SUPPORTING INFORMATION

Memantine Improved Cognitive Function and Altered Hippocampal and Cortical Proteome in Triple Transgenic Mouse Model of Alzheimer's Disease

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Table S-1. 233 proteins in the hippocampus that were significantly changed by memantine treatment.

Table S-1. 233 proteins in the hippocampus that were significantly changed by memantine treatment. These proteins have met the criteria, the ratio of memantine / AD in expression levels of at least 1.2-fold (up-regulation) or at least ＜0.83-fold (down-regulation) as defined in the experimental procedures.

Accession	Protein name	Description	Ratio			Unique	-10lgP
			AD/WT	Memantine/WT	Memantine/AD		
P48725	PCNT	Pericentrin, GN=Pcnt	0.79	2.83	3.58	1	66.89
Q5SX46	Q5SX46	Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment), GN=Slc25a11	1.48	4.12	2.78	1	200.12
E9QM77	E9QM77	Ataxin-2, GN=Atxn2	0.65	1.54	2.37	1	55.46
E9Q555	RN213	E3 ubiquitin-protein ligase RNF213, GN=Rnf213	0.8	1.88	2.35	1	65.4
P29387	GBB4	Guanine nucleotide-binding protein subunit beta-4, GN=Gnb4	1.15	2.62	2.28	2	172.11
Q5SGK3	AOXB	Aldehyde oxidase 2, GN=Aox2	1.53	3.36	2.20	1	19.72
Q80WM5	HPLN3	Hyaluronan and proteoglycan link protein 3, GN=Hapln3	0.9	1.97	2.19	1	97.78
Q9Z0J1	RECK	Reversion-inducing cysteine-rich protein with Kazal motifs, GN=Reck	1.1	2.19	1.99	1	20.71
P83510	TNIK	Traf2 and NCK-interacting protein kinase, GN=Tnik	1.26	2.49	1.98	2	173.49

Q9ERB0	SNP29	Synaptosomal-associated protein 29, GN=Snap29	0.89	1.75	1.97	3	91.63
Q9D1X0	NOL3	Nucleolar protein 3, GN=Nol3	0.79	1.41	1.78	2	109.74
Q8BGJ9	U2AF4	Splicing factor U2AF 26 kDa subunit, GN=U2af1l4	0.62	1.03	1.66	1	38.17
Q9D883	U2AF1	Splicing factor U2AF 35 kDa subunit, GN=U2af1	0.62	1.03	1.66	1	38.17
Q99JH7	CSTN3	Calsyntenin-3, GN=Clstn3	0.73	1.18	1.62	1	20.68
Q5HZI2	C2C4C	C2 calcium-dependent domain-containing protein 4C, GN=C2cd4cC2CD4	0.83	1.3	1.57	1	44.94
P56371	RAB4A	Ras-related protein Rab-4A, GN=Rab4a	1.15	1.78	1.55	1	115.33
P20065	TYB4	Thymosin beta-4, GN=Tmsb4x	1.14	1.75	1.54	4	134.25
A2ARZ7	A2ARZ7	RAB22A member RAS oncogene family isoform CRA_c, GN=Rab22a	0.98	1.5	1.53	2	89.67
Q9JMD0	ZN207	BUB3-interacting and GLEBS motif-containing protein ZNF207, GN=Znf207	0.79	1.2	1.52	1	71.53
A0A0J9YUM2	A0A0J9YUM2	Ras/Rap GTPase-activating protein SynGAP (Fragment), GN=Syngap1	1.41	2.14	1.52	1	323.14
Q9Z2H2	RGS6	Regulator of G-protein signaling 6, GN=Rgs6	0.99	1.5	1.52	3	112.67
A0A0A6YW90	A0A0A6YW90	Glutamate receptor 2, GN=Gria2	0.8	1.21	1.51	1	269.66
Q6NVD9	BFSP2	Phakinin, GN=Bfsp2	0.92	1.39	1.51	1	19.64
Q810U3	NFASC	Neurofascin, GN=Nfasc	1.01	1.51	1.50	1	326.06

P53702	CCHL	Cytochrome c-type heme lyase, GN=Hccs	0.68	1	1.47	1	62.75
O54781	SRPK2	SRSF protein kinase 2, GN=Srpk2	0.78	1.14	1.46	2	98.99
Q68EF0	RAB3I	Rab-3A-interacting protein, GN=Rab3ip	0.92	1.34	1.46	1	59.47
A0A1W2P7K6	A0A1W2P7K6	RAB3A interacting protein isoform CRA_b, GN=Rab3ip	0.92	1.34	1.46	1	59.47
P63054	PCP4	Purkinje cell protein 4, GN=Pcp4	0.82	1.17	1.43	1	112.09
D3YXH0	D3YXH0	Immunoglobulin superfamily member 5, GN=Igsf5	0.82	1.17	1.43	1	112.09
Q9D0J4	ARL2	ADP-rib, GN=ylation factor-like protein 2, GN=Arl2	0.87	1.24	1.43	1	86.81
Q8K4I3	ARHG6	Rho guanine nucleotide exchange factor 6, GN=Arhgef6	0.64	0.91	1.42	1	115.51
Q6Y685	TACC1	Transforming acidic coiled-coil-containing protein 1, GN=Tacc1	0.88	1.25	1.42	1	87.34
Q9JKX6	NUDT5	ADP-sugar pyrophosphatase, GN=Nudt5	1	1.42	1.42	1	84.38
Q921U8	SMTN	Smoothelin, GN=Smtn	0.79	1.12	1.42	1	37.61
A2A9C3	SZT2	KICSTOR complex protein SZT2, GN=Szt2	0.82	1.16	1.41	1	41.34
P97785	GFRA1	GDNF family receptor alpha-1, GN=Gfra1	0.99	1.4	1.41	2	69.39
O70456	1433S	14-3-3 protein sigma, GN=Sfn	1.04	1.47	1.41	1	135.38
B0F2B4	NLGN4	Neuroligin 4-like, GN=Nlgn4l	0.88	1.24	1.41	1	121.65
A0A0R4J034	A0A0R4J034	MCG129810 isoform CRA_c, GN=Pdxdc1	0.94	1.32	1.40	1	101.7

Q9WTP6	KAD2	Adenylate kinase 2 mitochondrial, GN=Ak2	0.96	1.34	1.40	2	144.13
Q9ESC8	AFF4	AF4/FMR2 family member 4, GN=Aff4	1.16	1.61	1.39	1	19.96
A0A0R4J1E3	A0A0R4J1E3	Drebrin, GN=Dbn1	0.86	1.19	1.38	1	256.64
E9Q9J6	E9Q9J6	Plectin (Fragment), GN=Plec	1.07	1.47	1.37	1	223.55
Q9CQY6	UQCC2	Ubiquinol-cytochrome-c reductase complex assembly factor 2, GN=Uqcc2	0.82	1.12	1.37	1	107.45
Q8BQZ4	RLGPB	Ral GTPase-activating protein subunit beta, GN=Ralgapb	1.15	1.57	1.37	1	101.97
Q9CQ45	NENF	Neudesin, GN=Nenf	0.86	1.17	1.36	1	51.5
Q8VE62	PAIP1	Polyadenylate-binding protein-interacting protein 1, GN=Paip1	0.87	1.18	1.36	3	88.99
Q9DB41	GHC2	Mitochondrial glutamate carrier 2, GN=Slc25a18	1.07	1.45	1.36	2	169.05
P50171	DHB8	Estradiol 17-beta-dehydrogenase 8, GN=Hsd17b8	0.99	1.34	1.35	2	189.78
J3QN87	J3QN87	Eukaryotic translation initiation factor 1 (Fragment), GN=Eif1	1.02	1.38	1.35	1	86.88
Q9DBN4	P33MX	Putative monooxygenase p33MONOX, GN=P33monox	0.94	1.27	1.35	1	36.83
Q9CQ40	RM49	39S rib, GN=omal protein L49 mitochondrial, GN=Mrpl49	1.15	1.55	1.35	1	62.99
Q9CX80	CYGB	Cytoglobin, GN=Cygb	0.72	0.97	1.35	2	65.15
Q8CJ40	CROCC	Rootletin, GN=Crocc	0.99	1.33	1.34	1	55.95

P50247	SAHH	Adenosylhomocysteinase, GN=Ahcy	1.03	1.38	1.34	11	189.07
Q9CQ19	MYL9	Myosin regulatory light polypeptide 9, GN=Myl9	0.8	1.07	1.34	1	147.23
H3BKU1	H3BKU1	Protein phosphatase 2 (Formerly 2A) regulatory subunit A (PR 65) beta isoform isoform CRA_b, GN=Ppp2r1b	1.43	1.91	1.34	1	199.62
Q64338	PDE1C	Calcium/calmodulin-dependent 3' 5'-cyclic nucleotide phosphodiesterase 1C, GN=Pde1c	0.88	1.17	1.33	1	72.4
Q62348	TSN	Translin, GE=Tsn	0.89	1.18	1.33	1	90.24
P61924	COPZ1	Coatomer subunit zeta-1, GN=Copz1	1.02	1.35	1.32	1	48.26
A0A140LHQ8	A0A140LHQ8	Phosphatidylinositol-binding clathrin assembly protein (Fragment), GN=Picalm	0.93	1.22	1.31	1	183.87
D3Z7J6	D3Z7J6	Translation initiation factor eIF-2B subunit beta (Fragment), GN=Eif2b2	0.9	1.18	1.31	1	19.96
P57722	PCBP3	Poly(rC)-binding protein 3, GN=Pcbp3	0.87	1.14	1.31	1	150.78
Q99NE5	RIMS1	Regulating synaptic membrane exocytosis protein 1, GN=Rims1	0.91	1.19	1.31	1	202.93
Q920N7	SYT12	Synaptotagmin-12, GN=Syt12	0.88	1.15	1.31	2	101.55
Q4V9Z5	SE6L2	Seizure 6-like protein 2, GN=Sez6l2	0.69	0.9	1.30	1	103.48
Q99P58	RB27B	Ras-related protein Rab-27B, GN=Rab27b	0.85	1.1	1.29	1	114.43
Q5SXY1	CYTSB	Cytospin-B, GN=Specc1	0.82	1.06	1.29	2	120.28

P24668	MPRD	Cation-dependent mannose-6-phosphate receptor, GN=M6pr	1.07	1.38	1.29	3	136.09
Q8BHE3	ATCAY	Caytaxin, GN=Atcay	0.94	1.21	1.29	3	164.01
P59279	RAB2B	Ras-related protein Rab-2B, GN=Rab2b	0.84	1.08	1.29	1	201.2
Q9D4E6	Q9D4E6	Polyadenylate-binding protein, GN=Pabpc6	0.99	1.27	1.28	1	184.45
Q80WQ2	VAC14	Protein VAC14 homolog, GN=Vac14	1.23	1.57	1.28	1	102.85
Q68ED7	CRTC1	CREB-regulated transcription coactivator 1, GN=Crtc1	0.8	1.02	1.28	2	123.79
Q9QXT0	CNPY2	Protein canopy homolog 2, GN=Cnpy2	0.88	1.12	1.27	2	142.4
O08582	GTPB1	GTP-binding protein 1, GN=Gtpbp1	0.92	1.17	1.27	4	122.49
Q80UM3	NAA15	N-alpha-acetyltransferase 15 NatA auxiliary subunit, GN=Naa15	0.96	1.22	1.27	7	98.88
P68181	KAPCB	cAMP-dependent protein kinase catalytic subunit beta, GN=Prkacb	0.85	1.08	1.27	3	166.15
Q8R010	AIMP2	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2, GN=Aimp2	0.85	1.08	1.27	2	128.04
P32848	PRVA	Parvalbumin alpha, GN=Pvalb	0.89	1.13	1.27	6	169.03
Q99J77	SIAS	Sialic acid synthase, GN=Nans	0.93	1.18	1.27	2	116.88
Q6P4T2	U520	U5 small nuclear ribonucleoprotein 200 kDa helicase, GN=Snrnp200	0.82	1.04	1.27	3	126.95
P31650	S6A11	Sodium- and chloride-dependent GABA transporter 3, GN=Slc6a11	0.97	1.23	1.27	6	193.18

Q80UW2	FBX2	F-box only protein 2, GN=Fbxo2	0.98	1.24	1.27	8	196.78
E9PYX6	E9PYX6	Sorbin and SH3 domain-containing protein 1, GN=Sorbs1	1.06	1.34	1.26	1	188.03
Q811G0	PTHB1	Protein PTHB1, GN=Bbs9	1.07	1.35	1.26	1	40.98
E0CXD4	E0CXD4	Protocadherin 1, GN=Pcdh1	0.73	0.92	1.26	1	175.79
Q8BGX2	TIM29	Mitochondrial import inner membrane translocase subunit Tim29, GN=Timm29	0.89	1.12	1.26	1	148.54
Q8CCT4	TCAL5	Transcription elongation factor A protein-like 5, GN=Tceal5	0.99	1.24	1.25	2	140.44
Q6PGN3	DCLK2	Serine/threonine-protein kinase DCLK2, GN=Dclk2	1.03	1.29	1.25	8	195.13
E0CYG3	E0CYG3	Sperm flagellar protein 2, GN=Spef2	0.76	0.95	1.25	1	26.76
Q8R191	SNG3	Synaptogyrin-3, GN=Syngr3	1.01	1.26	1.25	2	120.81
Q91Z61	DIRA1	GTP-binding protein Di-Ras1, GN=Diras1	1.01	1.26	1.25	3	118.17
A2AQJ8	A2AQJ8	Neutral alpha-glucosidase C, GN=Ganc	0.93	1.16	1.25	1	21.34
Q08331	CALB2	Calretinin, GN=Calb2	0.89	1.11	1.25	9	184.92
Q8CBY8	DCTN4	Dynactin subunit 4, GN=Dctn4	1.15	1.43	1.24	8	161.63
E9Q2W9	E9Q2W9	Alpha-actinin-4 (Fragment), GN=Actn4	0.83	1.03	1.24	1	270.34
P53996	CNBP	Cellular nucleic acid-binding protein, GN=Cnbp	1.08	1.34	1.24	1	94.04
Q8R5M8	CADM1	Cell adhesion molecule 1, GN=Cadm1	0.91	1.12	1.23	1	204.7

Q9CPU4	MGST3	Microsomal glutathione S-transferase 3, GN=Mgst3	0.91	1.12	1.23	2	97.46
Q8VHL1	SETD7	Histone-lysine N-methyltransferase SETD7, GN=Setd7	0.87	1.07	1.23	3	107.42
Q921E2	RAB31	Ras-related protein Rab-31, GN=Rab31	0.96	1.18	1.23	4	110.99
Q9Z2D3	DFNA5	Non-syndromic hearing impairment protein 5 homolog, GN=Dfna5	0.96	1.18	1.23	1	68.16
Q8R527	RHOQ	Rho-related GTP-binding protein RhoQ, GN=Rhoq	0.79	0.97	1.23	1	94.34
P63137	GBRB2	Gamma-aminobutyric acid receptor subunit beta-2, GN=Gabrb2	0.97	1.19	1.23	1	147.81
Q9CWE0	MFR1L	Mitochondrial fission regulator 1-like, GN=Mtfr1l	0.89	1.09	1.22	2	152.66
Q64253	LY6E	Lymphocyte antigen 6E, GN=Ly6e	0.98	1.2	1.22	1	41.3
E9PWG2	E9PWG2	Trafficking protein particle complex 8, GN=Trappc8	0.98	1.2	1.22	1	108.11
P11352	GPX1	Glutathione peroxidase 1, GN=Gpx1	0.9	1.1	1.22	4	134.33
Q9CZJ2	HS12B	Heat shock 70 kDa protein 12B, GN=Hspa12b	1.08	1.32	1.22	1	131.6
Q8CGA4	MTURN	Maturin, GN=Mturn	0.81	0.99	1.22	1	23.78
Q7SIG6	ASAP2	Arf-GAP with SH3 domain ANK repeat and PH domain-containing protein 2, GN=Asap2	0.95	1.16	1.22	1	86.75
A0A087WPR7	A0A087WPR7	Dystonin (Fragment), GN=Dst	0.68	0.83	1.22	1	92.07
P35569	IRS1	Insulin receptor substrate 1, GN=Irs1	1.18	1.44	1.22	1	19.6

Q9JHW2	NIT2	Omega-amidase NIT2, GN=Nit2	0.96	1.17	1.22	4	148.19
P12023	A4	Amyloid beta A4 protein, GN=App	1.83	2.23	1.22	13	254.95
Q3V132	ADT4	ADP/ATP translocase 4, GN=Slc25a31	0.87	1.06	1.22	1	136.77
Q8VCH8	UBXN4	UBX domain-containing protein 4, GN=Ubxn4	0.79	0.96	1.22	2	136.3
H3BJD6	H3BJD6	Protein phosphatase 1 regulatory (inhibitor) subunit 9A, GN=Ppp1r9a	1.07	1.3	1.21	6	201.42
P62715	PP2AB	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform, GN=Ppp2cb	0.84	1.02	1.21	1	229.03
Q9Z110	P5CS	Delta-1-pyrroline-5-carboxylate synthase, GN=Aldh18a1	0.84	1.02	1.21	2	117.19
P12787	COX5A	Cytochrome c oxidase subunit 5A mitochondrial, GN=Cox5a	0.94	1.14	1.21	11	216.43
Q91X72	HEMO	Hemopexin, GN=Hpx	0.8	0.97	1.21	3	71.12
Q8VBW6	ULA1	NEDD8-activating enzyme E1 regulatory subunit, GN=Nae1	1	1.21	1.21	6	140.6
P15532	NDKA	Nucleoside diphosphate kinase A, GN=Nme1	0.91	1.1	1.21	2	224.72
P53612	PGTB2	Geranylgeranyl transferase type-2 subunit beta, GN=Rabggtb	0.91	1.1	1.21	1	76.53
Q61768	KINH	Kinesin-1 heavy chain, GN=Kif5b	0.96	1.16	1.21	5	229.54
S4R294	S4R294	Protein PRRC2C, GN=Prrc2c	0.96	1.16	1.21	1	39.68
Q9DCM0	ETHE1	Persulfide dioxygenase ETHE1 mitochondrial, GN=Ethe1	1.25	1.51	1.21	1	103.82

P46097	SYT2	Synaptotagmin-2, GN=Syt2	1.02	1.23	1.21	5	177.57
P26041	MOES	Moesin, GN=Msn	0.98	1.18	1.20	3	188.43
P28352	APEX1	DNA-(apurinic or apyrimidinic site) lyase, GN=Apex1	0.98	1.18	1.20	2	107.21
P27661	H2AX	Histone H2AX, GN=H2afx	0.84	1.01	1.20	1	139.35
Q9DB73	NB5R1	NADH-cytochrome b5 reductase 1, GN=Cyb5r1	1.04	1.25	1.20	5	177.1
Q3TIR3	RIC8A	Synembryn-A, GN=Ric8a	1.09	1.31	1.20	1	146.96
Q8R555	CRAC1	Cartilage acidic protein 1, GN=Crtac1	1.09	1.31	1.20	1	53.89
Q9DBP5	KCY	UMP-CMP kinase, GN=Cmpk1	0.85	1.02	1.20	6	181.52
P84075	HPCA	Neuron-specific calcium-binding protein hippocalcin, GN=Hpca	0.99	0.82	0.83	5	206.59
A2BFF9	A2BFF9	Cytoplasmic dynein 1 intermediate chain 2, GN=Dync1i2	1.28	1.06	0.83	2	160.14
O08808	DIAP1	Protein diaphanous homolog 1, GN=Diaph1	1.16	0.96	0.83	2	132.11
A2A8L5	PTPRF	Receptor-type tyrosine-protein ph, GN=phatase F, GN=Ptprf	1.04	0.86	0.83	2	145.58
Q68FL6	SYMC	Methionine--tRNA ligase cytoplasmic, GN=Mars	1.02	0.84	0.82	3	79.3
Q3TRM8	HXK3	Hexokinase-3, GN=Hk3	1.58	1.3	0.82	1	83.68
Q60575	KIF1B	Kinesin-like protein KIF1B, GN=Kif1b	1.34	1.1	0.82	1	132.5
P55258	RAB8A	Ras-related protein Rab-8A, GN=Rab8a	1.11	0.91	0.82	1	170.35

P50571	GBRB1	Gamma-aminobutyric acid receptor subunit beta-1, GN=Gabrb1	1.44	1.18	0.82	1	141.79
Q9WUK4	RFC2	Replication factor C subunit 2, GN=Rfc2	0.92	0.75	0.82	1	19.92
G3UZJ2	G3UZJ2	Microtubule-associated protein (Fragment), GN=Map2	1.19	0.97	0.82	1	182.93
Q8VE70	PDC10	Programmed cell death protein 10, GN=Pdcd10	1.35	1.1	0.81	1	66.98
Q7TNB5	Q7TNB5	Glutamate receptor 1, GN=Gria1	1.08	0.88	0.81	1	259.16
Q02614	S30BP	SAP30-binding protein, GN=Sap30bp	1.29	1.05	0.81	1	62.9
P63087	PP1G	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit, GN=Ppp1cc	1.12	0.91	0.81	1	237.6
Q3UV17	K22O	Keratin type II cytoskeletal 2 oral, GN=Krt76	0.8	0.65	0.81	1	67.92
P47743	GRM8	Metabotropic glutamate receptor 8, GN=Grm8	1.22	0.99	0.81	1	42.57
Q8CBB6	Q8CBB6	Histone H2B, GN=Hist1h2bq	0.89	0.72	0.81	2	156.27
Q61036	PAK3	Serine/threonine-protein kinase PAK 3, GN=Pak3	0.99	0.8	0.81	2	197.78
P97952	SCN1B	Sodium channel subunit beta-1, GN=Scn1b	1.19	0.96	0.81	1	88.36
Q9DCH4	EIF3F	Eukaryotic translation initiation factor 3 subunit F, GN=Eif3f	1.39	1.12	0.81	3	97.58
O70274	TP4A2	Protein tyrosine phosphatase type IVA 2, GN=Ptp4a2	0.77	0.62	0.81	1	69.08
P35438	NMDZ1	Glutamate receptor ionotropic NMDA 1, GN=Grin1	1.18	0.95	0.81	12	210.43

F7AA26	F7AA26	Paralemmin A kinase anchor protein (Fragment), GN=Pakap	1.07	0.86	0.80	1	136.76
Q68FL4	SAHH3	Putative adenosylhomocysteinase 3, GN=Ahcyl2	1.06	0.85	0.80	4	226.66
F8WGT1	F8WGT1	Adenosylhomocysteinase, GN=Ahcyl2	1.06	0.85	0.80	4	226.66
Q8CDG3	VCIP1	Deubiquitinating protein VCIP135, GN=Vcpip1	1.21	0.97	0.80	3	105.33
Q3UH60	DIP2B	Disco-interacting protein 2 homolog B, GN=Dip2b	1.25	1	0.80	2	157.17
P61961	UFM1	Ubiquitin-fold modifier 1, GN=Ufm1	1.15	0.92	0.80	2	140.26
Q3UGY8	BIG3	Brefeldin A-inhibited guanine nucleotide-exchange protein 3, GN=Arfgef3	0.95	0.76	0.80	1	52.17
P60202	MYPR	Myelin proteolipid protein, GN=Plp1	1.33	1.06	0.80	18	258.66
Q6ZWZ6	Q6ZWZ6	40S ribosomal protein S12, GN=Rps12	1.18	0.94	0.80	4	128.21
Q61941	NNTM	NAD(P) transhydrogenase mitochondrial, GN=Nnt	1.67	1.33	0.80	6	162.78
Q4JIM5	ABL2	Abelson tyrosine-protein kinase 2, GN=Abl2	1.08	0.86	0.80	2	78.37
A2CES4	A2CES4	U2 small nuclear ribonucleoprotein B'' (Fragment), GN=Snrpb2	0.97	0.77	0.79	1	43.8
Q99KP3	CRYL1	Lambda-crystallin homolog, GN=Cryl1	1.35	1.07	0.79	1	111.55
Q9JK42	PDK2	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2 mitochondrial, GN=Pdk2	1.25	0.99	0.79	2	114.5
Q9EPK7	XPO7	Exportin-7, GN=Xpo7	1.24	0.98	0.79	2	169.57

Q8BYP3	RHOF	Rho-related GTP-binding protein RhoF, GN=Rhof	0.98	0.77	0.79	1	82.84
P43274	H14	Histone H1.4, GN=Hist1h1e	0.88	0.69	0.78	1	144.7
P30999	CTND1	Catenin delta-1, GN=Ctnnd1	1.11	0.87	0.78	2	129.83
A2A3W1	A2A3W1	Septin-6 (Fragment), GN=Sept6	1.06	0.83	0.78	1	180.86
Q91Y97	ALDOB	Fructose-bisphosphate aldolase B, GN=Aldob	1.15	0.9	0.78	1	86.3
P62313	LSM6	U6 snRNA-associated Sm-like protein LSm6, GN=Lsm6	0.78	0.61	0.78	1	51.97
F8VQ05	F8VQ05	FRY-like transcription coactivator, GN=Fryl	0.99	0.77	0.78	1	35.43
Q9CXT8	MPPB	Mitochondrial-processing peptidase subunit beta, GN=Pmpcb	1.8	1.4	0.78	1	75.23
P26339	CMGA	Chromogranin-A, GN=Chga	1.12	0.86	0.77	1	108.78
P29416	HEXA	Beta-hexosaminidase subunit alpha, GN=Hexa	1.12	0.86	0.77	2	119.68
Q3UX10	TBAL3	Tubulin alpha chain-like 3, GN=Tubal3	1.92	1.47	0.77	1	168.89
Q921M3	SF3B3	Splicing factor 3B subunit 3, GN=Sf3b3	1.19	0.91	0.76	5	107.65
Q91VM3	WIPI4	WD repeat domain phosphoinositide-interacting protein 4, GN=Wdr45	1.55	1.17	0.75	1	37.16
A0A140LJ36	A0A140LJ36	PRA1 family protein, GN=Gm45208	1.55	1.17	0.75	1	37.16
Q8VH51	RBM39	RNA-binding protein 39, GN=Rbm39	1.09	0.82	0.75	2	122.69
P04919	B3AT	Band 3 anion transport protein, GN=Slc4a1	1.03	0.77	0.75	1	65.68

D3YXB7	D3YXB7	Paraplegin, GN=Spg7	0.98	0.73	0.74	1	51.53
Q60738	ZNT1	Zinc transporter 1, GN=Slc30a1	0.82	0.61	0.74	1	75.79
Q9D6P8	CALL3	Calmodulin-like protein 3, GN=Calml3	1.44	1.07	0.74	1	168.04
Q8BH88	DEP1B	DEP domain-containing protein 1B, GN=Depdc1b	1.24	0.92	0.74	1	16.16
Q60749	KHDR1	KH domain-containing RNA-binding signal transduction-associated protein 1, GN=Khdrbs1	1.31	0.97	0.74	1	93.12
P62806	H4	Histone H4, GN=Hist1h4a	0.8	0.59	0.74	9	181.49
P28867	KPCD	Protein kinase C delta type, GN=Prkcd	1.39	1.02	0.73	1	79.34
Q6NVE9	PPTC7	Protein phosphatase PTC7 homolog, GN=Pptc7	1.16	0.85	0.73	1	88.49
A0A087WP80	A0A087WP80	Limbic system-associated membrane protein, GN=Lsamp	1.01	0.74	0.73	1	210.69
Q9D1H7	GET4	Golgi to ER traffic protein 4 homolog, GN=Get4	1.21	0.88	0.73	1	84.3
Q8BUK6	HOOK3	Protein Hook homolog 3, GN=Hook3	0.69	0.5	0.72	3	96.56
P46662	MERL	Merlin, GN=Nf2	0.98	0.71	0.72	1	55.06
Q8K4Z5	SF3A1	Splicing factor 3A subunit 1, GN=Sf3a1	1.2	0.86	0.72	1	50.56
Q99JB2	STML2	Stomatin-like protein 2 mitochondrial, GN=Stoml2	1.57	1.12	0.71	4	173.65
Q8BZA9	TIGAR	Fructose-2 6-bisphosphatase TIGAR, GN=Tigar	0.97	0.69	0.71	1	53.9

A0A0N4SVV8	A0A0N4SVV8	L-lactate dehydrogenase (Fragment), GN=Ldhb	1.86	1.31	0.70	1	171.63
P07309	TTHY	Transthyretin, GN=Ttr	1.04	0.73	0.70	3	136.58
Q8R086	SUOX	Sulfite oxidase mitochondrial, GN=Suox	0.91	0.63	0.69	1	92.73
Q9CQW2	ARL8B	ADP-ribosylation factor-like protein 8B, GN=Arl8b	1.35	0.93	0.69	1	168.84
O88879	APAF	Apoptotic protease-activating factor 1, GN=Apaf1	1.06	0.73	0.69	1	33.13
G3X8U3	G3X8U3	MCG6895, GN=2210016F16Rik	1.21	0.83	0.69	1	63.69
A0A0J9YVH8	A0A0J9YVH8	Ras/Rap GTPase-activating protein SynGAP (Fragment), GN=Syngap1	1.52	1.04	0.68	1	323.37
H3BJM7	H3BJM7	Arf-GAP with SH3 domain ANK repeat and PH domain-containing protein 1 (Fragment), GN=Asap1	1.46	0.98	0.67	1	70.88
E9PVS5	E9PVS5	MICoscomplex subunit MIC60 (Fragment), GN=Immt	1.5	0.99	0.66	1	193.01
F7ASU3	F7ASU3	Mitochondrial Rho GTPase 1 (Fragment), GN=Rhot1	0.91	0.6	0.66	1	87.14
Q99LE6	ABCF2	ATP-binding cassette sub-family F member 2, GN=Abcf2	1.37	0.9	0.66	1	41.14
E9PWE4	E9PWE4	Transcription factor E2-alpha, GN=Tcf3	0.96	0.63	0.66	1	19.66
H3BJQ8	H3BJQ8	Glypican-5, GN=Gpc5	1.21	0.79	0.65	1	22.79
A8DUK4	A8DUK4	Beta-globin, GN=Hbbt1	0.53	0.34	0.64	3	259.2
Q8CG72	ARHL2	Poly(ADP-ribose) glycohydrolase ARH3, GN=Adprhl2	1.47	0.93	0.63	1	43.86

B2RXC1	TPC11	Trafficking protein particle complex subunit 11, GN=Trappc11	1.48	0.92	0.62	1	80.57
P11679	K2C8	Keratin type II cytoskeletal 8, GN=Krt8	1.08	0.67	0.62	1	90.97
P43277	H13	Histone H1.3, GN=Hist1h1d	0.96	0.59	0.61	1	137.12
Q8BVG4	DPP9	Dipeptidyl peptidase 9, GN=Dpp9	1.64	0.98	0.60	1	72.07
A0A0R4J0U2	A0A0R4J0U2	Serine/threonine-protein phosphatase 4 regulatory subunit 2, GN=Ppp4r2	1.72	1.02	0.59	1	79.87
P28028	BRAF	Serine/threonine-protein kinase B-raf, GN=Braf	1.73	1.02	0.59	1	161.84
P48024	EIF1	Eukaryotic translation initiation factor 1, GN=Eif1	1.51	0.89	0.59	1	128.93
Q19AB2	Q19AB2	ROBO2 isoform b, GN=Robo2	1.19	0.7	0.59	1	49.02
Q8BTM8	FLNA	Filamin-A, GN=Flna	1.6	0.91	0.57	6	140.42
E9Q9N6	E9Q9N6	Non-specific serine/threonine protein kinase, GN=Mark2	1.53	0.67	0.44	1	143.16

Table S-2. The 40 proteins in the hippocampus that were changed significantly by memantine treatment.

Table S-2. The 40 proteins in the hippocampus that were changed significantly by memantine treatment. These proteins have met the criteria, the ratio of memantine / AD in expression levels of at least 1.5-fold (up-regulation) or at least ＜0.67-fold (down-regulation) as defined in the experimental procedures.

Accession	Protein name	Description	Ratio			Unique	-10lgP
			AD/WT	Memantine/WT	Memantine/AD		
P48725	PCNT	Pericentrin,GN=Pcnt	0.79	2.83	3.58	1	66.89
Q5SX46	Q5SX46	Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment),GN=Slc25a11	1.48	4.12	2.78	1	200.12
E9QM77	E9QM77	Ataxin-2,GN=Atxn2	0.65	1.54	2.37	1	55.46
E9Q555	RN213	E3 ubiquitin-protein ligase RNF213,GN=Rnf213	0.8	1.88	2.35	1	65.4
P29387	GBB4	Guanine nucleotide-binding protein subunit beta-4,GN=Gnb4	1.15	2.62	2.28	2	172.11
Q5SGK3	AOXB	Aldehyde oxidase 2,GN=Aox2	1.53	3.36	2.20	1	19.72
Q80WM5	HPLN3	Hyaluronan and proteoglycan link protein 3,GN=Hapln3	0.9	1.97	2.19	1	97.78
Q9Z0J1	RECK	Reversion-inducing cysteine-rich protein with Kazal motifs,GN=Reck	1.1	2.19	1.99	1	20.71
P83510	TNIK	Traf2 and NCK-interacting protein kinase,GN=Tnik	1.26	2.49	1.98	2	173.49

Q9ERB0	SNP29	Synaptosomal-associated protein 29,GN=Snap29	0.89	1.75	1.97	3	91.63
Q9D1X0	NOL3	Nucleolar protein 3,GN=Nol3	0.79	1.41	1.78	2	109.74
Q8BGJ9	U2AF4	Splicing factor U2AF 26 kDa subunit,GN=U2af1l4	0.62	1.03	1.66	1	38.17
Q9D883	U2AF1	Splicing factor U2AF 35 kDa subunit,GN=U2af1	0.62	1.03	1.66	1	38.17
Q99JH7	CSTN3	Calsyntenin-3,GN=Clstn3	0.73	1.18	1.62	1	20.68
Q5HZI2	C2C4C	C2 calcium-dependent domain-containing protein 4C,GN=C2cd4cC2CD4 family	0.83	1.3	1.57	1	44.94
P56371	RAB4A	Ras-related protein Rab-4A,GN=Rab4a	1.15	1.78	1.55	1	115.33
P20065	TYB4	Thymosin beta-4,GN=Tmsb4x	1.14	1.75	1.54	4	134.25
A2ARZ7	A2ARZ7	RAB22A member RAS oncogene family isoform CRA_c,GN=Rab22a	0.98	1.5	1.53	2	89.67
Q9JMD0	ZN207	BUB3-interacting and GLEBS motif-containing protein ZNF207,GN=Znf207	0.79	1.2	1.52	1	71.53
A0A0J9YUM2	A0A0J9YUM2	Ras/Rap GTPase-activating protein SynGAP (Fragment),GN=Syngap1	1.41	2.14	1.52	1	323.14
Q9Z2H2	RGS6	Regulator of G-protein signaling 6,GN=Rgs6	0.99	1.5	1.52	3	112.67
A0A0A6YW90	A0A0A6YW90	Glutamate receptor 2,GN=Gria2	0.8	1.21	1.51	1	269.66
Q6NVD9	BFSP2	Phakinin,GN=Bfsp2	0.92	1.39	1.51	1	19.64

E9PVS5	E9PVS5	MICOS complex subunit MIC60 (Fragment),GN=Immt	1.5	0.99	0.66	1	193.01
F7ASU3	F7ASU3	Mitochondrial Rho GTPase 1 (Fragment),GN=Rhot1	0.91	0.6	0.66	1	87.14
Q99LE6	ABCF2	ATP-binding cassette sub-family F member 2,GN=Abcf2	1.37	0.9	0.66	1	41.14
E9PWE4	E9PWE4	Transcription factor E2-alpha,GN=Tcf3	0.96	0.63	0.66	1	19.66
H3BJQ8	H3BJQ8	Glypican-5,GN=Gpc5	1.21	0.79	0.65	1	22.79
A8DUK4	A8DUK4	Beta-globin,GN=Hbbt1	0.53	0.34	0.64	3	259.2
Q8CG72	ARHL2	Poly(ADP-ribose) glycohydrolase ARH3,GN=Adprhl2	1.47	0.93	0.63	1	43.86
B2RXC1	TPC11	Trafficking protein particle complex subunit 11,GN=Trappc11	1.48	0.92	0.62	1	80.57
P11679	K2C8	Keratin type II cytoskeletal 8,GN=Krt8	1.08	0.67	0.62	1	90.97
P43277	H13	Histone H1.3,GN=Hist1h1d	0.96	0.59	0.61	1	137.12
Q8BVG4	DPP9	Dipeptidyl peptidase 9,GN=Dpp9	1.64	0.98	0.60	1	72.07

A0A0R4J0U2	A0A0R4J0U2	Serine/threonine-protein phosphatase 4 regulatory subunit 2,GN=Ppp4r2	1.72	1.02	0.59	1	79.87
P28028	BRAF	Serine/threonine-protein kinase B-raf,GN=Braf	1.73	1.02	0.59	1	161.84
P48024	EIF1	Eukaryotic translation initiation factor 1,GN=Eif1	1.51	0.89	0.59	1	128.93
Q19AB2	Q19AB2	ROBO2 isoform b,GN=Robo2	1.19	0.7	0.59	1	49.02
Q8BTM8	FLNA	Filamin-A,GN=Flna	1.6	0.91	0.57	6	140.42
E9Q9N6	E9Q9N6	Non-specific serine/threonine protein kinase,GN=Mark2	1.53	0.67	0.44	1	143.16

Table S-3. 342 proteins in the cerebral cortex that were significantly changed by memantine treatment.

Table S-3. 342 proteins in the cerebral cortex that were significantly changed by memantine treatment. These proteins have met the criteria, the ratio of memantine / AD in expression levels of at least 1.2-fold (up-regulation) or at least ＜0.83-fold (down-regulation) as defined in the experimental procedures.

Accession	Protein name	Description	Ratio			Unique	-10lgP
			AD/WT	Memantine/WT	Memantine/AD		
Q9CXT8	MPPB	Mitochondrial-processing peptidase subunit beta, GN=Pmpcb	0.98	2.64	2.69	1	89.76
P48725	PCNT	Pericentrin, GN=Pcnt	0.93	2.44	2.62	1	83.85
Q91X96	MSS4	Guanine nucleotide exchange factor MSS4, GN=Rabif	0.92	1.95	2.12	1	38.67
Q6X893	CTL1	Choline transporter-like protein 1, GN=Slc44a1	0.66	1.36	2.06	1	154.36
Q9CQB5	CISD2	CDGSH iron-sulfur domain-containing protein 2, GN=Cisd2	1.05	2.07	1.97	1	64.37
Q64010	CRK	Adapter molecule crk, GN=Crk	1.02	1.88	1.84	1	201.47
P50153	GBG4	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-4, GN=Gng4	0.73	1.33	1.82	2	111.86
Q8C129	LCAP	Leucyl-cystinyl aminopeptidase, GN=Lnpep	0.48	0.84	1.75	1	82.37
F6TYB7	F6TYB7	Myelin basic protein (Fragment), GN=Mbp	0.89	1.44	1.62	2	261.39
Q3TDN2	FAF2	FAS-associated factor 2, GN=Faf2	0.9	1.43	1.59	1	117.52

Q6PGB8	SMCA1	Probable global transcription activator SNF2L1, GN=Smarca1	0.96	1.5	1.56	1	66.05
P55258	RAB8A	Ras-related protein Rab-8A, GN=Rab8a	1.16	1.81	1.56	1	167.34
P83870	PHF5A	PHD finger-like domain-containing protein 5A, GN=Phf5a	0.38	0.59	1.55	1	72.42
Q9D4H1	EXOC2	Exocyst complex component 2, GN=Exoc2	0.94	1.45	1.54	1	128.79
B7ZCJ1	B7ZCJ1	Rho GTPase-activating protein 21, GN=Arhgap21	0.79	1.17	1.48	1	96.29
A0A1W2P772	A0A1W2P772	Plasma membrane calcium-transporting ATPase 1 (Fragment), GN=Atp2b1	0.55	0.81	1.47	1	191.19
D3Z0L4	D3Z0L4	MICOS complex subunit (Fragment), GN=Chchd3	0.89	1.31	1.47	1	128.02
Q80UU9	PGRC2	Membrane-associated progesterone receptor component 2, GN=Pgrmc2	0.73	1.06	1.45	1	109.61
O08677	KNG1	Kininogen-1, GN=Kng1	0.68	0.97	1.43	1	86.71
Q80UP3	DGKZ	Diacylglycerol kinase zeta, GN=Dgkz	1.04	1.48	1.42	2	127.01
Q03137	EPHA4	Ephrin type-A receptor 4, GN=Epha4	0.8	1.13	1.41	3	164.12
Q9D7X3	DUS3	Dual specificity protein phosphatase 3, GN=Dusp3	0.8	1.12	1.40	1	166.98
Q9D9V3	ECHD1	Ethylmalonyl-CoA decarboxylase, GN=Echdc1	1.17	1.61	1.38	1	145.5
Q91ZR1	RAB4B	Ras-related protein Rab-4B, GN=Rab4b	0.83	1.14	1.37	1	175.74
P61087	UBE2K	Ubiquitin-conjugating enzyme E2 K, GN=Ube2k	0.89	1.21	1.36	2	154.29

P28741	KIF3A	Kinesin-like protein KIF3A, GN=Kif3a	0.81	1.1	1.36	3	142
A0A140LIJ4	A0A140LIJ4	Dynein axonemal heavy chain 14, GN=Dnah14	0.96	1.3	1.35	1	81.01
Q3UHB8	CC177	Coiled-coil domain-containing protein 177, GN=Ccdc177	1.02	1.38	1.35	2	159.9
Q9DB25	ALG5	Dolichyl-phosphate beta-glucosyltransferase, GN=Alg5	0.71	0.96	1.35	1	49.53
Q9D8B4	NDUAB	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11, GN=Ndufa11	0.69	0.93	1.35	1	102.34
Q9DBS5	KLC4	Kinesin light chain 4, GN=Klc4	0.77	1.03	1.34	1	136.81
Q9CQC9	SAR1B	GTP-binding protein SAR1b, GN=Sar1b	0.75	1	1.33	1	143.58
F8WID5	F8WID5	Tropomyosin alpha-1 chain, GN=Tpm1	0.92	1.22	1.33	1	164.54
Q9EQF5	DPYS	Dihydropyrimidinase, GN=Dpys	0.71	0.94	1.32	1	47.12
S4R1C4	S4R1C4	Calcium-transporting ATPase, GN=Atp2b2	0.85	1.12	1.32	1	331.6
Q9CRC8	LRC40	Leucine-rich repeat-containing protein 40, GN=Lrrc40	0.92	1.21	1.32	1	116.9
F6V2U0	F6V2U0	Type I inositol 3 4-bisphosphate 4-phosphatase, GN=Inpp4a	0.7	0.91	1.30	1	186.05
O70250	PGAM2	Phosphoglycerate mutase 2, GN=Pgam2	1.2	1.55	1.29	1	152.71
Q9D662	SC23B	Protein transport protein Sec23B, GN=Sec23b	0.79	1.02	1.29	1	100.6
P16858	G3P	Glyceraldehyde-3-phosphate dehydrogenase, GN=Gapdh	0.83	1.07	1.29	4	368.99

Q7TNC4	LC7L2	Putative RNA-binding protein Luc7-like 2, GN=Luc7l2	0.92	1.18	1.28	1	132.05
Q9WTQ5	AKA12	A-kinase anchor protein 12, GN=Akap12	0.71	0.91	1.28	4	175.44
Q9WUT3	KS6A2	Ribosomal protein S6 kinase alpha-2, GN=Rps6ka2	0.82	1.05	1.28	2	90.79
Q9CTY5	MICU3	Calcium uptake protein 3 mitochondrial, GN=Micu3	0.87	1.11	1.28	1	86.62
Q9Z2W0	DNPEP	Aspartyl aminopeptidase, GN=Dnpep	0.84	1.07	1.27	3	162.68
Q9WUC3	LY6H	Lymphocyte antigen 6H, GN=Ly6h	1.05	1.33	1.27	2	123.58
F6RT34	F6RT34	Myelin basic protein (Fragment), GN=Mbp	1.07	1.35	1.26	3	280.79
O54946	DNJB6	DnaJ homolog subfamily B member 6, GN=Dnajb6	1.04	1.31	1.26	1	71.86
Q921Q7	RIN1	Ras and Rab interactor 1, GN=Rin1	0.85	1.07	1.26	2	72.47
A2A7S7	A2A7S7	Tyrosine--tRNA ligase, GN=Yars	1.05	1.32	1.26	1	206.01
Q5NCX5	NEUL4	Neuralized-like protein 4, GN=Neurl4	0.98	1.23	1.26	1	33.24
Q61074	PPM1G	Protein phosphatase 1G, GN=Ppm1g	0.95	1.19	1.25	2	146.75
P23819	GRIA2	Glutamate receptor 2, GN=Gria2	0.93	1.16	1.25	1	279.26
P03995	GFAP	Glial fibrillary acidic protein, GN=Gfap	0.85	1.06	1.25	18	266.3
Q80WM4	HPLN4	Hyaluronan and proteoglycan link protein 4, GN=Hapln4	0.99	1.23	1.24	1	95.84

Q8C754	VPS52	Vacuolar protein sorting-associated protein 52 homolog, GN=Vps52	0.92	1.14	1.24	2	66.35
Q9JIF0	ANM1	Protein arginine N-methyltransferase 1, GN=Prmt1	0.84	1.04	1.24	2	107.33
P80560	PTPR2	Receptor-type tyrosine-protein phosphatase N2, GN=Ptprn2	0.97	1.2	1.24	4	168.92
Q8VEJ9	VPS4A	Vacuolar protein sorting-associated protein 4A, GN=Vps4a	0.94	1.16	1.23	2	97.96
E9Q7Q3	E9Q7Q3	Tropomyosin alpha-3 chain, GN=Tpm3	0.94	1.16	1.23	1	211.99
E9PZ16	E9PZ16	Basement membrane-specific heparan sulfate proteoglycan core protein, GN=Hspg2	0.99	1.22	1.23	3	204.42
Q9QXK3	COPG2	Coatomer subunit gamma-2, GN=Copg2	0.82	1.01	1.23	1	105.49
A0A0N4SVT8	A0A0N4SVT8	DnaJ homolog subfamily B member 8 (Fragment), GN=Dnajb8	0.96	1.18	1.23	1	26.6
Q3UYG8	MACD2	O-acetyl-ADP-ribose deacetylase MACROD2, GN=Macrod2	1.02	1.25	1.23	1	109.24
P61961	UFM1	Ubiquitin-fold modifier 1, GN=Ufm1	1.03	1.26	1.22	2	69.67
P23927	CRYAB	Alpha-crystallin B chain, GN=Cryab	2.54	3.1	1.22	3	123.06
Q60790	RASA3	Ras GTPase-activating protein 3, GN=Rasa3	0.91	1.11	1.22	3	138.86
Q8BFQ8	GALD1	Glutamine amidotransferase-like class 1 domain-containing protein 1, GN=Gatd1	0.97	1.18	1.22	1	120.51
Q9JHG6	RCAN1	Calcipressin-1, GN=Rcan1	0.93	1.13	1.22	1	70.88

Q9JLR9	HIG1A	HIG1 domain family member 1A mitochondrial, GN=Higd1a	0.7	0.85	1.21	1	24.56
Q9QZB7	ARP10	Actin-related protein 10, GN=Actr10	0.98	1.19	1.21	2	124.82
A0A140LHX5	A0A140LHX5	Protein unc-13 homolog B, GN=Unc13b	1.03	1.25	1.21	1	109.9
Q99LS3	SERB	Phosphoserine phosphatase, GN=Psph	0.67	0.81	1.21	1	74.65
Q9WVK4	EHD1	EH domain-containing protein 1, GN=Ehd1	1.2	1.45	1.21	1	195.37
Q9DCS3	MECR	Enoyl-[acyl-carrier-protein] reductase mitochondrial, GN=Mecr	1.11	1.34	1.21	3	188.44
Q8K4R4	PITC1	Cytoplasmic phosphatidylinositol transfer protein 1, GN=Pitpnc1	0.97	1.17	1.21	3	140.07
Q9D061	ACBD6	Acyl-CoA-binding domain-containing protein 6, GN=Acbd6	0.97	1.17	1.21	2	140.28
O08530	S1PR1	Sphingosine 1-phosphate receptor 1, GN=S1pr1	0.83	1	1.20	1	78.29
P42208	NEDD5	Septin-2, GN=Sept2	0.95	1.14	1.20	4	182.32
Q9D906	ATG7	Ubiquitin-like modifier-activating enzyme ATG7, GN=Atg7	0.85	1.02	1.20	1	120.49
Q91Z67	SRGP2	SLIT-ROBO Rho GTPase-activating protein 2, GN=Srgap2	1	0.83	0.83	3	130.37
Q8K0D0	CDK17	Cyclin-dependent kinase 17, GN=Cdk17	1.29	1.07	0.83	1	125.94
Q922B2	SYDC	Aspartate--tRNA ligase cytoplasmic, GN=Dars	1.23	1.02	0.83	12	186.61
A2CG49	KALRN	Kalirin, GN=Kalrn	1.17	0.97	0.83	1	142.35

Q9DAW9	CNN3	Calponin-3, GN=Cnn3	1.17	0.97	0.83	1	131.59
F6VQ81	F6VQ81	Tumor protein D54 (Fragment), GN=Tpd52l2	1.11	0.92	0.83	3	147.89
Q922F4	TBB6	Tubulin beta-6 chain, GN=Tubb6	0.99	0.82	0.83	2	345.58
P62270	RS18	40S ribosomal protein S18, GN=Rps18	1.22	1.01	0.83	4	122.19
A2AEX6	A2AEX6	Four and a half LIM domains protein 1, GN=Fhl1	1.16	0.96	0.83	4	163.43
Q9CZR8	EFTS	Elongation factor Ts mitochondrial, GN=Tsfm	1.1	0.91	0.83	1	139.78
Q922Q4	P5CR2	Pyrroline-5-carboxylate reductase 2, GN=Pycr2	1.27	1.05	0.83	1	112.58
Q9CWE0	MFR1L	Mitochondrial fission regulator 1-like, GN=Mtfr1l	1.21	1	0.83	2	176.52
P41216	ACSL1	Long-chain-fatty-acid--CoA ligase 1, GN=Acsl1	1.38	1.14	0.83	8	157.07
Q9EPL8	IPO7	Importin-7, GN=Ipo7	1.03	0.85	0.83	4	143.62
O54901	OX2G	OX-2 membrane glycoprotein, GN=Cd200	1.2	0.99	0.83	4	150.49
Q8BH58	TIPRL	TIP41-like protein, GN=Tiprl	1.08	0.89	0.82	4	138.21
O88492	PLIN4	Perilipin-4, GN=Plin4	1.25	1.03	0.82	1	47
Q8BGH4	REEP1	Receptor expression-enhancing protein 1, GN=Reep1	1.25	1.03	0.82	2	126.61
Q9ESW4	AGK	Acylglycerol kinase mitochondrial, GN=Agk	1.19	0.98	0.82	11	229.63

Q59J78	MIMIT	Mimitin mitochondrial, GN=Ndufaf2	0.79	0.65	0.82	2	88.23
P14115	RL27A	60S ribosomal protein L27a, GN=Rpl27a	1.29	1.06	0.82	5	131.95
Q920E5	FPPS	Farnesyl pyrophosphate synthase, GN=Fdps	1.29	1.06	0.82	5	168.74
P47802	MTX1	Metaxin-1, GN=Mtx1	1.12	0.92	0.82	4	150.09
P70663	SPRL1	SPARC-like protein 1, GN=Sparcl1	1.4	1.15	0.82	3	213.02
Q8K0T7	UN13C	Protein unc-13 homolog C, GN=Unc13c	1.4	1.15	0.82	1	94.87
Q8C6E0	CFA36	Cilia- and flagella-associated protein 36, GN=Cfap36	1.23	1.01	0.82	1	131.4
Q8CGK7	GNAL	Guanine nucleotide-binding protein G(olf) subunit alpha, GN=Gnal	1.23	1.01	0.82	2	186.61
Q99KH8	STK24	Serine/threonine-protein kinase 24, GN=Stk24	1.23	1.01	0.82	3	168.92
Q9CYR0	SSBP	Single-stranded DNA-binding protein mitochondrial, GN=Ssbp1	1.23	1.01	0.82	2	102.39
E9Q3M9	E9Q3M9	RIKEN cDNA 2010300C02 gene, GN=2010300C02Rik	1.23	1.01	0.82	2	180.25
Q02248	CTNB1	Catenin beta-1, GN=Ctnnb1	0.95	0.78	0.82	1	230.08
P26339	CMGA	Chromogranin-A, GN=Chga	1.06	0.87	0.82	1	101.94
Q8VDQ1	PTGR2	Prostaglandin reductase 2, GN=Ptgr2	1.11	0.91	0.82	5	153.28
O88543	CSN3	COP9 signalosome complex subunit 3, GN=Cops3	1.21	0.99	0.82	4	144.6

P62192	PRS4	26S proteasome regulatory subunit 4, GN=Psmc1	1.21	0.99	0.82	8	205.76
A0A1B0GT12	A0A1B0GT12	Small conductance calcium-activated potassium channel protein 2, GN=Kcnn2	0.99	0.81	0.82	1	49.03
Q9D6S7	RRFM	Ribosome-recycling factor mitochondrial, GN=Mrrf	1.26	1.03	0.82	1	135.19
Q8C166	CPNE1	Copine-1, GN=Cpne1	1.15	0.94	0.82	2	104.7
Q99JY8	PLPP3	Phospholipid phosphatase 3, GN=Plpp3	1.25	1.02	0.82	3	74.11
Q8BHL3	TB10B	TBC1 domain family member 10B, GN=Tbc1d10b	1.51	1.23	0.81	1	105.27
P56395	CYB5	Cytochrome b5, GN=Cyb5a	1.13	0.92	0.81	3	163.17
Q91YH5	ATLA3	Atlastin-3, GN=Atl3	1.34	1.09	0.81	1	100.48
A2A8L5	PTPRF	Receptor-type tyrosine-protein phosphatase F, GN=Ptprf	1.07	0.87	0.81	2	159.56
Q8CFE4	SCYL2	SCY1-like protein 2, GN=Scyl2	1.07	0.87	0.81	2	112.42
Q924N4	S12A6	Solute carrier family 12 member 6, GN=Slc12a6	1.12	0.91	0.81	1	132.66
Q8C0C7	SYFA	Phenylalanine--tRNA ligase alpha subunit, GN=Farsa	1.17	0.95	0.81	6	170.04
E9PY39	E9PY39	Uncharacterized protein, GN=Gm20431	1.54	1.25	0.81	1	181.48
P08414	KCC4	Calcium/calmodulin-dependent protein kinase type IV, GN=Camk4	1.27	1.03	0.81	3	166.17
Q9WU84	CCS	Copper chaperone for superoxide dismutase, GN=Ccs	1.27	1.03	0.81	1	113.1

Q9CR00	PSMD9	26S proteasome non-ATPase regulatory subunit 9, GN=Psmd9	1.11	0.9	0.81	4	107.46
Q9D1D4	TMEDA	Transmembrane emp24 domain-containing protein 10, GN=Tmed10	1.16	0.94	0.81	3	132.69
Q9JII6	AK1A1	Alcohol dehydrogenase [NADP(+)], GN=Akr1a1	1.16	0.94	0.81	11	229.27
E9Q7G0	NUMA1	Nuclear mitotic apparatus protein 1, GN=Numa1	1.15	0.93	0.81	3	143.87
Q99JR1	SFXN1	Sideroflexin-1, GN=Sfxn1	1.15	0.93	0.81	4	206.93
Q60829	PPR1B	Protein phosphatase 1 regulatory subunit 1B, GN=Ppp1r1b	1.2	0.97	0.81	5	162.75
Q9DCP2	S38A3	Sodium-coupled neutral amino acid transporter 3, GN=Slc38a3	1.3	1.05	0.81	3	110.17
Q9JKC6	CEND	Cell cycle exit and neuronal differentiation protein 1, GN=Cend1	1.3	1.05	0.81	3	119.7
Q64338	PDE1C	Calcium/calmodulin-dependent 3' 5'-cyclic nucleotide phosphodiesterase 1C, GN=Pde1c	1.35	1.09	0.81	1	81.26
Q8R2Y0	ABHD6	Monoacylglycerol lipase ABHD6, GN=Abhd6	1.09	0.88	0.81	3	111.25
Q99JT1	GATB	Glutamyl-tRNA(Gln) amidotransferase subunit B mitochondrial, GN=Gatb	1.14	0.92	0.81	1	59.3
Q9CZR3	TM40L	Mitochondrial import receptor subunit TOM40B, GN=Tomm40l	0.88	0.71	0.81	1	86.58
Q9Z268	RASL1	RasGAP-activating-like protein 1, GN=Rasal1	0.88	0.71	0.81	9	223.64
Q8BJI1	S6A17	Sodium-dependent neutral amino acid transporter SLC6A17, GN=Slc6a17	1.19	0.96	0.81	4	187.93

Q922H2	PDK3	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3 mitochondrial, GN=Pdk3	1.24	1	0.81	4	165.42
Q6P1F6	2ABA	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform, GN=Ppp2r2a	1.29	1.04	0.81	3	205.92
Q05A62	DNAL1	Dynein light chain 1 axonemal, GN=Dnal1	0.98	0.79	0.81	1	74.68
Q9D6P8	CALL3	Calmodulin-like protein 3, GN=Calml3	1.08	0.87	0.81	1	172.36
Q14BI2	GRM2	Metabotropic glutamate receptor 2, GN=Grm2	1.13	0.91	0.81	5	197.26
Q8K097	LFG2	Protein lifeguard 2, GN=Faim2	1.23	0.99	0.80	1	70.68
O08848	RO60	60 kDa SS-A/Ro ribonucleoprotein, GN=Trove2	1.22	0.98	0.80	1	116.3
P16332	MUTA	Methylmalonyl-CoA mutase mitochondrial, GN=Mut	1.22	0.98	0.80	4	140.8
Q9DC16	ERGI1	Endoplasmic reticulum-Golgi intermediate compartment protein 1, GN=Ergic1	1.22	0.98	0.80	3	130.83
Q03157	APLP1	Amyloid-like protein 1, GN=Aplp1	1.16	0.93	0.80	1	133.65
Q3UYC0	PPM1H	Protein phosphatase 1H, GN=Ppm1h	1.21	0.97	0.80	8	204.76
Q64524	H2B2E	Histone H2B type 2-E, GN=Hist2h2be	1.26	1.01	0.80	1	168.34
Q8BFU3	RN214	RING finger protein 214, GN=Rnf214	1.36	1.09	0.80	4	180.9
A2ASQ1	AGRIN	Agrin, GN=Agrn	1	0.8	0.80	1	174.27

Q6P1B1	XPP1	Xaa-Pro aminopeptidase 1, GN=Xpnpep1	1.2	0.96	0.80	5	170.71
Q6P4T2	U520	U5 small nuclear ribonucleoprotein 200 kDa helicase, GN=Snrnp200	1.2	0.96	0.80	2	175.69
A3KFU8	A3KFU8	Polyadenylate-binding protein, GN=Pabpc4	0.95	0.76	0.80	2	191.35
Q3U214	MAST3	Microtubule-associated serine/threonine-protein kinase 3, GN=Mast3	1.19	0.95	0.80	1	98.21
Q6PAJ1	BCR	Breakpoint cluster region protein, GN=Bcr	1.14	0.91	0.80	5	145.44
O35609	SCAM3	Secretory carrier-associated membrane protein 3, GN=Scamp3	1.13	0.9	0.80	1	126.87
O88533	DDC	Aromatic-L-amino-acid decarboxylase, GN=Ddc	1.13	0.9	0.80	2	105.41
P97352	S10AD	Protein S100-A13, GN=S100a13	1.13	0.9	0.80	4	130.59
P28184	MT3	Metallothionein-3, GN=Mt3	1.62	1.29	0.80	1	65.93
Q9JHK4	PGTA	Geranylgeranyl transferase type-2 subunit alpha, GN=Rabggta	1.08	0.86	0.80	5	186.6
Q9ESN9	JIP3	C-Jun-amino-terminal kinase-interacting protein 3, GN=Mapk8ip3	1.47	1.17	0.80	2	150.61
Q8C181	MBNL2	Muscleblind-like protein 2, GN=Mbnl2	1.02	0.81	0.79	2	74.31
Q5F2E8	TAOK1	Serine/threonine-protein kinase TAO1, GN=Taok1	0.92	0.73	0.79	1	117.08
O70172	PI42A	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha, GN=Pip4k2a	1.16	0.92	0.79	2	186.43
E9Q2W9	E9Q2W9	Alpha-actinin-4 (Fragment), GN=Actn4	1.16	0.92	0.79	1	274.78

Q8BR63	F177A	Protein FAM177A1, GN=Fam177a1	1.74	1.38	0.79	1	114.22
Q3UVL4	VPS51	Vacuolar protein sorting-associated protein 51 homolog, GN=Vps51	1.11	0.88	0.79	3	133.3
Q99L13	3HIDH	3-hydroxyisobutyrate dehydrogenase mitochondrial, GN=Hibadh	1.35	1.07	0.79	4	182.05
P46471	PRS7	26S proteasome regulatory subunit 7, GN=Psmc2	1.2	0.95	0.79	11	210.98
A6H5Z3	EXC6B	Exocyst complex component 6B, GN=Exoc6b	1.53	1.21	0.79	1	116.3
Q64288	OMP	Olfactory marker protein, GN=Omp	1.29	1.02	0.79	4	160.44
P70206	PLXA1	Plexin-A1, GN=Plxna1	1.48	1.17	0.79	1	168.53
Q921M3	SF3B3	Splicing factor 3B subunit 3, GN=Sf3b3	1.24	0.98	0.79	4	154.78
Q8C729	F126B	Protein FAM126B, GN=Fam126b	1.14	0.9	0.79	3	149.8
Q9JHR7	IDE	Insulin-degrading enzyme, GN=Ide	0.95	0.75	0.79	2	85.94
Q8K1Z0	COQ9	Ubiquinone biosynthesis protein COQ9 mitochondrial, GN=Coq9	1.23	0.97	0.79	1	133.48
Q8CIQ7	DOCK3	Dedicator of cytokinesis protein 3, GN=Dock3	1.18	0.93	0.79	2	148.78
G3X922	G3X922	DnaJ heat shock protein family (Hsp40) member C13, GN=Dnajc13	1.18	0.93	0.79	1	117.85
Q60875	ARHG2	Rho guanine nucleotide exchange factor 2, GN=Arhgef2	1.32	1.04	0.79	8	220.88
Q4ACU6	SHAN3	SH3 and multiple ankyrin repeat domains protein 3, GN=Shank3	1.22	0.96	0.79	7	205.51

A2AJQ0	A2AJQ0	[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1 mitochondrial, GN=Pdp1	1.22	0.96	0.79	1	123.3
Q6ZWV7	RL35	60S ribosomal protein L35, GN=Rpl35	1.03	0.81	0.79	1	67.71
Q9Z0J4	NOS1	Nitric oxide synthase brain, GN=Nos1	1.03	0.81	0.79	6	92.13
Q91V77	Q91V77	Protein S100, GN=S100a1	1.03	0.81	0.79	1	105.07
Q9D8W7	OCAD2	OCIA domain-containing protein 2, GN=Ociad2	1.17	0.92	0.79	2	79.85
Q91YW3	DNJC3	DnaJ homolog subfamily C member 3, GN=Dnajc3	1.4	1.1	0.79	1	63.39
Q99J99	THTM	3-mercaptopyruvate sulfurtransferase, GN=Mpst	1.12	0.88	0.79	3	167.57
O08915	AIP	AH receptor-interacting protein, GN=Aip	0.79	0.62	0.78	1	150.37
Q6DFW4	NOP58	Nucleolar protein 58, GN=Nop58	1.3	1.02	0.78	4	145.8
Q8CJ19	MICA3	[F-actin]-methionine sulfoxide oxidase MICAL3, GN=Mical3	1.3	1.02	0.78	5	171.11
P23116	EIF3A	Eukaryotic translation initiation factor 3 subunit A, GN=Eif3a	1.16	0.91	0.78	8	190.78
Q9QUR6	PPCE	Prolyl endopeptidase, GN=Prep	1.43	1.12	0.78	4	187.84
Q7TQG5	Q7TQG5	Neogenin, GN=Neo1	0.83	0.65	0.78	1	93.92
O08914	FAAH1	Fatty-acid amide hydrolase 1, GN=Faah	1.52	1.19	0.78	1	132.94
P60764	RAC3	Ras-related C3 botulinum toxin substrate 3, GN=Rac3	1.24	0.97	0.78	2	159.95

Q8BKC5	IPO5	Importin-5, GN=Ipo5	1.19	0.93	0.78	4	166.87
Q9CZT8	RAB3B	Ras-related protein Rab-3B, GN=Rab3b	1.37	1.07	0.78	1	194.81
Q3UHA3	SPTCS	Spatacsin, GN=Spg11	1.09	0.85	0.78	1	34.12
Q8VHJ5	MARK1	Serine/threonine-protein kinase MARK1, GN=Mark1	1.18	0.92	0.78	2	189.11
Q3UZP4	SVIP	Small VCP/p97-interacting protein, GN=Svip	1.27	0.99	0.78	1	45.22
P43274	H14	Histone H1.4, GN=Hist1h1e	0.95	0.74	0.78	1	125.38
O35465	FKBP8	Peptidyl-prolyl cis-trans isomerase FKBP8, GN=Fkbp8	1.26	0.98	0.78	2	119.82
Q9ERG2	STRN3	Striatin-3, GN=Strn3	1.3	1.01	0.78	4	128.66
Q05BC3	EMAL1	Echinoderm microtubule-associated protein-like 1, GN=Eml1	1.12	0.87	0.78	1	138.4
Q61191	HCFC1	Host cell factor 1, GN=Hcfc1	1.15	0.89	0.77	1	121.14
Q68FF6	GIT1	ARF GTPase-activating protein GIT1, GN=Git1	1.15	0.89	0.77	1	189.25
P62911	RL32	60S ribosomal protein L32, GN=Rpl32	1.28	0.99	0.77	3	127.44
Q06890	CLUS	Clusterin, GN=Clu	1.28	0.99	0.77	7	192.02
Q8BWM0	PGES2	Prostaglandin E synthase 2, GN=Ptges2	1.28	0.99	0.77	4	155.79
Q80U56	AVL9	Late secretory pathway protein AVL9 homolog, GN=Avl9	1.23	0.95	0.77	2	116.79

Q8BXK8	AGAP1	Arf-GAP with GTPase ANK repeat and PH domain-containing protein 1, GN=Agap1	0.92	0.71	0.77	1	124.2
D3Z6P9	D3Z6P9	DEAD (Asp-Glu-Ala-Asp) box polypeptide 43, GN=Ddx43	1.05	0.81	0.77	1	22.13
Q9DB73	NB5R1	NADH-cytochrome b5 reductase 1, GN=Cyb5r1	1.31	1.01	0.77	3	121.5
P30681	HMGB2	High mobility group protein B2, GN=Hmgb2	1.22	0.94	0.77	1	100.67
Q9CS84	NRX1A	Neurexin-1, GN=Nrxn1	1.22	0.94	0.77	11	216.46
Q9JK81	MYG1	UPF0160 protein MYG1 mitochondrial, GN=Myg1	1.21	0.93	0.77	2	83.88
Q2PFD7	PSD3	PH and SEC7 domain-containing protein 3, GN=Psd3	1.25	0.96	0.77	1	255.19
D3YZZ5	D3YZZ5	Transmembrane p24-trafficking protein 7, GN=Tmed7	1.25	0.96	0.77	2	119
Q08642	PADI2	Protein-arginine deiminase type-2, GN=Padi2	1.24	0.95	0.77	3	135.66
Q9WU28	PFD5	Prefoldin subunit 5, GN=Pfdn5	1.28	0.98	0.77	3	136.98
Q8BP92	RCN2	Reticulocalbin-2, GN=Rcn2	1.02	0.78	0.76	2	164.72
Q6IR34	GPSM1	G-protein-signaling modulator 1, GN=Gpsm1	1.36	1.04	0.76	1	125.69
Q9Z130	HNRDL	Heterogeneous nuclear ribonucleoprotein D-like, GN=Hnrnpdl	1.31	1	0.76	2	134.99
O88746	TOM1	Target of Myb protein 1, GN=Tom1	1.39	1.06	0.76	1	92.93
Q99JR5	TINAL	Tubulointerstitial nephritis antigen-like, GN=Tinagl1	1.64	1.25	0.76	1	124.91

D3YZP9	CCDC6	Coiled-coil domain-containing protein 6, GN=Ccdc6	1.26	0.96	0.76	1	125.73
Q6PHS9	CA2D2	Voltage-dependent calcium channel subunit alpha-2/delta-2, GN=Cacna2d2	1.26	0.96	0.76	1	136.48
Q9WV18	GABR1	Gamma-aminobutyric acid type B receptor subunit 1, GN=Gabbr1	1.26	0.96	0.76	2	189.37
Q80WJ7	LYRIC	Protein LYRIC, GN=Mtdh	1.13	0.86	0.76	3	134.54
Q8CFI0	NED4L	E3 ubiquitin-protein ligase NEDD4-like, GN=Nedd4l	1.17	0.89	0.76	1	135.06
Q9D0T1	NH2L1	NHP2-like protein 1, GN=Snu13	1.33	1.01	0.76	2	90.59
Q05512	MARK2	Serine/threonine-protein kinase MARK2, GN=Mark2	1.16	0.88	0.76	3	235.34
P57722	PCBP3	Poly(rC)-binding protein 3, GN=Pcbp3	1.28	0.97	0.76	2	181.03
Q60709	Q60709	Amyloid-like protein 2, GN=Aplp2	1.03	0.78	0.76	1	104.22
Q8BXV2	BRI3B	BRI3-binding protein, GN=Bri3bp	1.4	1.06	0.76	1	98.21
Q9DC61	MPPA	Mitochondrial-processing peptidase subunit alpha, GN=Pmpca	1.15	0.87	0.76	1	80.45
O88809	DCX	Neuronal migration protein doublecortin, GN=Dcx	1.6	1.21	0.76	1	141.03
Q505F5	LRC47	Leucine-rich repeat-containing protein 47, GN=Lrrc47	1.27	0.96	0.76	7	201.29
Q9D554	SF3A3	Splicing factor 3A subunit 3, GN=Sf3a3	1.14	0.86	0.75	1	133.92
G3X972	G3X972	SEC24 related gene family member C (S. cerevisiae) isoform CRA_a, GN=Sec24c	1.18	0.89	0.75	2	173.46

Q9CQU3	RER1	Protein RER1, GN=Rer1	1.42	1.07	0.75	1	41.76
Q8K0E8	FIBB	Fibrinogen beta chain, GN=Fgb	1.33	1	0.75	1	170.36
Q3UGS4	MCRI1	Mapk-regulated corepressor-interacting protein 1, GN=Mcrip1	1.24	0.93	0.75	1	54.29
Q8VDP6	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase, GN=Cdipt	1.19	0.89	0.75	2	87.07
P13541	MYH3	Myosin-3, GN=Myh3	1.07	0.8	0.75	1	53.7
Q9ERT9	PPR1A	Protein phosphatase 1 regulatory subunit 1A, GN=Ppp1r1a	1.07	0.8	0.75	1	119.65
Q60902	EP15R	Epidermal growth factor receptor substrate 15-like 1, GN=Eps15l1	1.5	1.12	0.75	6	230
Q9R1R2	TRIM3	Tripartite motif-containing protein 3, GN=Trim3	1.46	1.09	0.75	1	134.38
F7BJK1	F7BJK1	Protocadherin 1 (Fragment), GN=Pcdh1	1.49	1.11	0.74	1	170.81
P05132	KAPCA	cAMP-dependent protein kinase catalytic subunit alpha, GN=Prkaca	0.98	0.73	0.74	1	154.04
O08919	NUMBL	Numb-like protein, GN=Numbl	1.21	0.9	0.74	4	204.38
Q922Q9	CHID1	Chitinase domain-containing protein 1, GN=Chid1	1.21	0.9	0.74	3	126.46
P70362	UFD1	Ubiquitin recognition factor in ER-associated degradation protein 1, GN=Ufd1	1.44	1.07	0.74	1	93.06
Q8VDP4	CCAR2	Cell cycle and apoptosis regulator protein 2, GN=Ccar2	1.31	0.97	0.74	4	151.89
Q61733	RT31	28S ribosomal protein S31 mitochondrial, GN=Mrps31	1.46	1.08	0.74	1	61.51

A0A1D5RL96	A0A1D5RL96	Uncharacterized protein, GN=A830010M20Rik	1.3	0.96	0.74	1	138.74
Q6ZPQ6	PITM2	Membrane-associated phosphatidylinositol transfer protein 2, GN=Pitpnm2	1.49	1.1	0.74	2	137.76
P58021	TM9S2	Transmembrane 9 superfamily member 2, GN=Tm9sf2	1.37	1.01	0.74	3	108.28
Q61290	CAC1E	Voltage-dependent R-type calcium channel subunit alpha-1E, GN=Cacna1e	1.29	0.95	0.74	2	166.94
Q9CZ04	CSN7A	COP9 signalosome complex subunit 7a, GN=Cops7a	1.36	1	0.74	2	117.15
Q9D8S4	ORN	Oligoribonuclease mitochondrial, GN=Rexo2	1.17	0.86	0.74	1	87.64
A2CG35	A2CG35	Ras-related protein Rab-12, GN=Rab12	1.13	0.83	0.73	2	137.61
Q9CQX8	RT36	28S ribosomal protein S36 mitochondrial, GN=Mrps36	1.31	0.96	0.73	1	117.77
Q9R020	ZRAB2	Zinc finger Ran-binding domain-containing protein 2, GN=Zranb2	1.25	0.91	0.73	1	50.07
Q8CGF6	WDR47	WD repeat-containing protein 47, GN=Wdr47	0.84	0.61	0.73	1	190.93
O35495	CDK14	Cyclin-dependent kinase 14, GN=Cdk14	1.38	1	0.72	2	93.54
G3X9K3	BIG1	Brefeldin A-inhibited guanine nucleotide-exchange protein 1, GN=Arfgef1	1.37	0.99	0.72	1	113.92
Q69Z26	CNTN4	Contactin-4, GN=Cntn4	1.47	1.06	0.72	3	106.38
Q8K2K6	AGFG1	Arf-GAP domain and FG repeat-containing protein 1, GN=Agfg1	1.29	0.93	0.72	2	128.25

Q3V132	ADT4	ADP/ATP translocase 4, GN=Slc25a31	1.03	0.74	0.72	1	164.35
Q9CR09	UFC1	Ubiquitin-fold modifier-conjugating enzyme 1, GN=Ufc1	1.17	0.84	0.72	1	40.44
Q08274	DMWD	Dystrophia myotonica WD repeat-containing protein, GN=Dmwd	1.24	0.89	0.72	1	92.86
P15864	H12	Histone H1.2, GN=Hist1h1c	1.06	0.76	0.72	2	127.31
Q91XF0	PNPO	Pyridoxine-5'-phosphate oxidase, GN=Pnpo	1.76	1.26	0.72	1	93.66
Q80TL1	ADCY2	Adenylate cyclase type 2, GN=Adcy2	1.44	1.03	0.72	1	137.21
Q68ED7	CRTC1	CREB-regulated transcription coactivator 1, GN=Crtc1	1.36	0.97	0.71	2	112.58
Q5SWU9	ACACA	Acetyl-CoA carboxylase 1, GN=Acaca	1.16	0.82	0.71	2	105.47
Q99LD9	EI2BB	Translation initiation factor eIF-2B subunit beta, GN=Eif2b2	1.39	0.98	0.71	2	100.06
A2A432	CUL4B	Cullin-4B, GN=Cul4b	1.22	0.86	0.70	1	145.59
Q8R1F1	NIBL1	Niban-like protein 1, GN=Fam129b	1.53	1.07	0.70	1	67.7
Q8BP48	MAP11	Methionine aminopeptidase 1, GN=Metap1	1.59	1.11	0.70	2	74.25
Q8BSN6	Q8BSN6	Putative uncharacterized protein, GN=Vamp4	1.19	0.83	0.70	1	94.8
Q501J6	DDX17	Probable ATP-dependent RNA helicase DDX17, GN=Ddx17	1.32	0.92	0.70	4	211.06
A0A087WNZ7	A0A087WNZ7	E3 ubiquitin-protein ligase TRIP12, GN=Trip12	1.32	0.92	0.70	1	76.38

O88696	CLPP	ATP-dependent Clp protease proteolytic subunit mitochondrial, GN=Clpp	1.45	1.01	0.70	1	125.11
Q9WVF8	TUSC2	Tumor suppressor candidate 2, GN=Tusc2	1.45	1.01	0.70	1	110.21
P49025	CTRO	Citron Rho-interacting kinase, GN=Cit	0.98	0.68	0.69	2	116.99
A2AJA9	CI172	Uncharacterized protein C9orf172 homolog, GN=Gm996	1.2	0.83	0.69	2	100.78
D3YWQ0	D3YWQ0	Diacylglycerol kinase, GN=Dgki	1.52	1.05	0.69	2	149.89
Q9R226	KHDR3	KH domain-containing RNA-binding signal transduction-associated protein 3, GN=Khdrbs3	1.22	0.84	0.69	2	121.77
P60824	CIRBP	Cold-inducible RNA-binding protein, GN=Cirbp	1.25	0.86	0.69	2	138.18
Q99JB2	STML2	Stomatin-like protein 2 mitochondrial, GN=Stoml2	1.25	0.86	0.69	1	175.35
Q9QXL1	KI21B	Kinesin-like protein KIF21B, GN=Kif21b	0.64	0.44	0.69	1	142.49
Q99KP3	CRYL1	Lambda-crystallin homolog, GN=Cryl1	1.37	0.94	0.69	1	109.61
Q9QZD8	DIC	Mitochondrial dicarboxylate carrier, GN=Slc25a10	1.33	0.91	0.68	2	121.54
Q3TCH7	CUL4A	Cullin-4A, GN=Cul4a	1.32	0.9	0.68	1	114.08
O08810	U5S1	116 kDa U5 small nuclear ribonucleoprotein component, GN=Eftud2	1.43	0.97	0.68	3	171.5
P35278	RAB5C	Ras-related protein Rab-5C, GN=Rab5c	1.49	1.01	0.68	2	176.31

Q8K0T4	KATL1	Katanin p60 ATPase-containing subunit A-like 1, GN=Katnal1	1.21	0.82	0.68	1	76.17
P97823	LYPA1	Acyl-protein thioesterase 1, GN=Lypla1	1.61	1.07	0.66	1	118.34
Q8R2Z3	S26A7	Anion exchange transporter, GN=Slc26a7	1.36	0.9	0.66	1	26.1
P56212	ARP19	cAMP-regulated phosphoprotein 19, GN=Arpp19	1.67	1.1	0.66	1	79.81
Q8BX94	OSBL2	Oxysterol-binding protein-related protein 2, GN=Osbpl2	1.51	0.99	0.66	1	62.67
Q80XI3	IF4G3	Eukaryotic translation initiation factor 4 gamma 3, GN=Eif4g3	1.34	0.87	0.65	3	143.96
P03888	NU1M	NADH-ubiquinone oxidoreductase chain 1, GN=Mtnd1	1.11	0.72	0.65	1	74.11
Q8R1S0	COQ6	Ubiquinone biosynthesis monooxygenase COQ6 mitochondrial, GN=Coq6	1.65	1.07	0.65	3	66.33
P50096	IMDH1	Inosine-5'-monophosphate dehydrogenase 1, GN=Impdh1	1.53	0.98	0.64	1	100.2
D3Z3B8	D3Z3B8	Disks large homolog 1, GN=Dlg1	0.99	0.63	0.64	1	223.24
Q0GNC1	INF2	Inverted formin-2, GN=Inf2	0.93	0.59	0.63	1	74.05
Q61033	LAP2A	Lamina-associated polypeptide 2 isoforms alpha/zeta, GN=Tmpo	1.33	0.84	0.63	2	115.13
A2ACM0	A2ACM0	Putative uncharacterized protein, GN=Rptor	1.58	0.99	0.63	1	124.14
Q3TCR7	Q3TCR7	Dynamin-2, GN=Dnm2	1.9	1.19	0.63	1	246.27
Q3U5Q7	CMPK2	UMP-CMP kinase 2 mitochondrial, GN=Cmpk2	1.55	0.97	0.63	1	102.4

Q9ES56	TPPC4		Trafficking protein particle complex subunit 4, GN=Trappc4	1.7	1.06	0.62	2	80.53
P97372	PSME2		Proteasome activator complex subunit 2, GN=Psme2	1.35	0.84	0.62	1	55.85
Q9DD18	DTD1		D-tyrosyl-tRNA(Tyr) deacylase 1, GN=Dtd1	1.24	0.77	0.62	1	80.82
Q3UMU9	HDGR2		Hepatoma-derived growth factor-related protein 2, GN=Hdgfl2	1.26	0.77	0.61	1	51.49
P48193		41	Protein 4.1, GN=Epb41	1.95	1.19	0.61	1	119.64
P62806	H4		Histone H4, GN=Hist1h4a	0.82	0.5	0.61	9	218.73
Q7TQK5	CCD93		Coiled-coil domain-containing protein 93, GN=Ccdc93	1.52	0.92	0.61	1	113.44
F8VQ05	F8VQ05		FRY-like transcription coactivator, GN=Fryl	1.65	0.98	0.59	1	80.5
P21300	ALD1		Aldose reductase-related protein 1, GN=Akr1b7	1.57	0.93	0.59	1	108.52
Q9WVA4	TAGL2		Transgelin-2, GN=Tagln2	1.78	1.04	0.58	3	167.3
E0CY16	E0CY16		Cell adhesion molecule 1, GN=Cadm1	1.7	0.99	0.58	1	196.6
Q9JMD3	STA10		START domain-containing protein 10, GN=Stard10	2.1	1.22	0.58	1	111.59
B2RWC4	B2RWC4		Gm88 protein, GN=Lrrc73	1.56	0.89	0.57	1	59.7
Q80VC9	CAMP3		Calmodulin-regulated spectrin-associated protein 3, GN=Camsap3	1.58	0.9	0.57	2	139.98
Q9D2V7	CORO7		Coronin-7, GN=Coro7	1.67	0.94	0.56	1	91.11

P33175	KIF5A	Kinesin heavy chain isoform 5A, GN=Kif5a	1.87	1.01	0.54	1	204.56
P28028	BRAF	Serine/threonine-protein kinase B-raf, GN=Braf	1.84	0.98	0.53	1	135.32
D3YXJ0	D3YXJ0	Diacylglycerol kinase, GN=Dgkh	1.61	0.85	0.53	2	130.16
A2AWT6	A2AWT6	Nucleolar transcription factor 1, GN=Ubtf	1.98	1.03	0.52	1	54.85
P97492	RGS14	Regulator of G-protein signaling 14, GN=Rgs14	1.52	0.79	0.52	1	71.21
A0A087WRT4	A0A087WRT4	FAT atypical cadherin 1, GN=Fat1	1.77	0.89	0.50	1	32.29
A8DUK4	A8DUK4	Beta-globin, GN=Hbbt1	0.71	0.33	0.46	4	273.67
P26041	MOES	Moesin, GN=Msn	2	0.82	0.41	1	188.76

Table S-4. The 50 proteins in the cerebral cortical that were changed significantly by memantine treatment.

Table S-4. The 50 proteins in the cerebral cortical that were changed significantly by memantine treatment. These proteins have met the criteria, the ratio of memantine / AD in expression levels of at least 1.5-fold (up-regulation) or at least ＜0.66-fold (down-regulation) as defined in the experimental procedures.

Accession	Protein name	Description	Ratio			Unique	-10lgP
			AD/WT	Memantine/WT	Memantine/AD		
Q9CXT8	MPPB	Mitochondrial-processing peptidase subunit beta, GN=Pmpcb	0.98	2.64	2.69	1	89.76
P48725	PCNT	Pericentrin, GN=Pcnt	0.93	2.44	2.62	1	83.85
Q91X96	MSS4	Guanine nucleotide exchange factor MSS4, GN=Rabif	0.92	1.95	2.12	1	38.67
Q6X893	CTL1	Choline transporter-like protein 1, GN=Slc44a1	0.66	1.36	2.06	1	154.36
Q9CQB5	CISD2	CDGSH iron-sulfur domain-containing protein 2, GN=Cisd2	1.05	2.07	1.97	1	64.37
Q64010	CRK	Adapter molecule crk, GN=Crk	1.02	1.88	1.84	1	201.47
P50153	GBG4	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-4, GN=Gng4	0.73	1.33	1.82	2	111.86
Q8C129	LCAP	Leucyl-cystinyl aminopeptidase, GN=Lnpep	0.48	0.84	1.75	1	82.37
F6TYB7	F6TYB7	Myelin basic protein (Fragment), GN=Mbp	0.89	1.44	1.62	2	261.39
Q3TDN2	FAF2	FAS-associated factor 2, GN=Faf2	0.9	1.43	1.59	1	117.52

Q6PGB8	SMCA1	Probable global transcription activator SNF2L1, GN=Smarca1	0.96	1.5	1.56	1	66.05
P55258	RAB8A	Ras-related protein Rab-8A, GN=Rab8a	1.16	1.81	1.56	1	167.34
P83870	PHF5A	PHD finger-like domain-containing protein 5A, GN=Phf5a	0.38	0.59	1.55	1	72.42
Q9D4H1	EXOC2	Exocyst complex component 2, GN=Exoc2	0.94	1.45	1.54	1	128.79
P97823	LYPA1	Acyl-protein thioesterase 1, GN=Lypla1	1.61	1.07	0.66	1	118.34
Q8R2Z3	S26A7	Anion exchange transporter, GN=Slc26a7	1.36	0.9	0.66	1	26.1
P56212	ARP19	cAMP-regulated phosphoprotein 19, GN=Arpp19	1.67	1.1	0.66	1	79.81
Q8BX94	OSBL2	Oxysterol-binding protein-related protein 2, GN=Osbpl2	1.51	0.99	0.66	1	62.67
Q80XI3	IF4G3	Eukaryotic translation initiation factor 4 gamma 3, GN=Eif4g3	1.34	0.87	0.65	3	143.96
P03888	NU1M	NADH-ubiquinone oxidoreductase chain 1, GN=Mtnd1	1.11	0.72	0.65	1	74.11
Q8R1S0	COQ6	Ubiquinone biosynthesis monooxygenase COQ6 mitochondrial, GN=Coq6	1.65	1.07	0.65	3	66.33
P50096	IMDH1	Inosine-5'-monophosphate dehydrogenase 1, GN=Impdh1	1.53	0.98	0.64	1	100.2
D3Z3B8	D3Z3B8	Disks large homolog 1, GN=Dlg1	0.99	0.63	0.64	1	223.24
Q0GNC1	INF2	Inverted formin-2, GN=Inf2	0.93	0.59	0.63	1	74.05
Q61033	LAP2A	Lamina-associated polypeptide 2 isoforms alpha/zeta, GN=Tmpo	1.33	0.84	0.63	2	115.13

A2ACM0	A2ACM0	Putative uncharacterized protein, GN=Rptor	1.58	0.99	0.63	1	124.14
Q3TCR7	Q3TCR7	Dynamin-2, GN=Dnm2	1.9	1.19	0.63	1	246.27
Q3U5Q7	CMPK2	UMP-CMP kinase 2 mitochondrial, GN=Cmpk2	1.55	0.97	0.63	1	102.4
Q9ES56	TPPC4	Trafficking protein particle complex subunit 4, GN=Trappc4	1.7	1.06	0.62	2	80.53
P97372	PSME2	Proteasome activator complex subunit 2, GN=Psme2	1.35	0.84	0.62	1	55.85
Q9DD18	DTD1	D-tyrosyl-tRNA(Tyr) deacylase 1, GN=Dtd1	1.24	0.77	0.62	1	80.82
Q3UMU9	HDGR2	Hepatoma-derived growth factor-related protein 2, GN=Hdgfl2	1.26	0.77	0.61	1	51.49
P48193	41	Protein 4.1, GN=Epb41	1.95	1.19	0.61	1	119.64
P62806	H4	Histone H4, GN=Hist1h4a	0.82	0.5	0.61	9	218.73
Q7TQK5	CCD93	Coiled-coil domain-containing protein 93, GN=Ccdc93	1.52	0.92	0.61	1	113.44
F8VQ05	F8VQ05	FRY-like transcription coactivator, GN=Fryl	1.65	0.98	0.59	1	80.5
P21300	ALD1	Aldose reductase-related protein 1, GN=Akr1b7	1.57	0.93	0.59	1	108.52
Q9WVA4	TAGL2	Transgelin-2, GN=Tagln2	1.78	1.04	0.58	3	167.3
E0CY16	E0CY16	Cell adhesion molecule 1, GN=Cadm1	1.7	0.99	0.58	1	196.6
Q9JMD3	STA10	START domain-containing protein 10, GN=Stard10	2.1	1.22	0.58	1	111.59

B2RWC4	B2RWC4	Gm88 protein, GN=Lrrc73	1.56	0.89	0.57	1	59.7
Q80VC9	CAMP3	Calmodulin-regulated spectrin-associated protein 3, GN=Camsap3	1.58	0.9	0.57	2	139.98
Q9D2V7	CORO7	Coronin-7, GN=Coro7	1.67	0.94	0.56	1	91.11
P33175	KIF5A	Kinesin heavy chain isoform 5A, GN=Kif5a	1.87	1.01	0.54	1	204.56
P28028	BRAF	Serine/threonine-protein kinase B-raf, GN=Braf	1.84	0.98	0.53	1	135.32
D3YXJ0	D3YXJ0	Diacylglycerol kinase, GN=Dgkh	1.61	0.85	0.53	2	130.16
A2AWT6	A2AWT6	Nucleolar transcription factor 1, GN=Ubtf	1.98	1.03	0.52	1	54.85
P97492	RGS14	Regulator of G-protein signaling 14, GN=Rgs14	1.52	0.79	0.52	1	71.21
A0A087WRT4	FAT atypical cadherin 1	FAT atypical cadherin 1, GN=Fat1	1.77	0.89	0.50	1	32.29
P26041	MOES	Moesin, GN=Msn	2	0.82	0.41	1	188.76