

Supplementary Table 1. Unique proteins with expression significantly altered in the hippocampus of rats of group of exposed to MeHg group (EG) vs. control group (CG).

^a Access Number	Protein name description	PLGS Score	Group	
			C	MeHg
Q6AXQ5	2',5'-phosphodiesterase 12	156.52	+	-
Q63570	26S proteasome regulatory subunit 6B	154.03	+	-
P0C2C0	39S ribosomal protein L22, mitochondrial	145.93	+	-
P62083	40S ribosomal protein S7	406.14	-	+
D3ZWR1	5', 3'-nucleotidase, cytosolic	156.77	+	-
P02401	60S acidic ribosomal protein P2	103.06	+	-
A7UAK3	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 3 splice variant	134.47	+	-
O35552	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	134.47	+	-
G3V8D5	6-phosphogluconolactonase	181.41	-	+
A0A0G2K6E7	AarF domain-containing kinase 5	123.95	+	-
Q7TP34	Ab2-450	98.65	+	-
A2VD09	Abi1 protein	143.58	-	+
Q7TPI4	Ac2-300	102.99	+	-
B3DMA6	Actin-like protein 9	353.7	-	+
Q99PD4	Actin-related protein 2/3 complex subunit 1A	4063.54	+	-
O88656	Actin-related protein 2/3 complex subunit 1B	154.25	+	-
B2GV73	Actin-related protein 2/3 complex subunit 3	440.4	+	-
B2RZ72	Actin-related protein 2/3 complex subunit 4	374.5	-	+
Q5XIK1	Actin-related protein T1	215.2	+	-
A0A0G2K2H6	Acyl-coenzyme A amino acid N-acyltransferase 1	135.57	-	+
Q6SKG1	Acyl-coenzyme A synthetase ACSM3, mitochondrial	120.42	+	-
Q63768	Adapter molecule crk	192.48	-	+
P69682	Adaptin ear-binding coat-associated protein 1	310.86	-	+

D3ZUY8	Adaptor protein complex AP-2, alpha 1 subunit (Predicted)	153.14	+	-
G3V8Q9	Adenomatous polyposis coli, isoform CRA_a	109.08	+	-
P70478	Adenomatous polyposis coli protein	109.08	+	-
G3V8T3	Adenosine deaminase, RNA-specific, isoform CRA_b	69.47	-	+
A0A0G2JUP2	Adhesion G protein-coupled receptor V1	152.69	+	-
Q7TP48	Adipocyte plasma membrane-associated protein	102.08	-	+
Q05962	ADP/ATP translocase 1	627.22	+	-
Q09073	ADP/ATP translocase 2	723.55	+	-
Q62924	A-kinase anchor protein 11	45.16	+	-
A0A0G2K548	A-kinase-anchoring protein 9	111.47	+	-
ADH1_YEAST	Alcohol dehydrogenase 1	734.08	+	-
P12711	Alcohol dehydrogenase class-3	174.15	+	-
Q6AYQ2	Aldo-keto reductase family 1 member C21	200.23	+	-
F1LQ80	Aldo-keto reductase family 1, member C2	200.23	+	-
Q5F2L1	Alpha-(1,3)-fucosyltransferase 10	70.44	+	-
Q09325	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	72.75	-	+
A0A0G2K8F6	Alpha-mannosidase	142.88	+	-
G3V6R0	Amino acid transporter	143.74	+	-
Q6AYS7	Aminoacylase-1A	122.1	-	+
F1M9V7	Aminopeptidase	115.66	-	+
F1M8D5	Amyotrophic lateral sclerosis 2 (Juvenile) chromosome region, candidate 13 (Predicted)	89.27	-	+
D3ZDK4	Angiopoietin-related protein 7-like	128.88	+	-
B2RYI5	Ankrd40 protein	84.78	-	+
B1WC29	Ankrd49 protein	206.35	-	+
M0RC04	Ankyrin repeat and MYND domain-containing 1	62.11	+	-
Q32Q00	Ankyrin repeat and SOCS box-containing 12	129.63	-	+
D4A6I3	Ankyrin repeat domain 13B	193.3	+	-

Q66HH8	Annexin	110.91	-	+
P14668	Annexin A5	110.91	-	+
O88321	Antisecretory factor	103.3	-	+
P62944	AP-2 complex subunit beta	100.21	+	-
Q8K4H4	Aprataxin	118.74	+	-
D3ZF86	ARFGEF family member 3	44.18	+	-
P09034	Argininosuccinate synthase	130.48	-	+
B0BN83	Armadillo repeat-containing protein 1	150.11	+	-
D3ZAQ1	ARP5 actin-related protein 5 homolog	73.83	-	+
F1M9V0	Ataxin 7-like 1	163.78	+	-
P19511	ATP synthase F(0) complex subunit B1, mitochondrial	434.16	+	-
P30835	ATP-dependent 6-phosphofructokinase, liver type	134.76	+	-
F1LNP1	AT-rich interaction domain 1B	54.88	-	+
F1LNQ2	Autophagy and beclin 1 regulator 1	309.3	+	-
D3ZFK6	Autophagy-related 16-like 1	50.01	-	+
D3ZMI4	Band 4.1-like protein 1	103.24	+	-
D3ZU26	Basic helix-loop-helix family, member e23	130.18	+	-
M0RCL1	BEN domain-containing 3	96.21	+	-
Q66HG3	Beta-Ala-His dipeptidase	60.4	+	-
P02524	Beta-crystallin B3	142.22	+	-
Q4FZV0	Beta-mannosidase	105.78	-	+
G3V7X7	BRCA1-associated RING domain protein 1	109.12	-	+
A0A0G2JYH8	Brevican core protein	195.93	-	+
F1M8A0	Butyrophilin-like 5	81.85	+	-
Q8R490	Cadherin 13	67.08	-	+
Q767I2	Cadherin-related neuronal receptor 10	51.97	+	-
P07171	Calbindin	155.83	-	+
D3ZW89	Calcium binding protein 5 (Predicted), isoform CRA_b	171.9	+	-

O70150	Calcium/calmodulin-dependent protein kinase type 1B	145.75	-	+
F1LNC7	Calcium-activated potassium channel subunit alpha-1	142.13	+	-
Q66HR5	Calcium-binding and coiled-coil domain-containing protein 1	626.87	+	-
M0R793	Calcium-binding protein 2	492.41	+	-
Q5BK10	Calpain-13	97.58	+	-
P27321	Calpastatin	91.55	-	+
P47728	Calretinin	102.82	+	-
D3ZZR7	Cancer/testis antigen 2	172.83	+	-
M0R6B1	Caprin family member 2	71.44	+	-
B5DFG6	Car13 protein	74.58	+	-
P10959	Carboxylesterase 1C	126.65	+	-
Q6IRK9	Carboxypeptidase Q	134.16	+	-
A0A0H2UHQ2	Casein kinase 1, gamma 2, isoform CRA_b	68.91	-	+
Q62762	Casein kinase I isoform gamma-2	73.7	-	+
Q9JHK1	Caspase 9, isoform CRA_a	156.18	+	-
A0A0G2JT93	Catenin (Cadherin associated protein), beta 1, isoform	105.39	+	-
Q9WU82	Catenin beta-1	105.39	+	-
P00787	Cathepsin B	71.49	-	+
P24268	Cathepsin D	110.66	-	+
A0A0G2K5S0	Cation channel sperm-associated auxiliary subunit gamma	46.29	-	+
Q5PQL2	CCR4-NOT transcription complex subunit 9	94.68	+	-
Q4V884	CDC16 cell division cycle 16 homolog (<i>S. cerevisiae</i>)	73.15	-	+
M0R837	CDK5 regulatory subunit-associated protein 1-like 1	93.55	-	+
A0A0G2JT88	Cell division cycle 16	71.94	-	+
Q62623	Cell division cycle protein 20 homolog	127.96	+	-
D3ZZ61	Centrosomal protein 68	94.8	+	-
F7EXF4	Centrosomal protein 85-like	85.87	-	+
A0A0G2KBC1	Centrosomal protein POC5	37.47	+	-

O54735	cGMP-specific 3',5'-cyclic phosphodiesterase	88.43	-	+
E9PT11	Chromobox 6	264.58	+	-
Q4V8E4	Cilia- and flagella-associated protein 36	97.1	-	+
D4AD05	Ciliary rootlet coiled-coil, rootletin	56.01	+	-
A0A0G2K0B6	Clathrin coat assembly protein AP180	170.84	+	-
A0A0G2JZ07	Clusterin	120.52	+	-
Q3ZRW7	Clusterin-like protein 1	142.22	+	-
B2GV96	Coiled-coil domain-containing 115	216.01	+	-
Q6PEB9	Coiled-coil domain-containing protein 127	118.71	+	-
D3ZTE2	Coiled-coil domain-containing protein 132-like	116.94	-	+
Q3ZAV0	Coiled-coil domain-containing protein 60	130.51	-	+
F1M6Q3	Collagen type IV alpha 2 chain	99.47	+	-
D3ZZT9	Collagen type XIV alpha 1 chain	42.52	+	-
P23097	Collagenase 3	63.41	-	+
A0A0G2KBC4	Colony stimulating factor 1 receptor	39.75	+	-
G3V6K0	COMM domain containing 5, isoform CRA_a	108.41	-	+
Q9ERR2	COMM domain-containing protein 5	108.41	-	+
A0A1B0GWS5	Complement C5	52.97	-	+
F1LND1	Component of oligomeric golgi complex 1	47.82	+	-
Q63198	Contactin-1	158.73	+	-
Q62682	Contactin-3	70.77	-	+
Q0V8T3	Contactin-associated protein like 5-4	120.07	-	+
F1LMS4	Contactin-associated protein-like 5-3	120.07	-	+
P61203	COP9 signalosome complex subunit 2	97.65	+	-
O35828	Coronin-7	102.37	+	-
D3ZGE6	Cortactin, isoform CRA_c	253.81	-	+
Q9EQH5	C-terminal-binding protein 2	182.75	-	+
G3V897	CTR9 homolog, Paf1/RNA polymerase II complex component	73.04	-	+

D4A0E3	C-type (Calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 1 (Cartilage-derived) (Predicted)	110.4	-	+
D4AD02	C-type lectin domain family 9 member A	191.58	-	+
A0A0G2K685	Cyclic nucleotide-gated channel beta 1	39.76	+	-
M0R9G9	Cysteine protease	190.89	-	+
P36201	Cysteine-rich protein 2	204.28	-	+
P00406	Cytochrome c oxidase subunit 2	147.34	+	-
P10888	Cytochrome c oxidase subunit 4 isoform 1, mitochondria	158.65	+	-
D3ZFAQ8	Cytochrome c-1	664.73	+	-
P20814	Cytochrome P450 2C13, male-specific	91.28	-	+
P10633	Cytochrome P450 2D1	97.9	-	+
G3V8J2	Cytochrome P450 family 8 subfamily B member 1	131.45	+	-
F1LR47	Cytochrome P450, family 2, subfamily C, polypeptide 6, variant 1	113.73	+	-
F1LRG0	Cytochrome P450, family 21, subfamily a, polypeptide 1	146.75	+	-
F1M5X7	Dachsous cadherin-related 2	73.64	-	+
F1M8Y4	DEP domain-containing MTOR-interacting protein	97.04	-	+
D3ZSZ6	Diacylglycerol kinase	43.87	-	+
Q63707	Dihydroorotate dehydrogenase (quinone), mitochondrial	165.14	+	-
Q8K4B7	Dimethylaniline monooxygenase [N-oxide-forming] 4	101.79	+	-
Q5U2X4	Dipeptidase 3	58.76	-	+
Q5U2P0	DIS3-like exonuclease 1	66.33	+	-
D3ZIL9	DIS3-like exonuclease 2	115.84	+	-
O88797	Disabled homolog 2	83.88	-	+
Q91ZV2	Discoidin, CUB and LCCL domain-containing protein 2	64.8	-	+
A0A0G2KB74	Disco-interacting protein 2 homolog A	69.48	-	+
D3ZZB0	Disco-interacting protein 2 homolog C	38.18	-	+
Q62936	Disks large homolog 3	189.88	+	-
P31016	Disks large homolog 4	59.2	+	-

G3V616	Divalent cation tolerant protein CUTA, isoform CRA_b	416.8	-	+
Q6AXY4	DNA polymerase delta subunit 2	71.82	+	-
D3ZYP7	DNA polymerase gamma 2, accessory subunit	127.54	+	-
D3ZJ19	DNA-binding protein SATB	110.88	+	-
Q5YKV6	DnaJ (Hsp40) related, subfamily B, member 13	107.75	+	-
D3ZTT0	Double homeobox B-like 1	147.76	+	-
D3Z9E7	Double PHD fingers 3	38.17	+	-
P55266	Double-stranded RNA-specific adenosine deaminase	69.47	-	+
M0RD87	Dual specificity phosphatase-like 15 (Predicted), isoform CRA_b	148.58	-	+
B4F7B7	Dual specificity protein phosphatase 15	369.01	-	+
Q64346	Dual specificity protein phosphatase 6	144.48	+	-
D4A8U7	Dynactin 1, isoform CRA_a	119.37	+	-
P28023	Dynactin subunit 1	119.37	+	-
Q6AYH5	Dynactin subunit 2	181.4	-	+
Q66HC9	Dynein intermediate chain 2, axonemal	47.16	-	+
P63170	Dynein light chain 1, cytoplasmic	349.23	+	-
A0A0G2JU43	Dynein light chain 1-like	291.02	+	-
Q78P75	Dynein light chain 2, cytoplasmic	291.02	+	-
P62628	Dynein light chain roadblock-type 1	896.47	-	+
Q6MFZ5	E3 ubiquitin-protein ligase TRIM39	203.8	+	-
D3ZD71	EF-hand domain-containing 1	54.38	+	-
Q811U3	ELKS/Rab6-interacting/CAST family member 1	51.15	-	+
Q68FR6	Elongation factor 1-gamma	210.79	+	-
P05197	Elongation factor 2	185.76	+	-
Q9QYU2	Elongation factor Ts, mitochondrial	103.34	+	-
P52555	Endoplasmic reticulum resident protein 29	231.78	-	+
Q3ZAV8	Enhancer of mRNA-decapping protein 4	55.99	+	-
Q5PPH0	Enolase-phosphatase E1	207.25	-	+

D3ZDH4	Eph receptor A1	136.87	+	-
F1LX55	EPH receptor A10	89.98	+	-
Q4V882	Ephrin type-A receptor 7	142.44	+	-
Q6MG84	Epidermal growth factor-like protein 8	114.3	-	+
B2RYD2	Epithelial splicing regulatory protein 1	62.8	-	+
F1LTS8	Epoxide hydrolase	53.35	-	+
D4A994	ER membrane protein complex subunit 1	101.26	+	-
B5DF57	Erythrocyte membrane protein band 4.2	53.9	+	-
P56571	ES1 protein homolog, mitochondrial	199.96	+	-
Q4G061	Eukaryotic translation initiation factor 3 subunit B	40.92	-	+
P24942	Excitatory amino acid transporter 1	104.54	+	-
P31596	Excitatory amino acid transporter 2	182.18	+	-
Q5XI32	F-actin-capping protein subunit beta	839.91	+	-
D3ZW60	Family with sequence similarity 179, member B	32.97	+	-
D3ZPE2	Family with sequence similarity 222, member B	120.37	+	-
D3ZH34	Family with sequence similarity 46, member A	83.79	-	+
B0BN65	Family with sequence similarity 49, member A	108.17	+	-
D3ZX03	Fanconi anemia core complex-associated protein 100	129.62	+	-
G3V774	F-box only protein 2	251.11	-	+
D3ZFK8	FERM, ARH/RhoGEF and pleckstrin domain protein 2	96.25	+	-
F1LTM1	Ferritin	155.36	+	-
F8WG20	First gene upstream of Nt5dc3	126.88	+	-
D3ZJ81	Follistatin-like 4	81.95	-	+
D4A433	Forkhead box O4	73.66	-	+
D4A4Y9	Formin 1	62.14	-	+
D3ZX41	Formyl peptide receptor,-related sequence 3	147.8	+	-
P00884	Fructose-bisphosphate aldolase B	154.3	+	-
P25093	Fumarylacetoacetase	128.33	+	-

F1LU70	G patch domain containing 1 (Predicted), isoform CRA_a	86.32	-	+
P11762	Galectin-1	394.58	+	-
Q62847	Gamma-adducin	57.52	+	-
F1M498	Gastrokine 3	187.55	+	-
Q6AY96	General transcription factor IIF subunit 1	105.48	-	+
D3ZD80	General transcription factor IIIC subunit 4	48.99	-	+
Q6QLN3	Glioma tumor suppressor candidate region gene 2	139.47	+	-
B5DEZ6	Glucosamine-6-phosphate isomerase	152.66	+	-
Q6TXE9	Glutamyl-prolyl-tRNA synthetase	41.5	-	+
D4ADD7	Glutaredoxin 5	321.83	+	-
F7F2H5	Glutathione S-transferase	91.39	-	+
P00502	Glutathione S-transferase alpha-1	91.39	-	+
P04903	Glutathione S-transferase alpha-2	91.39	-	+
P04904	Glutathione S-transferase alpha-3	91.39	-	+
Q9Z1B2	Glutathione S-transferase Mu 5	75.42	-	+
A0A096MJ04	Glutathione S-transferase omega 1, isoform CRA_a	113.08	+	-
Q6AXR6	Glutathione S-transferase omega 1, isoform CRA_b	234.44	+	-
Q9Z339	Glutathione S-transferase omega-1	234.44	+	-
A0A0G2JTY5	Glutathione S-transferase omega-2	121.36	+	-
F1LNI0	Glycerol-3-phosphate dehydrogenase	142.38	+	-
P35571	Glycerol-3-phosphate dehydrogenase, mitochondrial	142.38	+	-
B1H250	Glycine-N-acyltransferase-like 1	91.23	-	+
A0A0G2JXP1	Glycogenin-1	157.77	-	+
D3ZJB2	Glycoprotein integral membrane 1	248.19	-	+
G3V8B1	Glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_a	107.14	-	+
A0A0H2UHS9	GRAM domain containing 1A, isoform CRA_a	58.28	+	-
Q3KR56	GRAM domain-containing protein 1A	59.71	+	-
P62994	Growth factor receptor-bound protein 2	460.34	-	+

A0A0G2K665	GTPase-activating protein testicular GAP1	69.29	+	-
A0A0G2JX90	GTPase-activating Rap/RanGAP domain-like 3	109.05	-	+
P62828	GTP-binding nuclear protein Ran	314.94	-	+
Q8K586	GTP-binding nuclear protein Ran, testis-specific isoform	115.73	-	+
Q63942	GTP-binding protein Rab-3D	798.01	+	-
P20595	Guanylate cyclase soluble subunit beta-1	125.39	-	+
Q6AYR6	Haloacid dehalogenase-like hydrolase domain-containing protein 2	282.7	+	-
D3ZC55	Heat shock 70kDa protein 12A (Predicted), isoform CRA_a	122.08	-	+
B4F772	Heat shock 70kDa protein 4-like (Predicted), isoform CRA_b	75.22	-	+
A0A0G2JTT6	HECT and RLD domain-containing E3 ubiquitin protein ligase family member 1	114.94	+	-
D3ZLS5	HECT domain E3 ubiquitin protein ligase 1	120.97	+	-
D4ADZ6	Helicase with zinc finger	120.01	+	-
P23711	Heme oxygenase 2	102.3	+	-
D4A6A2	Heterogeneous nuclear ribonucleoprotein A3	247.64	+	-
Q794E4	Heterogeneous nuclear ribonucleoprotein F	113.7	-	+
G3V9Q3	Heterogeneous nuclear ribonucleoprotein H	134.98	-	+
Q6AY09	Heterogeneous nuclear ribonucleoprotein H2	134.98	-	+
P05708	Hexokinase-1	200.11	+	-
D4A0C3	HID1 domain-containing	85.49	-	+
B2GV65	HIG1 domain family, member 2A	305.69	-	+
D3ZU87	HIG1 hypoxia inducible domain family, member 2A-like 1	217.83	-	+
P63159	High mobility group protein B1	151.7	-	+
D3ZCR3	High-mobility group (nonhistone chromosomal) protein 1-like 1	151.7	-	+
Q569C4	Histone deacetylase 10	84.49	-	+
F1MAL8	HMG-box containing 3	70.96	+	-
D4AA38	Holocarboxylase synthetase	105.79	-	+
G3V6Y1	Homeo box B8 (Mapped)	257.76	-	+
A6YP92	Homeobox protein ARX	170.39	-	+

P18863	Homeobox protein Hox-B8	257.76	-	+
P18866	Homeobox protein Hox-C8	257.76	-	+
D4A8N6	Hypothetical protein LOC690422	139.63	-	+
P27605	Hypoxanthine-guanine phosphoribosyltransferase	240.78	+	-
P20760	Ig gamma-2A chain C region	197.4	+	-
Q6IE24	Inactive ubiquitin carboxyl-terminal hydrolase 54	46.05	-	+
D3ZN51	Integrin subunit alpha 9	80.46	-	+
M0R9Z5	Interferon regulatory factor 2-binding protein 2	60.78	-	+
Q4V797	Interferon-gamma-inducible GTPase Ifgga1 protein	168.28	-	+
Q5FVQ6	Interferon-gamma-inducible GTPase Ifgga3 protein	187.13	-	+
M0RAS6	Interferon-inducible GTPase 1-like	187.13	-	+
B2RYH5	Interleukin-1 receptor-associated kinase 1	95.69	+	-
D3ZBV8	Interleukin-1 receptor-associated kinase 1-binding protein 1	117.09	-	+
G3V760	Intestinal cell kinase, isoform CRA_a	116.8	+	-
A0A0G2JVF8	Intraflagellar transport protein 172 homolog	131.56	-	+
Q8VI04	Isoaspartyl peptidase/L-asparaginase	269.31	+	-
A0A0G2JZH2	Isoleucine--tRNA ligase, cytoplasmic-like	209.7	+	-
F1LS86	Isoleucine-tRNA synthetase (Predicted)	231.25	+	-
A0A0G2JVL8	Isoleucyl-tRNA synthetase	231.25	+	-
D4A1C2	Junction adhesion molecule-like	83.75	-	+
F1M5A4	Katanin p60 ATPase-containing subunit A-like 2	146.69	+	-
P57790	Kelch-like ECH-associated protein 1	67.9	-	+
A0A096MJ07	Keratin, type I cytoskeletal 9	156.81	-	+
A0A0G2K509	Keratin, type II cytoskeletal 5	108.7	-	+
M0RD15	Keratin-associated protein 27-1	140.31	-	+
Q9EQG6	Kinase D-interacting substrate of 220 kDa	59.85	+	-
Q70AM4	Kinesin 13B	52.29	+	-
A0A0G2K8Z9	Kinesin family member 13B	52.29	+	-

F1M4A4	Kinesin family member 1A	48.5	-	+
Q2PQA9	Kinesin-1 heavy chain	92.47	+	-
D3ZI07	Kinesin-like protein	114.63	+	-
Q62909	Kinesin-like protein KIF2C	90.33	-	+
G3V8Z6	KRIT1, ankyrin repeat-containing	91.33	+	-
D4AC69	Leishmanolysin-like (Metallopeptidase M8 family) (Predicted), isoform CRA_a	46.85	+	-
B1H234	Leucine-rich repeat transmembrane protein FLRT3	153.8	+	-
Q5FVI3	Leucine-rich repeat-containing protein 57	128.28	+	-
F8WFF9	Leucine-rich repeat-containing protein 57-like	110.4	+	-
Q66H93	LOC100125386 protein	795.65	+	-
D3ZX48	LON peptidase N-terminal domain and ring finger 2	105.26	-	+
Q66H35	Lung adenoma susceptibility protein 2 homolog	102.18	-	+
Q5XI99	Lysosome-associated membrane glycoprotein 3	91.07	-	+
Q00495	Macrophage colony-stimulating factor 1 receptor	39.75	+	-
F1M5N4	Malic enzyme	171.15	+	-
G3V742	Matrix metalloproteinase	48.9	-	+
A1EC81	Matrix metalloproteinase 28	164.3	-	+
D3ZVH5	MDM2 proto-oncogene	97.21	-	+
P41243	Megakaryocyte-associated tyrosine-protein kinase	129.25	+	-
F1M6Z3	Melanoma antigen preferentially-expressed in tumors-like	169.19	+	-
A0A0G2KA58	Melanoma inhibitory activity 2	102.98	+	-
A0A0U1RS09	Microtubule-associated protein 2	273.37	+	-
Q6XVN8	Microtubule-associated proteins 1A/1B light chain 3A	417.97	-	+
A0A0G2K9L9	Midasin AAA ATPase 1	92	-	+
A0A0G2K5W5	MINDY lysine 48 deubiquitinase 4B, pseudogene	100.02	+	-
P84817	Mitochondrial fission 1 protein	307.92	-	+
Q5FVG4	Mitochondrial glutamate carrier 1-like	122.46	+	-
Q505J6	Mitochondrial glutamate carrier 2	137.34	+	-

D3ZPN5	Mitochondrial poly(A) polymerase	126.77	-	+
Q66H23	Mitoferrin-1	156.12	+	-
P63086	Mitogen-activated protein kinase 1	112.38	+	-
P21708	Mitogen-activated protein kinase 3	141.63	+	-
G3V9J9	Mitogen-activated protein kinase 4	157.98	+	-
P27704	Mitogen-activated protein kinase 6	35.23	+	-
G3V840	Mitogen-activated protein kinase kinase kinase 8	109.65	-	+
D3Z899	Mitoguardin 2	155.54	+	-
D4AAP6	MN1 proto-oncogene, transcriptional regulator	89.09	+	-
Q6Y306	Multidrug resistance-associated protein 9	58.24	-	+
D4A1Q3	Myb/SANT DNA-binding domain-containing 1	156.63	+	-
Q69CM7	MYCBP-associated protein	68.39	-	+
P07722	Myelin-associated glycoprotein	204.93	+	-
Q63345	Myelin-oligodendrocyte glycoprotein	237.62	+	-
Q9R1J4	Myocilin	169.24	-	+
A0A0G2K5P5	Myomesin 1	119.94	+	-
F1LMU0	Myosin heavy chain 1	42.65	+	-
A0A0G2K2W5	Myosin light chain 7	124.18	-	+
Q64122	Myosin regulatory light polypeptide 9	76.42	-	+
Q29RW1	Myosin-4	44.75	+	-
B2RYX0	Naca protein	108.02	+	-
B0BNE6	NADH dehydrogenase (Ubiquinone) Fe-S protein 8 (Predicted), isoform CRA_a	96.21	+	-
G3V644	NADH dehydrogenase (Ubiquinone) flavoprotein 3-like, isoform CRA_a	157.77	-	+
Q6PCU8	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	384.96	-	+
Q641Y2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	165.83	+	-
Q5XIF3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	108.11	-	+
P52504	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	748.22	-	+
D4A1F8	Nanos C2HC-type zinc finger 1	150.55	+	-

A0A0G2K1B7	NEDD4 binding protein 2-like 1	260.02	-	+
D4A1D7	Neurexophilin and PC-esterase domain family, member 2	93	-	+
O35095	Neurochondrin	215.49	+	-
P97685	Neurofascin	41.07	-	+
Q9WU34	Neuronal-specific septin-3	334.4	-	+
F1LP80	Neurosecretory protein VGF	240.33	-	+
A7E3N2	Neutrophil cytosol factor 2	119.66	-	+
Q80Z29	Nicotinamide phosphoribosyltransferase	62.76	+	-
G3V6L2	NIMA-related kinase 2	99.84	+	-
P29476	Nitric oxide synthase, brain	60.24	-	+
B1H280	NK2 homeobox 6	116.94	-	+
D3ZKI9	NOP9 nucleolar protein	62.29	-	+
O35987	NSFL1 cofactor p47	234.34	-	+
D3ZU59	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (Predicted), isoform CRA_a	101.62	-	+
Q9EPU2	Nuclear receptor coactivator 3	55.34	-	+
Q6AYD9	Nucleoside diphosphate-linked moiety X motif 19	100.13	-	+
P70563	Nucleoside diphosphate-linked moiety X motif 6	128.63	-	+
A0A0G2K226	NudC domain-containing 3	314.58	-	+
D4A232	Olfactory receptor	194.13	+	-
Q56A26	Oligodendrocytic myelin paranodal and inner loop protein	284.8	+	-
Q8R5M4	Optineurin	113.87	-	+
D4A6R6	Otoancorin	99.41	+	-
D3ZUC9	Oxidative-stress responsive 1 (Predicted)	181.71	-	+
P63014	Paired mesoderm homeobox protein 1	299.16	-	+
Q32PZ0	PAK1-interacting protein 1	101.25	+	-
P04550	Parathymosin	398.02	-	+
Q5PQT0	PAS domain containing serine/threonine kinase, isoform CRA_a	45.2	+	-

Q4V8F6	Pcbp2 protein	135.67	+	-
F1LPA6	Peptidyl arginine deiminase, type II, isoform CRA_a	66.41	+	-
D3ZUZ9	Peptidyl-prolyl cis-trans isomerase	167.27	-	+
D3ZMY8	Pericentrin	73.32	-	+
M0RA08	Perilipin	82.67	-	+
Q6IRH6	Phosphate carrier protein, mitochondrial	150.02	+	-
Q6IMX4	Phosphatidic acid phosphatase type 2B	118.5	+	-
Q8R2H5	Phosphatidylinositol-glycan-specific phospholipase D	107.14	-	+
G3V7V8	Phosphodiesterase	82.35	-	+
Q499Q4	Phosphoglucomutase-1	256.17	+	-
D4A4M4	Phosphoinositide-interacting regulator of transient receptor potential channels	188.24	-	+
D3ZA44	Phospholipase A2, group IIE	473.97	+	-
Q5FVH2	Phospholipase D3	97.59	+	-
E9PSV5	Phosphoserine aminotransferase	188.21	-	+
P63004	Platelet-activating factor acetylhydrolase IB subunit alpha	201.16	+	-
D4A2Q3	Pleckstrin and Sec7 domain-containing 3	92.29	-	+
D3ZW91	POC1 centriolar protein homolog B	88.78	+	-
Q6AYU5	Poly(rC)-binding protein 2	135.67	+	-
Q6AY48	Poly(rC)-binding protein 3	135.67	+	-
B4F7D3	Polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like	235.94	-	+
Q66H20	Polypyrimidine tract-binding protein 2	210.48	-	+
Q9JK96	Potassium voltage-gated channel subfamily KQT member 4	88.97	+	-
O88758	Potassium voltage-gated channel subfamily S member 1	120.75	-	+
P09626	Potassium-transporting ATPase alpha chain 1	169.91	+	-
B1WCA0	Ppm1d protein	49.33	-	+
D3ZP38	Predicted gene 1758	240.86	+	-
Q64060	Probable ATP-dependent RNA helicase DDX4	165.04	+	-
F7FA48	Progesterone receptor	159.9	+	-

F7EPE0	Prosaposin	155.98	-	+
D4AE56	Prostaglandin E synthase 2	72.89	-	+
P83868	Prostaglandin E synthase 3	292.53	-	+
P35355	Prostaglandin G/H synthase 2	45.56	+	-
F1M6I7	Proteasome subunit alpha type	288.76	-	+
P17220	Proteasome subunit alpha type-2	194.94	-	+
P48004	Proteasome subunit alpha type-7	158.59	-	+
Q6PDW4	Proteasome subunit beta type	110.34	-	+
P18421	Proteasome subunit beta type-1	118.36	-	+
Q6MGD0	Protein CutA	416.8	-	+
Q6AYM4	Protein DPCD	265.4	+	-
F1LS98	Protein kinase C	131.56	+	-
P05696	Protein kinase C alpha type	131.56	+	-
P68403	Protein kinase C beta type	106.29	+	-
P63319	Protein kinase C gamma type	150.02	+	-
G3V9L2	Protein kinase LYK5, isoform CRA_c	169.22	+	-
Q8K3F3	Protein phosphatase 1 regulatory subunit 14B	278.55	+	-
Q66HR9	Protein phosphatase 1 regulatory subunit 32	100.64	+	-
P0C7L8	Protein phosphatase 1 regulatory subunit 3E	333.76	+	-
Q5HZV9	Protein phosphatase 1 regulatory subunit 7	762.39	-	+
A0A0G2JV26	Protein phosphatase 4, regulatory subunit 4	149.08	+	-
B0BMY7	Protein tyrosine kinase 9-like (A6-related protein) (Predicted), isoform CRA_b	110.91	+	-
D4A497	Protocadherin 11 X-linked	68.2	+	-
Q68HB8	Protocadherin 7	82.84	-	+
Q63132	Proto-oncogene tyrosine-protein kinase ROS	35.23	+	-
D3ZM38	Putative uncharacterized protein RGD1565972_predicted	92.1	-	+
F7EPH4	Pyrophosphatase (inorganic) 1	157.69	-	+
P52873	Pyruvate carboxylase, mitochondrial	106.88	-	+

Q5RKJ9	RAB10, member RAS oncogene family	798.01	+	-
A0A0G2JYK2	Rab11 family-interacting protein 1	144.46	+	-
B0BMW0	RAB14, member RAS oncogene family	864.64	+	-
E9PU16	RAB1A, member RAS oncogene family	798.01	+	-
G3V6H0	RAB1B, member RAS oncogene family-like	798.01	+	-
A0A0G2JTT4	RAB30, member RAS oncogene family	914.26	+	-
F1LW77	RAB33B, member RAS oncogene family	180.14	+	-
D4A0G7	RAB37, member RAS oncogene family	798.01	+	-
D3ZZP2	RAB39, member RAS oncogene family (Predicted)	179.48	+	-
F1LVC3	RAB6B, member RAS oncogene family	179.48	+	-
D4ADQ7	RAD21 cohesin complex component-like 1	79.76	-	+
Q62796	RalA-binding protein 1	50.82	-	+
D4A2G9	RAN-binding protein 1	431.08	-	+
Q9QYJ2	Ras GTPase-activating protein 3	128.92	+	-
Q63486	Ras-related GTP-binding protein A	44.41	+	-
Q63487	Ras-related GTP-binding protein B	126.57	+	-
P35281	Ras-related protein Rab-10	798.01	+	-
P35284	Ras-related protein Rab-12	798.01	+	-
P61107	Ras-related protein Rab-14	864.64	+	-
P35289	Ras-related protein Rab-15	801.55	+	-
Q6NYB7	Ras-related protein Rab-1A	798.01	+	-
P10536	Ras-related protein Rab-1B	798.01	+	-
P51156	Ras-related protein Rab-26	798.01	+	-
Q5U316	Ras-related protein Rab-35	798.01	+	-
P63012	Ras-related protein Rab-3A	798.01	+	-
Q63941	Ras-related protein Rab-3B	798.01	+	-
P62824	Ras-related protein Rab-3C	798.01	+	-
Q53B90	Ras-related protein Rab-43	798.01	+	-

P05714	Ras-related protein Rab-4A	918.58	+	-
P51146	Ras-related protein Rab-4B	798.01	+	-
Q9WVB1	Ras-related protein Rab-6A	179.48	+	-
P35280	Ras-related protein Rab-8A	798.01	+	-
P70550	Ras-related protein Rab-8B	798.01	+	-
D3Z9I5	RCG25530, isoform CRA_c	69.63	-	+
D4A1L6	RCG26910, isoform CRA_b	163.09	+	-
D4AEF5	RCG31107	50.23	-	+
B0BNM4	RCG33221, isoform CRA_c	152.24	-	+
A0A0H2UHP9	RCG39700, isoform CRA_d	179.48	+	-
D4AEK4	RCG49713	97.63	-	+
D3ZGZ4	RCG49718	85.04	-	+
Q1KMU0	RCG52183	43.56	+	-
F1LYG2	RCG54282	63.52	-	+
D4A3D2	RCG56113, isoform CRA_a	148.23	+	-
D3Z8H5	RCG65904-like	58	+	-
Q9Z2P5	Receptor-interacting serine/threonine-protein kinase 3	72.04	-	+
A0A0G2JYG7	Receptor-type tyrosine-protein phosphatase R	112.2	+	-
O70521	Regulator of G-protein signaling 19	220.18	+	-
E9PT49	Regulatory factor X, 7	87.48	-	+
B4F778	Replication factor C (Activator 1) 4 (Predicted), isoform	100.14	-	+
B5DF29	Replication factor C (Activator 1) 5	92.36	-	+
Q64548	Reticulon-1	122.75	+	-
Q4KM26	RGD1311345 protein	265.21	+	-
D4A5K8	RGD1559600	396.03	+	-
A1A5Q3	RGD1560775 protein	145.48	+	-
A0A0H2UHP2	RGD1561415	188.19	+	-
B2RYG3	RGD1565149 protein	108.78	+	-

A2VD15	RGD1566036 protein	135.64	+	-
Q5FVG9	Rho family GTPase 1	146.48	+	-
M0R5V4	Rho GTPase-activating protein 19	80.1	-	+
F1LUU6	Rho guanine nucleotide exchange factor 38	61.06	-	+
D3ZN03	Ribosomal protein P2-like	103.06	+	-
D3Z8E0	Ribosomal protein S6 kinase	59.34	+	-
D3ZY39	Ribosomal RNA-processing 1B	128.7	+	-
D3ZXH1	RIKEN cDNA 2310003L06 gene	63.07	-	+
D3ZYQ9	Ring finger protein 20	39.42	+	-
D3ZRG6	Ring finger protein 6	119.8	-	+
D3ZND9	RIO kinase 3	157.11	+	-
A0A0G2KAG6	RNA polymerase III subunit G-like	235.94	-	+
Q68FS8	RNA terminal phosphate cyclase domain 1	157.88	-	+
A0A0G2K1R3	Scaffolding protein involved in DNA repair	126.22	+	-
B5DFD3	Schip1 protein	49.88	+	-
D4A2D6	Schlafen 2	209.71	+	-
D3ZHJ3	Semaphorin 3B	94.95	+	-
A0JN02	Sept4 protein	180.16	+	-
E9PST0	Septin 4	180.16	+	-
D4A2H2	Serine palmitoyltransferase, long chain base subunit 1	76.8	-	+
D3ZKU3	Serine/threonine kinase 35	113.29	+	-
D4A648	Serine/threonine kinase 4	112.51	+	-
O08875	Serine/threonine-protein kinase DCLK1	212.87	+	-
Q62726	Serine/threonine-protein kinase ICK	116.8	+	-
P35465	Serine/threonine-protein kinase PAK 1	243.67	-	+
Q64303	Serine/threonine-protein kinase PAK 2	158.43	-	+
Q62829	Serine/threonine-protein kinase PAK 3	154.37	-	+
G3V8M5	Serine/threonine-protein phosphatase	112.53	-	+

A0A0G2K5X0	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B	281.04	+	-
P97888	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B gamma isoform	281.04	+	-
Q4QQT4	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	87.95	-	+
P63331	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	109.77	+	-
Q5BJ92	Serine/threonine-protein phosphatase 4 catalytic subunit	112.53	-	+
Q6P799	Serine--tRNA ligase, cytoplasmic	71.88	-	+
D3ZHH8	Serum response factor	71.24	+	-
Q9JLU4	SH3 and multiple ankyrin repeat domains protein 3	148.57	-	+
D3ZPJ0	Shisa family member 7	60.01	-	+
A0A0G2KAW2	Signal-induced proliferation-associated 1 like 1, isoform CRA_b	88.72	+	-
O35412	Signal-induced proliferation-associated 1-like protein 1	88.72	+	-
F1M611	Similar to 2610034M16Rik protein	143.33	+	-
D4A4D5	Similar to 60S acidic ribosomal protein P2	103.06	+	-
D3ZWL0	Similar to 60S ribosomal protein L32	156.25	-	+
F7FKF2	Similar to Ab1-351	148.06	-	+
F7FM32	Similar to CG9752-PA	265.21	+	-
D3ZY56	Similar to divalent cation tolerant protein CUTA	328.44	+	-
M0R509	Similar to hypothetical protein C130079G13	82.56	-	+
F1LX85	Similar to K04F10.2	62.63	-	+
F1LTP9	Similar to MAP/microtubule affinity-regulating kinase 4 (MAP/microtubule affinity-regulating kinase-like 1)	154.77	-	+
D3ZHA7	Similar to Myosin light chain 1 slow a (Predicted)	106.15	+	-
F1LVY7	Similar to RIKEN cDNA 4732496O08	85.54	-	+
A0A0G2K442	Similar to RIKEN cDNA 4930579C12 gene	145.48	+	-
F1LTK7	Similar to sentrin 15	161.51	-	+
D3ZMV1	Similar to Src-like adaptor protein-2 (Predicted)	157.09	-	+
D4AA19	Similar to T-cell activation Rho GTPase-activating protein isoform b	163.11	-	+
D3ZJ47	Similar to UPF0258 protein KIAA1024	114.41	+	-

D3ZLP9	Sin3A-associated protein 130	168.15	+	-
G3V970	SIX homeobox 1	93.94	-	+
D4ABU3	SLAM family member 7	112.64	+	-
D3ZS24	SLAM family member 8	110.96	-	+
F1LQU9	Small G protein-signaling modulator 3	174.32	-	+
F1LYZ6	Small nuclear RNA-activating complex, polypeptide 4	43.15	+	-
P60192	SNARE-associated protein Snapin	415.08	+	-
Q63553	SNF-related serine/threonine-protein kinase	44.34	+	-
F1LRK1	Sodium/potassium-transporting ATPase subunit alpha	169.91	+	-
G3V8G0	Solute carrier family 12 member 3	105.15	-	+
D3ZKX5	Solute carrier family 15, member 5	161.65	-	+
F1LZW6	Solute carrier family 25 member 13	132.24	+	-
D4A961	Solute carrier family 25, member 48	186.06	-	+
G3V6S0	Spectrin beta chain	230.85	+	-
A0JPP4	Sperm equatorial segment protein 1	107.69	-	+
D4A6T1	Spermatogenesis associated 5 (Predicted), isoform CRA_a	96.67	+	-
A0A0G2K0I1	Spermatogenesis-associated 5	96.67	+	-
Q6PEC4	S-phase kinase-associated protein 1	807.13	-	+
Q564G3	Sphingolipid delta(4)-desaturase/C4-monooxygenase DES2	295.2	+	-
A0A0G2K8K0	Splicing factor proline and glutamine rich	140.13	-	+
Q9JKL7	Splicing regulatory glutamine/lysine-rich protein 1	123.02	+	-
A0A0G2KAV7	SprT-like domain-containing protein Spartan	115.91	-	+
Q9QXY2	SRC kinase signaling inhibitor 1	87.85	-	+
Q66HL2	Src substrate cortactin	253.81	-	+
Q9ET50	Staufen double-stranded RNA-binding protein 1	57.65	+	-
Q7TNZ6	STE20-related kinase adapter protein alpha	169.22	+	-
F1LN57	Sterile alpha motif domain-containing protein 14	113.24	+	-
Q64562	Steroid 21-hydroxylase	156.13	+	-

P56720	Sterol regulatory element-binding protein 1	60.16	+	-
P70483	Striatin	64.71	-	+
F1LPV8	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial	329.47	-	+
P07825	Synaptophysin	2871.56	+	-
G3V6M3	Synaptotagmin II	132.14	+	-
P29101	Synaptotagmin-2	132.14	+	-
P47861	Synaptotagmin-5	158.37	+	-
F1LSG8	Syndetin	167.2	-	+
Q9Z158	Syntaxin-17	144.57	+	-
D3ZTQ2	T cell immunoreceptor with Ig and ITIM domains	204.79	-	+
D3ZA84	Talin 2	122.2	-	+
D3ZN60	Tau tubulin kinase 1 (Predicted)	115.02	-	+
A0A0G2JYZ1	Tau tubulin kinase 2	115.02	-	+
Q7TST9	T-box transcription factor TBX3	53.38	-	+
A0A0G2JYT7	T-complex protein 10b	131.77	+	-
D3ZMN0	Testis specific gene A13 (Predicted)	303.71	+	-
Q4V7F0	Tetratricopeptide repeat protein 23	151.83	-	+
Q6P3V7	Tetratricopeptide repeat protein 41	126.88	+	-
Q920J4	Thioredoxin-like protein 1	142.68	-	+
Q80WE6	TNF superfamily member 9	172.13	+	-
B1WC25	Tra2a protein	212.27	+	-
Q5XIC7	Transcription elongation factor A N-terminal and central domain-containing protein 2	118.21	+	-
D4A3I4	Transcription factor BTF3	308.18	-	+
Q68A21	Transcriptional activator protein Pur-beta	417.57	-	+
Q64428	Trifunctional enzyme subunit alpha, mitochondrial	137.34	+	-
D3ZA88	Tripartite motif-containing 34	119.83	-	+
D4A3L4	Tripartite motif-containing 6	98.44	+	-

D4A0T1	tRNA-dihydrouridine synthase	50.46	-	+
Q642B1	TSPY-like 1	123.59	-	+
P22934	Tumor necrosis factor receptor superfamily member 1A	178.39	+	-
Q5FVG7	Tyrosine-protein kinase	87.04	-	+
P57097	Tyrosine-protein kinase Mer	63.42	-	+
Q63159	Ubiquinone biosynthesis O-methyltransferase, mitochondrial	259.6	+	-
B2GUX4	Ubiquitin carboxyl-terminal hydrolase 21	108.84	-	+
Q4VSI4	Ubiquitin carboxyl-terminal hydrolase 7	87.06	-	+
D3ZFY8	Ubiquitin-conjugating enzyme E2 variant 1-like	795.65	+	-
Q7M767	Ubiquitin-conjugating enzyme E2 variant 2	795.65	+	-
Q4V8I9	UDP-glucose pyrophosphorylase 2	168.61	+	-
D3ZRJ5	Uncharacterized LOC100910852	58	+	-
A0A0G2K5H8	Uncharacterized protein	135.53	+	-
A0A0G2JW95	Uncharacterized protein	68.27	+	-
M0R8M5	Uncharacterized protein	74.92	+	-
E9PSU5	Uncharacterized protein	247.64	+	-
A0A0G2JV25	Uncharacterized protein	142.58	+	-
M0RCJ6	Uncharacterized protein	361.15	+	-
F1LUW0	Uncharacterized protein	300.84	+	-
M0RDR2	Uncharacterized protein	240.33	-	+
A0A0G2K9B5	Uncharacterized protein	69.05	-	+
D3ZXR5	Uncharacterized protein	151.7	-	+
A0A0G2K0Z2	Uncharacterized protein	256.95	-	+
A0A0G2K6D3	Uncharacterized protein	81.74	-	+
F1M3U2	Uncharacterized protein	82.77	-	+
F1M6B2	Uncharacterized protein	113.66	-	+
F1M269	Uncharacterized protein	132.87	-	+
A0A0H2UHJ3	Uncharacterized protein	100.54	-	+

A0A0G2K3G4	Uncharacterized protein	89.37	-	+
D3ZAQ5	Uncharacterized protein C16orf86 homolog	188.19	+	-
Q6AXP4	Uncharacterized protein C2orf81 homolog	105.8	-	+
Q63357	Unconventional myosin-I δ	41	-	+
B2RZ78	Vacuolar protein sorting-associated protein 29	456.87	-	+
A0A0G2K944	Versican core protein	82.41	-	+
Q63666	Vesicle-associated membrane protein 1	308.24	-	+
Q5J3M1	Vomeroneasal type-1 receptor	68.49	-	+
D4ADT3	WAPL cohesin release factor	44.39	+	-
D4A106	WD repeat domain 3	142.16	-	+
D3ZQ02	WD repeat domain 37	109.13	+	-
D4A0M9	WD repeat domain 64	55.69	-	+
F1LYQ6	WD repeat domain 97	107.17	+	-
Q4V8G4	WD repeat-containing and planar cell polarity effector protein fritz homolog	111.37	-	+
Q5BJU7	Wiskott-Aldrich syndrome protein family member 1	148.26	-	+
B1WC00	Zfr protein	313.63	+	-
D3ZYC1	Zinc finger protein 507	143.63	+	-
Q499R0	Zinc finger protein 518A	60.05	-	+
F1LV88	Zinc finger protein 7	791.67	-	+
D3ZAE8	Zinc finger protein 780B, pseudogene 1	656.42	+	-
Q3MHS2	Zinc finger protein 830	83	-	+
M0R740	Zinc finger protein 865-like	112.84	+	-
P56163	Zinc finger protein neuro-d4	47.74	+	-
Q562A2	Zinc finger RNA-binding protein	316.77	+	-
D4A1E1	Zinc finger, MYND domain containing 15 (Predicted), isoform CRA_a	66.93	-	+

^aAccession ID according to Uniport.org database. Signs of + or – indicates presence or absence of the protein in one of the groups.