

11. Anhang

11.1. Tabelle S1

Parkin 2 Monate

Tabelle S1: Proteinspots, die in der vorliegenden Arbeit bei den jeweiligen Mausmodellen identifiziert wurden

Spot-nummer	% KO zu WT	p-Wert	Mowse Score	Sequenzabdeckung (%)	Anzahl gefundener Peptide	Theoretische Masse	Theoretischer pI	Ensemble ID	Swiss-prot ID	Gen-symbol	NCBI Accessnummer	Protein Name
9362	-19,72	0,0250	90	42	7	13362	5,52	NP_079657.1	Q9D1K2	Atp6v1f	gi 16758754	ATPase, H transporting, lysosomal V1 subunit F
9408	-12,02	0,0425	70	57	8	13362	5,52	NP_079657.1	Q9D1K2	Atp6v1f	gi 16758754	ATPase, H transporting, lysosomal V1 subunit F
9012	-14,93	0,0101	119	77	9	12425	9,24	BAB29375.1	O55042	Snca	gi 12852348	synuclein, alpha
8394	-15,66	0,0401	75	39	5	21837	5,30	NP_780774.1	Q4VAA2	Cdv3	gi 148689123	carnitine deficiency-associated gene expressed in ventricle 3, isoform CRA_b
8168	-11,85	0,0204	80	27	10	48265	5,52	CAM24398.1	A2ALV1	Sh3gl2	gi 123229396	SH3-domain GRB2-like 2
7620	-12,67	0,0043	202	39	19	60764	6,04	BAE29191.1	Q3UDS0	Hspa8	gi 74211667	heat shock protein 8
2314	-17,88	0,0063	127	67	10	14948	8,46	NP_035202.1	P62962	Pfn1	gi 6755040	profilin 1
2271	-5,93	0,0049	84	45	7	13768	6,36	NP_032274.1	P70349	Hint1	gi 33468857	histidine triad nucleotide binding protein 1
2096	-9,04	0,0026	75	46	16	17960	7,74	NP_032933.1	P17742	Ppia	gi 6679439	peptidylprolyl isomerase A
2148	-12,78	0,0017	169	79	11	17298	6,78	EDL15910.1			gi 148683963	mCG145251
2092	-15,54	0,0217	74	44	7	14083	9,13	CAI35365.1	Q5NC80	Nme1	gi 56800495	Nucleoside diphosphate kinase (EC 2.7.4.6) (Fragment)
1781	-10,07	0,0103	130	66	16	23463	8,13				gi 576133,	Chain A, 1.8 Angstroms Molecular Structure Of Mouse Liver Class Pi Glutathione S-Transferase Comple

1737	-13,67	0,0445	87	42	9	26696	6,90	NP_033441.1	P17751	Tpi1	gi 6678413	triosephosphate isomerase 1
1583	-7,12	0,0203	82	48	13	28814	6,67	NP_075907.2	Q9DBJ1	Pgam1	gi 114326546	phosphoglycerate mutase 1
1290	-10,93	0,0397	86	33	10	30737	8,62	NP_035824.1	Q60932	Vdac1	gi 6755963	voltage-dependent anion channel 1
1289	-11,62	0,0003	148	53	13	30737	8,62	NP_035824.1	Q60932	Vdac1	gi 6755963	voltage-dependent anion channel 1
1054	-8,72	0,0056	75	41	17	37328	9,91	NP_059077.1	Q9R020	Zranb2	gi 74315981	zinc finger, RAN-binding domain containing 2
1087	-8,96	0,0039	67	22	7	40798	9,00	BAE29370.1	P05202	Got2	gi 74213886	glutamate oxaloacetate transaminase 2, mitochondrial
1058	-8,29	0,0042	108	26	11	47381	9,13	NP_034455.1	P05202	Got2	gi 6754036	glutamate oxaloacetate transaminase 2, mitochondrial
961	12,11	0,0202	175	42	14	39370	6,67	NP_033787.2	P05063	Aldoc	gi 60687506	aldolase 3, C isoform
900	-8,43	0,0035	191	52	23	44522	8,02	NP_032854.2	P09411	Pgk1	gi 70778976	phosphoglycerate kinase 1
717	-8,43	0,0044	79	29	12	46143	6,31	2CMJ_A			gi 149241012	Chain A, Crystal Structure Of Mouse Cytosolic Isocitrate Dehydrogenase
513	-11,89	0,0027	86	30	15	54238	7,99	NP_031887.2	O08749	Dld	gi 31982856	dihydrolipoamide dehydrogenase
446	19,02	0,0019	71	21	12	62542	6,4	NP_058017.1	Q60864	Stip1	gi 14389431	stress-induced phosphoprotein 1
211	-4,38	0,0153	278	38	28	85295	8,08	BAE25770.1	Q99KI0	Aco2	gi 74188189	aconitase 2, mitochondrial

Parkin 8 Monate

Spot-nummer	% KO zu WT	p-Wert	Mowse Score	Sequenzabdeckung (%)	Anzahl gefundener Peptide	Theoretische Masse	Theoretischer pI	Ensemble ID	Swiss-prot ID	Gen-symbol	NCBI Access nummer	Protein Name
1	-38,10	0,0170	430	35	7	26784	5,07	NP_080270.2	Q8C845	Efhd2	gi 31981086	EF hand domain containing 2
2	-54,88	0,0461	403	29	6	22952	8,65	O55234.2	O55234	Psmb5	gi 3914434	Proteasome subunit beta type 5 precursor
3	-292,76	0,0489	97	11	2	17850	8,68	NP_003338.1	P68036	UBE2L3	gi 4507789	ubiquitin-conjugating enzyme E2L3 isoform 1
4	-22,49	0,0247	691	19	12	79698	5,51	NP_663493.1	Q91VD9	Ndufs1	gi 21704020	NADH dehydrogenase (ubiquinone) Fe-S protein 1
5	-27,72	0,0389	498	27	8	40992	5,56	CAA31455.1	P63260	Actg1	gi 809561	gamma-actin
6	-26,74	0,0360	486	52	8	23618	4,63	NP_032109.1	P06837	Gap43	gi 6679935	growth associated protein 43
7	-68,75	0,0370	217	15	4	37309	5,6	AAC72250.1	P62880	Gnb2	gi 984551	G protein beta 2 subunit
8	-27,86	0,0057	234	28	4	21051	5,18	NP_038574.2	Q9R257	Hebp1	gi 7305137	heme binding protein 1
9	-141,15	0,0030	95	9	2	20796	5,24	Q9CPU0.3	Q9CPU0	Glo1	gi 21362640	Lactoylglutathione lyase (Methylglyoxalase)
10	-84,49	0,0347	396	37	7	24822	5,14	Q9R0P9.1	Q9R122	Uchl1	gi 61098212	ubiquitin carboxy-terminal hydrolase L1

PINK1 Striatum

Spot-nummer	% KO zu WT	p-Wert	Mowse Score	Sequenzabdeckung (%)	Anzahl gefundener Peptide	Theoretische Masse	Theoretischer pI	Ensemble ID	Swiss-prot ID	Gen-symbol	NCBI Accessnummer	Protein Name
1829	28	0,0307	136	7	3	41492	5,53	NP_038692.1	Q62419	Sh3g11	gi 7305485	SH3-domain GRB2-like 1
1403	31	0,0245	428	26	8	31237	8,76	AAH02178.1	Q8BH95	Echs1	gi 12805413	Echs1 protein
1932	32	0,0048	84	5	2	40992	5,56	AAA37167.1	P63260	Actg1	gi 809561	gamma-actin
2683	32	0,0098	183	18	4	29627	5,66	AAH03328.1	Q99LD8	Ddah2	gi 13097102	Ddah2 protein
833	34	0,0097	144	9	3	39307	6,47	AAH08184.1	P05063	Aldoc	gi 14198249	Fructose-bisphosphate aldolase C
2416	34	0,0109	163	12	4	37363	6,57	NP_035658.1	Q93092	Taldo1	gi 33859640	transaldolase 1
1529	36	0,0214	38	4	1	26679	6,9	CAA37420.1	P17751	Tpi1	gi 54855	triosephosphate isomerase
849	-36	0,0133	37	1	1	80423	5,56	NP_031890.1	Q62108	Dlg4	gi 6681195	postsynaptic density protein 95
743	37	0,0002	235	12	5	46974	8,39	NP_034027.1	P30275	Ckmt1	gi 6753428	creatine kinase, mitochondrial 1, ubiquitous
742	37	0,0151	221	10	4	50902	8,88	NP_766599.1	P54071	Idh2	gi 27370516	isocitrate dehydrogenase 2 (NADP+), mitochondrial
1125	37	0,0079	222	12	4	35588	8,93	AAA39509.1	P08249	Mdh2	gi 387422	malate dehydrogenase
2336	37	0,0012	53	4	1	36549	5,7	NP_032518.1	P16125	Ldhb	gi 6678674	lactate dehydrogenase 2, B chain
1976	40	0,0046	93	6	2	40763	5,23	AAH12963.1	Q9QYG0	Ndr2	gi 15277976	N-myc downstream regulated gene 2
692	42	0,0142	371	21	8	47094	9,08	NP_034053.1	P16330	Cnp	gi 6753476	cyclic nucleotide phosphodiesterase 1
1707	42	0,0035	436	16	8	52214	5,56	NP_032206.1	P51855	Gss	gi 6680117	glutathione synthetase
1815	42	0,0018	465	25	8	42686	5,4	NP_067248.1	Q04447	Ckb	gi 10946574	creatine kinase, brain

1971	42	0,001 0	299	21	6	46215	5,65	AAC64398.1	Q9Z2I9	Sucla2	gi 3766201	ATP-specific succinyl-CoA synthetase beta subunit
1945	43	0,002 5	56	1	1	95984	4,76	NP_032717.2	P08553	Nefm	gi 112363107	Neurofilament triplet M protein
2881	45	0,000 8	46	3	1	24822	5,33	NP_035800.1	Q9R0P9	Uchl1	gi 6755929	ubiquitin carboxy-terminal hydrolase L1
1192	54	0,001 6	395	21	7	33983	8,66	NP_081095.2	Q99L04	Dhrs1	gi 31980844	dehydrogenase/reductase (SDR family) member 1

PINK1 Mittelhirn

Spot-nummer	% KO zu WT	p-Wert	Mowse Score	Sequenzabdeckung (%)	Anzahl gefundener Peptide	Theoretische Masse	Theoretischer pI	Ensemble ID	Swiss-prot ID	Gen-symbol	NCBI Access number	Protein Name
8791	-34,88	0,04	157	16	3	24822	5,14	NP_058933.2	Q00981	Uchl1	gi 61098212	ubiquitin carboxy-terminal hydrolase L1
8599	-31,03	0,003	545	46	11	33296	5,28	BAB28324.1	Q9CPV4	Glod4	gi 12849397	Glyoxalase domain-containing protein 4
8563	-43,8	0,031	193	18	3	29997	5,12	NP_031922.1	Q61166	Mapre1	gi 7106301	microtubule-associated protein, RP/EB family, member 1
8678	-18,18	0,015	91	8	2	25476	5,57	AAH56211.1	Q61206	Pafah1b2	gi 33440467	Platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit
8447	-34,38	0,018	602	45	9	25084	5,07	NP_080270.2	Q8C845	Efh2	gi 31981086	EF hand domain containing 2
8509	-15,81	0,01	145	11	3	36454	6,16	AAA37423.1	P14152	Mdh1	gi 387129	cytosolic malate dehydrogenase
8425	41,39	0,037	196	19	4	34195	5,91	NP_031501.1	Q5M8R8	Arbp	gi 6671569	acidic ribosomal phosphoprotein P0
8469	-12,85	0,021	497	32	11	38912	6,41	NP_077183.1	Q9D051	Pdhb	gi 18152793	pyruvate dehydrogenase (lipoamide) beta
8467	-24,22	0,046	708	42	10	33536	6,41	NP_062606.1	A2APW8	Napb	gi 29789104	N-ethylmaleimide sensitive fusion protein attachment protein beta
8040	-61,35	0,007	140	6	2	51745	5,58	NP_542124.1	Q91YJ2	Snx4	gi 18017596	sorting nexin 4
8135	64,11	0,049	158	13	3	50506	5,93	AAH53381.1	Q5RKT4	Gdi2	gi 55931021	Gdi2 protein
8157	-30,85	0,047	861	43	13	47267	4,99	NP_038537.1	P17183	Eno2	gi 7305027	enolase 2, gamma neuronal
7642	-23,97	0,021	669	13	10	117734	5,43	NP_033483.1	A6H6S6	Uba1	gi 6678483	ubiquitin-activating enzyme E1, Chr X
7682	-29,79	0,018	328	9	5	80712	5,83	AAH23143.2	P13020	Gsn	gi 18606238	Gsn protein
7709	-28,25	0,007	62	9	1	45618	5,47	AAH30891.1	Q8K2L6	Rap1gap	gi 21410877	Rap1gap protein
2667	-26,22	0,013	522	23	8	47382	9,05	AAB91426.1	P05202	Got-2	gi 2690302	aspartate aminotransferase precursor
2672	-51,51	0,029	61	3	1	42517	8,22	AAH37729.1	Q3ULJ0	Gpd1l	gi 22902419	Gpd1l protein
2672	-51,51	0,029	51	3	1	43244	8,22	AAG32038.1	Q8VDQ8	Sir2L2	gi 11141704	SIR2L2
2695	-43,75	0,001	69	4	1	35787	8,69	ABD77187.1	P16858	GAPDH	gi 89573923	glyceraldehyde-3-phosphate

												dehydrogenase
2701	-49,83	0,003	55	6	1	36519	8,69	ABD77187.1	P16858	GAPDH	gi 89573923	glyceraldehyde-3-phosphate dehydrogenase
2715	-41,16	0,002	340	19	5	35787	8,44	NP_032110.1	A6H6A8	Gapdh	gi 6679937	similar to glyceraldehyde-3-phosphate dehydrogenase
2811	-21,79	0,005	855	51	10	30737	8,62	NP_035824.1	Q60932	Vdac1	gi 6755963	voltage-dependent anion channel 1
2824	20,79	0,039	88	9	2	34953	9,45	NP_063932.1	Q9WUM5	Suclg1	gi 9845299	succinate-CoA ligase, GDP-forming, alpha subunit
2874	-42,04	0,014	205	14	2	30737	8,62	NP_035824.1	Q60932	Vdac1	gi 6755963	voltage-dependent anion channel 1
15175	-38,69	0,046	151	14	3	36475	7,62	NP_034829.1	P06151	Ldha	gi 6754524	lactate dehydrogenase 1, A chain
15175	-38,69	0,046	107	20	1	30737	8,96	NP_035824.1	Q60932	Vdac1	gi 6755963	voltage-dependent anion channel 1
15178	-38,69	0,016	455	29	6	35018	8,42	NP_663590.2	Q99LC5	Etfa	gi 21759113	Electron transfer flavoprotein subunit alpha, mitochondrial precursor (Alpha-ETF)
15593	-33,99	0,025	224	20	4	30733	8,96	NP_035826.1	Q60931	Vdac3	gi 6755967	voltage-dependent anion channel 3
2634	-46,99	0,001	88	4	1	40316	9,34	NP_079573.1	Q9DCS3	Mecr	gi 13384652	trans-2-enoyl-CoA reductase, mitochondrial precursor
2654	-19,19	0,041	533	23	8	47382	9,05	AAB91426.1	P05202	Got-2	gi 2690302	aspartate aminotransferase precursor
2563	-21,35	0,019	1158	59	17	39331	8,31	NP_031464.1	Q5FWB7	Aldoa	gi 6671539	aldolase 1, A isoform
23769	-54,44	0,007	318	9	5	74523	8,43	NP_766024.1	A2BFG0	Slc25a12	gi 27369581	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
23825	-26,67	0,016	177	12	3	62142	6,39	CAA70300.1	P97427	Ulip3	gi 1915915	Ulip3 protein
23877	-38,64	0,034	70	2	1	52418	7,62	NP_038709.1	Q64332	Syn2	gi 8567410	synapsin II
2465	-22,58	0,003	123	14	1	46974	8,39	NP_034027.1	P30275	Ckmt1	gi 6753428	creatine kinase, mitochondrial 1, ubiquitous

PINK1 Kortex

Spot-nummer	% KO zu WT	p-Wert	Mowse Score	Sequenzabdeckung (%)	Anzahl gefundener Peptide	Theoretische Masse	Theoretischer pI	Ensemble ID	Swiss-prot ID	Gen-symbol	NCBI Accessnummer	Protein Name
1404	38,89	0,0008	156	51	18	31514	7,66	NP_035658.1	Q93092	Taldo1	gi 148686116	transaldolase 1, isoform CRA_e
1295	26,83	0,0011	86	42	7	11317	5,73	AAH87888.1	Q5M8R7	Ldhb	gi 56789289	Ldhb protein
3972	35,45	0,0019	237	54	27	39161	5,79	CAA27396.1	P60710	Actb	gi 49868	put. beta-actin (aa 27-375)
3979	31,88	0,0028	230	56	24	41724	5,30	CAA31455.1	P63260	Actg1	gi 809561	gamma-actin
3951	23,77	0,0386	107	26	12	51913	6,52	AAL87533.1	Q8R436	Gss	gi 19547889	glutathione synthetase
857	31,56	8,80E-06	98	35	13	49877	4,96	NP_033474.1	P68373	Tuba1c	gi 6678469	tubulin, alpha 1C
718	23,92	0,0019	180	35	23	68074	5,32	AAH66191.1	P63017	Hspa8	gi 42542422	Heat shock protein 8
2041	30,77	0,0022	176	73	14	14948	8,46	NP_035202.1	P62962	Pfn1	gi 6755040	profilin 1
1864	21,69	0,0006	91	48	9	17197	6,84	NP_032730.1	P15532	Nme1	gi 37700232	nucleoside-diphosphate kinase 1
1839	29,77	0,0006	99	53	12	17960	7,74	NP_032933.1	P17742	Ppia	gi 6679439	peptidylprolyl isomerase A
1494	-33,67	0,0004	124	47	11	24625	8,57	BAA77360.1	Q9WTP7	Ak3	gi 4760600	adenylate kinase isozyme 3
1347	61,88	6,80E-05	114	32	13	32621	9,57	AAH26525.1	Q9JLZ3	Auh	gi 20072952	Auh protein
1559	24,26	0,0228	64	23	5	18915	6,82	CAM16506.1	B1AXW5	Prdx1	gi 123230136	peroxiredoxin 1
1441	38,99	0,0006	147	42	9	26696	6,90	NP_033441.1	P17751	Tpi1	gi 6678413	triosephosphate isomerase 1
1216	119,96	0,0007	126	42	15	30237	8,86	NP_001106209.1	Q3UD06	Atp5c1	gi 163838648	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit isoform b
	119,96	0,0007	74	40	13	31093	8,54	NP_083033.1	Q9DC07	Nebi	gi 21311871	nebulin
1041	44,32	0,0009	31	20	4	24445	8,76	CAM20025.1	A2ALE2		gi 123210063	novel protein
921	33,26	0,0005	211	60	23	35787	8,44	NP_032110.1	P16858	Gapdh	gi 6679937	glyceraldehyde-3-phosphate dehydrogenase
1051	47,09	0,0019	161	62	15	30737	8,62		Q60932	Vdac1	gi 6755963	voltage-dependent anion channel 1
761	51,99	0,0050	179	43	17	39331	8,31	NP_031464.1	P05064	Aldoa	gi 6671539	aldolase 1, A isoform
699	-25,8	0,0057	130	28	16	51703	8,72	NP_080720.1	Q9CZU6	Cs	gi 13385942	citrate synthase
763	61,99	0,0112	130	30	12	46219	6,68	NP_034454.2	Q3UJH8	Got1	gi 160298209	glutamate oxaloacetate transaminase 1, soluble

702	-22,03	0,0026	130	30	12	46219	6,68	NP_034454.2	Q3UJH8	Got1	gi 160298209	glutamate oxaloacetate transaminase 1, soluble
772	54,29	0,0050	130	39	17	44508	7,53	AAA70267.1	P09411	Pgk1	gi 202423	phosphoglycerate kinase
736	-22,74	0,0122	265	58	28	44522	8,02	NP_032854.2	P09411	Pgk1	gi 70778976	phosphoglycerate kinase 1
2565	24,5	0,0005	227	37	24	56416	8,35	NP_766549.2	P61922	Abat	gi 37202121	4-aminobutyrate aminotransferase
593	26,43	0,0062	139	43	16	39757	5,86	AAH56611.1	Q6PHC1	Eno1	gi 34784434	Eno1 protein
443	25,64	0,0017	168	42	17	54474	6,44	NP_032010.2	Q61553	Fscn1	gi 113680348	fascin homolog 1, actin bundling protein
375	23,48	0,0058	225	40	24	62142	6,39	CAA70300.1	P97427	Dpysl1	gi 1915915	Ulip3 protein
286	88,65	0,0058	151	34	20	62142	6,39	CAA70300.1	P97427	Dpysl1	gi 1915915	Ulip3 protein
	88,65	0,0058	65	26	11	60545	6,54	AAG28459.1	P40142	Tkt	gi 11066098	transketolase

MPTP 1d C57BL6/J

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782	-52,89	0,016	535	21	10	50981	5,36	NP_034396.1	Q9R111	Gda	gi 6753960	guanine deaminase
5080	-14,82	0,049	76	37	7	23560	9,46	NP_878259.1	Q7TQD2	Tppp	gi 33469051	tubulin polymerization-promoting protein
4327	-24,84	0,027	90	21	10	62728	7,75	NP_032181.1	P06745	Gpi	gi 6680067	glucose phosphate isomerase 1
4183	-24,07	0,021	180	36	23	67659	6,62	NP_033321.2	O08599	Stxbp1	gi 6678179	syntaxin binding protein 1
4860	-16,75	0,004	175	62	18	30737	8,62	NP_035824.1	Q60932	Vdac1	gi 6755963	voltage-dependent anion channel 1
4178	-18,64	0,023	86	32	23	67526	6,49	NP_037170.1	P61765	Stxbp1	gi 6981602	syntaxin binding protein 1
4178	-18,64	0,023	66	17	23	133329	7,80	NP_034696.2	Q4U212	Inpp5d	gi 1209068	SH2-containing inositol-phosphatase
1338	-27,13	0,005	526	37	8	26394	4,74	NP_036097.1	Q3UPK6	Psm5	gi 7106387	proteasome (prosome, macropain) subunit, alpha type 5
5673	-21,06	0,020	421	30	9	34993	5,88	NP_742146.1	Q8K183	Pdxk	gi 26006861	pyridoxal (pyridoxine, vitamin B6) kinase
5673	-21,06	0,020	77	5	2	31361	5,64	NP_081269.1	Q9CWS0	Ddah1	gi 38371755	dimethylarginine dimethylaminohydrolyase 1
5673	-21,06	0,020	41	2	1	54295	8,46	BAC39931.1	Q8BIU1	Chdh	gi 26352602	Choline dehydrogenase, mitochondrial precursor
6352	-14,38	0,018	86	23	7	43968	6,79	NP_077752.1	Q99PL6	Ubx1	gi 16741117	Ubx1 protein
1629	-24,04	0,001	224	23	5	17264	5,76	NP_062615.1	Q545B6	Stmn1	gi 9789995	stathmin 1
1629	-24,04	0,001	42	0	1	124373	6,77	NP_032865.1	P42337	Pik3ca	gi 6679317	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide
5105	-14,27	0,027	92	41	10	23560	9,46	NP_878259.1	Q7TQD2	Tppp	gi 33469051	tubulin polymerization-promoting protein
4151	-16,15	0,001	104	23	12	67588	7,23	NP_033414.1	P40142	Tkt	gi 6678359	transketolase
1339	-17,78	0,015	637	57	10	23300	4,66	NP_035558.1	P60879	Snap25	gi 6755588	synaptosomal-associated protein 25
6294	-22,89	0,026	68	11	1	12853	5,27	NP_032124.1	P62774	Mtpn	gi 6679961	myotrophin
5129	-11,86	0,022	73	38	9	25340	9,80	NP_663570.1	Q91VT4	Cbr4	gi 21704190	carbonic reductase 4
5020		0,027	201	37	19	32621	9,51	NP_057918.2	Q9JLZ3	Auh	gi 20072952	Auh protein
1634	-19,45	0,012	53	6	1	17264	5,76	NP_062615.1	Q545B6	Stmn1	gi 9789995	stathmin 1
4638	-10,59	0,007	137	61	17	35695	6,71	NP_033788.3	P45376	Akr1b1	gi 3046247	aldose reductase

4554	-10,19	0,012	142	57	16	39331	8,31	NP_031464.1	Q5FWB7	Aldoa	gi 6671539	aldolase 1, A isoform
4554	-10,19	0,012	95	36	14	42168	8,76	NP_570954.1	Q91VA7	Idh3b	gi 18700024	isocitrate dehydrogenase 3, beta subunit
5816	-16,05	0,032	436	51	9	17264	5,76	NP_062615.1	Q545B6	Stmn1	gi 9789995	stathmin 1
5724	-18,79	0,030	462	45	7	14476	4,74	NP_033247.1	O55042	Snca	gi 6678047	synuclein, alpha
1163	-15,44	0,022	343	21	6	30325	5,04	NP_076253.1	Q9QZ06	Tollip	gi 13591860	toll interacting protein
1647	-15,33	0,029	119		2	15394	5,09	NP_034076.1	P84086	Cplx2	gi 6753508	complexin 2 .
4748	-7,77	0,006	215	65	18	35589	8,93	NP_032643.2	P08249	Mdh2	gi 31982186	malate dehydrogenase 2, NAD (mitochondrial)
4556	-7,89	0,000	64	29	6	30404	8,73	XP_926838.1		LOC633657	gi 82956953	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3 isoform 4
4188	-7,78	0,010	114	25	14	67659	6,62	NP_033321.2	O08599	Stxbp1	gi 6678179	syntaxin binding protein 1
809	-11,56	0,005	227	11	3	42981	5,69	NP_032707.2	Q62433	Ndrp1	gi 6754810	N-myc downstream regulated gene 1
809	-11,56	0,005	134	8	2	35397	6,08	AAD00176.1	Q9Z1D1	Eif3s4	gi 4097873	eIF3-p44
4800	-9,09	0,021	162	50	12	31299	6,70	NP_058599.1	Q9R0P3	Esd	gi 13937355	esterase D/formylglutathione hydrolase
4221	-8,09	0,040	119	22	11	62142	6,39	NP_031791.3	P97427	Crmp1	gi 1915915	Ulip3 protein
5219	-9,98	0,020	73	32	5	20343	6,95	NP_062692.1	Q9WUL7	Arl3	gi 12084691	Chain A, Crystal Structure Of Murine Arl3-Gdp
5813	-12,75	0,022	152	16	2	16278	5,47	NP_080645.1	Q9CPW4	Arpc5	gi 62510460	Actin-related protein 2/3 complex subunit 5
4809	-9,98	0,013	99	43	12	37459	8,91	BAE28433.1	Q3UFX6	Mgll	gi 74201613	unnamed protein product
714	-9,79	0,008	574	27	10	50134	4,94	AAA40500.1	P05213	Tuba2	gi 202210	alpha-tubulin isotype M-alpha-2
714	-9,79	0,008	374	18	7	49761	4,95	NP_033473.1	P68368	Tuba4a	gi 6678467	tubulin, alpha 4
714	-9,79	0,008	222	11	4	53689	5,06	CAA39807.1	P20152	Vim	gi 55408	vimentin
856	-8,63	0,039	183	9	3	49784	4,64	AAK68859.1	Q91VI7	Rnh1	gi 31981748	ribonuclease/angiogenin inhibitor 1
6345	-5,59	0,014	168	39	17	59758	8,10	BAE21910.1	Q3UZE7	Cat	gi 74228849	unnamed protein product
5619	-4,88	0,029	162	70	13	14948	8,46	NP_035202.1	P62962	Pfn1	gi 6755040	profilin 1
4361	-5,41	0,017	83	25	11	50422	9,11	NP_031932.1	P62631	Eef1a2	gi 6681273	eukaryotic translation elongation factor 1 alpha 2
4361	-5,41	0,017	80	24	10	50140	9,04	NP_034236.2	P10126	Eef1a1	gi 13278382	Eukaryotic translation elongation factor 1 alpha 1

679	-7,81	0,003	415	17	8	57108	4,79	AAA39906.1	P09103	P4hb	gi 129729	Protein disulfide-isomerase precursor (PDI)
679	-7,81	0,003	166	9	2	45862	5,44	NP_033273.1	Q00898	Serpina1e	gi 6678087	serine (or cysteine) proteinase inhibitor, clade A, member 1e
679	-7,81	0,003	51	3	1	49639	4,78	NP_035785.1	P99024	Tubb5	gi 7106439	tubulin, beta 5
679	-7,81	0,003	44	0	1	191727	8,08	AAA37182.1	Q01341	Adcy6	gi 191727	adenylyl cyclase, type 6
4816	-4,22	0,039	137	61	15	30737	8,62	NP_035824.1	Q60932	Vdac1	gi 6755963	voltage-dependent anion channel 1
4816	-4,22	0,039	109	48	14	31713	7,44	NP_035825.1	Q60930	Vdac2	gi 6755965	voltage-dependent anion channel 2
1917	-8,85	0,034	83		1	9725	4,7	AAH66015.1	Q6NZQ3	Snrpf	GI:41946811	small nuclear ribonucleoprotein polypeptide F
707	-6,29	0,014	534	19	9	49639	4,78	NP_035785.1	P99024	Tubb5	gi 7106439	tubulin, beta 5
707	-6,29	0,014	532	20	9	49783	4,79	AAH05547.1	P68372	Tubb2c	gi 13542680	Tubulin, beta 2c
707	-6,29	0,014	515	19	9	49921	4,78	NP_076205.1	Q9CWF2	Tubb2b	gi 21746161	tubulin, beta
707	-6,29	0,014	411	16	7	50386	4,82	NP_075768.1	Q9ERD7	Tubb3	gi 12963615	tubulin, beta 3
707	-6,29	0,014	143	9	3	49877	4,96	NP_033474.1	P68373	Tuba1c	gi 6678469	tubulin, alpha 6
707	-6,29	0,014	114	7	2	49761	4,95	NP_033473.1	P68368	Tuba4a	gi 6678467	tubulin, alpha 4
882	-6,54	0,030	901	45	15	40992	5,56	CAA31455.1	P63260	Actb	gi 809561	gamma-actin
882	-6,54	0,030	886	47	15	39161	5,78	CAA27396.1	P63260	Actb	gi 49868	put. beta-actin (aa 27-375)
882	-6,54	0,030	876	42	15	41773	5,9	AAA37168.1	P63260	ACTG	gi 54036677	Actin, cytoplasmic 2 (Gamma-actin)
882	-6,54	0,030	823	41	14	41742	5,29	NP_031419.1	P60710	ACTB	gi 46397334	Actin, cytoplasmic 1 (Beta-actin)
882	-6,54	0,030	89	8	1	19450	4,76	NP_033455.1	P63028	Tpt1	gi 6678437	tumor protein, translationally-controlled 1
4275	-3,59	0,024	108	40	18	55953	8,73	NP_077150.1	Q9D0K2	Oxct1	gi 18266680	3-oxoacid CoA transferase 1
4275	-3,59	0,024	106	38	18	56150	7,14	NP_077754.2	Q9CPY7	Lap3	gi 31981147	leucine aminopeptidase 3
275	-5,86	0,014	820	19	13	94021	5,13	AAH03770.1	Q99L75	Hspa4	gi 13277753	Heat shock protein 4
5217	4,21	0,044	1227	28	20	94325	5,5	AAC52610.1	P48722	Hspa41	gi 1098541	osmotic stress protein 94
1382	4,89	0,033	236	20	4	19450	4,76	NP_033455.1	P63028	Tpt1	gi 6678437	tumor protein, translationally-controlled 1
744	5,08	0,002	1280	45	19	56632	5,24	AAH37127.1	P56480	Atp5b	gi 23272966	Atp5b protein
744	5,08	0,002	162	12	3	39161	5,78	CAA27396.1	P60710	Actb	gi 49868	put. beta-actin (aa 27-375)
821	5,63	0,030	562	35	10	42686	5,4	NP_067248.1	Q04447	Ckb	gi 10946574	creatine kinase, brain
821	5,63	0,030	45	9	1	13658	7,82	AAK16238.1	P60521	GBRL2	gi 31542873	gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2

1446	5,96	0,011	189	22	3	20847	5,19	AAB06983.1	P70296	PEBP-1	gi 1517864	phosphatidylethanolamine binding protein
1213	5,36	0,041	434	27	7	27813	4,63	AAH39635.1	O70251	Eef1b2	gi 24586721	eukaryotic translation elongation factor 1 beta 2
446	5,45	0,016	906	26	15	79726	5,51	BAC29641.1	Q91VD9	Ndufs1	gi 26331822	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor (Complex I-75kD)
5475	4,07	0,002	225	69	15	21884	9,10	NP_036151.1	P99029	Prdx5	gi 6755114	peroxiredoxin 5 precursor
855	6,42	0,022	731	43	12	42686	5,4	NP_067248.1	Q04447	Ckb	gi 10946574	creatine kinase, brain
480	6,98	0,046	658	16	12	79698	5,51	NP_663493.1	Q91VD9	Ndufs1	gi 21704020	NADH dehydrogenase (ubiquinone) Fe-S protein 1
5703	4,87	0,009	90	56	10	13351	7,82	NP_080890.1	Q9CPP6	Ndufa5	gi 13386100	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5
822	8,21	0,028	376	20	6	41492	5,53	NP_038692.1	Q62419	Sh3gl1	gi 7305485	SH3-domain GRB2-like 1
822	8,21	0,028	167	9	3	42686	5,4	NP_067248.1	Q04447	Ckb	gi 10946574	creatine kinase, brain
822	8,21	0,028	37	3	1	25245	8,7	NP_064336.1	Q3SXX2	Clcf1	gi 9910314	cardiotrophin-like cytokine factor 1
5668	8,26	0,020	557	24	10	37754	5,42	NP_075629.2	Q9CQM9	Txn12	gi 31981269	thioredoxin-like 2
5668	8,26	0,020	52	6	1	20049	5,14	AAH05788.1	Q99JN5	Cnn3	gi 13543244	Cnn3 protein
5668	8,26	0,020	38	0	1	124373	6,77	NP_032865.1	P42337	Pik3ca	gi 6679317	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide
5796	7,16	0,039	110	90	10	9321	9,52	NP_035016.1	Q62425	Ndufa4	gi 33563266	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4
5771	8,87	0,015	103	45	7	9321	9,52	NP_035016.1	Q62425	Ndufa4	gi 33563266	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4
1129	9,98	0,043	123	15	2	24560	4,65	NP_084090.1	Q9D7S9	Chmp5	gi 13386442	chromatin modifying protein 5
1129	9,98	0,043	134	9	2	29646	5,06	NP_997611.1	Q8BHL8	Psmf1	gi 47078287	proteasome inhibitor subunit 1 isoform a
481	8,82	0,007	1026	25	17	79726	5,51	BAC29641.1	Q91VD9	Ndufs1	gi 26331822	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor (Complex I-75kD)
3901	9,45	0,042	340	8	5	79698	5,51	NP_663493.1	Q91VD9	Ndufs1	gi 21704020	NADH dehydrogenase (ubiquinone) Fe-S protein 1
6110	12,08	0,007	189	25	2	15112	4,93	AAH14803.1	P63040	Cplx1	gi 31542416	complexin 1
5465	5,61	0,024	136	64	13	17076	9,38	BAB26955.2	Q7TMF3	Ndufa12	gi 47117166	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

4529	-11,14	0,010	215	42	19	42721	6,21	NP_998779.2	Q9Z2Q6	Sept5	gi 83305642	Septin-5 (Peanut-like protein 1) (Cell division control-related protein 1)
4120	7,12	0,033	135	37	33	82617	9,24	NP_849209.1	Q8BMS1	Hadha	gi 33859811	mitochondrial trifunctional protein, alpha subunit
5335	-8,64	0,047	111	49	8	16970	6,32	NP_083085.1	Q9D898	Arpc5l	gi 21312654	actin related protein 2/3 complex, subunit 5-like
4528	8,44	0,012	157	57	17	39370	6,67	NP_033787.2	P05063	Aldoc	gi 60687506	aldolase 3, C isoform
4528	8,44	0,012	70	31	10	46202	6,68	NP_034454.1	P05201	Got1	gi 6754034	glutamate oxaloacetate transaminase 1, soluble
4519	-8,70	0,041	131	36	15	49626	6,88	BAE43095.1	Q3T9C9	Acot2	gi 74196709	unnamed protein product
1223	16,26	0,004	472	27	8	38912	6,41	NP_077183.1	Q9D051	Pdhb	gi 18152793	pyruvate dehydrogenase (lipoamide) beta
4576	10,36	0,023	244	58	26	39370	6,67	NP_033787.2	P05063	Aldoc	gi 60687506	aldolase 3, C isoform
544	18,47	0,035	1146	31	20	61471	4,62	NP_035040.1	P08551	Nefl	gi 39204499	neurofilament, light polypeptide
544	18,47	0,035	46	2	1	69684	5,58	P17156	S10859	HSP70	gi 109946	dnaK-type molecular chaperone HSP70.2
4558	10,78	0,003	121	40	15	46203	6,68	NP_034454.1	P05201	Got1	gi 871422	aspartate aminotransferase
4558	10,78	0,003	81	36	11	39370	6,67	NP_033787.2	P05063	Aldoc	gi 60687506	aldolase 3, C isoform
144	18,61	0,026	270	35	30	95728	4,76	AAI19603.1	P08553	Nefm	gi 111185724	Nef3 protein
144	18,61	0,026	692	15	13	95728	4,76	AAI19603.1	P08553	Nefm	gi 111185724	Nef3 protein
536	16,42	0,032	401	19	7	58641	4,85	NP_689420.1	Q8R317	Ubqln1	gi 22726191	ubiquilin 1 isoform 2
536	16,42	0,032	154	5	3	61485	4,63	AAA39814.1	P08551	NFL	gi 200038	neurofilament-L
129	18,66	0,039	205	29	24	95728	4,76	AAI19603.1	P08553	Nefm	gi 111185724	Nef3 protein
164	19,10	0,021	275	37	32	95728	4,76	AAI19603.1	P08553	Nefm	gi 111185724	Nef3 protein
125	19,54	0,031	222	31	25	95728	4,76	AAI19603.1	P08553	Nefm	gi 111185724	Nef3 protein
6138	21,80	0,042	303	51	5	11923	5,02	NP_038673.2	P32848	Pvalb	gi 31980767	parvalbumin
5688	16,93	0,008	81	51	5	11039	6,82	NP_031819.1	Q62426	Cstb	gi 6681071	cystatin B
3899	22,57	0,023	378	11	7	79698	5,51	NP_663493.1	Q91VD9	Ndufs1	gi 21704020	NADH dehydrogenase (ubiquinone) Fe-S protein 1
4119	26,76	0,041	72	20	15	67694	6,34	BAE34156.1	Q3TZQ2	Msn	gi 74186081	unnamed protein product

MPTP 7d C57BL6/J

Spot-nummer	% KO zu WT	p-Wert	Mowse Score	Sequenzabdeckung (%)	Anzahl gefundener Peptide	Theoretische Masse	Theoretischer pI	Ensemble ID	Swiss-prot ID	Gen-symbol	NCBI Accessnummer	Protein Name
693	-53,62	0,041	117	33	11	35322	6,11	NP_075602.2	Q8R3P0	Aspa	gi 31560279	aspartoacylase (aminoacylase) 2
1736	-24,69	0,013	223	95	14	15753	7,14	NP_032246.2	P02088	Hbb-b1	gi 12846921	unnamed protein product
4455	-41,51	0,033	96	36	7	28711	5,44	NP_038913.1	Q9QYB1	Clic4	gi 7304963	chloride intracellular channel 4 (mitochondrial)
1645	-41,51	0,014	64	35	5	14154	9,24	NP_077182.1	Q9CQ54	Ndufc2	gi 18859597	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2
1691	-33,40	0,022	90	57	11	11915	7,88	NP_032045.1	P26883	Fkbp1a	gi 6679803	FK506 binding protein 1a
1691	-33,40	0,022	83	66	9	15607	7,27	NP_032246.2	P02088	Hbb-b1	gi 18655687	Chain B, Chimeric HumanMOUSE CARBONMONOXY HEMOGLOBIN
4305	-35,91	0,022	264	57	20	26784	5,07	NP_080270.2	Q8C845	Efhd2	gi 31981086	EF hand domain containing 2
4451	-32,21	0,018	86	37	9	24249	4,67	NP_694723.1	Q8JZL3	Thtpa	gi 23346499	thiamine triphosphatase
1712	-18,82	0,011	163	77	13	15607	7,27	NP_032246.2	P02088	Hbb-b1	gi 18655687	Chain B, Chimeric HumanMOUSE CARBONMONOXY HEMOGLOBIN
1671	-26,68	0,025	203	95	15	15607	7,27	NP_032246.2	P02088	Hbb-b1	gi 18655687	Chain B, Chimeric HumanMOUSE CARBONMONOXY HEMOGLOBIN
1723	-20,37	0,026	133	91	9	15103	7,96	BAB27381.1	Q9CY06	Hba-a1	gi 12846963	unnamed protein product
807	-17,76	0,019	71	23	5	30512	9,35	XP_896535.1	Q9CX86	Hnrpa0	gi 82950644	PREDICTED: heterogeneous nuclear ribonucleoprotein A0 isoform 2
1710	-23,31	0,048	141	83	11	15103	7,96	BAB27381.1	Q9CY06	Hba-a1	gi 12846963	unnamed protein product
3454	-14,87	0,007	250	53	35	68678	5,75	NP_033784.2	P07724	Alb1	gi 33859506	albumin 1
3454	-14,87	0,007	80	31	17	62239	5,95	NP_034085.2	O08553	Dpysl2	gi 40254595	dihydropyrimidinase-like 2
222	-10,93	0,001	148	27	25	85400	6,73	NP_062677.1	Q9WUA3	Pfcp	gi 9790051	phosphofructokinase, platelet
3450	-13,04	0,003	97	22	10	68678	5,75	NP_033784.2	P07724	Alb1	gi 33859506	albumin 1
694	-13,25	0,017	141	45	12	35815	8,44	NP_032110.1	P16858	Gapdh	gi 62201487	Similar to glyceraldehyde-3-phosphate dehydrogenase

698	-10,63	0,039	142	54	24	35815	8,44	NP_032110.1	P16858	Gapdh	gi 62201487	Similar to glyceraldehyde-3-phosphate dehydrogenase
698	-10,63	0,039	63	40	11	33445	7,71	NP_033463.1	P52196	Tst	gi 6678449	thiosulfate sulfurtransferase, mitochondrial
2289	-6,56	0,028	320	68	27	46219	6,68	NP_034454.2	Q3UJH8	Got1	gi 74138724	unnamed protein product
1028	-7,20	0,022	74	13	11	104516	5,22	NP_082191.1	Q5SWR1	Ap2b1	gi 21313640	adaptor-related protein complex 2, beta 1 subunit isoform b
4486	-7,21	0,028	188	64	17	28711	5,44	NP_038913.1	Q9QYB1	Clic4	gi 7304963	chloride intracellular channel 4 (mitochondrial)
3857	-6,57	0,039	188	50	17	46628	6,50	XP_001052621.1	Q61598	Gdi2	gi 94394631	PREDICTED: guanosine diphosphate (GDP) dissociation inhibitor 2 isoform 1
755	-5,87	0,020	235	62	17	35589	8,93	NP_032643.2	P08249	Mdh2	gi 31982186	malate dehydrogenase 2, NAD (mitochondrial)
1373	-8,39	0,044	120	52	9	17352	6,97	NP_032731.1	Q01768	Nme2	gi 6679078	nucleoside-diphosphate kinase 2
1870	-10,75	0,022	94	54	6	10065	8,96	NP_079904.1	P56391	Cox6b1	gi 13385090	cytochrome c oxidase, subunit Vib polypeptide 1
2565	3,11	0,026	288	48	27	47381	9,13	NP_034455.1	P05202	Got2	gi 6754036	glutamate oxaloacetate transaminase 2, mitochondrial
2564	3,77	0,044	255	55	29	47381	9,13	NP_034455.1	P05202	Got2	gi 6754036	glutamate oxaloacetate transaminase 2, mitochondrial
772	4,72	0,027	251	67	22	35589	8,93	NP_032643.2	P08249	Mdh2	gi 31982186	malate dehydrogenase 2, NAD (mitochondrial)
269	5,49	0,007	200	41	24	61477	6,62	NP_075534.1	Q9EQF6	Dpysl5	gi 12746424	dihydropyrimidinase-like 5
3532	5,73	0,046	103	21	11	50944	5,39	NP_079555.1	P61979	Hnrpk	gi 13384620	heterogeneous nuclear ribonucleoprotein K
3622	6,93	0,041	168	43	17	49877	4,96	NP_033474.1	P68373	Tuba1c	gi 6678469	tubulin, alpha 6
3622	6,93	0,041	63	22	9	49554	4,78	NP_006078.2	P04350	Tubb4	gi 21361322	tubulin, beta 4
4551	6,00	0,003	105	35	10	25080	5,81	NP_598661.1	Q99LS3	Psph	gi 19527116	phosphoserine phosphatase
3533	6,43	0,011	199	27	20	67903	8,81	NP_663589.2	Q8BMF4	Dlat	gi 31542559	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)
786	6,50	0,011	218	67	21	35589	8,93	NP_032643.2	P08249	Mdh2	gi 31982186	malate dehydrogenase 2, NAD (mitochondrial)
2167	6,74	0,033	198	51	25	54322	9,12	BAE27597.1	Q3UIA9	Fh1	gi 74150922	unnamed protein product
2167	6,74	0,033	118	43	19	43204	8,49	NP_032836.1	P35486	Pdha1	gi 6679261	pyruvate dehydrogenase E1 alpha 1

3522	9,33	0,008	169	39	23	67903	8,81	NP_663589.2	Q8BMF4	Dlat	gi 31542559	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)
3941	9,27	0,022	203	57	28	42686	5,40	NP_067248.1	Q04447	Ckb	gi 10946574	creatine kinase, brain
4345	8,65	0,003	155	52	18	30609	5,69	NP_004921.1	P47756	Capzb	gi 4826659	F-actin capping protein beta subunit
3614	12,39	0,015	173	39	15	50104	4,94	NP_035783.1	P68369	Tuba1a	gi 6755901	tubulin, alpha 1
4562	14,56	0,003	95	27	8	26784	5,07	NP_080270.2	Q8C845	Efh2	gi 31981086	EF hand domain containing 2
2277	15,29	0,028	244	55	22	49477	7,23	NP_766333.1	Q8BFR5	Tufm	gi 27370092	Tu translation elongation factor, mitochondrial
4766	14,33	0,004	131	46	11	21053	5,53	NP_034369.1	P09528	Fth1	gi 6753912	ferritin heavy chain 1
841	15,70	0,008	112	52	12	30737	8,62	NP_035824.1	Q60932	Vdac1	gi 6755963	voltage-dependent anion channel 1
952	13,74	0,027	127	45	10	30864	8,96	AAH89336.1	Q5EBQ0	Vdac3	gi 59807690	Voltage-dependent anion channel 3
780	19,72	0,007	192	56	21	32440	8,74	NP_872591.1	O88569	Hnrpa2b1	gi 32880197	heterogeneous nuclear ribonucleoprotein A2/B1 isoform 2
1022	33,32	0,014	77	38	11	31454	8,76	NP_444349.1	Q8BH95	Echs1	gi 29789289	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial

MPTP 1d L1cam C57BL6/J

Spot-nummer	% KO zu WT	p-Wert	Mowse Score	Sequenzabdeckung (%)	Anzahl gefundener Peptide	Theoretische Masse	Theoretischer pI	Ensemble ID	Swiss-prot ID	Gen-symbol	NCBI Accessnummer	Protein Name
769	-34,78	0,012	44	1	1	56344	5,14	AAB86421.1	P56480	Atp5b	gi 2623222	ATP synthase beta-subunit
1757	-40,25	0,048	148	25	3	14476	4,74	NP_033247.1	O55042	Snca	gi 6678047	synuclein, alpha
3493	-33,80	0,001	56	7	1	13363	5,3	NP_079657.1	Q9D1K2	Atp6v1f	gi 12834081	ATPase, H ⁺ transporting, V1 subunit F
3931	-32,27	0,006	667	27	11	56632	5,24	AAH37127.1	P56480	Atp5b	gi 23272966	Atp5b protein
1716	-29,37	0,005	571	38	9	14043	4,38	NP_291088.1	Q91ZZ3	Sncb	gi 15809030	synuclein, beta
3928	-29,11	0,014	171	4	3	56344	5,14	AAB86421.1	P56480	Atp5b	gi 2623222	ATP synthase beta-subunit
3929	-25,54	0,024	734	24	12	56632	5,24	AAH37127.1	P56480	Atp5b	gi 23272966	Atp5b protein
1029	-22,25	0,003	106	7	2	39547	5,28	AAF31669.1	Q9JKK7	Tmod2	gi 6934242	tropomodulin 2
780	-21,08	0,002	252	9	5	44090	5,14	NP_081427.1	Q99KJ8	Dctn2	gi 28076935	dynactin 2
1135	-21,20	0,004	50	3	1	50944	5,39	NP_079555.1	P61979	Hnrpk	gi 13384620	heterogeneous nuclear ribonucleoprotein K
2058	-22,76	0,018	75	10	1	10470	5,02	NP_542126.1	Q91VW3	Sh3bgrl3	gi 18017602	SH3 domain binding glutamic acid-rich protein-like 3
206	-31,42	0,039	128	35	17	74052	9,81	NP_038708.3	O88935	Syn1	gi 73920802	Synapsin-1 (Synapsin I)
1154	-31,46	0,010	98	37	7	23560	9,46	NP_878259.1	Q7TQD2	Tppp	gi 33469051	tubulin polymerization-promoting protein
1129	-28,14	0,005	116	37	8	23560	9,46	NP_878259.1	Q7TQD2	Tppp	gi 33469051	tubulin polymerization-promoting protein
3336	-16,25	0,014	478	12	7	72412	5,09	BAA11462.1	P20029	Hspa5	gi 1304157	78 kDa glucose-regulated protein
616	-25,77	0,012	86	26	8	39628	9,10	NP_666242.2	Q8BG05	Hnrpa3	gi 31559916	heterogeneous nuclear ribonucleoprotein A3 isoform b
1325	-19,98	0,033	68	28	5	16970	6,32	NP_083085.1	Q9D898	Arpc5l	gi 21312654	actin related protein 2/3 complex, subunit 5-like
1936	-25,66	0,017	78	59	6	8967	6,59	NP_032709.1	P29595	Nedd8	gi 6679034	neural precursor cell expressed, developmentally down-regulated gene 8
874	-22,04	0,025	218	55	20	33276	9,83	NP_009204.1	Q99623	Phb2	gi 6005854	prohibitin 2
1239	-20,97	0,035	134	61	19	22456	6,84	NP_062728.1	Q9R1Q8	Tagln3	gi 9790125	transgelin 3
892	-13,01	0,006	116	7	2	32698	4,74	NP_035159.2	P14206	Rpsa	gi 125970	40S ribosomal protein SA (p40) (34/67 kDa laminin receptor)

1128	-21,38	0,007	66	41	7	23560	9,46	NP_878259.1	Q7TQD2	Tppp	gi 33469051	tubulin polymerization-promoting protein
1441	-23,75	0,048	84	53	11	18509	8,14	NP_062745.1	Q9R0P5	Dstn	gi 9790219	destrin
1441	-23,75	0,048	66	32	7	17960	7,74	NP_032933.1	P17742	Ppia	gi 6679439	peptidylprolyl isomerase A
1441	-23,75	0,048	52	50	6	17352	6,97	NP_032731.1	Q01768	Nme2	gi 6679078	nucleoside-diphosphate kinase 2
891	-17,63	0,022	148	53	19	26141	8,44	NP_031536.2	P50518	Atp6v1e1	gi 45504359	vacuolar H+ ATPase E1
843	-24,45	0,041	167	61	17	30737	8,62	NP_035824.1	Q60932	Vdac1	gi 6755963	voltage-dependent anion channel 1
1582	-12,31	0,022	361	44	6	18738	5,52	NP_082138.1	Q9DCX2	Atp5h	gi 21313679	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d
1582	-12,31	0,022	44	8	1	18510	5,33	XP_136323.1	B1ASE2	LOC240853	gi 20830329	PREDICTED: similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d isoform 1
1955	-11,06	0,047	100	16	2	16020	6,08	NP_031773.2	P12787	Cox5a	gi 117099	Cytochrome c oxidase subunit 5A, mitochondrial precursor
886	-23,77	0,030	281	72	28	26141	8,44	NP_031536.2	P50518	Atp6v1e1	gi 45504359	vacuolar H+ ATPase E1
680	-11,01	0,024	366	11	5	60918	5,67	NP_034607.2	P63038	Hspd1	gi 31981679	heat shock protein 1 (chaperonin)
680	-11,01	0,024	50	4	1	39575	5,06	XP_983732.1	Q803B0	hspd1	gi 94373522	PREDICTED: similar to heat shock protein 1 (chaperonin)
1436	-15,56	0,032	76	36	8	14035	8,67	NP_065615.1	Q8R3R8	Gabarapl1	gi 10181206	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1
1637	-8,43	0,016	113	10	2	21792	5,2	AAA69475.1	Q61171	tpx	gi 885932	peroxidase
1430	-11,13	0,035	92	51	7	18815	8,77	AAI07209.1	Q3KNM9	Apoo	gi 76825443	0610008C08Rik protein
1430	-11,13	0,035	56	20	5	22162	8,26	NP_035164.1	B1AXW7	Prdx1	gi 6754976	peroxiredoxin 1
675	-7,46	0,045	462	17	8	60918	5,67	NP_034607.2	P63038	Hspd1	gi 31981679	heat shock protein 1 (chaperonin)
675	-7,46	0,045	129	6	2	39575	5,06	XP_983732.1	Q803B0	hspd1	gi 94373522	PREDICTED: similar to heat shock protein 1 (chaperonin)
1770	-14,28	0,047	72	33	6	25014	5,72	NP_796230.1	Q8BG37	Prdx6-rs1	gi 116643146	peroxiredoxin 6, related sequence 1

420	-12,04	0,023	434	65	44	59716	9,22	NP_031531.1	Q03265	Atp5a1	gi 6680748	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1
1049	-9,02	0,001	252	81	30	28814	6,67	XP_985088.1	Q9DBJ1	Pgam1	gi 94369185	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B)
1296	-6,67	0,021	101	36	8	23260	9,48	NP_079992.1	Q91WK1	Spryd4	gi 58037095	SPRY domain containing 4
1757	-7,27	0,013	114	58	9	13351	7,82	NP_080890.1	Q9CPP6	Ndufa5	gi 13386100	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5
555	-7,02	0,034	299	52	30	48205	9,26	NP_080175.1	Q9DB77	Uqcr2	gi 22267442	ubiquinol cytochrome c reductase core protein 2
1512	-5,42	0,030	139	62	14	17197	6,84	NP_032730.1	P15532	Nme1	gi 37700232	nucleoside-diphosphate kinase 1
2496	8,40	0,047	124	35	15	50132	9,10	AAA50406.1	P10126	Eef1a1	gi 556301	elongation factor Tu
2110	9,51	0,036	404	63	40	67588	7,23	NP_033414.1	P40142	Tkt	gi 6678359	transketolase
354	11,75	0,023	197	41	24	54238	7,99	NP_031887.2	O08749	Dld	gi 31982856	dihydroliipoamide dehydrogenase
354	11,75	0,023	97	40	16	43138	5,88	NP_035229.2	P52480	Pkm2	gi 74212815	unnamed protein product
2055	12,38	0,049	300	40	31	85410	8,08	NP_542364.1	Q99KI0	Aco2	gi 18079339	aconitase 2, mitochondrial
349	11,85	0,049	114	36	17	57808	7,18	NP_035229.2	P52480	Pkm2	gi 2506796	pyruvate kinase 3
349	11,85	0,049	90	27	13	54238	7,99	NP_031887.2	O08749	Dld	gi 31982856	dihydroliipoamide dehydrogenase
339	13,16	0,032	311	64	35	57808	7,18	NP_035229.2	P52480	Pkm2	gi 2506796	pyruvate kinase 3
2059	12,33	0,049	290	44	37	85410	8,08	NP_542364.1	Q99KI0	Aco2	gi 18079339	aconitase 2, mitochondrial
2117	12,04	0,038	250	52	33	61477	6,62	NP_075534.1	Q9EQF6	Dpysl5	gi 12746424	dihydropyrimidinase-like 5
2113	13,15	0,045	208	40	24	67588	7,23	NP_033414.1	P40142	Tkt	gi 6678359	transketolase
2113	13,15	0,045	189	49	31	61477	6,62	NP_075534.1	Q9EQF6	Dpysl5	gi 12746424	dihydropyrimidinase-like 5
508	11,19	0,047	160	41	19	42092	6,64	NP_032157.2	P15105	Glul	gi 31982332	glutamine synthetase
2057	14,71	0,011	351	48	38	85410	8,08	NP_542364.1	Q99KI0	Aco2	gi 18079339	aconitase 2, mitochondrial
267	15,13	0,021	216	48	29	68692	6,32	AAH31728.1	O08599	Stxbp1	gi 4507297	syntaxin binding protein 1 isoform a
445	14,88	0,046	207	48	26	56416	8,35	NP_766549.2	P61922	Abat	gi 37202121	4-aminobutyrate aminotransferase
203	16,33	0,041	105	27	16	79432	8,76	NP_032318.2	P51660	Hsd17b4	gi 31982273	hydroxysteroid (17-beta) dehydrogenase 4
230	17,59	0,014	324	47	33	82617	9,24	NP_849209.1	Q8BMS1	Hadha	gi 33859811	mitochondrial trifunctional protein, alpha subunit

231	18,88	0,021	335	45	39	82617	9,24	NP_849209.1	Q8BMS1	Hadha	gi 33859811	mitochondrial trifunctional protein, alpha subunit
208	20,78	0,042	217	29	21	85249	8,24	NP_067489.2	Q99K08	Pfkm	gi 31981185	phosphofructokinase, muscle
119	23,65	0,013	120	15	14	116375	6,36	NP_035086.2	Q60597	Ogdh	gi 85861164	oxoglutarate dehydrogenase (lipoamide)
1644	25,76	0,004	90	51	7	14154	9,24	NP_077182.1	Q9CQ54	Ndufc2	gi 18859597	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2
550	23,16	0,032	240	39	20	44626	8,71	BAA07622.1	P16330	Cnp1	gi 2160434	2',3'-cyclic-nucleotide 3'-phosphodiesterase I
480	15,53	0,018	118	4	2	62132	5,95	CAA71370.1	O08553	Ulip2	gi 1915913	Ulip2 protein
125	26,02	0,027	137	21	15	102025	7,08	NP_062750.2	Q78PY7	Snd1	gi 77404392	staphylococcal nuclease domain containing 1
947	22,81	0,015	277	12	6	41758	5,23	AAA37167.1	P68033	Aczc1	gi 387090	alpha-cardiac actin
562	31,78	0,028	278	48	26	44626	8,71	BAA07622.1	P16330	Cnp1	gi 2160434	2',3'-cyclic-nucleotide 3'-phosphodiesterase I
478	25,83	0,006	90	3	2	68648	5,75	NP_033784.2	P07724	Alb	gi 5915682	Serum albumin precursor
996	91,76	0,004	66	34	7	40578	7,63	NP_077159.1	Q99LC3	Ndufa10	gi 13195624	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10

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Spot-nummer	% KO zu WT	p-Wert	Mowse Score	Sequenzabdeckung (%)	Anzahl gefundener Peptide	Theoretische Masse	Theoretischer pI	Ensemble ID	Swissprot ID	Gen-symbol	NCBI Accessnummer	Protein Name
2007	-32,75	0,008	147	33	2	15122	4,93	NP_031782.2	P63040	Cplx1	gi 31542416	complexin 1
1313	-59,25	0,037	618	40	11	26784	5,07	NP_080270.2	Q8C845	Efhd2	gi 31981086	EF hand domain containing 2
1856	-45,71	0,007	291	31	5	19784	4,9	NP_062278.2	Q9R1K9	Cetn2	gi 10257421	centrin 2
1290	-49,82	0,018	420	29	8	26784	5,07	NP_080270.2	Q8C845	Efhd2	gi 31981086	EF hand domain containing 2
1290	-49,82	0,018	42	0	1	152498	5,67	NP_032503.2	Q61595	Ktn1	gi 6678650	kinectin 1
196	-41,17	0,046	723	24	12	69992	9,84	AAD09833.1	O88935	SynI	gi 3599473	synapsin Ib
196	-41,17	0,046	35	1	1	63191	5,23	NP_032011.2	Q8CBR3	Fancc	gi 111185909	Fanconi anemia, complementation group C
1367	-50,29	0,045	410	30	7	29003	4,75	CAA37782.1	P21107	Tpm5	gi 54912	Tropomyosin 5
1919	-42,44	0,004	71	8	1	17264	5,76	NP_062615.1	Q545B6	Stmn1	gi 9789995	stathmin 1
1905	-46,31	0,003	117	15	2	17264	5,76	NP_062615.1	Q545B6	Stmn1	gi 9789995	stathmin 1
801	-42,19	0,004	887	36	14	56632	5,24	AAH37127.1	P56480	Atp5b	gi 23272966	Atp5b protein
1899	-38,15	0,003	334	39	7	17264	5,76	NP_062615.1	Q545B6	Stmn1	gi 9789995	stathmin 1
1054	-41,98	0,002	553	25	10	39547	5,28	AAF31669.1	Q9JKK7	Tmod2	gi 6934242	tropomodulin 2
1054	-41,98	0,002	67	3	1	41492	5,53	NP_038692.1	Q62419	Sh3gl1	gi 7305485	SH3-domain GRB2-like 1
2170	-37,61	0,002	476	63	8	13362	5,52	NP_079657.1	Q9D1K2	Atp6v1f	gi 21314824	ATPase, H ⁺ transporting, V1 subunit F
1882	-43,56	0,016	815	61	11	14476	4,74	NP_033247.1	O55042	Snca	gi 6678047	synuclein, alpha
2108	-30,18	0,001	294	41	5	14810	6,11	NP_034304.1	Q5EBJ0	Fabp3	gi 6753810	fatty acid binding protein 3, muscle and heart
2108	-30,18	0,001	62	10	1	13363	5,3	NP_079657.1	Q9D1K2	Atp6v1f	gi 21314824	ATPase, H ⁺ transporting, V1 subunit F
2108	-30,18	0,001	38	0	1	172305	5,33	NP_803423.2	Q6P1D7	Btbd12	gi 42734487	BTB (POZ) domain containing 12
814	-37,01	0,009	1141	41	17	56632	5,24	AAH37127.1	P56480	Atp5b	gi 23272966	Atp5b protein
1898	-31,39	0,006	256	32	5	17264	5,76	NP_062615.1	Q545B6	Stmn1	gi 9789995	stathmin 1

1050	-32,13	0,001	753	42	14	39852	5,33	NP_062408.2	Q62420	Sh3gl2	gi 10720274	SH3-containing GRB2-like protein 2 (Endophilin-1) (Endophilin-A1)
1050	-32,13	0,001	118	6	2	39613	6,27	NP_083849.1	Q9D6R2	Idh3a	gi 18250284	isocitrate dehydrogenase 3 (NAD+) alpha
1154	-30,78	0,014	392	42	7	23560	9,46	NP_878259.1	Q7TQD2	Tppp	gi 33469051	tubulin polymerization-promoting protein
2126	-27,75	0,009	257	30	4	14810	6,11	NP_034304.1	Q5EBJ0	Fabp3	gi 6753810	fatty acid binding protein 3, muscle and heart
811	-29,62	0,001	1396	49	20	56632	5,24	AAH37127.1	P56480	Atp5b	gi 23272966	Atp5b protein
1137	-28,98	0,016	251	27	5	23560	9,46	NP_878259.1	Q7TQD2	Tppp	gi 33469051	tubulin polymerization-promoting protein
1152	-28,24	0,021	95	7	1	23560	9,46	NP_878259.1	Q7TQD2	Tppp	gi 33469051	tubulin polymerization-promoting protein
1392	-32,36	0,005	362	29	5	16970	6,32	NP_083085.1	Q9D898	Arpc5l	gi 21312654	actin related protein 2/3 complex, subunit 5-like
1141	-27,81	0,044	442	45	7	23560	9,46	NP_878259.1	Q7TQD2	Tppp	gi 33469051	tubulin polymerization-promoting protein
1380	-24,50	0,015	312	36	5	20542	8,98	NP_081178.1	Q9DB27	Mcts1	gi 21312175	malignant T cell amplified sequence 1
1380	-24,50	0,015	41	15	1	25107	8,55	XP_001001534.1	P97799	Nrsn1	gi 94398256	PREDICTED: similar to vesicular membrane protein p24
751	-19,57	0,007	531	33	9	23087	5,11	AAC52639.1	Q61792	MLN50	gi 1407651	Lasp-1
751	-19,57	0,007	42	0	1	154079	9,25	NP_001028936.1	Q3V0G6	4931408 C20 Rik	gi 85702059	hypothetical protein LOC210940
1832	-30,69	0,001	498	52	6	14043	4,38	NP_291088.1	Q91ZZ3	Sncb	gi 15809030	synuclein, beta
1832	-30,69	0,001	373	36	6	14476	4,74	NP_033247.1	O55042	Snca	gi 6678047	synuclein, alpha
2210	32,47	0	45	21	1	10969	6,58	NP_080223.1	P62627	Dynlrb1	gi 21735425	dynein, cytoplasmic, light chain 2A
1926	-26,36	0,025	124	21	2	10655	9,96	NP_034076.1	P84086	Cplx2	gi 6753508	complexin 2
2050	-32,99	0,016	160	25	3	15022	6,55	NP_062283.1	Q9JJV2	Pfn2	gi 9506971	profilin 2
2014	-20,30	0,013	178	17	3	17619	5,03	BAB27577.1	Q9D0J2	Atp5d	gi 12847456	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit precursor
2014	-20,30	0,013	162	21	3	16950	4,46	NP_034990.1	Q60605	Myl6	gi 33620739	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle

927	-21,57	0,018	727	49	12	26141	8,44	NP_031536.2	P50518	Atp6v1e 1	gi 45504359	vacuolar H+ ATPase E1
1373	-23,34	0,003	325	23	6	29872	8,14	NP_035317.1	P70195	Psmb7	gi 6755206	proteasome (prosome, macropain) subunit, beta type 7
1399	-24,58	0,048	359	29	6	28841	4,79	AAH92045.1	Q58E70	Tpm3	gi 62027399	Tpm3 protein
934	-12,99	0,008	274	16	5	34874	6,05	NP_032660.1	P14873	MAP1B	gi 126745	microtubule-associated protein 1 B
1578	-26,03	0	444	36	6	29113	5,47	AAH08241.1	P99026	Psmb4	gi 14198355	Proteasome (prosome, macropain) subunit, beta type 4
2055	-30,40	0,01	155	16	2	15045	4,94	NP_035193.1	Q62048	Pea15a	gi 21426847	phosphoprotein enriched in astrocytes 15 isoform 2
2055	-30,40	0,01	124	13	2	17619	5,03	BAB27577.1	Q9D0J2	Atp5d	gi 12847456	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit precursor
1171		0,037	309	27	5	23560	9,46	NP_878259.1	Q7TQD2	Tppp	gi 33469051	tubulin polymerization-promoting protein
1172	-20,43	0,037	246	22	4	23560	9,46	NP_878259.1	Q7TQD2	Tppp	gi 33469051	tubulin polymerization-promoting protein
464	-18,43	0,009	1605	49	27	59716	9,22	NP_031531.1	Q03265	Atp5a1	gi 6680748	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1
970	-19,17	0,005	570	27	9	34355	6,37	NP_080669.1	Q8K2T1	Nmral1	gi 24431937	NmrA-like family domain containing 1
970	-19,17	0,005	165	11	2	26571	9,28	NP_031536.2	P50518	Atp6v1e 1	gi 1718091	Vacuolar ATP synthase subunit E (V-ATPase E subunit)
970	-19,17	0,005	67	5	1	28919	6,19	AAG13955.1	Q9DBJ1	Pgam1	gi 10179944	phosphoglycerate mutase 1
1081	-22,08	0,018	673	46	12	25132	9,29	NP_038930.1	Q62446	Fkbp3	gi 7305061	FK506 binding protein 3
891	-20,05	0,045	356	14	5	47267	4,99	NP_038537.1	P17183	Eno2	gi 7305027	enolase 2, gamma neuronal
891	-20,05	0,045	277	14	5	49518	5,09	AAH05783.1	Q99JN8	Psmc3	gi 13543237	Proteasome (prosome, macropain) 26S subunit, ATPase 3
891	-20,05	0,045	39	4	1	38334	5,17	NP_035078.1	A2A9F5	Nudc	gi 6754910	nuclear distribution gene C homolog
1833	-30,61	0	301	33	5	14043	4,38	NP_291088.1	Q91ZZ3	Sncb	gi 15809030	synuclein, beta
670	-25,82	0,012	1428	43	23	55349	5,35	AAH18383.1	P46660	Ina	gi 17390900	Ina protein
670	-25,82	0,012	1274	37	20	55836	5,16	AAA62617.1	P46660	Ina	gi 508538	alpha-internexin

2233	-25,04	0,001	64	11	1	12194	5,05	AAH66015.1	Q6NZQ3	Snrpf	gi 41946811	Snrpf protein
2200	-20,58	0,003	390	67	7	10956	7,93	NP_032329.1	Q4KL76	Hspe1	gi 6680309	heat shock protein 1 (chaperonin 10)
2435	-17,18	0,006	233	17	4	23568	5,15	AAA16195.1	P34022	RanBP1	gi 431422	Ran/TC4 Binding Protein
1068	-18,46	0,014	759	58	12	28814	6,67	XP_985088.1	Q9DBJ1	Pgam1	gi 94369185	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B) (PGAM-B)
607	-20,98	0,018	294	12	5	50944	5,39	NP_079555.1	P61979	Hnrpk	gi 13384620	heterogeneous nuclear ribonucleoprotein K
2242	-19,33	0,002	127	15	2	10298	5,89	NP_038927.2	A2ATS2	Timm10	gi 7305575	translocase of inner mitochondrial membrane 13 homolog a
550	-15,24	0,03	648	22	11	54336	9,12	NP_034339.1	P97807	Fh1	gi 33859554	fumarate hydratase 1
550	-15,24	0,03	66	18	1	12232	8,31	AAA79963.1	O88935	SYN1	gi 1041085	synapsin I
1480	-16,63	0,031	268	20	5	31353	4,94	NP_031612.1	Q08331	Calb2	gi 34098931	calbindin 2
1562	-17,68	0,005	451	35	8	25222	5,89	NP_032189.1	Q60631	Grb2	gi 6680083	growth factor receptor bound protein 2
1562	-17,68	0,005	41	0	1	112700	6,85	AAN52484.1	Q80UH5	Nod2	gi 29838691	NOD2
1562	-17,68	0,005	40	1	1	67276	5,96	AAH46591.1	Q80VQ1	Lrrc1	gi 28302239	Lrrc1 protein
1481	-15,33	0,01	255	19	5	31353	4,94	NP_031612.1	Q08331	Calb2	gi 34098931	calbindin 2
1439	-13,96	0,011	156	12	3	28805	5,9	NP_080405.1	P57759	Erp29	gi 19526463	endoplasmic reticulum protein ERp29 precursor
1447	-14,58	0,011	89	3	2	70600	4,69	NP_033155.1	Q03517	Scg2	gi 6677865	secretogranin II
529	-18,01	0,007	1530	41	23	72377	5,07	AAA76734.1	P20029	Hspa5	gi 2506545	78 kDa glucose-regulated protein precursor (GRP 78)
455	-13,98	0,024	1503	44	24	59716	9,22	NP_031531.1	Q03265	Atp5a1	gi 6680748	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1
526	-15,69	0,028	1769	46	28	72377	5,07	AAA76734.1	P20029	Hspa5	gi 2506545	78 kDa glucose-regulated protein precursor (GRP 78)
1636	-12,89	0,001	298	39	5	13658	7,82	NP_080969.2	P60521	Gabarapl2	gi 31542873	gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2
1988	-13,32	0,004	253	42	5	17171	5,71	NP_542127.1	P61089	Ube2n	gi 18017605	ubiquitin-conjugating enzyme E2N

1988	-13,32	0,004	96	13	1	10956	7,93	NP_032329.1	Q4KL76	Hspe1	gi 6680309	heat shock protein 1 (chaperonin 10)
1540	-14,12	0,02	576	63	10	15752	6,03	AAA40121.1	P08228	Sod-1	gi 201006	Cu/Zn-superoxide dismutase
1469	-13,05	0,028	348	22	6	23393	5,12	NP_598557.3	Q99PT1	Arhgdia	gi 31982030	Rho GDP dissociation inhibitor (GDI) alpha
1469	-13,05	0,028	170	24	3	18738	5,52	NP_082138.1	B1ASE1	Atp5h	gi 21313679	ATP synthase, H ⁺ transporting, mitochondrial F ₀ complex, subunit d
1469	-13,05	0,028	59	5	1	23568	5,15	AAA16195.1	P34022	RanBP1	gi 431422	Htf9-a/RanBP1
1095	-14,82	0,004	661	34	11	34710	5,31	NP_082293.1	Q9CWZ7	Napg	gi 110625902	N-ethylmaleimide sensitive fusion protein attachment protein gamma
1095	-14,82	0,004	45	4	1	32540	4,62	NP_032748.1	Q5SQB7	Npm1	gi 6679108	nucleophosmin 1
1095	-14,82	0,004	45	8	1	13524	5,5	CAA44500.1	Q61621	Gnb1	gi 51116	G-protein beta subunit
1592	-15,71	0,006	545	43	9	27298	7	NP_082664.1	Q9D6J6	Ndufv2	gi 20178012	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial precursor
1592	-15,71	0,006	61	1	1	80208	5,24	CAA53178.1	Q62469	Itga2	gi 556846	alpha 2 integrin
1592	-15,71	0,006	49	66	1	1514	4,38	NP_082664.1	Q9D6J6	Ndufv2	gi 20178012	NADH-ubiquinone oxidoreductase 24 kDa subunit
2045	-16,06	0,002	345	44	5	14266	5,55	NP_062720.1	P56812	Pdcd5	gi 9790259	programmed cell death 5
2045	-16,06	0,002	334	39	6	12750	5,24	NP_033347.1	Q5I0U7	Tbca	gi 6678225	tubulin cofactor a
1913	-14,43	0,033	48	5	1	16292	4,85	CAI35154.1	P63242	Eif5a	gi 56800106	eukaryotic translation initiation factor 5A
1134	-14,04	0,01	142	10	2	27764	8,76	AAB57689.1	O08756	Erab	gi 2078284	amyloid beta-peptide binding protein
1134	-14,04	0,01	101	6	2	29349	8,91	NP_079986.1	Q9CR68	Uqcrfs1	gi 13385168	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
1134	-14,04	0,01	61	4	1	25700	6,9	NP_032209.1	P15626	Gstm2	gi 6680121	glutathione S-transferase, mu 2
1455	-8,44	0,031	615	56	10	18548	8,22	NP_031713.1	P18760	Cfl1	gi 6680924	cofilin 1, non-muscle
1455	-8,44	0,031	39	2	1	37275	4,83	AAC52892.1	P70353	Nfyc	gi 1669496	transcription factor NF-YC subunit
1696	-13,43	0,011	395	31	7	21792	5,2	AAA69475.1	Q61171	tpx	gi 885932	peroxidase
1997	-13,11	0,007	205	25	4	17171	5,71	NP_542127.1	P61089	Ube2n	gi 18017605	ubiquitin-conjugating enzyme E2N
1123	-13,00	0,005	611	34	10	34710	5,31	NP_082293.1	Q9CWZ7	Napg	gi 110625902	N-ethylmaleimide sensitive fusion protein attachment protein gamma
1123	-13,00	0,005	57	4	1	32540	4,62	NP_032748.1	Q61937	Npm1	gi 6679108	nucleophosmin 1

733	-12,35	0,019	1103	30	18	60903	5,91	CAA38762.1	P63038	Hspd1	gi 51455	heat shock protein 65
733	-12,35	0,019	275	12	5	39575	5,06	XP_983732.1	Q803B0	hspd1	gi 94373522	PREDICTED: similar to heat shock protein 1 (chaperonin)
1211	-16,05	0,035	122	14	2	22996	8,54	NP_796329.1	Q8BLJ3	Plcx3	gi 28893495	phosphatidylinositol-specific phospholipase C, X domain containing 3
1150	-10,60	0,05	552	26	9	32912	9,31	CAA04635.1	O55126	Gbas	gi 17380131	Protein NipSnap2 (Glioblastoma amplified sequence)
934	-22,52	0,035	693	56	9	23618	4,63	NP_032109.1	P06837	Gap43	gi 6679935	growth associated protein 43
934	-22,52	0,035	127	8	2	42686	5,4	NP_067248.1	Q04447	Ckb	gi 10946574	creatine kinase, brain
934	-22,52	0,035	67	8	1	32128	4,54	NP_084248.2	Q5EBJ4	Ernm	gi 60097931	hypothetical protein LOC77767
1626	-11,58	0,024	553	63	10	18738	5,52	NP_082138.1	Q9DCX2	Atp5h	gi 21313679	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d
1626	-11,58	0,024	153	13	3	18510	5,33	XP_136323.1	B1ASE2	LOC240853	gi 20830329	PREDICTED: similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d isoform 1
1078	-10,70	0,047	283	17	6	39852	5,33	NP_062408.2	Q62420	Sh3gl2	gi 10720274	SH3-containing GRB2-like protein 2 (Endophilin-1) (Endophilin-A1)
1078	-10,70	0,047	239	10	4	39613	6,27	NP_083849.1	Q9D6R2	Idh3a	gi 18250284	isocitrate dehydrogenase 3 (NAD+) alpha
1229	-11,17	0,043	275	32	4	21970	7,67	NP_075661.1	Q9CQJ8	Ndufb9	gi 29789148	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9
1229	-11,17	0,043	168	14	3	24663	8,29	CAA56702.1	O09061	Psmb1	gi 1165123	component C5 of proteasome
1229	-11,17	0,043	42	0	1	97981	9,29	AAC71052.1	Q9Z1X4	Ilf3	gi 3834675	interleukin enhancer binding factor 3
1229	-11,17	0,043	42	3	1	28073	9	NP_613067.1	Q9D172	D10Jhu81e	gi 20070420	es1 protein
2125	-10,27	0,002	430	39	8	16020	6,08	NP_031773.2	P12787	Cox5a	gi 117099	Cytochrome c oxidase subunit 5A, mitochondrial precursor

2121	-11,33	0,005	226	22	4	16020	6,08	NP_031773.2	P12787	Cox5a	gi 117099	Cytochrome c oxidase subunit 5A, mitochondrial precursor
2121	-11,33	0,005	224	31	4	11668	4,8	NP_035790.1	A2AV97	Txn1	gi 6755911	thioredoxin 1
428	-9,82	0,011	1188	30	22	83848	6,18	NP_083949.2	Q8CAQ8	Immt	gi 70608131	inner membrane protein, mitochondrial
1028	-11,08	0,046	255	15	5	39852	5,33	NP_062408.2	Q62420	Sh3gl2	gi 10720274	SH3-containing GRB2-like protein 2 (Endophilin-1)
1028	-11,08	0,046	245	11	3	39547	5,28	AAF31669.1	Q9JKK7	Tmod2	gi 6934242	tropomodulin 2
1028	-11,08	0,046	212	10	4	37991	5,27	NP_084156.2	Q3TG36	Zadh1	gi 85719320	zinc binding alcohol dehydrogenase, domain containing 1
1028	-11,08	0,046	57	6	1	29621	5,97	NP_080543.2	Q9CR95	Necap1	gi 27229051	adaptin-ear-binding coat-associated protein 1
1028	-11,08	0,046	42	6	1	33881	5,35	NP_035351.1	O35295	Purb	gi 6755252	purine rich element binding protein B
883	-10,72	0,038	893	44	13	47267	4,99	NP_038537.1	P17183	Eno2	gi 7305027	enolase 2, gamma neuronal
1678	-7,56	0,016	241	34	4	14506	6,81	NP_035425.2	Q6ZWZ6	Rps12	gi 40254577	ribosomal protein S12
1432	-7,65	0,035	656	31	12	35075	5,36	NP_061359.2	P61982	Ywhag	gi 31543976	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide
1080	-6,92	0,024	843	49	13	28814	6,67	XP_985088.1	Q9DBJ1	Pgam1	gi 94369185	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B)
1080	-6,92	0,024	115	13	2	25554	7,67	NP_077198.1	Q8BVI4	Qdpr	gi 21312520	quininoid dihydropteridine reductase
1080	-6,92	0,024	40	3	1	31128	5,17	NP_705809.1	P35802	Gpm6a	gi 23957686	glycoprotein m6a
1139	-6,71	0,028	715	56	12	24625	8,57	BAA77360.1	Q9WTP7	mAK3	gi 4760600	adenylate kinase isozyme 3
1139	-6,71	0,028	187	13	4	32858	9,06	AAH23146.1	Q8R164	Bphl	gi 18606328	Biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)

884	-8,24	0,048	912	45	14	47267	4,99	NP_038537.1	P17183	Eno2	gi 7305027	enolase 2, gamma neuronal
1107	-14,80	0,043	223	17	4	25953	7,71	NP_034488.1	P10649	Gstm1	gi 6754084	glutathione S-transferase, mu 1
1107	-14,80	0,043	178	11	4	29349	8,91	NP_079986.1	Q9CR68	Uqcrfs1	gi 13385168	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
1524	-6,26	0,01	487	59	10	18672	8,44	AAA39826.1	P15532	Nme1	gi 387496	tumor metastatic process-associated protein NM23
1524	-6,26	0,01	130	13	2	17224	6,23	NP_034340.1	O89106	Fhit	gi 6753862	fragile histidine triad
1524	-6,26	0,01	130	16	2	15955	6,23	AAA40121.1	P08228	Sod-1	gi 201006	Cu/Zn-superoxide dismutase
880	-7,41	0,046	801	36	13	47267	4,99	NP_038537.1	P17183	Eno2	gi 7305027	enolase 2, gamma neuronal
1537	-5,19	0,006	138	22	3	14263	8,74	NP_080011.1	A2AVS1	Map1lc3a	gi 23956148	microtubule-associated protein 1 light chain 3 alpha
1537	-5,19	0,006	37	15	1	25107	8,55	XP_001001534.1	P97799	Nrsn1	gi 94398256	PREDICTED: similar to vesicular membrane protein p24
613	5,45	0,009	186	10	4	51703	8,72	NP_080720.1	Q9CZU6	Cs	gi 13385942	citrate synthase
613	5,45	0,009	170	8	3	47376	7,75	NP_080060.1	Q9CZP5	Bcs1l	gi 21313544	BCS1-like
613	5,45	0,009	119	6	2	39331	8,31	NP_031464.1	Q5FWB7	Aldoa	gi 6671539	aldolase 1, A isoform
613	5,45	0,009	87	3	1	48205	9,26	NP_080175.1	Q9DB77	Uqcrc2	gi 22267442	ubiquinol cytochrome c reductase core protein 2
614	6,27	0,006	833	43	13	39331	8,31	NP_031464.1	Q5FWB7	Aldoa	gi 6671539	aldolase 1, A isoform
614	6,27	0,006	563	29	10	42168	8,76	NP_570954.1	Q91VA7	Idh3b	gi 18700024	isocitrate dehydrogenase 3, beta subunit
572	5,43	0,018	583	23	10	46974	8,39	NP_034027.1	P30275	Ckmt1	gi 6753428	creatine kinase, mitochondrial 1, ubiquitous
572	5,43	0,018	252	9	3	50902	8,88	NP_766599.1	P54071	Idh2	gi 27370516	isocitrate dehydrogenase 2 (NADP+), mitochondrial
572	5,43	0,018	76	3	1	48616	8,82	AAB04679.1	Q60759	Gcdh	gi 2492632	Glutaryl-CoA dehydrogenase, mitochondrial precursor (GCD)
422	6,43	0,048	703	26	11	56106	7,62	AAK13495.1	Q9CPY7	Lap	gi 13161142	leucine aminopeptidase
422	6,43	0,048	515	22	8	55953	8,73	NP_077150.1	Q9D0K2	Oxct1	gi 18266680	3-oxoacid CoA transferase 1
422	6,43	0,048	277	11	5	52418	7,62	NP_038709.1	Q64332	Syn2	gi 8567410	synapsin II
422	6,43	0,048	229	13	4	51542	7,16	NP_031624.1	P40124	Cap1	gi 6671666	CAP, adenylate cyclase-associated protein 1

422	6,43	0,048	69	2	1	59716	9,22	NP_031531.1	Q03265	Atp5a1	gi 6680748	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1
672	6,84	0,032	770	37	13	39370	6,67	NP_033787.2	B1AQE0	Aldoc	gi 60687506	aldolase 3, C isoform
672	6,84	0,032	401	16	7	46203	6,68	CAA30275.1	P05201	Got1	gi 871422	aspartate aminotransferase
1720	6,34	0,025	378	52	6	14948	8,46	NP_035202.1	P62962	Pfn1	gi 6755040	profilin 1
760	6,73	0,003	307	20	5	37305	9,46	BAC31624.1	Q8BRQ9	Sfxn5	gi 30519995	sideroflexin 5
743	8,07	0,046	462	21	8	57108	4,79	CAA29759.1	P09103	P4hb	gi 129729	Protein disulfide-isomerase precursor (PDI)
743	8,07	0,046	128	6	2	54291	4,83	NP_035752.1	O88746	Tom1	gi 6755847	target of myb1 homolog
743	8,07	0,046	43	10	1	13944	4,16	AAA40510.1	P99024	Tubb5	gi 202231	beta-tubulin
897	7,04	0,019	676	47	8	30737	8,62	NP_035824.1	Q60932	Vdac1	gi 6755963	voltage-dependent anion channel 1
897	7,04	0,019	675	45	10	31713	7,44	NP_035825.1	Q60930	Vdac2	gi 6755965	voltage-dependent anion channel 2
425	8,62	0,027	1134	36	18	59614	7,95	BAA81878.1	P80313	Cct7	gi 549060	T-complex protein 1 subunit eta (TCP-1-eta)
425	8,62	0,027	101	5	2	51542	7,16	NP_031624.1	P40124	Cap1	gi 6671666	CAP, adenylate cyclase-associated protein 1
471	7,85	0,026	649	29	12	50802	8,51	NP_598427.1	Q91YT0	Ndufv1	gi 19526814	NADH dehydrogenase (ubiquinone) flavoprotein 1
471	7,85	0,026	167	7	2	46640	6,97	NP_038653.1	P63005	Pafah1b1	gi 7305363	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit
471	7,85	0,026	88	5	1	46974	8,39	NP_034027.1	P30275	Ckmt1	gi 6753428	creatine kinase, mitochondrial 1, ubiquitous
389	10,00	0,005	1408	43	23	57878	7,18	CAA65761.1	P52480	Pkm2	gi 1405933	M2-type pyruvate kinase
389	10,00	0,005	1334	54	21	57808	7,18	NP_035229.2	P52480	Pkm2	gi 31981562	pyruvate kinase 3
389	10,00	0,005	167	7	3	54178	7,97	AAC53170.1	O08749	Dld	gi 2078522	dihydrolipoamide dehydrogenase
677	8,58	0,048	976	44	16	39370	6,67	NP_033787.2	B1AQE0	Aldoc	gi 60687506	aldolase 3, C isoform
677	8,58	0,048	443	27	7	37531	7,16	NP_579926.1	Q91V12	Acot7	gi 19923052	acyl-CoA thioesterase 7
677	8,58	0,048	140	7	3	39331	8,31	NP_031464.1	P05064	Aldoa	gi 6671539	aldolase 1, A isoform
677	8,58	0,048	86	4	1	44508	7,53	NP_032854.2	P09411	Pgk1	gi 129903	Phosphoglycerate kinase 1
571	8,60	0,013	597	24	11	46555	8,36	NP_031520.1	P16460	Ass1	gi 6996911	argininosuccinate synthetase
571	8,60	0,013	419	19	7	46974	8,39	NP_034027.1	P30275	Ckmt1	gi 6753428	creatine kinase, mitochondrial 1, ubiquitous

571	8,60	0,013	410	22	7	44701	7,64	NP_080218.1	Q9CZ30	Gtpbp9	gi 21313144	GTP-binding protein PTD004 isoform a
571	8,60	0,013	163	6	2	48616	8,82	AAB04679.1	Q60759	Gcdh	gi 2492632	Glutaryl-CoA dehydrogenase, mitochondrial precursor (GCD)
571	8,60	0,013	38	2	1	34223	5,24	AAH48718.1	Q80ZM0	Cep63	gi 28913749	Cep63 protein
266	9,55	0,018	1032	30	18	67588	7,23	NP_033414.1	P40142	Tkt	gi 6678359	transketolase
266	9,55	0,018	802	25	12	61477	6,62	NP_075534.1	Q9EQF6	Dpysl5	gi 12746424	dihydropyrimidinase-like 5
266	9,55	0,018	99	4	2	60085	6,65	NP_796275.2	Q8R081	Hnrpl	gi 33667042	heterogeneous nuclear ribonucleoprotein L
266	9,55	0,018	980	30	18	67588	7,23	NP_033414.1	P40142	Tkt	gi 6678359	transketolase
266	9,55	0,018	338	12	5	60085	6,65	NP_796275.2	Q8R081	Hnrpl	gi 33667042	heterogeneous nuclear ribonucleoprotein L
266	9,55	0,018	232	10	4	61477	6,62	NP_075534.1	Q9EQF6	Dpysl5	gi 12746424	dihydropyrimidinase-like 5
702	8,99	0,009	649	22	12	47723	9,05	AAA37265.1	P05202	Got2	gi 192050	mitochondrial aspartate aminotransferase
702	8,99	0,009	105	6	1	35787	8,44	NP_032110.1	P16858	Gapdh	gi 6679937	similar to glyceraldehyde-3-phosphate dehydrogenase
702	8,99	0,009	40	2	1	33200	4,81	BAC30832.1	Q8BRX3	Btbd12	gi 27503115	Btbd12 protein
554	10,90	0,043	480	20	9	62239	5,95	NP_034085.2	O08553	Dpysl2	gi 40254595	dihydropyrimidinase-like 2
554	10,90	0,043	38	1	1	68648	5,75	NP_033784.2	P07724	Alb	gi 5915682	Serum albumin precursor
746	10,79	0,029	482	28	7	35787	8,44	NP_032110.1	P16858	Gapdh	gi 6679937	similar to glyceraldehyde-3-phosphate dehydrogenase
746	10,79	0,029	289	17	5	35574	8,83	NP_032643.2	P08249	Mdh2	gi 126897	Malate dehydrogenase, mitochondrial precursor
399	10,37	0,01	1401	50	24	57808	7,18	NP_035229.2	P52480	Pkm2	gi 31981562	pyruvate kinase 3
399	10,37	0,01	1243	61	21	57808	7,18	NP_035229.2	P52480	Pkm2	gi 31981562	pyruvate kinase 3
399	10,37	0,01	37	3	1	101716	9,05	NP_035912.2	Q8BGP4	Adamts5	gi 6752976	a disintegrin-like and metalloprotease with thrombospondin type 1 motif,
792	10,90	0,014	618	19	11	56502	7,53	NP_033786.1	P47738	Aldh2	gi 6753036	aldehyde dehydrogenase 2, mitochondrial
983	9,24	0,045	436	32	6	30864	8,96	AAH89336.1	Q5EBQ0	Vdac3	gi 59807690	Voltage-dependent anion channel 3
697	9,94	0,008	676	25	12	47723	9,05	AAA37265.1	P05202	Got2	gi 192050	mitochondrial aspartate aminotransferase

697	9,94	0,008	45	2	1	33200	4,81	BAC30832.1	Q8BRX3	Btbd12	gi 27503115	Btbd12 protein (BTB (POZ) domain containing 12)
974	13,84	0,031	786	40	13	40992	5,56	CAA31455.1	P63260	Actg1	gi 809561	gamma-actin
974	13,84	0,031	709	38	12	39161	5,78	CAA27396.1	P60710	Actb	gi 49868	put. beta-actin (aa 27-375)
974	13,84	0,031	60	3	1	61485	4,63	AAA39814.1	P08551	NFL	gi 200038	neurofilament-L
399	10,37	0,01	173	17	3	29621	5,97	NP_080543.2	Q9CR95	Necap1	gi 27229051	adaptin-ear-binding coat-associated protein 1
399	10,37	0,01	64	3	1	39613	6,27	NP_083849.1	Q9D6R2	Idh3a	gi 18250284	isocitrate dehydrogenase 3 (NAD ⁺) alpha
468	10,84	0,004	560	26	10	46640	6,97	NP_038653.1	P63005	Pafah1b1	gi 7305363	platelet-activating factor acetylhydrolase, isoform 1b, beta 1 subunit
468	10,84	0,004	247	10	4	50802	8,51	NP_598427.1	Q91YT0	Ndufv1	gi 19526814	NADH dehydrogenase (ubiquinone) flavoprotein 1
424	12,50	0,017	814	32	15	58030	8,24	NP_033967.1	P80315	Cct4	gi 6753322	chaperonin subunit 4 (delta)
424	12,50	0,017	431	13	6	61340	8,2	NP_084302.1	Q3ULD5	Mccc2	gi 73622267	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)
424	12,50	0,017	341	13	6	52418	7,62	NP_038709.1	Q64332	Syn2	gi 8567410	synapsin II
424	12,50	0,017	106	6	2	61298	8,05	NP_032159.1	P26443	Glud1	gi 6680027	glutamate dehydrogenase 1
424	12,50	0,017	98	4	2	57824	7,58	BAA07457.1	P52480	Pkm2	gi 551295	pyruvate kinase M
424	12,50	0,017	62	2	1	54178	7,97	AAC53170.1	O08749	Dld	gi 2078522	dihydrolipoamide dehydrogenase
2956	12,98	0,022	370	11	6	80827	5,53		A32621		gi 90508	gelsolin, cytosolic - mouse
379	12,39	0,005	1420	41	22	57878	7,18	CAA65761.1	P52480	Pkm2	gi 1405933	M2-type pyruvate kinase
379	12,39	0,005	1391	54	21	57808	7,18	NP_035229.2	P52480	Pkm2	gi 31981562	pyruvate kinase 3
379	12,39	0,005	43	2	1	55214	6,77	NP_663397.1	Q99LF4	D10Wsu 52e	gi 81880226	UPF0027 protein C22orf28 homolog
388	13,45	0,044	292	9	5	80827	5,53		A32621		gi 90508	gelsolin, cytosolic - mouse
388	13,45	0,044	37	15	1	25107	8,55	XP_0010015 34.1	P97799	Nrsn1	gi 94398256	PREDICTED: similar to vesicular membrane protein p24
2921	13,79	0,046	1418	30	22	89252	5,14	NP_033529.2	Q01853	Vcp	gi 400712	Transitional endoplasmic reticulum ATPase
295	13,44	0,004	619	17	10	68692	6,32	AAH31728.1	O08599	Stxbp1	gi 21594764	Stxbp1 protein
295	13,44	0,004	45	2	1	72280	7,11	AAH11301.1	Q8K2B3	Sdha	gi 15030102	Sdha protein

184	13,62	0,012	437	11	8	82561	6,94	AAH08570.1	Q922B8	Ddx1	gi 14250287	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1
320A	13,08	0,007	701	29	14	57968	6,63	NP_033968.1	P80317	Cct6a	gi 6753324	chaperonin subunit 6a (zeta)
320A	13,08	0,007	70	3	1	57824	7,58	BAA07457.1	P52480	Pkm2	gi 551295	pyruvate kinase M
320B	13,08	0,007	792	33	13	64117	6,3	NP_080471.1	Q9CWX9	Atic	gi 27229048	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
692	11,98	0,026	726	28	12	47723	9,05	AAA37265.1	P05202	Got2	gi 192050	mitochondrial aspartate aminotransferase
692	11,98	0,026	40	2	1	33200	4,81	BAC30832.1	Q8BRX3	Btbd12	gi 27503115	Btbd12 protein
454	12,49	0,034	519	20	10	50422	9,11	NP_031932.1	P62631	Eef1a2	gi 6681273	eukaryotic translation elongation factor 1 alpha 2
454	12,49	0,034	513	25	10	50086	9,1	NP_034236.2	P10126	Eef1a1	gi 126032329	eukaryotic translation elongation factor 1 alpha 1
454	12,49	0,034	39	6	1	16125	10,95	AAH58348.1	Q6PE14	Unc13a	gi 34849707	Unc13a protein
454	12,49	0,034	39	3	1	28307	11,83	XP_919182.2			gi 94411169	PREDICTED: hypothetical protein LOC76613
548	14,93	0,002	609	23	10	62239	5,95	NP_034085.2	O08553	Dpysl2	gi 40254595	dihydropyrimidinase-like 2
582	12,75	0,002	524	26	10	42587	6,19	NP_058556.1	P61164	Actr1a	gi 8392847	ARP1 actin-related protein 1 homolog A .
734	18,69	0,023	555	29	9	49168	5,89	NP_067485.1	O35737	Hnrph1	gi 10946928	heterogeneous nuclear ribonucleoprotein H1
486	13,99	0,002	769	33	14	55933	8,53	NP_766120.1	Q8BWF0	Aldh5a1	gi 27369748	aldehyde dehydrogenase family 5, subfamily A1
534	15,85	0,044	844	33	14	62239	5,95	NP_034085.2	O08553	Dpysl2	gi 40254595	dihydropyrimidinase-like 2
534	15,85	0,044	187	7	4	68688	5,78	CAA09617.1	P07724	Alb	gi 3647327	serum albumin
978	17,30	0,001	686	36	12	40992	5,56	CAA31455.1	P63260	Actg1	gi 809561	gamma-actin
978	17,30	0,001	624	32	11	41758	5,23	AAA37167.1	P68033	Actc1	gi 387090	alpha-cardiac actin
978	17,30	0,001	613	34	11	39161	5,78	CAA27396.1	P60710	Actb	gi 49868	put. beta-actin (aa 27-375)
267	14,27	0,032	450	11	8	73371	7,88	NP_083270.1	Q8BH04	Pck2	gi 28077029	mitochondrial phosphoenolpyruvate carboxykinase 2
267	14,27	0,032	252	6	4	72280	7,11	AAH11301.1	Q8K2B3	Sdha	gi 15030102	Sdha protein
267	14,27	0,032	68	2	1	66365	6,11	NP_035845.1	O88342	Wdr1	gi 6755995	WD repeat domain 1

233	15,54	0,03	683	15	12	82618	9,24	NP_849209.1	Q8BMS1	Hadha	gi 33859811	mitochondrial trifunctional protein, alpha subunit
233	15,54	0,03	72	18	1	12232	8,31	AAA79963.1	O88935	SYN1	gi 1041085	synapsin I
717	13,06	0,01	815	30	13	47723	9,05	AAA37265.1	P05202	Got2	gi 192050	mitochondrial aspartate aminotransferase
717	13,06	0,01	40	2	1	33200	4,81	BAC30832.1	Q8BRX3	Btbd12	gi 27503115	Btbd12 protein
298	15,75	0,001	778	24	14	72280	7,11	AAH11301.1	Q8K2B3	Sdha	gi 15030102	Sdha protein
298	15,75	0,001	72	2	1	67659	6,62	NP_033321.2	O08599	Stxbp1	gi 6678179	syntaxin binding protein 1
298	15,75	0,001	45	1	1	73371	7,88	NP_083270.1	Q8BH04	Pck2	gi 28077029	mitochondrial phosphoenolpyruvate carboxykinase 2
693	14,03	0,032	718	29	13	47381	9,13	NP_034455.1	P05202	Got2	gi 6754036	glutamate oxaloacetate transaminase 2, mitochondrial
870	16,64	0,032	226	12	4	42287	5,58	AAH29064.1	Q8BVQ5	Ppme1	gi 20809834	Protein phosphatase methylesterase 1
913	16,00	0,014	758	39	12	42686	5,4	NP_067248.1	Q04447	Ckb	gi 10946574	creatine kinase, brain
2904	17,64	0,024	1415	33	23	94021	5,13	AAH03770.1	Q99L75	Hspa4	gi 13277753	Heat shock protein 4
166	17,22	0,004	1017	26	18	85410	8,08	NP_542364.1	Q99KI0	Aco2	gi 18079339	aconitase 2, mitochondrial
1546	20,37	0,03	248	20	5	24855	5,71	NP_031479.1	O08709	Prdx6	gi 3219774	Peroxiredoxin-6 (Antioxidant protein 2)
1546	20,37	0,03	231	19	5	28109	7,15	NP_031478.1	P20108	Prdx3	gi 6680690	peroxiredoxin 3
1546	20,37	0,03	56	6	1	24559	8,62	AAH16106.1	Q8C0M9	Asrgl1	gi 16359292	Asrgl1 protein
180	18,14	0,008	1371	32	22	85410	8,08	NP_542364.1	Q99KI0	Aco2	gi 18079339	aconitase 2, mitochondrial
750	18,08	0,026	976	32	16	56384	5,57	NP_031535.2	P62814	Atp6v1b2	gi 19705578	vacuolar H+ATPase B2
750	18,08	0,026	44	2	1	46696	7,59	S14538			gi 110056	transition protein - mouse
231	16,70	0,018	909	23	14	82618	9,24	NP_849209.1	Q8BMS1	Hadha	gi 33859811	mitochondrial trifunctional protein, alpha subunit
632	19,38	0,029	748	32	13	50479	4,96	AAL60197.1	P50396	Gdi1	gi 18139889	guanosine diphosphate dissociation inhibitor 1
158	16,82	0,004	1231	32	20	85410	8,08	NP_542364.1	Q99KI0	Aco2	gi 18079339	aconitase 2, mitochondrial
461	16,64	0	989	32	15	56416	8,35	NP_766549.2	P61922	Abat	gi 37202121	4-aminobutyrate aminotransferase
159	17,58	0,004	1252	33	22	85410	8,08	NP_542364.1	Q99KI0	Aco2	gi 18079339	aconitase 2, mitochondrial
481	15,19	0,04	431	16	8	50132	9,1	AAA50406.1	P10126	Eef1a1	gi 556301	elongation factor Tu

822	15,88	0,008	895	49	15	35589	8,93	NP_032643.2	P08249	Mdh2	gi 31982186	malate dehydrogenase 2, NAD (mitochondrial)
2951	19,74	0,012	796	20	14	94429	5,53	BAA08446.1	P48722	Hspa41	gi 705391	APG-1
2951	19,74	0,012	42	1	1	103190	7,94	NP_651540.1	Q9VB72	Gm969	gi 94406335	PREDICTED: similar to CG5882-PA
287	18,47	0,003	795	19	13	74523	8,43	NP_766024.1	Q8BH59	Slc25a12	gi 27369581	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
293	18,98	0,001	919	32	16	68692	6,32	AAH31728.1	O08599	Stxbp1	gi 21594764	Stxbp1 protein
293	18,98	0,001	81	2	1	58280	6,16	AAC72373.1	Q8K2B3	Sdha	gi 3851614	succinate dehydrogenase Fp subunit
286	18,28	0,004	810	29	14	61477	6,62	NP_075534.1	Q9EQF6	Dpysl5	gi 12746424	dihydropyrimidinase-like 5
286	18,28	0,004	447	16	8	67588	7,23	NP_033414.1	P40142	Tkt	gi 6678359	transketolase
2950	21,13	0,017	1071	26	19	94325	5,5	AAC52610.1	P48722	Osp94	gi 1098541	osmotic stress protein 94
518	20,78	0,009	1109	33	20	83848	6,18	NP_083949.2	Q8CAQ8	Immt	gi 70608131	inner membrane protein, mitochondrial
518	20,78	0,009	37	15	1	25107	8,55	XP_001001534.1	P97799	Nrsn1	gi 94398256	PREDICTED: similar to vesicular membrane protein p24
333	21,74	0,023	1004	26	18	94325	5,5	AAC52610.1	P48722	Osp94	gi 1098541	osmotic stress protein 94
591	19,92	0,048	39	15	1	25107	8,55	XP_001001534.1	P97799	Nrsn1	gi 94398256	PREDICTED: similar to vesicular membrane protein p24
544	23,98	0,009	482	12	8	80159	6,25	NP_080784.1	Q9CQN1	Trap1	gi 13385998	TNF receptor-associated protein 1
476	19,51	0,014	834	28	14	56416	8,35	NP_766549.2	P61922	Abat	gi 37202121	4-aminobutyrate aminotransferase
153	23,06	0	153	4	3	98078	7,23	CAA43455.1	P28271	Aco1	gi 52736	iron response element binding protein
1103	21,51	0,01	362	24	6	34993	5,88	NP_742146.1	Q8K183	Pdxk	gi 26006861	pyridoxal (pyridoxine, vitamin B6) kinase
211	23,96	0,001	1155	27	20	85215	8,24	S53317	P47857	Pfkm	gi 13638207	6-phosphofructokinase, muscle type (Phosphofructokinase 1)
849	22,81	0,022	197	11	3	42981	5,69	NP_032707.2	Q62433	Ndrp1	gi 6754810	N-myc downstream regulated gene 1
849	22,81	0,022	112	4	2	47095	6,37	NP_075608.2	P17182	Eno1	gi 12963491	enolase 1, alpha non-neuron
216	26,15	0,002	438	10	7	85215	8,24	S53317	P47857	Pfkm	gi 13638207	6-phosphofructokinase, muscle type (Phosphofructokinase 1)

213	24,16	0,001	368	11	6	85396	6,73	AAF75700.1	Q9WUA3	Pfkc	gi 8489537	phosphofruktokinase-1 C isozyme
209	27,16	0,001	706	17	12	85215	8,24	S53317	P47857	Pfkm	gi 13638207	6-phosphofruktokinase, muscle type (Phosphofruktokinase 1)
712	25,86	0,004	471	15	7	56549	6,12	NP_058662.2	Q61753	Phgdh	gi 52353955	3-phosphoglycerate dehydrogenase
150	26,63	0,003	1021	23	19	93495	6,42	AAH60707.1	Q6P9L9	Eef2	gi 38511951	Eef2 protein
150	26,63	0,003	693	15	13	101136	6,7	AAL99692.1	Q8R013	Dcs	gi 19850913	C1-tetrahydrofolate synthase
206	26,95	0,003	576	14	10	85215	8,24	S53317	P47857	Pfkm	gi 13638207	6-phosphofruktokinase, muscle type (Phosphofruktokinase 1)
736	24,22	0,025	460	23	7	43010	8,16	NP_666220.1	Q8QZS1	Hibch	gi 22122625	3-hydroxyisobutyryl-Coenzyme A hydrolase
736	24,22	0,025	405	29	8	35282	6,06	AAF76459.1	Q8R3P0	Aspa	gi 8570166	aspartoacylase ASPA
736	24,22	0,025	66	3	1	35159	6,36	NP_001073293.1		Hnrnp3	gi 94388237	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein H3 isoform a isoform 6
142	28,58	0,002	348	5	4	99250	6,64	BAA84944.1	Q78PY7	Snd1	gi 6009521	p100 co-activator
151	28,66	0,001	686	13	11	101136	6,7	AAL99692.1	Q8R013	Dcs	gi 19850913	C1-tetrahydrofolate synthase
1703	33,99	0,008	198	18	4	21792	5,2	AAA69475.1	Q61171	tpx	gi 885932	peroxidase
589	28,95	0,004	341	19	6	42758	9,17	NP_032349.1	P70404	Idh3g	gi 6680345	isocitrate dehydrogenase 3 (NAD+), gamma
589	28,95	0,004	117	5	2	47382	9,05	AAB91426.1	P05202	Got-2	gi 2690302	aspartate aminotransferase precursor
589	28,95	0,004	41	1	1	196175	9,6	NP_001106844.1	Q80Z38	Shank2	gi 94381425	PREDICTED: similar to SH3/ankyrin domain gene 2 isoform a isoform 6
139	35,82	0,001	211	5	4	117683	6,52	AAH57354.1	Q60597	Ogdh	gi 34785384	Ogdh protein
487	33,80	0,035	637	30	11	49310	6,36	NP_001009818.1	Q8C1B7	Sept11	gi 57634518	septin 11
487	33,80	0,035	316	11	5	59716	9,22	NP_031531.1	Q03265	Atp5a1	gi 6680748	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1
595	36,88	0,012	491	23	9	42758	9,17	NP_032349.1	P70404	Idh3g	gi 6680345	isocitrate dehydrogenase 3 (NAD+), gamma

595	36,88	0,012	236	10	4	47382	9,05	AAB91426.1	P05202	Got-2	gi 2690302	aspartate aminotransferase precursor
595	36,88	0,012	102	6	2	42674	9,56	NP_064430.1	O35435	Dhodh	gi 9910194	dihydroorotate dehydrogenase
595	36,88	0,012	37	5	1	13322	8,89	NP_079880.1	Q9CZH3	Psmg3	gi 21313432	hypothetical protein LOC66506
1160	41,61	0,009	268	13	4	36549	5,7	NP_032518.1	P16125	Ldhb	gi 6678674	lactate dehydrogenase 2, B chain
1539	48,79	0,03	201	23	3	25063	5,21	BAA84083.1	Q9R0P9	Uchl1	gi 5834486	UCH-L1
1680	76,23	0,037	175	13	4	24023	5,89	NP_659119.2	Q8K3J1	Ndufs8	gi 46195430	NADH dehydrogenase (ubiquinone) Fe-S protein 8
1680	76,23	0,037	88	8	1	21834	5,19	NP_035693.3	Q61171	Prdx2	gi 31560539	peroxiredoxin 2

11.2. Tabelle S2**Tabelle S2:** Proteinvergleich mit der Literatur und verschiedenen Neurodegenerativen Erkrankungen.

Proteinname	Erkrankung	Modell aus dieser Arbeit	Modell und/oder Gewebe aus Literatur	Referenz
ENERGIE METABOLISMUS				
Fructose-bisphosphate aldolase C	PD	Parkin	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005 Prabakaran et al.
	SCZD		menschl. Gehirn	2004
ATP synthase b chain, mitochondrial	PD	L1cam	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005 Tilleman et al.
	AD		Tau transgene Maus	2002a
Dihydrolipoamide dehydrogenase	PD	Parkin, L1cam	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005 Tilleman et al.
	AD		Tau transgene Maus	2002a
Succinate dehydrogenase flavoprotein subunit	PD	L1cam	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005 Tilleman et al.
	AD		GSK3b transgene Maus	2002b

Enolase gamma	PD	PINK1, L1cam	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005
	AD		menschl. Gehirn	Schonberger et al. 2001
	SCZD		menschl. Gehirn	Prabakaran et al. 2004
	AD		Tau transgene Maus	Tilleman et al. 2002a
Glyceraldehyde 3-phosphate dehydrogenase	PD	PINK1, B6, L1cam	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005
	AD		menschl. Gehirn	Schonberger et al. 2001
	PD		MPTP Maus mitochondriale SN	Jin et al. 2005
	SCZD		menschl. Gehirn	Prabakaran et al. 2004
	AD		Tau transgene Maus	Tilleman et al. 2002a
Pyruvat dehydrogenase E1 component a subunit	PD	B6	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005
	SCZD		menschl. Gehirn	Prabakaran et al. 2004

PD		MPTP Maus mitochondriale SN	Jin et al. 2005
PD		Parkin KO Maus, ventrales Mittelhirn	Palacino et al. 2004

SIGNAL TRANSDUKTION

Dihydropyrimidinase-related protein-2	PD	B6, L1cam	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005
	AD		menschl. Gehirn	Tsuji et al. 2002
	AD		menschl. Gehirn	Schonberger et al. 2001
	AD		menschl. Gehirn	Kanninen et al. 2004
	SCZD		menschl. Gehirn	Prabakaran et al. 2004
	AD-PD		menschl. Gehirn	Choi et al. 2004a
	AD		menschl. Gehirn	Castegna et al. 2002b
	AD		GSK3b transgene Maus	Tilleman et al. 2002b

VESIKULAR TRAFFICKING

N-ethylmaleimide sensitive fusion protein	PD	PINK1, L1cam	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005
	AD		menschl. Gehirn	Schonberger et al. 2001

	SCZD		menschl. Gehirn	Prabakaran et al. 2004
	AD		GSK3b transgene Maus	Tilleman et al. 2002b
Syntaxin-binding protein 1	PD	B6, L1cam	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005
	PD		MPTP Maus mitochondriale SN	Jin et al. 2005
<hr/> CYTOSKELETT				
Tubulin a chain	PD	PINK1, B6	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005
	AD		GSK3b transgene Maus	Tilleman et al. 2002b
	SCZD		menschl. Gehirn	Prabakaran et al. 2004
<hr/> PROTEINABBAU				
Ubiquitin carboxyterminal hydrolase L1	PD	Parkin, PINK1, L1cam	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005
	SCZD		menschl. Gehirn	Schonberger et al. 2001
	PD-AD		menschl. Gehirn	Choi et al. 2004a
	DS		Maus ES Zellen	Kadota et al. 2004

	AD		menschl. Gehirn	Castegna et al. 2002a
AMINOSÄURE SYNTHESE				
Glutamin synthetase	PD	L1cam	Parkin KO Maus, Kortex, Striatum	Periquet et al. 2005 Tilleman et al.
	AD		GSK3b transgene Maus	2002b Castegna et al.
	AD		menschl. Gehirn	2002a