0.53	2.565	0.368	269.1
16		R.NAVTQEFGPVPDTAR.Y	1601.79	2	0.0006	0.80	3.279	0.482	292.0
17		K.IVYGHLDDPANQEIER.G	1868.91	3	0.002	0.86	3.659	0.562	367.3
18		R.DGYAQILR.D	935.49	2	0.002	0.86	2.462	0.327	739.7
23		K.IVYGHLDDPANQEIER.G	1868.91	3	0.0006	0.91	3.939	0.557	627.6
26		R.DGYAQILR.D	935.49	2	0.001	0.88	2.506	0.279	822.9
32		K.IVYGHLDDPANQEIER.G	1868.91	3	0.004	0.88	3.992	0.509	436.7
34		R.DGYAQILR.D	935.49	2	0.001	0.76	2.355	0.275	582.8
35		R.NAVTQEFGPVPDTAR.Y	1601.79	2	0.006	0.63	2.635	0.514	213.9
41		K.IVYGHLDDPANQEIER.G	1868.91	3	0.001	0.78	3.312	0.479	350.9
43		K.SQFTITPGSEQIR.A	1463.75	2	0.002	0.61	2.382	0.421	337.4
45		R.DGYAQILR.D	935.49	2	0.001	0.85	2.714	0.245	734.2
49		K.FKLEAPDADELPR.A	1500.77	3	8e-007	0.95	3.909	0.453	1386.5
50		R.NAVTQEFGPVPDTAR.Y	1601.79	2	3e-005	0.77	2.887	0.591	268.8
56		R.NAVTQEFGPVPDTAR.Y	1601.79	2	6e-005	0.67	2.588	0.568	237.9
59		K.FKLEAPDADELPR.A	1500.77	3	0.003	0.68	2.611	0.423	544.8
74		K.VAM*SHFEPSEYIR.Y	1581.74	3	0.0001	0.41	2.629	0.292	271.6
84		K.FKLEAPDADELPR.A	1500.77	3	0.007	0.70	2.702	0.396	632.7
91		K.FKLEAPDADELPR.A	1500.77	3	0.008	0.72	2.888	0.408	500.2
Alpha-enolase	P17182				1e-005	0.8	20.1	0.0	0
67		K.DATNVGDEGGFAPNILENK.E	1960.92	2	0.003	0.48	2.200	0.576	206.3
78		R.AAVPSGASTGIYEALELR.D	1804.94	2	1e-005	0.43	2.314	0.465	55.4
128		K.DATNVGDEGGFAPNILENK.E	1960.92	2	0.003	0.36	2.110	0.538	169.7
185		K.DATNVGDEGGFAPNILENK.E	1960.92	3	0.001	0.40	2.625	0.321	304.1
246		K.DATNVGDEGGFAPNILENK.E	1960.92	3	0.004	0.50	2.728	0.479	206.3
254		K.DATNVGDEGGFAPNILENK.E	1960.92	3	0.05	0.60	2.834	0.425	384.7
ATP synthase subunit alpha, mitochondrial	Q03265				1e-007	2.5	40.1	0.0	0
12		K.AVDSLVPIGR.G	1026.59	2	0.04	0.60	2.514	0.283	371.0
22		R.ILGADTSVDLEETGR.V	1575.79	2	0.0006	0.47	2.381	0.521	201.5
53		K.AVDSLVPIGR.G	1026.59	2	7e-005	0.62	2.238	0.264	460.7
65		R.ILGADTSVDLEETGR.V	1575.79	2	1e-007	0.80	2.740	0.513	579.0
71		R.ILGADTSVDLEETGR.V	1575.79	2	3e-007	0.90	2.811	0.672	781.5
81		R.VVDALGNAIDGK.G	1171.63	2	0.02	0.56	2.156	0.479	348.9
84		K.TGTAEM*SSILEER.I	1439.67	2	0.0004	0.53	2.102	0.539	357.1
89		R.VVDALGNAIDGK.G	1171.63	2	0.01	0.53	2.073	0.387	361.1
95		K.TGTAEM*SSILEER.I	1439.67	2	0.0009	0.72	2.425	0.558	394.6
ATP synthase subunit alpha, mitochondrial	Q03265				2e-007	2.9	40.2	0.0	0
3		K.AVDSLVPIGR.G	1026.59	2	0.02	0.60	2.337	0.332	386.6
4		R.VLSIGDGIAR.V	1000.58	2	0.002	0.60	2.272	0.142	476.3
8		R.VVDALGNAIDGK.G	1171.63	2	3e-006	0.96	3.640	0.584	1075.6

16		R.VVDALGNAIDGK.G	1171.63	2	0.0003	0.91	3.161	0.478	789.0
25		R.VVDALGNAIDGK.G	1171.63	2	0.0004	0.92	3.234	0.536	814.8
35		R.VVDALGNAIDGK.G	1171.63	2	0.0002	0.76	2.680	0.414	521.5
44		R.VVDALGNAIDGK.G	1171.63	2	0.003	0.75	2.533	0.462	435.2
51		R.ILGADTSVDLEETGR.V	1575.79	2	8e-006	0.63	2.342	0.614	321.6
67		R.ILGADTSVDLEETGR.V	1575.79	2	2e-007	0.70	2.371	0.642	449.0
83		R.ILGADTSVDLEETGR.V	1575.79	2	4e-006	0.62	2.554	0.425	435.3
ATP synthase subunit d, mitochondrial	Q9DCX2				5e-007	2.2	30.2	0.0	0
18		K.PGLVDDFEK.K	1019.50	2	0.0008	0.80	2.364	0.388	733.7
24		R.ANVAKPGLVDDFEK.K	1502.78	3	0.0003	0.78	2.565	0.586	402.4
33		R.ANVAKPGLVDDFEK.K	1502.78	3	0.02	0.62	2.593	0.567	210.8
53 - 57		R.ANVAKPGLVDDFEKK.Y	1630.88	3	5e-007	0.84	3.105	0.483	555.7
99		K.PGLVDDFEK.K	1019.50	2	0.001	0.83	2.422	0.504	634.7
124		K.PGLVDDFEK.K	1019.50	2	0.0007	0.77	2.011	0.463	639.5
186		K.PGLVDDFEK.K	1019.50	2	0.0002	0.62	2.053	0.371	507.4
194		K.PGLVDDFEK.K	1019.50	2	0.001	0.72	2.098	0.332	690.6
245		R.ANVAKPGLVDDFEKK.Y	1630.88	3	0.0003	0.44	2.546	0.445	188.4
Calbindin	P12658				0.0002	1.7	20.1	0.0	0
8		K.LAEYTDLM*LK.L	1212.62	2	0.0002	0.83	2.382	0.518	613.5
9		K.SFVDQYGQR.D	1099.52	2	0.0006	0.84	2.235	0.484	636.1
18		K.SFVDQYGQR.D	1099.52	2	0.01	0.67	2.080	0.455	412.5
52		K.SFVDQYGQR.D	1099.52	2	0.002	0.64	2.218	0.231	515.7
67		K.LAEYTDLM*LK.L	1212.62	2	0.0003	0.86	2.506	0.559	679.0
Cytochrome c oxidase subunit 5A, mitochondrial	P12787				2e-005	2.3	30.2	0.0	0
4		R.LNDFASAVR.I	992.52	2	6e-005	0.83	2.725	0.230	662.4
7		K.GM*NTLVGYDLVPEPK.I	1648.83	2	0.001	0.72	2.832	0.523	345.8
14		R.LNDFASAVR.I	992.52	2	2e-005	0.89	3.056	0.222	812.2
23		R.LNDFASAVR.I	992.52	2	3e-005	0.92	3.196	0.242	993.0
32		R.LNDFASAVR.I	992.52	2	0.0004	0.91	2.901	0.264	979.0
34		K.GM*NTLVGYDLVPEPK.I	1648.83	2	2e-005	0.83	3.054	0.464	483.4
56		R.LNDFASAVR.I	992.52	2	0.0008	0.92	3.175	0.208	1069.5
85		R.KGM*NTLVGYDLVPEPK.I	1776.92	3	0.002	0.64	2.576	0.513	302.8
Fructose-bisphosphate aldolase C	P05063				3e-008	3.3	40.2	0.0	0
4		K.GILAADESVGSM*AK.R	1364.67	2	6e-008	0.96	4.384	0.175	1708.1
7		R.DNAGAATEEFIK.R	1265.60	2	1e-005	0.95	3.443	0.517	1070.8
9		R.LSQIGVENTEENR.R	1488.73	2	5e-006	0.84	2.723	0.418	677.3
13		K.GILAADESVGSM*AK.R	1364.67	2	3e-008	0.96	4.638	0.116	1825.9
15		R.DNAGAATEEFIK.R	1265.60	2	2e-006	0.90	3.251	0.438	729.7
16		R.QVLFSADDR.V	1050.52	2	0.002	0.69	2.085	0.496	211.2

22		K.GILAADESVGSM*AK.R	1364.67	2	8e-008	0.96	4.546	0.173	1872
24		R.DNAGAATEEFIK.R	1265.60	2	8e-005	0.84	3.188	0.442	564.2
31		K.GILAADESVGSM*AK.R	1364.67	2	2e-006	0.93	4.376	0.167	1241.1
33		R.QVLFSADDR.V	1050.52	2	0.006	0.41	2.002	0.281	165.9
34		R.DNAGAATEEFIK.R	1265.60	2	7e-005	0.82	3.095	0.410	519.8
40		K.GILAADESVGSM*AK.R	1364.67	2	4e-006	0.74	3.138	0.126	775.7
42		R.DNAGAATEEFIK.R	1265.60	2	2e-005	0.62	2.274	0.487	388.0
62 - 84		R.LSQIGVENTEENR.R	1488.73	2	9e-007	0.80	2.819	0.395	544.5
Glyceraldehyde-3-phosphate dehydrogenase	P16858				1e-007	2.6	30.2	0.0	0
41		R.VVDLM*AYM*ASK.-	1259.60	2	1e-006	0.96	3.582	0.543	1117.2
44		R.VVDLM*AYM*ASKE.-	1388.64	2	3e-007	0.95	3.617	0.581	1083.9
46		K.PITIFQER.D	1003.56	2	0.0003	0.67	2.243	0.354	312.9
49		R.VVDLM*AYM*ASK.-	1259.60	2	3e-006	0.96	3.536	0.541	1092.9
51		R.VVDLM*AYM*ASKE.-	1388.64	2	1e-007	0.97	3.666	0.493	1653.4
58		R.VVDLM*AYM*ASK.-	1259.60	2	4e-007	0.96	3.719	0.558	1254.4
61		R.VVDLM*AYM*ASKE.-	1388.64	2	7e-007	0.97	4.016	0.553	1317.2
67		R.VVDLM*AYM*ASK.-	1259.60	2	2e-007	0.97	3.920	0.612	1330.8
70		R.VVDLM*AYM*ASKE.-	1388.64	2	6e-006	0.97	4.103	0.549	1402.7
77		R.VVDLM*AYM*ASKE.-	1388.64	2	7e-007	0.96	3.852	0.519	1295.2
87		K.PITIFQER.D	1003.56	2	0.0002	0.70	2.389	0.353	321.8
Heat shock protein HSP 90-alpha	P07901				2e-007	3.2	34.2	0.0	0
4		-.TLTIVDTGIGM*TK.-	1365.73	2	4e-006	0.91	3.354	0.280	1090.4
9		K.ADLINNLGTIAK.S	1242.71	2	2e-006	0.72	2.681	0.254	531.9
17		-.GVVDSEDLPLNISR.-	1513.79	2	2e-005	0.88	3.559	0.193	770.2
25		K.ADLINNLGTIAK.S	1242.71	2	2e-006	0.88	3.430	0.356	671.2
26		-.GVVDSEDLPLNISR.-	1513.79	2	0.001	0.84	3.698	0.170	667.6
34		K.ADLINNLGTIAK.S	1242.71	2	3e-007	0.90	3.168	0.390	798.3
36		-.GVVDSEDLPLNISR.-	1513.79	2	2e-007	0.88	3.411	0.304	744.2
43		-.GVVDSEDLPLNISR.-	1513.79	2	5e-006	0.90	3.618	0.241	811.6
44		K.ADLINNLGTIAK.S	1242.71	2	3e-007	0.78	2.970	0.289	545.7
49		K.ADLINNLGTIAK.S	1242.71	2	4e-007	0.89	3.360	0.305	807.0
50		-.GVVDSEDLPLNISR.-	1513.79	2	3e-005	0.87	3.532	0.242	730.6
111		K.DQVANSAFVER.L	1235.60	2	0.02	0.49	2.074	0.399	396.6
Synaptosomal-associated protein 25-A	P60879				2e-006	2.4	30.2	0.0	0
5		R.TLVM*LDEQGEQLER.I	1676.82	2	5e-006	0.65	2.719	0.281	340.4
18		R.TLVM*LDEQGEQLER.I	1676.82	2	2e-006	0.89	3.322	0.399	604.1
45		R.TLVM*LDEQGEQLER.I	1676.82	2	2e-006	0.90	3.515	0.406	577.4
50		R.TLVM*LDEQGEQLER.I	1676.82	2	0.0001	0.85	3.344	0.427	443.1
53		R.M*LQLVEESK.D	1092.56	2	0.02	0.65	2.154	0.334	362.6
57		R.TLVM*LDEQGEQLER.I	1676.82	2	7e-005	0.87	3.399	0.478	428.1

68		R.M*LQLVEESK.D	1092.56	2	0.006	0.83	2.177	0.362	659.1
84		-.M*LQLVEESK.-	1092.56	2	0.04	0.68	2.116	0.314	550.6
93		R.M*LQLVEESK.D	1092.56	2	0.05	0.63	2.299	0.231	437.9
Glutamate dehydrogenase 1, mitochondrial	P26443				3e-005	6.4	80.1	0.0	0
16		R.YSTDVSVDEVK.A	1241.59	2	0.001	0.88	2.490	0.707	407.2
24		K.HGGTIPVVPTAEFQDR.I	1723.88	3	0.008	0.75	2.758	0.380	573.9
27		K.YNLGLDLR.T	963.53	2	0.0001	0.93	2.730	0.457	969.7
35		R.YSTDVSVDEVK.A	1241.59	2	3e-005	0.84	2.430	0.605	341.8
36		K.YNLGLDLR.T	963.53	2	9e-005	0.94	2.621	0.603	928.9
43		R.YSTDVSVDEVK.A	1241.59	2	0.02	0.85	2.624	0.600	424.6
44 - 47		K.YNLGLDLR.T	963.53	2	0.0008	0.94	2.952	0.561	978.0
48		R.YSTDVSVDEVK.A	1241.59	2	0.002	0.86	2.386	0.635	425.4
52		R.TAAYVNAIEK.V	1079.57	2	0.007	0.88	2.526	0.613	548.7
54		R.DSNYHLLM*SVQESLER.K	1936.91	3	0.004	0.42	2.557	0.320	282.2
58		K.YNLGLDLR.T	963.53	2	0.0001	0.94	2.874	0.594	954.6
60		R.TAAYVNAIEK.V	1079.57	2	6e-005	0.93	2.852	0.599	763.3
67		R.TAAYVNAIEK.V	1079.57	2	0.02	0.92	2.657	0.562	818.3
69		K.DIVHSGLAYTM*ER.S	1507.72	3	0.002	0.91	2.794	0.476	1381.1
77		R.TAAYVNAIEK.V	1079.57	2	0.04	0.87	2.638	0.558	550.6
80		R.DSNYHLLM*SVQESLER.K	1936.91	3	0.001	0.50	2.591	0.381	274.4
83		R.TAAYVNAIEK.V	1079.57	2	0.008	0.86	2.652	0.627	438.9
88		K.CAVVDVPFGGAK.A	1219.61	2	0.03	0.87	2.846	0.458	795.7
133		R.DDGSWEVIEGYR.A	1425.63	2	4e-005	0.73	2.187	0.704	441.6
142		R.DDGSWEVIEGYR.A	1425.63	2	4e-005	0.69	2.321	0.539	408.2
165		R.DDGSWEVIEGYR.A	1425.63	2	0.0008	0.78	2.146	0.706	494.1
Cofilin 1	P18760				2e-009	2.7	40.2	0.0	0
9		K.LGGSAVISLEGKPL.-	1340.78	2	0.0003	0.83	3.056	0.382	566.0
18		R.YALYDATYETK.E	1337.63	2	0.0003	0.83	2.978	0.475	494.1
27		K.LGGSAVISLEGKPL.-	1340.78	2	0.007	0.63	2.073	0.363	463.4
47		K.LGGSAVISLEGKPL.-	1340.78	2	0.005	0.52	2.185	0.391	316.1
50		R.YALYDATYETK.E	1337.63	2	0.0004	0.82	2.672	0.429	578.9
55		K.NIILEEGKEILVGDVGQTVDDPYTTFVK.M	3092.60	3	1e-008	0.94	4.814	0.554	828.8
59		K.LGGSAVISLEGKPL.-	1340.78	2	0.01	0.32	2.003	0.294	275.9
64		K.NIILEEGKEILVGDVGQTVDDPYTTFVK.M	3092.60	3	2e-009	0.88	3.706	0.565	579.0
69		R.YALYDATYETK.E	1337.63	2	0.0001	0.67	2.364	0.350	435.9
86		R.YALYDATYETK.E	1337.63	2	0.0003	0.75	2.802	0.317	514.8
100		K.NIILEEGKEILVGDVGQTVDDPYTTFVK.M	3092.60	3	5e-007	0.87	3.565	0.585	532.8
125		K.NIILEEGKEILVGDVGQTVDDPYTTFVK.M	3092.60	3	2e-005	0.59	2.833	0.372	288.3
130		R.YALYDATYETK.E	1337.63	2	0.0004	0.85	2.819	0.441	611.9
274		K.EILVGDVGQTVDDPYTTFVK.M	2196.11	2	0.0008	0.31	2.145	0.446	161.7

Cofilin 1	P18760				6e-006	2.1	30.2	0.0	0
8		R.FDAGELITQR.E	1149.59	2	0.0001	0.97	3.807	0.368	1871.1
16		R.FDAGELITQR.E	1149.59	2	6e-006	0.94	3.082	0.322	1308.2
27		R.FDAGELITQR.E	1149.59	2	0.0002	0.86	2.626	0.337	913.6
35		R.FDAGELITQR.E	1149.59	2	0.0005	0.87	2.729	0.266	978.2
53		R.FDAGELITQR.E	1149.59	2	0.003	0.92	3.181	0.257	1259
87		R.IYTSIGEDYDER.V	1460.65	2	0.002	0.54	2.017	0.570	243.8
102		K.AAELIANSLATAGDGLIELR.K	1998.09	3	0.01	0.67	3.012	0.403	488.1
115		K.AAELIANSLATAGDGLIELR.K	1998.09	3	0.04	0.61	2.815	0.375	461.7
131		K.AAELIANSLATAGDGLIELR.K	1998.09	3	0.007	0.67	2.964	0.336	545.7
ATP synthase subunit alpha, mitochondrial	Q03265				2e-006	2.6	42.1	0.0	0
7		R.VVDALGNAIDGK.G	1171.63	2	0.0008	0.83	2.574	0.526	546.7
9		K.AVDSLVPIGR.G	1026.59	2	0.01	0.48	2.152	0.339	344.8
10		R.ILGADTSVDLEETGR.V	1575.79	2	5e-006	0.59	2.327	0.552	331.5
16		R.VVDALGNAIDGK.G	1171.63	2	0.0009	0.91	2.923	0.490	831.0
19		R.ILGADTSVDLEETGR.V	1575.79	2	0.0002	0.73	2.395	0.584	438.2
25		R.VVDALGNAIDGK.G	1171.63	2	0.0006	0.91	2.877	0.526	797.3
26		-.TSIAIDTIINQK.-	1316.74	2	0.002	0.19	2.205	-	353.2
27		K.TGTAEM*SSILEER.I	1439.67	2	0.0006	0.38	2.027	0.425	266.3
34		R.VVDALGNAIDGK.G	1171.63	2	0.03	0.87	2.980	0.420	684.1
37		R.ILGADTSVDLEETGR.V	1575.79	2	2e-006	0.65	2.324	0.532	414.7
43		R.VVDALGNAIDGK.G	1171.63	2	0.006	0.89	2.881	0.523	670.7
46		K.TGTAEM*SSILEER.I	1439.67	2	0.0003	0.50	2.076	0.523	318.9
53		K.TGTAEM*SSILEER.I	1439.67	2	7e-005	0.51	2.317	0.515	225.5
54 - 57		R.ILGADTSVDLEETGR.V	1575.79	2	3e-006	0.73	2.720	0.442	543.1
61		K.TGTAEM*SSILEER.I	1439.67	2	4e-006	0.44	2.117	0.477	242.8
79		-.TSIAIDTIINQK.-	1316.74	2	0.02	0.46	2.235	-	514.4
86		-.TSIAIDTIINQK.-	1316.74	2	0.007	0.18	2.071	-	286.9
Cytochrome c oxidase, subunit 5A	P12787				5e-008	2.3	30.2	16.4	0
7		R.LNDFASAVR.I	992.52	2	4e-005	0.89	2.965	0.312	711.6
9		K.GM*NTLVGYDLVPEPK.I	1648.83	2	1e-005	0.91	3.694	0.530	647.1
14		R.LNDFASAVR.I	992.52	2	2e-005	0.84	2.796	0.249	644.7
17		K.GM*NTLVGYDLVPEPK.I	1648.83	2	5e-008	0.92	3.657	0.495	764.3
24		R.LNDFASAVR.I	992.52	2	7e-005	0.86	3.104	0.232	665.9
27		K.GM*NTLVGYDLVPEPK.I	1648.83	2	6e-005	0.85	3.181	0.484	528.7
34		R.LNDFASAVR.I	992.52	2	0.0003	0.89	3.158	0.204	816.9
36		K.GM*NTLVGYDLVPEPK.I	1648.83	2	1e-005	0.82	3.081	0.493	485.4
43		R.LNDFASAVR.I	992.52	2	0.0008	0.89	3.170	0.234	797.3
45		K.GM*NTLVGYDLVPEPK.I	1648.83	2	2e-006	0.89	3.092	0.566	640.5
68		R.KGM*NTLVGYDLVPEPK.I	1776.92	3	0.0002	0.56	2.540	0.411	318.0

Dynamin 1	P39053				2e-009	9.1	108.2	0.0	0
8		K.SSVLENFVGR.D	1107.58	2	0.0002	0.62	2.357	0.154	615.3
9		K.VPVGDQPPDIEFQIR.D	1709.89	2	8e-006	0.57	2.486	0.431	266.8
17		K.SSVLENFVGR.D	1107.58	2	0.0002	0.76	2.582	0.212	676.5
18		K.VPVGDQPPDIEFQIR.D	1709.89	2	0.0006	0.72	2.676	0.444	353.6
25		-.LQSQLLSIEK.-	1158.67	2	0.05	0.49	2.013	0.188	344.9
27		K.SSVLENFVGR.D	1107.58	2	6e-005	0.83	2.684	0.166	897.1
36		R.NLVDSYM*AIVNK.T	1382.70	2	0.0009	0.81	2.809	0.466	489.3
45		R.NLVDSYM*AIVNK.T	1382.70	2	8e-005	0.91	3.054	0.467	720.9
51		K.VPVGDQPPDIEFQIR.D	1709.89	2	4e-007	0.87	3.132	0.476	497.8
54		K.DITAALAAER.K	1030.55	2	0.0001	0.96	3.390	0.354	1673.2
58		K.VPVGDQPPDIEFQIR.D	1709.89	2	0.0005	0.52	2.321	0.423	265.5
60		R.NLVDSYM*AIVNK.T	1382.70	2	2e-006	0.93	3.226	0.555	792.3
62		R.GM*EDLIPLVNR.L	1272.66	2	0.0002	0.87	2.654	0.593	445.2
67		R.GM*EDLIPLVNR.L	1272.66	2	0.001	0.68	2.422	0.427	290.7
70		K.VPVGDQPPDIEFQIR.D	1709.89	2	8e-009	0.90	3.362	0.526	602.9
71		R.NLVDSYM*AIVNK.T	1382.70	2	0.002	0.87	2.987	0.511	583.7
76		R.GM*EDLIPLVNR.L	1272.66	2	0.0002	0.74	2.544	0.472	325.6
77		R.NLVDSYM*AIVNK.T	1382.70	2	8e-005	0.90	3.102	0.500	655.1
80		K.TSGNQDEILVIR.K	1344.71	2	2e-005	0.62	2.576	0.337	333.5
81		K.DITAALAAER.K	1030.55	2	0.0003	0.95	3.249	0.376	1476
86		K.DITAALAAER.K	1030.55	2	0.001	0.96	3.223	0.385	1684.4
88		K.TSGNQDEILVIR.K	1344.71	2	7e-005	0.85	3.005	0.367	555.3
96		K.TSGNQDEILVIR.K	1344.71	2	0.0001	0.75	2.926	0.338	409.4
99		R.DM*LM*QFVTK.E	1144.54	2	0.004	0.88	2.576	0.241	950.7
105		K.DITAALAAER.K	1030.55	2	0.0002	0.94	3.135	0.299	1399.5
106		K.ALLQM*VQQFAVDFEK.R	1782.91	2	1e-007	0.90	3.031	0.614	474.1
107		K.LDLM*DEGTDAR.D	1251.55	2	3e-006	0.78	2.375	0.368	535.7
108		K.TSGNQDEILVIR.K	1344.71	2	4e-005	0.77	2.648	0.348	499.3
112		K.TSGNQDEILVIR.K	1344.71	2	0.0002	0.69	2.652	0.313	414.6
113		K.LDLM*DEGTDAR.D	1251.55	2	0.003	0.66	2.453	0.348	373.2
114		R.DM*LM*QFVTK.E	1144.54	2	0.001	0.88	2.601	0.272	870.5
120		K.SSVLENFVGR.D	1107.58	2	0.0004	0.79	2.356	0.185	843.6
123		K.DITAALAAER.K	1030.55	2	3e-005	0.95	3.218	0.357	1521.5
124		R.DM*LM*QFVTK.E	1144.54	2	0.03	0.85	2.363	0.302	854.9
140		K.LDLM*DEGTDAR.D	1251.55	2	0.0002	0.67	2.326	0.406	370.9
146		K.SSVLENFVGR.D	1107.58	2	3e-005	0.81	2.531	0.170	882.0
147		K.LDLM*DEGTDAR.D	1251.55	2	0.009	0.57	2.097	0.327	379.5
150		K.ALLQM*VQQFAVDFEK.R	1782.91	2	2e-009	0.96	3.965	0.601	933.3
156		K.ALLQM*VQQFAVDFEK.R	1782.91	2	8e-005	0.82	2.884	0.532	365.6
165		K.ALLQM*VQQFAVDFEK.R	1782.91	2	4e-006	0.91	3.347	0.608	521.1
178		K.ALLQM*VQQFAVDFEK.R	1782.91	3	2e-008	0.82	3.392	0.220	922.3
191		R.DM*LM*QFVTK.E	1144.54	2	0.005	0.84	2.430	0.274	772.5

203		K.ALLQM*VQQFAVDFEK.R	1782.91	3	8e-005	0.57	2.895	0.161	574.7
211		R.DM*LM*QFVTK.E	1144.54	2	0.01	0.88	2.601	0.215	986.7
212		R.LQDAFSAIGQNADLDLPQIAVVGGQSAGK.S	2883.48	3	5e-006	0.87	3.781	0.585	458.5
215		K.ALLQM*VQQFAVDFEK.R	1782.91	3	1e-008	0.85	3.360	0.308	945.2
235		R.LQDAFSAIGQNADLDLPQIAVVGGQSAGK.S	2883.48	3	0.0002	0.58	2.868	0.362	306.9
Glutamine synthetase	P15105				0.001	1.4	18.2	0.0	0
49		R.LTGFHETSNINDFSAGVANR.G	2150.03	3	0.001	0.73	3.135	0.524	331.3
58		R.LTGFHETSNINDFSAGVANR.G	2150.03	3	0.006	0.89	3.841	0.568	715.8
80		R.LTGFHETSNINDFSAGVANR.G	2150.03	3	0.009	0.67	2.932	0.533	311.4
84		-.RPSANCDPYAVTEAIVR.-	1918.94	3	0.007	0.70	2.705	0.455	542.6
106		R.LTGFHETSNINDFSAGVANR.G	2150.03	3	0.002	0.81	3.342	0.551	445.3
Hemoglobin subunit beta	P02088				5e-008	2.4	30.1	0.0	0
4		K.DFTPAAQAAFQK.V	1294.64	2	6e-005	0.81	2.543	0.430	478.6
12		K.DFTPAAQAAFQK.V	1294.64	2	0.0005	0.71	2.485	0.434	353.8
21		K.DFTPAAQAAFQK.V	1294.64	2	0.0003	0.67	2.502	0.441	312.8
22		K.VNSDEVGGEALGR.L	1302.63	2	6e-008	0.93	2.993	0.463	1123.7
30		K.VNSDEVGGEALGR.L	1302.63	2	2e-007	0.78	2.146	0.500	698.8
31		K.DFTPAAQAAFQK.V	1294.64	2	0.0003	0.76	2.245	0.487	404.8
39		K.DFTPAAQAAFQK.V	1294.64	2	1e-005	0.74	2.459	0.389	431.1
42		K.VNSDEVGGEALGR.L	1302.63	2	9e-007	0.92	2.846	0.459	1121.7
47		K.VNSDEVGGEALGR.L	1302.63	2	5e-008	0.94	2.783	0.452	1461.2
88		K.VVAGVATALAHK.Y	1136.68	2	0.0003	0.75	2.336	0.535	432.8
116		K.VVAGVATALAHK.Y	1136.68	2	3e-006	0.72	2.461	0.429	476.1
124		K.VVAGVATALAHK.Y	1136.68	2	0.001	0.54	2.170	0.494	273.1
133		K.VVAGVATALAHK.Y	1136.68	2	6e-005	0.71	2.398	0.597	248.5
Peptidyl-prolyl cis-trans isomerase A	P17742				2e-005	1.6	18.1	0.0	0
13		R.VSFELFADK.V	1055.54	2	0.0002	0.55	2.044	0.369	310.0
21		R.VSFELFADK.V	1055.54	2	0.0009	0.55	2.059	0.209	436.8
23		-.FEDENFILK.-	1154.57	2	0.001	0.76	2.409	0.220	444.0
31		R.VSFELFADK.V	1055.54	2	2e-005	0.85	2.632	0.218	683.5
41		R.VSFELFADK.V	1055.54	2	0.002	0.72	2.445	0.183	600.7
Alpha-enolase	P17182				7e-008	5.1	74.2	0.0	0
18		R.GNPTVEVDLYTAK.G	1406.72	2	2e-007	0.74	3.025	0.203	318.6
28		R.GNPTVEVDLYTAK.G	1406.72	2	7e-008	0.75	3.048	0.138	359.1
50		R.GNPTVEVDLYTAK.G	1406.72	2	2e-006	0.70	3.024	0.136	323.2
53		-.IDKLM*IEM*DGTENK.-	1668.78	3	0.0004	0.89	3.627	0.533	562.4
58		R.GNPTVEVDLYTAK.G	1406.72	2	1e-007	0.74	3.038	0.206	319.5
59		-.IDKLM*IEM*DGTENK.-	1668.78	3	0.0005	0.83	3.069	0.448	603.3
66		R.GNPTVEVDLYTAK.G	1406.72	2	1e-006	0.69	2.944	0.224	276.4

69		-.IDKLM*IEM*DGTENK.-	1668.78	3	0.002	0.90	3.548	0.567	648.8
76		-.IDKLM*IEM*DGTENK.-	1668.78	3	0.006	0.93	3.684	0.590	828.5
80		K.GVSQAVEHINK.T	1181.63	2	1e-005	0.94	3.336	0.526	946.9
84		-.IDKLM*IEM*DGTENK.-	1668.78	3	0.0006	0.89	3.345	0.560	683.3
90		K.GVSQAVEHINK.T	1181.63	2	0.0003	0.90	2.928	0.467	686.9
95		K.GVSQAVEHINK.T	1181.63	2	0.0001	0.90	2.987	0.409	796.1
98		-.LM*IEM*DGTENK.-	1312.58	2	0.01	0.50	2.170	0.211	207.9
106		K.GVSQAVEHINK.T	1181.63	2	0.001	0.82	2.876	0.410	517.2
109		K.LAM*QEFM*ILPVGASSFR.E	1928.96	3	0.002	0.60	3.260	0.203	434.3
111		K.GVSQAVEHINK.T	1181.63	2	4e-006	0.87	2.863	0.437	647.5
113		-.LM*IEM*DGTENK.-	1312.58	2	0.03	0.52	2.098	0.247	225.8
117		K.LAM*QEFM*ILPVGASSFR.E	1928.96	3	0.03	0.47	2.540	0.153	506.7
121		-.LM*IEM*DGTENK.-	1312.58	2	0.008	0.56	2.231	0.258	233.1
127		R.SGKYDLDFK.S	1072.53	3	0.05	0.75	2.725	0.351	569.6
130		K.LAM*QEFM*ILPVGASSFR.E	1928.96	3	0.004	0.45	2.677	0.149	487.4
136		-.LAM*QEFM*ILPVGASSFR.-	1928.96	2	0.0007	0.19	2.670	0.568	216.0
139		K.LAM*QEFM*ILPVGASSFR.E	1928.96	3	0.0004	0.64	3.067	0.124	625.3
213		K.AGYTDQVVIGM*DVAASEFYR.S	2208.03	2	0.003	0.54	2.571	0.519	208.2
225		K.AGYTDQVVIGM*DVAASEFYR.S	2208.03	2	0.004	0.45	2.248	0.444	256.2
263		K.AGYTDQVVIGM*DVAASEFYR.S	2208.03	2	2e-005	0.46	2.341	0.500	203.5
Pyruvate kinase isozymes M1/M2	P52480				4e-008	8.2	100.2	0.0	0
6		R.LDIDSAPITAR.N	1171.63	2	0.01	0.84	2.850	0.373	625.3
8		R.VNLAM*DVGK.A	962.50	2	0.0002	0.88	2.487	0.516	644.4
16		R.LDIDSAPITAR.N	1171.63	2	0.0006	0.86	2.848	0.402	664.8
17		R.VNLAM*DVGK.A	962.50	2	2e-005	0.93	2.775	0.451	913.8
18		R.RFDEILEASDGIM*VAR.G	1837.91	3	2e-005	0.93	4.125	0.436	1077.3
25		R.LDIDSAPITAR.N	1171.63	2	0.001	0.90	3.111	0.441	736.4
26		R.VNLAM*DVGK.A	962.50	2	0.0003	0.93	2.962	0.507	817.2
27		R.RFDEILEASDGIM*VAR.G	1837.91	3	1e-006	0.94	4.236	0.381	1266.4
34		R.LDIDSAPITAR.N	1171.63	2	0.0005	0.92	3.301	0.413	821.3
35		R.VNLAM*DVGK.A	962.50	2	4e-005	0.93	2.878	0.392	923.9
36		R.RFDEILEASDGIM*VAR.G	1837.91	3	3e-006	0.93	4.410	0.495	827.9
43		R.LDIDSAPITAR.N	1171.63	2	0.0002	0.93	3.314	0.463	801.0
44		R.VNLAM*DVGK.A	962.50	2	0.0001	0.92	2.708	0.515	834.3
45 - 47		R.RFDEILEASDGIM*VAR.G	1837.91	3	7e-006	0.96	4.790	0.458	1260.1
49		K.KGVNLPGAAVDLPAVSEK.D	1764.99	3	0.003	0.82	3.029	0.428	780.9
56		K.KGVNLPGAAVDLPAVSEK.D	1764.99	3	0.007	0.67	3.071	0.378	438.2
60		K.GVNLPGAAVDLPAVSEK.D	1636.89	2	4e-007	0.92	3.646	0.563	598.2
61		K.IYVDDGLISLQVK.Q	1462.82	2	4e-008	0.96	3.881	0.317	1622
66		K.KGVNLPGAAVDLPAVSEK.D	1764.99	3	0.0002	0.79	3.101	0.408	669.0
68		K.IYVDDGLISLQVK.Q	1462.82	2	6e-006	0.94	3.789	0.279	1150.4
70		K.GVNLPGAAVDLPAVSEK.D	1636.89	2	1e-006	0.88	3.185	0.602	461.5

77	K.IYVDDGLISLQVK.Q	1462.82	2	6e-007	0.96	4.323	0.378	1426.8
80	K.GVNLPGAAVDLPAVSEK.D	1636.89	2	4e-007	0.92	3.552	0.653	556.7
83	K.KGVNLPGAAVDLPAVSEK.D	1764.99	3	0.004	0.72	3.249	0.353	487.9
85	K.IYVDDGLISLQVK.Q	1462.82	2	1e-006	0.96	4.018	0.302	1511.7
86	K.GVNLPGAAVDLPAVSEK.D	1636.89	2	1e-005	0.85	3.326	0.538	422.4
89	R.EATESFASDPILYRPVAVALDTK.G	2493.29	3	0.001	0.47	2.776	0.436	150.4
92	K.IYVDDGLISLQVK.Q	1462.82	2	8e-008	0.97	4.051	0.441	1904.7
95	K.GVNLPGAAVDLPAVSEK.D	1636.89	2	5e-007	0.93	4.065	0.564	637.8
98	R.AGKPVICATQM*LESM*IK.K	1908.96	3	0.01	0.85	3.821	0.448	534.8
113	R.AGKPVICATQM*LESM*IK.K	1908.96	3	0.0002	0.74	3.293	0.451	344.5
120	R.AGKPVICATQM*LESM*IK.K	1908.96	3	0.003	0.70	3.047	0.397	436.3
125	R.PVAVALDTK.G	913.54	2	0.001	0.80	2.820	0.180	599.6
131	R.AGKPVICATQM*LESM*IK.K	1908.96	3	0.009	0.75	3.149	0.469	417.5
135	R.PVAVALDTK.G	913.54	2	0.04	0.63	2.045	0.330	446.6
141	R.PVAVALDTK.G	913.54	2	0.002	0.66	2.237	0.213	464.9
143	R.EATESFASDPILYR.P	1598.77	2	0.0006	0.24	2.047	0.351	233.4
147	R.PVAVALDTK.G	913.54	2	0.01	0.47	2.159	0.267	305.6
156	R.PVAVALDTK.G	913.54	2	0.01	0.45	2.178	0.239	318.0
174	R.EATESFASDPILYR.P	1598.77	2	6e-006	0.74	2.398	0.574	496.6
194	K.KGVNLPGAAVDLPAVSEK.D	1764.99	2	0.002	0.33	2.209	0.423	197.9