Functional ontology	Specific function	Spot No.	Protein name	Gene name	SwissProt Accession No.	Theor. Mw (kDa)	Theor. pI	fold changes in protein	p-value (ANOVA)
CNS development/cytoskeletal		47	14-3-3 gamma	Ywhag	P61982	28.26	4.80	1.04	0.029
		10	14-3-3 protein epsilon	Ywhae	P62259	29.17	4.63	-1.22	0.015
		21	14-3-3 protein epsilon	Ywhae	P62259	29.17	4.63	-1.12	0.040
		6	Dihydropyrimidase related protein 2	Dpysl2	O08553	62.28	5.95	-1.38	0.029
		26	Dihydropyrimidase related protein 2	Dpysl2	O08553	62.28	5.95	-1.10	0.006
		25	Dihydropyrimidase related protein 3	Dpysl3	Q62188	61.94	6.04	-1.10	0.008
		44	Dihydropyrimidase related protein 3	Dpysl3	Q62188	61.94	6.04	-1.06	0.028
		3	Profilin 1	Pfn1	P62962	14.96	8.46	1.45	0.030
	Cytoskeletal components	13	Actin, cytoplasmic 2	Actg1	P63260	41.79	5.31	1.19	0.040
		32	Alpha internexin	Ina	P46660	55.71	5.20	-1.03	0.014
		15	Neurofilament light polypeptide	Nefl	P08551	61.51	4.62	-1.18	0.037
		39	Tubulin alpha 4 chain	Tuba4a	P68368	49.92	4.95	1.14	0.016
		14	Tubulin beta 2A chain	Tubb2a	Q7TMM9	49.91	4.78	1.18	0.001
		24	Tubulin beta 2A chain	Tubb2a	Q7TMM9	49.91	4.78	-1.12	0.004
Cellular Trafficking		9	Septin 5	Sept5	Q9Z2Q6	42.75	6.21	-1.23	0.007
		7	Signal transducing adapter molecule 1	Stam	P70297	59.77	4.73	-1.31	0.033
		8	Neuron specific calcium binding protein hippocalcin	Hpca	P84075	22.43	4.87	1.25	0.044
		30	Synapsin 2	Syn2	Q64332	63.37	8.59	1.06	0.003
Protein modifications	Biosynthesis	37	40S ribosomal protein S12	Rps12	P63323	14.53	6.82	-1.22	0.023
		20	Elongation factor 1 beta	Eef1b	O70251	24.69	4.53	1.12	0.048
	Catabolism	33	26S protease regulatory subunit 6A	PSMC3	P17980	49.49	4.87	-1.12	0.048
		35	Proteasome subunit alpha type-5	Psma5	Q9Z2U1	26.39	4.70	1.04	0.050
	Phosphatase	19	ERB-B receptor feedback inhibitor	Errfi1	Q99Jz7	80.04	7.80	-1.13	0.046
		40	Low molecular weight phosphotyrosine protein phosphatase	Acp1	Q9D358	18.19	6.30	1.12	0.050
Stress response	Heat shock	43	Heat shock cognate 71 kDa protein	Hspa8	P63017	70.87	5.38	1.08	0.032
		45	Heat shock cognate protein, 71 kDa	Hspa8	P63017	70.83	5.37	-1.06	0.035
		22	Endoplasmin	Hsp90b1	P08113	94.13	4.74	1.11	0.033
		29	Stress 70 protein, mitochondrial	Hspa9	P38647	73.53	5.91	-1.07	0.046
		31	Stress 70 protein, mitochondrial	Hspa9	P38647	73.53	5.91	-1.03	0.024
	Redox homeostasis	34	Protein DJ 1	Park7	Q99LX0	20.02	6.32	1.07	0.050
		5	Peroxiredoxin 2	Prdx2	Q61171	21.78	5.20	1.41	0.001
		2	Peroxiredoxin 5, mitochondrial	Prdx5	P99029	21.90	9.09	1.57	0.043
		27	Protein disulfide isomerase A3	Pdia3	P27773	56.68	5.88	-1.09	0.023
Calcium sensing		23	Calcineurin subunit B type	Ppp3r1	Q63810	19.30	4.64	1.1	0.006
		11	Calretinin	Calb2	Q08331	31.35	4.90	1.21	0.005
Energy metabolism	Mitochondrial ATP production	28	Aldehyde dehydrogenase X, mitochondrial	Aldh1b1	Q9CZS1	57.55	6.59	1.09	0.035
		1	ATP synthase subunit beta, mitochondrial	Atp5b	P56480	56.30	5.19	1.59	0.036
		4	Isocitrate dehydrogenase (NAD] subunit alpha, mitochondrial	IDH3A	P50213	39.64	6.46	1.43	0.027
		12	Isocitrate dehydrogenase (NAD] subunit alpha, mitochondrial	Idh3a	Q9D6R2	39.64	6.27	1.2	0.029
		46	Isocitrate dehydrogenase (NAD] subunit alpha, mitochondrial	Idh3a	Q9D6R2	39.63	6.27	-1.05	0.037
		42	Isovaleryl CoA dehydrogenase, mitochondrial	Ivd	Q9JHI5	46.33	8.53	1.08	0.004
		16	Gamma enolase	Eno2	P17183	47.30	4.99	1.17	0.021
		18	Gamma enolase	Eno2	P17183	47.30	4.99	1.14	0.0323
Myelination		17	Galactokinase	Galk1	Q9R0N0	42.18	5.17	-1.13	0.007
		38	Myelin basic protein	Mbp	P04370	27.17	9.57	1.2	0.044
Other		36	Heterogenous nuclear riboprotein K	Hnrnpk	P61979	50.94	5.40	1.03	0.049
		41	SH3 domain binding glutamic acid rich like protein 2	Sh3bgrl2	Q8BG73	12.26	5.49	1.34	0.014