



Research article

Brain proteomics links oxidative stress with metabolic and cellular stress response proteins in behavioural alteration of Alzheimer’s disease model rats

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Supplementary Materials

Table 1. List of differentially expressed and significantly regulated proteins (log fold change > 1.5, p < 0.05).

No.	Protein	Swiss-Prot ID	M. wt. (KDa)	p value	AD vs. C	
					Regulation	Log FC
1	Carbamoyl-phosphate synthase [ammonia], mitochondrial	P07756	165.78	2.13E-04	down	-2.73
2	Serum albumin	P02770	70.73	1.61E-08	up	1.87
3	Alpha-1-inhibitor 3	P14046	165.14	3.78E-04	up	1.77
4	Murinoglobulin-1	Q03626	166.69	0.002112	up	1.62
5	Complement C3	M0RBF1	187.86	0.001387	up	1.77

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No.	Protein	Swiss-Prot ID	M. wt. (kDa)	p value	AD vs. C	
					Regulation	Log FC
6	Heat shock cognate 71 kDa protein	P63018	71.10	8.89E-07	up	2.22
7	Heat shock-related 70 kDa protein 2	P14659	69.93	3.03E-06	up	2.20
8	78 kDa glucose-regulated protein	P06761	72.52	1.84E-04	up	1.87
9	Serotransferrin	P12346	78.56	9.83E-08	up	2.60
10	ATP synthase subunit beta, mitochondrial	P10719	56.35	4.42E-04		
11	Protein Dsp	F1LMV6	334.78	1.06E-11	down	-16.47
12	Glutamate dehydrogenase 1, mitochondrial	P10860	61.76	7.85E-11	down	-15.35
13	Serpina3n-like protein	E0A3N4	48.21	7.49E-04	up	2.41
14	Clathrin heavy chain	F1M779	193.32	8.61E-04		
15	Rat apolipoprotein E protein	Q65ZS7	38.38	5.54E-05	up	1.53
16	60 kDa heat shock protein, mitochondrial	P63039	61.13	2.03E-05		
17	Synapsin-1	P09951	74.16	5.39E-07	up	2.80
18	Synapsin-2	Q63537	63.74	7.18E-05	up	2.33
19	Argininosuccinate synthase	P09034	46.78	0.002866		
20	Junction plakoglobin	Q6P0K8	82.54	8.13E-15	down	-16.85
21	Glial fibrillary acidic protein	P47819	50.01	3.78E-04	down	-2.16
22	Keratin, type II cytoskeletal 8	Q10758	54.02	2.68E-04	down	-3.70
23	Protein Kb15	G3V908	57.95	3.34E-06	down	-2.55
24	Keratin, type II cytoskeletal 73	Q6IG03	61.01	0.003322		
25	Vitamin D-binding protein	P04276	55.14	1.56E-05		
26	Keratin, type II cytoskeletal 5	Q6P6Q2	62.00	9.67E-06	down	-2.55
27	Keratin, type II cytoskeletal 6A	Q4FZU2	59.59	1.16E-06	down	-1.81
28	Keratin, type II cytoskeletal 1	Q6IMF3	65.23	1.49E-06	down	-1.79
29	Keratin, type II cytoskeletal 2 epidermal	M3ZCQ4	69.69	4.72E-04	down	-2.38
30	Neurofilament heavy polypeptide	P16884	115.66	0.006005	down	-1.90
31	Heat shock protein HSP 90-alpha	P82995	85.21	2.71E-04	up	1.64
32	Heat shock protein HSP 90-beta	P34058	83.62	1.84E-04	up	1.71
33	Endoplasmic	A0A0A0MY09	93.18	8.06E-10	up	16.38
34	Neurofilament light polypeptide	P19527	61.39	0.004508		
35	Apolipoprotein A-I	P04639	30.12	2.34E-08		
36	Phosphoglycerate kinase 1	P16617	44.94	8.24E-06		
37	Myosin-4	Q29RW1	223.79	0.022195	up	8.68
38	Protein Myh2	F1LRV9	224.31	0.021982	up	8.68
39	Uncharacterized protein	G3V6E1	220.89	0.021238	up	8.68
40	Hemopexin	P20059	52.09	0.00618	up	2.12

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No.	Protein	Swiss-Prot ID	M. wt. (KDa)	p value	AD vs. C	
					Regulation	Log FC
41	Protein Atp6v1a	D4A133	68.61	0.016075	up	1.88
42	LOC367586 protein	Q5M7V3	51.63	7.19E-06	up	2.18
43	Gamma-enolase	P07323	47.54	6.12E-05	up	1.74
44	Cytochrome b-c1 complex subunit 2, mitochondrial	P32551	48.45	1.80E-05		
45	14-3-3 protein zeta/delta	P63102	27.94	2.73E-04	up	2.19
46	14-3-3 protein theta	P68255	28.06	0.0126	up	1.91
47	14-3-3 protein eta	P68511	28.38	0.00353	up	2.03
48	14-3-3 protein gamma	P61983	28.47	0.019343	up	1.69
49	14-3-3 protein beta/alpha	P35213	28.17	0.008179	up	1.86
50	Keratin, type I cytoskeletal 10	Q6IFW6	56.73	2.55E-05	down	-1.79
51	Keratin, type I cytoskeletal 14	Q6IFV1	52.97	0.026066	down	-1.54
52	Keratin, type I cytoskeletal 17	Q6IFU8	48.41	0.015524	down	-1.82
53	Keratin, type I cytoskeletal 42	Q6IFU7	50.55	0.021279	down	-2.25
54	Keratin, type I cytoskeletal 13	Q6IFV4	48.13	0.002573	down	-2.85
55	Hexokinase-1	P05708	103.60	0.010358	up	1.72
56	Cytosolic 10-formyltetrahydrofolate dehydrogenase	P28037	99.79	1.58E-14		
57	Malate dehydrogenase, cytoplasmic	O88989	36.65	6.06E-05		
58	ADH-like protein	Q8K571	40.63	4.68E-04	down	-1.83
59	Aconitate hydratase, mitochondrial	Q9ER34	86.17	0.002837	up	1.89
60	Vesicle-fusing ATPase	Q9QUL6	83.22	3.10E-04	up	3.99
61	Non-erythroid spectrin beta	Q6XD99	274.49	0.008846		
62	Creatine kinase B-type	P07335	43.01	1.90E-04		
63	Isoform 2 of Haptoglobin	P06866-2	43.10	3.70E-04	up	2.51
64	Hemoglobin subunit beta-1	P02091	16.09	2.52E-05		
65	Hemoglobin subunit beta-2	P11517	16.10	2.85E-04		
66	Glyceraldehyde-3-phosphate dehydrogenase	P04797	36.11	3.42E-06		
67	Calcium/calmodulin-dependent protein kinase type II subunit alpha	P11275	54.68	6.49E-05	up	1.69
68	Calcium/calmodulin-dependent protein kinase type II subunit beta	F1LN18	65.95	7.09E-05	up	1.80
69	Triosephosphate isomerase	P48500	27.36	9.13E-05	up	4.57
70	Hydroxymethylglutaryl-CoA synthase, mitochondrial	P22791	57.37	2.35E-05		
71	3-oxo-5-beta-steroid 4-dehydrogenase	P31210	37.66	1.62E-12		
72	Aldo-keto reductase family 1, member C1 (Dihydrodiol dehydrogenase 1 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	Q3MHS3	37.52	3.44E-09		

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No.	Protein	Swiss-Prot ID	M. wt. (KDa)	p value	AD vs. C	
					Regulation	Log FC
73	Protein Akr1c19	D3ZEL2	37.40	8.26E-12		
74	3-alpha-hydroxysteroid dehydrogenase	P23457	37.54	2.78E-10		
75	17beta-hydroxysteroid dehydrogenase	Q2MHD9	37.53	3.31E-12		
76	2',3'-cyclic-nucleotide 3'-phosphodiesterase	P13233	47.67	0.003737	up	1.12
77	Syntaxin-1B	P61265	33.47	3.15E-13		
78	Citrate synthase, mitochondrial	Q8VHF5	52.21	1.20E-06	up	2.07
79	Fructose-bisphosphate aldolase C	P09117	39.68	0.003252	up	2.34
80	Dimethylglycine dehydrogenase	Q5RKL4	96.26	8.18E-10		
81	Alpha-2-HS-glycoprotein	P24090	38.78	2.14E-04		
82	4-hydroxyphenylpyruvate dioxygenase	P32755	45.34	3.43E-08		
83	Glutathione S-transferase Yb-3	P08009	25.85	0.011535	up	2.76
84	Glutathione S-transferase Mu 1	G3V983	26.07	0.015353	up	2.53
85	Glutathione S-transferase Mu 5	Q9Z1B2	27.08	0.048973	up	12.15
86	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	Q02253	58.26	1.29E-10	down	-14.14
87	Stress-70 protein, mitochondrial	P48721	74.14	2.76E-10	up	17.35
88	Phosphoglycerate mutase 1	P25113	28.95	0.002031	up	2.40
89	Protein Slc25a12 (Fragment)	F1LX07	74.68	0.001387	up	2.34
90	Ornithine carbamoyltransferase, mitochondrial	P00481	39.94	0.012683		
91	Creatine kinase, mitochondrial 1, ubiquitous	Q5BJT9	47.36	1.38E-04	up	2.87
92	Protein disulfide-isomerase A3	P11598	57.08	0.014876	down	-4.50
93	Ceruloplasmin	G3V7K3	121.46	6.50E-08	up	16.66
94	Transthyretin	P02767	15.83	6.59E-05		
95	Protein disulfide-isomerase	P04785	57.35	0.015887	down	-8.78
96	Prohibitin-2	Q5XIH7	33.31	0.006005		
97	Synaptotagmin-1	P21707	47.74	1.15E-04		
98	Thiosulfate sulfurtransferase	P24329	33.63	0.017788	down	-4.82
99	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	P49432	39.32	5.02E-04		
100	ADP-ribosylation factor 1	P84079	20.75	0.031895	up	10.53
101	ADP/ATP translocase 1	Q05962	33.22	0.002509	up	1.56
102	ADP/ATP translocase 2	Q09073	33.13	0.010116	up	1.52
103	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	Q5BK63	42.67	3.82E-04		
104	Uricase	P09118	35.16	6.58E-09		

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No.	Protein	Swiss-Prot ID	M. wt. (KDa)	p value	AD vs. C	
					Regulation	Log FC
105	Carbonic anhydrase 3	P14141	29.72	1.35E-13		
106	Isoform 2 of Voltage-dependent anion-selective channel protein 3	Q9R1Z0-2	31.33	0.012938		
107	Voltage-dependent anion-selective channel protein 2	P81155	32.37	0.046547		
108	Isocitrate dehydrogenase [NADP], mitochondrial	P56574	51.42	8.24E-08	up	15.68
109	Sulfotransferase 1A1	P17988	34.19	6.02E-11		
110	Pyruvate carboxylase, mitochondrial	P52873	130.52	5.76E-11		
111	Isoform LMW of Kininogen-1	P08934-2	48.97	0.031895	down	-11.08
112	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	P08461	67.68	0.002564	up	1.63
113	Carboxylesterase 1E	Q63108	62.00	0.02349	down	-15.15
114	Neurochondrin	O35095	80.41	2.09E-09	up	17.00
115	Regucalcin	Q03336	33.96	7.05E-10		
116	Syntaxin 1A	Q9QXG3	33.38	1.09E-08		
117	Inter-alpha-inhibitor H4 heavy chain	O35802	103.95	0.007122	up	1.57
118	Glucose-6-phosphate isomerase	Q6P6V0	63.00	7.39E-05		
119	Peroxiredoxin-6	O35244	24.88	2.59E-11	up	16.62
120	Protein Serpina4	Q5M8C3	48.16	2.74E-09	down	-15.24
121	Myristoylated alanine-rich C-kinase substrate	F1LMW7	29.95	8.86E-11	up	14.82
122	LOC500183 protein	Q4KM66	26.03	5.19E-04		
123	Neural cell adhesion molecule 1	P13596	95.46	0.036474	down	-5.39
124	CRP	H6X2V9	25.76	4.70E-05		
125	Aa1249	Q7TMA9	117.83	1.11E-04		
126	Uncharacterized protein (Fragment)	F1LPQ6	39.33	5.62E-04	up	3.35
127	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	P63329	59.33	3.14E-05	up	1.93
128	Annexin	Q66HH8	35.83	0.02747	down	-9.43
129	Sarcosine dehydrogenase, mitochondrial	Q64380	102.64	5.51E-12		
130	Fatty acid-binding protein, liver	P02692	14.33	6.71E-07	down	-17.25
131	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Q9WVK7	34.56	9.88E-11		
132	Elongation factor 1-alpha 1	P62630	50.46	0.048974		
133	Heat shock 70kDa protein 12A (Predicted), isoform CRA_a	D3ZC55	75.17	9.72E-08	up	16.07
134	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	Q66HF1	80.38	5.57E-10	up	16.66
135	Clusterin	G3V836	52.05	1.64E-16	down	-15.71

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No.	Protein	Swiss-Prot ID	M. wt. (KDa)	p value	AD vs. C	
					Regulation	Log FC
136	Amino acid transporter	Q8K5B5	61.43	1.00E-05	up	2.12
137	Sodium/potassium-transporting ATPase subunit beta-1	P07340	35.60	3.87E-04		
138	Protein Hoga1	D4A2K1	34.81	6.43E-11		
139	Mitochondrial 2-oxoglutarate/malate carrier protein	P97700	34.42	2.19E-07	down	-16.70
140	ATP synthase subunit O, mitochondrial	Q06647	23.45	3.83E-11	up	17.23
141	Proteasome subunit beta type	G3V7Q6	28.73	2.40E-09		
142	60S acidic ribosomal protein P0	P19945	34.39	2.93E-09		
143	Corticosteroid 11-beta-dehydrogenase isozyme 1	P16232	32.11	1.40E-12		
144	Slc25a3 protein	Q6IRH6	40.08	4.06E-04	up	1.98
145	Glutathione S-transferase	B6DYP7	25.72	3.95E-14		
146	ATP synthase subunit gamma	Q6PCU0	33.11	2.93E-09	down	-16.32
147	Protein Tppp	D3ZQL7	23.72	4.52E-09	up	17.35
148	Acetyl-Coenzyme A dehydrogenase, medium chain	G3V796	46.97	3.78E-11	up	16.44
149	Transitional endoplasmic reticulum ATPase	P46462	90.03	7.98E-09	up	15.11
150	Histone H4	P62804	11.37	7.39E-06		
151	Ras-related protein Rab-2A	P05712	23.71	2.27E-09	up	17.04
152	Alpha-1,4 glucan phosphorylase	B2GV03	97.46	0.041384	up	10.01
153	Glycogen phosphorylase, liver form	P09811	97.94	0.041384	up	9.96
154	ATP synthase F(0) complex subunit B1, mitochondrial	P19511	28.98	3.71E-09	up	18.18
155	Kynurenine--oxoglutarate transaminase 3	Q58FK9	51.61	4.02E-09	up	15.50
156	Carboxylesterase 1D	P16303	62.43	8.73E-10		
157	Cofilin-1	P45592	18.76	0.048974	up	5.87
158	Prothrombin	P18292	71.84	1.44E-08	down	-14.11
159	Succinyl-CoA ligase subunit beta	F1LM47	50.65	1.89E-07	up	14.44
160	ATPase, H ⁺ transporting, V1 subunit E isoform 1, isoform CRA_a	G3V7L8	26.20	4.93E-09	down	-15.88
161	Protein LOC100909412	F7FIH7	21.20	0.021638	down	-18.30
162	Peroxisomal trans-2-enoyl-CoA reductase	A0A096MIT3	33.45	1.99E-09		
163	Protein Aldh8a1	D3ZXY4	54.30	6.05E-13		
164	Inter-alpha-trypsin inhibitor heavy chain H3	Q63416	99.44	2.50E-09	up	16.20
165	Delta-1-pyrroline-5-carboxylate dehydrogenase, itochondrial	R9PY10	165.64	4.86E-12		
166	Bucs1 protein	B5DFA3	66.04	6.22E-11		

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No.	Protein	Swiss-Prot ID	M. wt. (KDa)	p value	AD vs. C	
					Regulation	Log FC
167	Prohibitin	P67779	29.88	0.039269	down	-10.25
168	Cytochrome b5	P00173	15.35	2.68E-09	down	-18.20
169	Carbonic anhydrase 2	P27139	29.28	2.93E-09	down	-16.12
170	S-adenosylmethionine synthase isoform type-1	P13444	44.27	7.71E-09		
171	Superoxide dismutase [Cu-Zn]	P07632	16.08	2.68E-09	down	-17.61
172	D-dopachrome decarboxylase	P80254	13.25	2.63E-08	down	-18.54
173	Peroxiredoxin-2	P35704	21.95	0.009422		
174	Ras-related C3 botulinum toxin substrate 1	Q6RUV5	21.85	5.65E-10		
175	4-aminobutyrate aminotransferase, mitochondrial	P50554	57.20	0.031895	up	17.04
176	Transgelin-3	P37805	22.67	3.46E-13		
177	Carbonic anhydrase 1	B0BNN3	28.36	6.12E-09	down	-15.19
178	Polyubiquitin-C	Q63429	91.20	9.52E-06		
179	ATPase, H ⁺ transporting, V1 subunit D, isoform CRA_c	Q6P503	28.31	0.023331	down	-4.75
180	Nicotinamide nucleotide transhydrogenase	Q5BJZ3	114.61	8.31E-10		
181	Peroxiredoxin-1	Q63716	22.34	0.041384	up	10.70
182	Dihydropteridine reductase	P11348	25.78	4.40E-11		
183	Electron transfer flavoprotein subunit beta	Q68FU3	27.92	5.49E-10		
184	3-hydroxyacyl-CoA dehydrogenase type-2	B0BMW2	27.42	9.91E-09		
185	Beta-soluble NSF attachment protein	F8WFM2	33.90	3.83E-08		
186	Isoform 2 of Clathrin coat assembly protein AP180	Q05140-2	91.66	0.003282		
187	Peroxiredoxin-5, mitochondrial	Q9R063	22.52	2.98E-10	down	-15.52
188	RCG55639, isoform CRA_c	Q5DT04	60.46	1.06E-11		
189	Ubiquitin thioesterase OTUB1	B2RYG6	31.50	1.79E-06		
190	Thy-1 membrane glycoprotein	P01830	18.40	5.99E-10	up	18.40
191	Protein LOC100362298 (Fragment)	D3ZM33	17.97	3.85E-08	down	-17.04
192	Ig lambda-2 chain C region	P20767	11.49	3.47E-08	up	1.76
193	Superoxide dismutase [Mn], mitochondrial	P07895	24.90	0.023666	up	17.78
194	Neuromodulin	P07936	23.72	0.042242	down	-4.57
195	Septin-2	Q91Y81	41.76	7.80E-10		
196	Glycine N-methyltransferase	M0RDH0	32.99	0.021703	up	4.37
197	Ras-related protein Rab-5A	M0RC99	23.85	0.047559	up	10.75
198	SAP	H6X338	26.32	9.78E-16	down	-15.08

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No.	Protein	Swiss-Prot ID	M. wt. (KDa)	p value	AD vs. C	
					Regulation	Log FC
199	Histone H2B	D3ZNH4	15.49	1.79E-04		
200	Protein kinase C and casein kinase substrate in neurons protein 1	Q9Z0W5	50.79	2.63E-08	down	-15.20
201	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	O35077	38.14	6.25E-09		
202	Dihydrolipoyl dehydrogenase, mitochondrial	Q6P6R2	54.61	8.61E-07	down	-13.72
203	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	Q5EBC3	101.66	9.63E-10		
204	40S ribosomal protein SA	P38983	32.94	1.27E-08	up	14.88
205	Nucleoside diphosphate kinase B	P19804	17.40	1.52E-06	down	-15.99
206	Corticosteroid-binding globulin	P31211	44.84	0.01144	up	3.83
207	Ras-related protein Rap-1A	P62836	21.33	0.04164	up	5.30
208	Glutathione S-transferase pi	B6DYQ7	23.67	0.021118	up	18.00
209	Long-chain-fatty-acid--CoA ligase 1	P18163	79.20	6.02E-09		
210	Alpha-centractin	P85515	42.73	0.002136	up	1.57
211	Neurofascin	R9PY05	138.87	0.024378	down	-9.67
212	Peptidyl-prolyl cis-trans isomerase A	P10111	18.10	1.63E-11		
213	Ras-related protein Ral-A	P63322	23.72	1.62E-12		
214	Pyridoxal phosphate phosphatase	Q8VD52	33.51	1.70E-07	down	-12.59
215	Liver carboxylesterase 4	Q64573	62.71	7.71E-09		
216	Prostaglandin reductase 1	P97584	36.00	2.07E-08		
217	Leucine-rich repeat-containing protein 59	Q5RJR8	35.33	5.20E-07		
218	Protein Stard10	Q5BJN1	33.30	1.61E-11		
219	Isoform 2 of Septin-5	Q9JIM9-2	44.38	1.09E-11		
220	Ras-related protein Rab-7a	P09527	23.79	1.85E-05	up	17.05
221	Glutathione peroxidase 3	P23764	25.50	3.51E-10	down	-14.39
222	60S ribosomal protein L13	P41123	24.37	7.23E-09		
223	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	Q01205	49.27	0.048973	down	-9.95
224	Igh-6 protein	Q569B3	69.10	6.13E-08	up	17.87
225	Ras-related protein Rab-11B	O35509	24.60	3.01E-11	up	17.25
226	Adaptor protein complex AP-2, alpha 1 subunit (Predicted)	D3ZUY8	108.76	0.015656	up	8.52
227	AP-2 complex subunit alpha-2	Q66HM2	105.08	1.27E-07	up	15.74
228	10 kDa heat shock protein, mitochondrial	P26772	10.90	0.046951	down	-17.23

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No.	Protein	Swiss-Prot ID	M. wt. (KDa)	p value	AD vs. C	
					Regulation	Log FC
229	Excitatory amino acid transporter 1	P24942	59.87	5.51E-10	up	17.81
230	Protein LOC100365958	F7FHR5	36.08	2.52E-12		
231	Transcriptional activator protein Pur-alpha	F1LPS8	33.85	9.89E-06	up	14.55
232	ATP synthase subunit d, mitochondrial	P31399	18.82	4.37E-15		
233	Protein Syngr3	D4ABK1	21.65	5.17E-05	up	2.32
234	Protein Serpinf2	Q68FT8	55.12	0.043573	up	9.14
235	Protein Dsg1	D3ZM39	115.05	0	down	-17.41
236	Formimidoyltransferase-cyclodeaminase	O88618	59.54	1.37E-14		
237	Histone H2A type 4	Q00728	14.28	6.63E-05		
238	Protein LOC100362339	D4A6G6	16.12	1.09E-05	down	-14.51
239	Ras-related protein Rab-18	Q5EB77	23.26	6.58E-09		
240	40S ribosomal protein S2	P27952	31.52	6.39E-10		
241	T-complex protein 1 subunit gamma	Q6P502	61.22	7.20E-10	down	-14.22
242	Isoform 2 of Vacuolar protein sorting-associated protein 29	B2RZ78-2	21.06	1.99E-11		
243	NADH dehydrogenase (Ubiquinone) Fe-S protein 7	Q5RJN0	24.23	7.25E-11		
244	2,4-dienoyl CoA reductase 1, mitochondrial, isoform CRA_a	G3V734	36.42	3.26E-08		
245	Alpha-aminoadipic semialdehyde dehydrogenase	Q64057	59.26	9.72E-10		
246	Pyruvate dehydrogenase E1 component subunit alpha	D4A5G8	44.31	1.23E-08	up	15.82
247	V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	A0JN17	21.72	4.28E-10		
248	Vesicle associated membrane protein 2B	Q9WUW2	14.57	2.49E-11	up	17.92
249	Protein RGD1561381	D3ZZQ8	16.93	0.012683	up	18.01
250	Alcohol dehydrogenase [NADP(+)]	P51635	36.73	7.23E-09		
251	Microsomal glutathione S-transferase	B6DYQ4	17.53	1.67E-12		
252	Calmodulin	P62161	16.84	6.58E-06	up	14.19
253	Tenascin R, isoform CRA_b	A0A096MJ E6	151.94	1.20E-09	up	17.23
254	Catechol-O-methyltransferase	F2W8B0	29.83	1.57E-10		
255	Protein LOC100911847	Q6PDV6	16.44	2.74E-09	down	-16.89
256	Aldose reductase	P07943	36.25	0.026749	down	-9.56
257	ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit d1	Q5M7T6	40.76	5.74E-06	up	1.50
258	Reticulon-3	Q6RJR6	102.09	8.51E-09		
259	RCG62292, isoform CRA_a	B5DEL9	22.13	1.56E-08		

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No.	Protein	Swiss-Prot ID	M. wt. (KDa)	p value	AD vs. C	
					Regulation	Log FC
260	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	Q99NA5	40.07	5.22E-08	up	16.78
261	Histone H3.1	Q6LED0	15.52	2.15E-09	down	-17.58
262	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	P19234	27.72	3.01E-11	up	15.95
263	Isoform Syn2 of Alpha-synuclein	P37377-2	15.87	1.05E-11		
264	Isoform Gamma-2 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	P63088-2	39.25	4.55E-08		
265	Cytosol aminopeptidase	Q68FS4	56.55	8.73E-11		
266	Synaptogyrin-1	Q62876	25.90	0.038714	down	-10.26
267	RCG25732, isoform CRA_b	B5DEM5	23.89	6.22E-11		
268	NAD-dependent protein deacetylase sirtuin-2	Q5RJQ4	39.95	0.034961	up	5.26
269	Glutathione peroxidase 1	P04041	22.33	1.73E-13		
270	Aflatoxin B1 aldehyde reductase member 2	Q8CG45	41.13	3.46E-13		
271	Park7 protein	Q5BK3	23.02	2.52E-12		
272	Hyaluronan and proteoglycan link protein 1	A1A5N6	40.89	0.02627	down	-10.20
273	3-hydroxyanthranilate 3,4-dioxygenase	P46953	32.87	5.62E-11		
274	40S ribosomal protein S8	Q6TXJ0	27.00	2.13E-07		
275	Protein disulfide-isomerase A6	Q63081	48.57	3.44E-09		
276	Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	Q68G41	32.38	1.50E-07		
277	Synaptophysin	P07825	33.60	1.22E-12	up	16.92
278	Reticulon-1	Q64548	83.40	9.38E-11	down	0.00
279	Beta-ureidopropionase	Q03248	44.61	3.50E-12	up	17.07
280	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans), isoform CRA_b	G3V728	33.63	1.22E-12		
281	Calreticulin	P18418	48.17	4.55E-09		
282	Pgm1 protein (Fragment)	A1A5L2	63.63	1.43E-09	down	-14.45
283	Visinin-like 1	Q56A29	22.34	1.02E-08		
284	ES1 protein homolog, mitochondrial	P56571	28.51	6.39E-11		
285	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	P29147	38.60	2.19E-10		
286	Isovaleryl-CoA dehydrogenase, mitochondrial	P12007	46.89	1.69E-06	up	16.95
287	Protein LOC100364509	D3ZV50	22.76	9.76E-07		

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No.	Protein	Swiss-Prot ID	M. wt. (KDa)	p value	AD vs. C	
					Regulation	Log FC
288	Protein LOC301861	D3ZEF5	44.32	8.61E-04	up	1.56
289	Cytosolic acyl coenzyme A thioester hydrolase	Q64559	43.19	0.037845	down	-9.31

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