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Supplemental Information

GDE2-Dependent Activation

of Canonical Wnt Signaling in Neurons

Regulates Oligodendrocyte Maturation

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DIV3 OLs WT Gde2KO

Figure S1. Related to Figure 1. GDE2 is expressed in neurons and OLs.

(A) Western blot of cortical extracts from WT animals at postnatal day 7 (P7), P10 and P14. GAPDH is a loading control, NFH is expressed in axons and provides a readout of neurons in brain tissue. Arrow indicates GDE2. Asterisk indicates a nonspecific band. Graph quantifying Western data from P7-P14. a.u. = arbitrary units. **p = 0.0013. n = 3 P7, 4 P10, 3 P14, 1-way ANOVA. (B) Western blot and quantification of GDE2 protein expression at 1 and 2 months (m) of age. ns p = 0.182. n = 3 for each timepoint, two-tailed unpaired t-test. (C) Cortical coronal sections showing *Gde2* transcript distribution. CC: corpus callosum, SS: somatosensory cortex. Cortical layers are marked by dotted lines. Boxed areas 1 and 2 are magnified in right panels. Scale bar: 100 µm, insets 10 µm (D) Western blot of DIV3 cortical neuronal cultures. Arrow marks GDE2. Actin is a loading control. (E) qPCR of *Gde2* transcripts normalized to *Gapdh* mRNA. *p = 0.0021. n = 3 sets of WT, *Gde2KO* OPCs, and WT OLs, 1-way ANOVA. (F) Western blot shows GDE2 is expressed in WT OLs (marked by arrow). Actin is a loading control. All graphs: Mean \pm sem.



Figure S2. Related to Figure 2. GDE2 loss impairs OL maturation.

(A) Coronal section of P15 mouse cortex, hatched lines mark cortical boundaries. Cortical layers I-VI are marked. (B) Schematic showing the progression of OL maturation coincident with marker expression. (C) Coronal section of P7 mouse cortex (CTX) and corpus callosum (CC). Hatched line marks boundary between CTX and CC. Inset box shows magnified image of proliferating OPCs (white, Ki67+Sox10+Olig2+). (D) Graphs guantifying the number of proliferating OPCs (Ki67+Sox10+Olig2+) CC ns p = 0.9981 and CTX ns p = 0.6352, n = 4 WT, 3 Gde2KO. Two tailed unpaired Student's t-test. (E) Coronal section of P11 mouse CTX and CC. Hatched line demarcates the CC. Inset box shows magnified image of immature (TCF4+CC1-) and mature OLs (CC1+). (F) Graphs guantifying the number of immature OLs (TCF4+CC1-). CC ns p =0.2306 and CTX ns p = 0.8021, n = 3 WT, 5 Gde2KO. Two tailed unpaired Student's t-test. (G) Graphs guantifying number of CC1+ cells in boxed areas in rostral, middle and caudal regions of mouse P11 CC and CTX as shown in schematic. Data for middle regions are the same as in Figure 2B and are reproduced here for comparison purposes. CC: *p rostral = 0.013 ***p middle = 0.0007 **p caudal = 0.0072; CTX: *p rostral = 0.0004 ***p middle = 0.0035 **p caudal = 0.0063. n = 3 WT 5 *Gde2KO*. Two tailed unpaired Student's t-test. All graphs: Mean + sem. Scale bars: (A, C, E) 100 μm, insets (C, E) 5 μm.



Figure S3. Related to Figure 2. *Gde2* KOs show recovery of myelin protein but have decreased myelination of large-diameter axons.

(A, C) Coronal sections of mouse cortex (CTX) and corpus callosum (CC). Hatched lines delineate the CC. Insets show high magnification of mature OLs. Scale bars: 100 µm insets: 10 µm in A and C. (B, D) Graphs quantifying numbers of ASPA+ OLs in CC and CTX. (B) CC *p = 0.0275 and CTX **p = 0.0028, n = 4 WT, 5 Gde2KO (D) CC ns p = 0.539 and CTX ns p = 0.4373, n = 3 WT, 4 Gde2KO. (E) Western blot of cortical extracts from P28 animals. Graphs guantifying myelin associated proteins MBP ns p = 0.5198, MOG ns p = 0.1035 n = 4 WT, 4 Gde2KO. (F) Representative TEM images of 10 week WT and Gde2KO animals. * marks exemplar unmyelinated larger-diameter axon in Gde2KO condition. Scale bar: (Top) 1 µm, (Bottom) 200 nm, Inset 100 nm. Graphs quantifying axon numbers (ns p = 0.3905) and the percentage of axons with diameters between 1.5 and $2\mu m$ (ns p = 0.1649) and larger than $2\mu m$ (ns p = 0.8323). Although the percentage of myelinated axons between 1.5 and 2µm is equivalent between WT and *Gde2KO* animals (ns p = 0.9667), the percentage of myelinated axons with diameters larger than 2µm is dramatically reduced (*p = 0.0206) n = 3 WT, 3 Gde2KO. Diameters of axons greater than 0.5 μ m (ns p = 0.5977) and g-ratios of myelinated axons with diameters larger than 1.5 μ m are unchanged between WT and *Gde2KO* animals (ns p = 0.156). Each point refers to individual myelinated axons from 3 WT and 3 Gde2KO. All graphs Mean + sem, two tailed unpaired t-test.





Figure S4. Related to Figure 4. Characterization of neuron-OPC co-cultures.

(A) Immunocytochemical staining of DIV3 cortical neuronal cultures. Scale bar: 50 µm. Graphs quantifying percentage neurons (β -tubulin III+) and astrocytes in DIV3 WT and *Gde2KO* cortical neuronal cultures (β -tubulin III+ ns p = 0.6243; GFAP+ ns p = 0.6093; n = 3 WT 3 *Gde2KO*). (B) Graph quantifying the number of Olig2+ cells after neuron-OPC co-culture (ns p = 0.1235, n = 4 WT neuron-WT OPC co-cultures, 4 *Gde2KO* neuron-WT OPC co-cultures). Two tailed unpaired Student's t-test. All graphs: Mean <u>+</u> sem. (C) Graph of fluorescence changes (Δ F/F0) in DIV3 WT and *Gde2KO* neurons loaded with the calcium indicator Fluo-4 over a 3.5 minute period. Each data point represents mean value of Δ F/F0 from at least 11 recordings per group at a given time. Arrowhead marks the time of Ionomycin addition, which permeabilizes the membrane and acts as a positive control. (D) Western blot of DIV14 cortical neurons treated with bicuculine for specified times. Bar denotes GDE2. Graph quantifying GDE2 protein levels show no change in expression after stimulation. 1 way ANOVA ns p = 0.4692, n = 3 for each timepoint.



Figure S5. Related to Figure 5. Canonical Wnt signaling is reduced when GDE2 is disrupted. (A) Volcano plot showing differentially expressed genes between WT and Gde2KO spinal cord. (B) Gene ontology analysis using p-value (< 0.05) highlights Wnt signaling pathways are disrupted in absence of GDE2. (C) List of known Wnt target genes that are altered in Gde2KO condition. (D) Analysis of Wnt-reporter animals (Wnt-eGFP) show that canonical Wnt signaling (eGFP) is high at P7 and P11 but is minimal at P28. Hatched line marks the boundary between cortex and corpus callosum. (E) Graphs quantifying the percentage of reporter gene expression in Wnt-eGFP mice at P7, P11 and P28 in neurons (NeuN+) and oligodendroglia (Olig2+) in corpus callosum (CC) and cortex (CTX). GFP+NeuN+ ***p < 0.0001, GFP+Olig2+ CC **p = 0.0027, GFP+Olig2+ CTX ***p < 0.0001. n = 3 P7, 3 P11, 3 P28, 1-way ANOVA. Data for P11 are the same as presented in Figure 4F and 4H (WT) and are included here for comparison purposes. (F) Coronal sections of P11 WT; Wnt-eGFP and Gde2KO; Wnt-eGFP animals (G) Graphs guantifying GFP+ cells in CC and CTX. CC **p = 0.004, CTX **p = 0.007, n = 3 WT; Wnt-eGFP, 4 Gde2KO;Wnt-eGFP, two-tailed unpaired t-test. (H) Representative image of P11 cortex of Wnt-eGFP mice. Arrowheads mark TCF4+CC1- immature OLs, arrows mark mature CC1+ OLs; both populations do not co-express eGFP. All graphs: Mean + sem. Scale bar: (D, F) 100 µm, (H) 20µm.



Lane 4: Gde2-/-; Ctnnbflex3/+; NexCre

Figure S6. Related to Figure 6. Genetic stabilization of β -catenin in neurons does not change total Olig2+ cells.

(A) Western blot of P14 cortical extracts. Open arrowhead marks WT β -catenin; black arrowhead marks β -catenin deleted for exon 3. Actin is used as a loading control. (B) Graphs quantifying the number of Olig2+ cells in P11 corpus callosum (CC) and cortex (CTX). ns CC p = 0.1608 (1-way ANOVA/Bonferroni's multiple comparison test), ns CTX p = 0.6109 (1-way ANOVA/Bonferroni's multiple comparison test), ns CTX p = 0.6109 (1-way ANOVA/Bonferroni's multiple comparison test). n = 4 *WT*; β -cat^{ex3}, 3 *Gde2KO*; β -cat^{ex3}; 4 *Gde2KO*;N- β -cat^{ex3}. All graphs: Mean <u>+</u> sem.



Figure S7. Related to Figure 5. Stabilization of β -catenin in OPCs does not rescue *Gde2KO* OL maturation.

(A, C) Coronal sections of P11 mouse cortex (CTX) and corpus callosum (CC). Hatched lines in panel C outlines CC boundaries. (B) Graphs quantifying the number of Olig2+ cells in CC and CTX. CC ns p = 0.0601, **p = 0.0011, two-tailed unpaired t- test; CTX ns p = 0.1235, 1-way ANOVA Bonferroni's multiple comparison test, all 3 genotypes. n = 3 *WT;β-cat^{ex3}*, 3 *Gde2KO;β-cat^{ex3}*, 6 *Gde2KO;O-β-cat^{ex3}*. (D) Graph quantifying the number of MBP+Olig2+ cells *p = 0.0132, **p = 0.0073, n = 3 *WT;β-cat^{ex3}*, 3 *Gde2KO;β-cat^{ex3}*, 6 *Gde2KO;O-β-cat^{ex3}*. Two tailed unpaired Student's t-test. (E) Graphs quantifying number of CC1+ OLs. CC *p = 0.0132, **p = 0.0012; CTX *p = 0.0242, ***p = 0.0008, n = 3 *WT;β-cat^{ex3}*, 3 *Gde2KO;β-cat^{ex3}*, 6 *Gde2KO;O-β-cat^{ex3}*. Two tailed unpaired Student's t-test. All graphs: Mean <u>+</u> sem. Scale bars: 100 µm.

Α		,
Protein name	Gene name	KO/WT ratio
Glypican-1;Secreted glypican-1	Gpc1	0.82
Glypican-2;Secreted glypican-2	Gpc2	0.91
Semaphorin-7A	Sema7a	0.94
Cadherin-13	Cdh13	0.95
Contactin-2 (a.k.a. TAG-1)	Cntn2	1.05
Neural cell adhesion molecule 1	Ncam1	1.11
RGM domain family member B	Rgmb	1.22
Lipoprotein lipase	Lpl	1.23
Repulsive guidance molecule A	Rgma	1.25
Contactin-1	Cntn1	1.25
Neural cell adhesion molecule 2	Ncam2	1.40

В		
Protein name	Gene name	KO/WT ratio
Carboxypeptidase B2	Cpb2	0.33
Phosphatidylethanolamine-binding protein 1	Pebp1	0.43
Receptor-type tyrosine-protein phosphatase zeta	Ptprz1	0.44
Gamma-glutamyl hydrolase	Ggh	0.47
Follistatin-related protein 5	Fstl5	0.50
Glucose-6-phosphate isomerase	Gpi	0.51
ProSAAS	Pcsk1n	0.53
Noelin	Olfm1	0.53
Glia-derived nexin	Serpine2	0.54
Complement C5	C5	0.57
Collagen alpha-1(I) chain	Col1a1	3.98



Figure S8. Related to Figure 7. Candidate mechanisms for GDE2-dependent OL maturation. (A) List of GPI-anchored proteins identified in WT and Gde2KO CM by mass spectrometry. (B) List of secreted and extracellular matrix proteins identified in WT and Gde2KO CM by mass spectrometry. RPTPzeta (phosphacan) is highlighted in red. (C) Western blot of WT neuronal CM showing effective depletion of phosphacan using neuronal phosphacan antibodies conjugated to protein-L (D) Representative images of WT OPCs after culturing with WT neuronal CM and WT neuronal CM depleted for phosphacan. (E) Graphs quantifying the percentage of MBP+Olig2+ OLs (normalized to WT CM) in WT OPC cultures grown with WT neuronal CM or phosphacan depleted WT neuronal CM. Top panel ***p<0.0001, n = 5 WT CM, 5 Phosphacan depleted CM, two tailed unpaired t-test. All 3 stages of OL maturation are also affected (2-way ANOVA ***p < 0.0001; Bonferroni correction Stage 1 ***p <0.001; Stage 2 ***p <0.001; Stage 3 ***p <0.001; n = 5 WT CM, 5 Phosphacan depleted CM. No change in OPC maturation is observed between WT neuronal CM or WT neuronal CM preincubated with protein L alone. Bottom panel ns p = 0.1456, n = 3 WT CM, 3 Protein L incubated CM, two tailed unpaired t-test. Similarly, stages of OL maturation are unchanged (2-way ANOVA ns p = 0.1262; Bonferroni correction Stage 1 ns p >0.05; Stage 2 ns p >0.05; Stage 3 ns p >0.05; n = 5 WT CM, 5 Phosphacan depleted CM.(F) Model for GDE2 regulation of OL maturation. GDE2 stimulates canonical Wnt signaling in neurons. Wnt activation leads to release of neuronally-derived factors such as phosphacan, which act on neighboring OPCs or immature OLs to promote their maturation into myelinating oligodendrocytes.

Table S1: Cell counts for in vitro cultures. Refers to Figure 4, Figure 7, and Figure S8.

Fig 4	B/F			D/F			D		
	DIV3+4 coculture	WT	Gde2KO	DIV3+4 CM	WТ	Gde2KO	DIV3 CM	WТ	Gde2KC
	Olia2+	2959	3030	Olia2+	1251	1126	Olia2+	730	907
	MBP stage 1	159	89	MBP stage 1	251	194	MBP stage 1	50	60
	MBP_stage 2	116	43	MBP stage 2	219	147	MBP stage 2	71	51
	MBP Stage 3	53	18	MBP Stage 3	62	30	MBP Stage 3	48	27
	total MBP+	328	152	total MBP+	532	371	total MBP+	169	138
E : 7D									
FIG 7B		CdagKOre Catex3 CM	CHOIN & Cot ^{ex3} CM						
	Olian	Guezno,p-Cai Civi							
		936	094						
	MBP_stage 1	65	100						
	MBP_stage 2	26	43						
	MBP_Stage 3	17	28						
	total MBP+	108	171						
Fig S8E									
		CM	CM phsophacan depleted		CM	CM protein L			
	Olig2+	2189	2815	Olig2+	1007	869			
	MBP_stage 1	290	306	MBP_stage 1	132	97			
	MBP_stage 2	377	278	MBP_stage 2	132	140			
	MBP_Stage 3	189	138	MBP_Stage 3	61	67			
	total MBP+	856	722	total MBP+	325	304			

Table S3: Related to Supplemental Figure 8. List of proteins showing > 40% differential enrichment in *Gde2KO* CM.

Number of altered protein expression: 149

			Sequence	Sequence	LFQ intensity	LFQ intensity	Ratio
Protein IDs	Protein names	Gene names	coverage KO [%]	coverage WT [%]	ко	wт	(KO/WT)
A8DUK4	beta-globin	Hbbt1	60.9	58.2	3.67E+06	3.93E+08	0.0093385
Q80ZV4	Cadherin-4	Cdh4	3.6	3.6	3.59E+05	6.73E+06	0.0533103
P35979	60S ribosomal protein L12	Olfm1	9.7	9.7	3.50E+05	3.35E+06	0.104707
Q3TLP8	Ras-related C3 botulinum toxin substrate 1	Rac1	9.45	12.3	1.22E+06	1.16E+07	0.1055619
P58283	E3 ubiquitin-protein ligase RNF216	Rnf216	0.8	0.8	7.20E+05	5.81E+06	0.1241085
Q6ZWQ9	Myosin regulatory light chain 12B	Myl12a	17.4	9.3	2.92E+06	2.11E+07	0.1384735
P48678	Prelamin-A/C	Lmna	1.8	0.75	7.71E+04	3.94E+05	0.1955637
F6VYE2	Zinc finger MYM-type protein 4	Zmym4	0.7	0.7	3.81E+07	1.28E+08	0.2985482
G5E866	Splicing factor 3B subunit 1	Sf3b1	0.35	1.1	6.29E+05	2.08E+06	0.3018324
Q99JI6	Ras-related protein Rap-1b	Rap1b	11.15	11.15	2.20E+06	7.24E+06	0.304105
P62897	Cytochrome c, somatic	Cycs	17.15	17.15	1.47E+06	4.78E+06	0.3074461
P32233	Developmentally-regulated GTP-binding protein 1	Drg1	4.4	4.4	4.55E+05	1.37E+06	0.3315903
Q2KIG3	Carboxypeptidase B2	Cpb2	2.6	2.15	2.81E+05	8.34E+05	0.3367496
P19253	60S ribosomal protein L13a	Rpl13a	8.1	8.1	1.20E+06	3.52E+06	0.3409558
P97350	Plakophilin-1	Pkp1	2.25	2.25	2.43E+06	6.66E+06	0.3647232
P62242	40S ribosomal protein S8	Rps8	8.9	7.2	7.11E+05	1.75E+06	0.4058655
Q3UHN9	Bifunctional heparan sulfate N-deacetylase	Ndst1	0.8	1.6	9.53E+05	2.35E+06	0.4063519
A0A087WPL5	ATP-dependent RNA helicase A	Dhx9	0.6	0.85	4.55E+05	1.11E+06	0.4094201
Q8QZY9	Splicing factor 3B subunit 4	Sf3b4	1.65	3.3	2.16E+06	5.03E+06	0.4288
P70296	Phosphatidylethanolamine-binding protein 1	Pebp1	32.6	29.15	4.56E+07	1.05E+08	0.4363098
Q62189	U1 small nuclear ribonucleoprotein A	Snrpa	9.55	9.55	7.22E+06	1.64E+07	0.4395122
B9EKR1	Receptor-type tyrosine-protein phosphatase zeta	Ptprz1	7.05	6.8	1.08E+08	2.43E+08	0.445375
Q9DBG3	AP-2 complex subunit beta;AP complex subunit beta	Ap2b1	2	1.3	2.06E+06	4.55E+06	0.4524362
Q60648	Ganglioside GM2 activator	Gm2a	8.8	4.4	1.39E+06	2.98E+06	0.4666868
Q9CXV9	DCN1-like protein 5	Dcun1d5	6.3	6.3	3.76E+07	8.06E+07	0.466781
Q9Z0L8	Gamma-glutamyl hydrolase	Ggh	12.9	12.9	6.49E+06	1.37E+07	0.4751144
P80317	T-complex protein 1 subunit zeta	Cct6a	4.35	2.85	1.13E+06	2.35E+06	0.4792104
B1AX58	Plastin-3	Pls3	0.7	1.4	8.46E+05	1.76E+06	0.4811927
Q9R1P3	Proteasome subunit beta type-2	Psmb2	6.2	9.95	8.15E+06	1.65E+07	0.4936686
Q8R093	Uridine phosphorylase	Upp2	4.2	2.1	5.18E+07	1.03E+08	0.5007006
Q8BFR2	Follistatin-related protein 5	Fstl5	8	9.8	1.04E+07	2.08E+07	0.5017444
Q9EST1	Gasdermin-A	Gsdma	1	2.6	1.80E+06	3.50E+06	0.5148759
Q91V64	Isochorismatase domain-containing protein 1	lsoc1	5.2	10.4	1.33E+06	2.58E+06	0.5164249
P06745	Glucose-6-phosphate isomerase	Gpi	5.2	5.2	9.57E+05	1.84E+06	0.518811
Q9CQU0	Thioredoxin domain-containing protein 12	Txndc12	6.45	4.4	1.93E+06	3.68E+06	0.5235417
Q08331	Calretinin	Calb2	11.8	11.8	3.97E+06	7.51E+06	0.5290136
Q9QXV0	ProSAAS	Pcsk1n	12.2	10.5	9.84E+06	1.85E+07	0.53233
A3KGE4	Noelin	Olfm1	4.3	4.3	7.73E+05	1.44E+06	0.5356937
Q3TKX1	V-type proton ATPase subunit S1	Atp6ap1	14.2	14.2	1.28E+07	2.37E+07	0.5403885
Q9DAY9	Nucleophosmin	Npm1	4.1	14	1.17E+07	2.15E+07	0.5426547
Q07235	Glia-derived nexin	Serpine2	13.35	13.35	5.49E+06	1.00E+07	0.5480371
Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein	Sh3bgrl	25	18	7.48E+06	1.36E+07	0.548844
P61164	Alpha-centractin	Actr1a	2.95	7.85	1.46E+06	2.65E+06	0.550069
P61358	60S ribosomal protein L27	Rpl27	7.35	10.65	2.31E+06	4.20E+06	0.5504141
009061	Proteasome subunit beta type-1	Psmb1	14.15	18.3	1.62E+07	2.92E+07	0.5534894
Q5RKN9	F-actin-capping protein subunit alpha-1	Capza1	13.6	13.6	4.36E+06	7.85E+06	0.5548677
E9PYH2	Cytosolic acyl coenzyme A thioester hydrolase	Acot7	8.3	6.75	6.44E+06	1.15E+07	0.559416
P24369	Peptidyi-prolyi cis-trans isomerase B	Ppib	18.05	16	2.04E+07	3.62E+07	0.5644408
Q9D1C8	Vacuolar protein sorting-associated protein 28 homolog	Vps28	2.75	5.5	7.42E+05	1.31E+06	0.5652669
Q31X55	Actin-related protein 2/3 complex subunit 4	Arpc4	20.25	17.9	1.39E+07	2.44E+07	0.569117
P62702	40S ribosomal protein S4	Gm15013	5.1	8.1	7.23E+06	1.27E+07	0.569801
54K1Nb	40S ribosomal protein S18	Rps18	22.9	18.7	1.08E+07	1.88E+07	0.5729743
P00084		C5	1.05	1.05	2.07E+06	3.60E+06	0.5752787
D326E4	Enolase,Gamma-enolase	Enoz	0.30	7.9	4.40E+05	7.04E+05	0.5833966
P50247	Adenosylhomocysteinase	Ahcy	9	9	5.44E+06	9.19E+06	0.5925307
P20029	ro kuja glucose-regulated proteiň	rispao Streen 2	1.25	9.4	2.20E+06	3.08E+06	0.5991105
F 33821	Statumm-2	Sullinz Noom2	14.0	14.0	2.0/E+U/	1.91E+07	1.400/286
035136	Adia as astis	NCamz Adia a s	3.0	3.0	2.09E+06	1.49E+06	1.4047028
060994	Auponecum	Adipoq Stip1	10.75	10.75	1.19E+07	3.10E+07	1.4090303
	Suess-induced-phosphoprotein 1	Sup I	2.9 12.0	2.9 17.0	0.30E+Ub	3.01E+Ub	1.4100147
	Actual reactine-rich nuclear phosphoprotein 32 tamily member A	Aripsza Apre	13.9	0.0	1.19E+07	0.300+00	1.4150217
003002	Transaldalasa	Taldo1	0.9	0.5	1.010+00	0.075+07	1 4202020
000 136	THUMP domain-containing protein 1	Thumpd1	8 45	73	2 465-06	1 72 5+06	1 /3/270
000PT1	Rho GDP-dissociation inhibitor 1	Arbadio	20.40	30.15	2.40L+00 8.03E±07	5.58E±07	1 /302266
061500		Cdio	17.75	16.05	5.03LTUI	4.075.07	1 4504440
866100		Guiz	11.10	10.90	5.91E+U/	4.0/ =+0/	1.4504449
A2A4I8	Amine oxidase	AOC3	1.9	1.9	1.04E+08	7.17E+07	1.45059
P08030	Adenine prosphoridosyltransferase	Арп	10	1.2	4.33E+06	2.986+06	1.4560516
P21460		USt3	21.5	27.5	5.//E+08	3.93E+08	1.4677356
P35441	I nrombospondin-1	INDS1	4.8	5	0.15E+06	4.14E+06	1.4860469
P04444	Hemoglobin Subunit beta-H1	HDD-DN1	21.1	21.1	7.56E+06	5.08E+06	1.4896048
PU2104	nemoglobin subunit epsilon-Y2	ribb-y Dala	40.15	39.15	2.39E+08	1.601+08	1.4902499
Q8CBG6	b-pnospnogluconolactonase	rgis	1.2	10.9	4.86E+06	3.26E+06	1.4918735
050450	nigh mobility group protein B1	rimgp1	24.3	24	5.03E+07	3.3/E+U/	1.4921339
Q304E2	L-laciale denydrogenase	LUNA	J∠.J	32.3	1.43E+U8	9.01E+U/	1.502/012
F 34022	Transpecific G i Pase-activating protein	Tach2	0.1	10.0	3.39E+Ub	3.30E+Ub	1.504/218
P02009	Franscription elongation factor B polypeptide 2	TCED2	20.20	45.0	1.9UE+Ub	3.24E+U0	1.50/0908
010251	LIUNYAUUH IACIUF I-Dela	Δtrn	0.55	0.55	0.12E+Ub	4.U3E+U0	1.5109003

GAUFF Relationar poten Pylrob Hole (2) Loss (2) <thloss (2)<="" th=""> Loss (2) <thloss (2)<="" th=""> <thloss (2)<="" th=""></thloss></thloss></thloss>	A2AI62	Hephaestin	Heph	0.9	0.9	6.04E+07	3.94E+07	1.5319845
Oper Terrison Advact 6.8 4.2 6.8.4.5.0 6.186-05 4.186-05 4.186-05 4.186-05 4.186-05 P1113 Exclusion in Start Chain 1 Every 1 5.3.5 1.27.6 2.15.4.00 1.5.244-05 1.5.244-05 1.5.244-05 1.5.244-05 1.5.244-05 1.5.24 1.5.25 1.15.25 1.15.25 1.15.24	Q5XJF6	Ribosomal protein	Rpl10a	12.4	12.4	1.26E+07	8.16E+06	1.5469304
P31618 Larnie B2 L	Q9WTP6	Adenvlate kinase 2	Ak2	6.9	4.2	6.54E+05	4.19E+05	1.560639
Elengaton factor 1 algona 1 Extra 12.7s 2.12.7s 2.12.8s 3.35.400 1.57.13785 035086 Classical IIII algonal Carl 1 1.45 16.55 1.57.14835 1.57.14835 035086 Classical IIII algonal Carl 1.45 16.55 1.55.16	P21619	Lamin-B2	Lmnb2	2.3	1.15	8.17E+05	5.23E+05	1.5621844
Gastine Cartini have organic/latini have organic Out 10.53 10.13 60.8477 1.8216-07 1.8216-07 1.8216-07 1.811276 GBORD Conscionality proxim Carty 1 1.61 6.15 7.054-00 1.056-00 1.756-00 1.056-00 1.756-00 1.056-00 1.756-00	P10126	Elongation factor 1-alpha 1	Eef1a1	15.35	12.75	2.10E+09	1.33E+09	1.5713376
SecOse Conduction Conf1 14.4s 15.5s 15.54-50 5.65-50 15.55 BORH JD Diright protein 2 Arboz 14.25 16.85 5.776-60 3.667-60 1.650775 BORH JD Diright protein 2 Arboz 14.25 16.85 0.7744-50 1.650775 BORH JD Diright protein 2 Protein 2 1.7744-50 1.650775 1.677545 BORH JD Protein 2 Protein 2 2.8 0.067-60 1.177-60 1.677545 PS5568 AP-1 complex makunit mu-1 Aptron 5.8 4.05 0.067-60 1.672546 1.682591 FE2BL Z Protection 1 State AP 1.682476 1.682476 1.682591 1.68267 1.882476 1.188506 1.682591 1.68267 1.882477 1.188556 1.68267 1.882477 1.188556 1.68267 1.882477 1.188556 1.68267 1.882477 1.188556 1.68267 1.882477 1.188556 1.68267 1.882477 1.188556 1.68267 1.882477	Q5SXR6	Clathrin heavy chain;Clathrin heavy chain 1	Cltc	10.55	10.15	6.69E+07	4.26E+07	1.5719838
Op/Link Op/Link Circl 6.15 6.15 6.375-06 3.88-08 1.880708 C300CDD Fphorphophophophophony April 5.8 1.781-07 7.064-03 1.687005 C300CDD Fphorphophophophophony April 5.8 5.8 7.281-07 7.064-03 1.687005 C300CDD Fphorphophophophony April 5.8 5.8 7.281-05 3.061-03 1.697034 C300CDD Fphorphophophony April 5.8 5.8 1.881-08 3.061-08 1.682031 C40111 Prode 2.8 2.6 0.061-08 3.061-08 1.682031 C40110 C420 2.6 0.0741-08 0.0741-08 0.0741-08 1.680031 C30110 C420-074 1.8 1.8 1.682031 1.4 1.4 3.281-06 1.7124076 C30110 C420-077 0.7 0.581-05 3.061-07 1.728076 C30110 C420-077 0.7 0.581-06 1.7724076 1.7724076	Q9CQ16	Coactosin-like protein	Cotl1	14.45	16.55	1.03E+08	6.50E+07	1.5812476
BigMIRP Psyloc Field 14.25 18.86 1.78E-07 11.1E-07 10.807085 CBRLDO 6.5 propaginorsa dorutogramas, documo signa Part 8.8 6.5 7.8E+06 4.87246 10.001017 CBRLDO Propagine subunit mu1 Aprint 5.8 4.05 1.02E+06 4.774-05 16.02244 FEZEL 2.3.Bispatitin protein ligas MB1 Mb7 2.6 2.6 1.98E+09 1.9	Q6P1J1	Dihydropyrimidinase-related protein 1	Crmp1	6.15	6.15	5.37E+06	3.38E+06	1.5860785
000C00 Exploration (Unit of the second	B2M1R7	Poly(rC)-binding protein 2	Pcbp2	14.25	13.85	1.76E+07	1.11E+07	1.5870965
DBBH200 Protein FAMMA FilmeRight 5.5 4.5 1.5 4.5 1.000220 DBB150 APT 5.8 4.05 1.961-00 1.772-06 1.022204 DBB110 DB101 2.5 2.5 1.561-00 1.562-00 1.	Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating	Pad	5.8	5.8	1.23E+07	7.69E+06	1.6018917
P35866 AP-1 complex subunit mu-1 Ap frant 5.8 4.05 1.082-06 1.127-06 1.022014 FR2BL2 E3 ubiquities protein ligase MB1 Mb1 2.5 2.5 1.086-03 1.086-03 1.082014 G20307 Cougulation factor A-R in F21 2.8 1.8 3.784-06 2.288-06 1.082324 G20307 Cougulation factor A-R in F21 2.1 2.1 0.000 3.084-06 1.082324 G20307 Cougulation factor A-R in F24 2.5 1.65.0 9.844-06 3.084-08 1.793806 G20307 Hatore H3 MAGDig 3 1.4 1.4 3.284-06 1.793806 G20307 Hatore H3 Insertion Vm0 3.8 3.8 2.384-06 3.764-05 1.793806 G20307 Nancordentino Vm0 3.8 3.8 3.8 2.384+06 1.793806 G2040 Art A.3 3.84-06 3.384+06 1.793805 G20301 Anopolicion AnyrD	Q8BHZ0	Protein FAM49A	Fam49a	8.5	6.5	7.84E+05	4.87E+05	1.6099238
Déch111 Perconnadionn-2 Pérdiz 25 Sofie-log 1582/191 CR2LL ES document-orten ingase MB1 Mof 2.5 1.95 3.78E-06 2.28E+06 1.685/0231 CAULYI Coogulation factor AC4-14 <i>El-Mar2</i> 1.85 3.77E+06 5.77E+06	P35585	AP-1 complex subunit mu-1	Ap1m1	5.8	4.05	1.90E+06	1.17E+06	1.627294
FigBle_2 23 ubquiling notion 198E-100 198E-200 197E-200 197E-200 </td <td>Q61171</td> <td>Peroxiredoxin-2</td> <td>Prdx2</td> <td>25</td> <td>25</td> <td>5.06E+08</td> <td>3.10E+08</td> <td>1.6326191</td>	Q61171	Peroxiredoxin-2	Prdx2	25	25	5.06E+08	3.10E+08	1.6326191
D3U3UT Conjunition frame A Prio 1.8 3.78E-80 2.28E-80 1.6852281 08UTU Eukoric Instanto fraudo d'Al Effedaz 2.2 2.165 9.76-80 5.75E-80 7.752227 7.752327 7.752327 7.752327 7.752327 7.757202 7.755909 7.752909 7.752909 7.752909 7.752909 7.752909 7.752909 7.752900 7.718 7.78 7	F6ZBL2	E3 ubiguitin-protein ligase MIB1	Mib1	2.5	2.5	1.95E+09	1.18E+09	1.6437232
Obs/Proj. Eukaryotic nutation had/or 4A-4 EffAac PEA27 Historn H1.3 MiethTrid 15.5 24.84-06 15.72-06 18.800383 091VU/U Carbowic ester hydrolase Cest1 2.1 2.1 6.05.6-07 3.34E-07 17.109886 EDGEB C-Jun-amno eleminal knase-interacting protein 3 Maplabip.1 1.4 1.4 3.22E-07 1.36E-07 1.7353405 DBGP00 Protocolimin-20 Proto 0.8 0.3 2.92E-07 1.7353405 DBGP00 Protocolimin-20 Proto 0.8 0.3 2.92E-07 1.7553401 DBGP00 Protocolimin-20 Proto 1.94 1.4 1.4 3.55E+06 1.97550901 P17807 Lyoparmo C-1 MprI 2.3 3.1 3.55E+06 1.97550901 1.77509010 DBG304 AlpfE Respontator2 Alpr2 4.76 4.455 3.55E+06 1.985401 1.7852002 DBG304 AlpfE Respontator2 Alpr2 1.74 7.4 4.455 7.44560 3.58E+06 <td>Q3U3V1</td> <td>Coagulation factor X</td> <td>F10</td> <td>1.8</td> <td>1.8</td> <td>3.78E+06</td> <td>2.28E+06</td> <td>1.6583261</td>	Q3U3V1	Coagulation factor X	F10	1.8	1.8	3.78E+06	2.28E+06	1.6583261
P43277 Historie H1.3. Historie H1.3. Historie H1.3. Energy and the set of	Q8BTU6	Eukarvotic initiation factor 4A-II	Eif4a2	24.2	21.65	9.47E+06	5.57E+06	1.6980858
OpHVUD Catchooyle sett hydroiase Cref if AS3a 15.5 19.3 5.76-08 3.36E-07 17.748708 ESOGER C-Lun-amino terminal kinase-intracting protein 3 MapkBg3 1.4 1.4 3.28E-07 1.80E-07 1.7284708 ESOGER C-Lun-amino terminal kinase-intracting protein 3 MapkBg3 1.4 1.4 3.28E-07 1.7358431 P28788 Wronectin Vin 3.8 3.8 2.38E-06 1.35E+06 1.7575263 P28789 Vinconctin Vinho 3.8 3.8 2.38E-07 1.753841 P17897 Lytacyme C-1 Lyt 8.1 8.1 3.06E-06 1.38E+07 1.755841 P17897 Lytacyme C-1 Lyt 8.1 8.1 3.4 6.48E-07 1.755841 P178920 Acin Acin Acin 7.75660 1.98E-06 1.8027027 P02029 Acin Acin Acin 5.8E-06 1.88E-06 1.8026456 P02029 Acin Soff acin 1.84E-06 1.80	P43277	Histone H1.3	Hist1h1d	18.55	18.55	2.84E+08	1.67E+08	1.6982031
EDC227 Histone H3 HYSter 15.55 19.3 C/0E-608 3.0E-608 17.248/076 DS06B6 C-Lum-anno-terminal kinase-interacting protein 3 MapRight 3 1.4 1.4 3.251-07 16.561-05 3.75E+65 1.7583305 DS07B6 Mironeclin Vin 3.8 3.8 2.861-06 1.5752425 DS07B0 Viscontin Vinhab 2.0.9 23.15 4.20E+07 2.755240 DS07B0 Lyzy prote C-1 Lyz f 8.1 8.1 8.1 3.66E+06 1.7565005 DS03B4 Ayrelf P oport Inclu? Ayrel 5 5 1.724707 1.7242076 DS03B4 Ayrelf P oport Inclu? Ayrel 5 1.7245076 1.28622027 PS03B5 Adstinuonal protein S7 Apgr 7 1.6 4.466 3.36E+06 1.8062401 DS03B4 Ayrelf P oport Inclu? Apgr 7 1.7 2.1 7 1.724206 DS03B4 Ayrelf P oport Inclu? Apgr 7 1.7 7.71666 1.826407 </td <td>Q91WU0</td> <td>Carboxylic ester hydrolase</td> <td>Ces1f</td> <td>2.1</td> <td>2.1</td> <td>6.60E+07</td> <td>3.84E+07</td> <td>1.7195086</td>	Q91WU0	Carboxylic ester hydrolase	Ces1f	2.1	2.1	6.60E+07	3.84E+07	1.7195086
EGOGBBQ C-Lum-ammontal hunae-intracting proton 3 Mag/Bg/2 1.4 1.4 1.4 2.23E+07 1.86E+07 1.733480 P28788 Wronectin Vin 3.8 3.8 3.8 2.98E+06 1.35E+06 1.7573280 P28788 Wronectin Vin/ba 2.0 2.315 4.20E+07 2.38E+07 1.7538641 P17897 Lyacxyme C-1 Lyz1 8.1 8.1 3.0E+06 1.7575080 S3304 AlvyREF coport factor 2.72 AlvyRC 5 5 1.72E+06 1.80262027 P62002 Alton AlvyREF Algort 4.7 6 4.465 3.55E+06 1.8267027 P62002 Alton Alton Algort 7.8 7.78 5.7E+06 1.8267027 P62002 Alton Algort Algort 7.8 5.7E+06 1.8267027 P62004 Alton J.7 1.46 3.4E+06 1.8277042 CART Pranto 6.8 3.4 6.4	E0CZ27	Histone H3	H3f3a	15.55	19.3	5.70E+08	3.30E+08	1,7248706
OpBIEQ Protocadherni-20 Protocadherni-20 Protocadherni-20 Protocadherni-20 Profestal Virtuab 2.8 7.7 6.656+06 3.786+06 1.7863232 QBCCV0 143-3 proton bedrialpha Wirbab 2.0.9 2.3.1 3.56+06 1.7873225 QBCCV0 143-3 proton bedrialpha Wirbab 2.0.9 2.3.1 3.56406 1.985+06 1.7875026 P17897 Lyscome C-1 Npr1 2.3.3 3.1 3.556+06 1.985+06 1.7875026 S0304 AlyrREF export factor 2 AlyrR2 5 5 1.756+07 3.784+06 1.866240 P18206 Actin Actin AlyrR2 2.1 2.1 2.1 3.456+06 1.866240 P18206 Actin State 1.0 3.5 7.784+06 1.8672641 1.8672641 P17807 Numepin-2 State 2 2.861-06 1.8872641 1.8872641 OAVERS1 Heterogeneous nuclear rebund beprotein S7 Apr2 9.1 7.7 7.716+06 1.8962547 <td>E9Q6B6</td> <td>C-Jun-amino-terminal kinase-interacting protein 3</td> <td>Mapk8ip3</td> <td>1.4</td> <td>1.4</td> <td>3.23E+07</td> <td>1.86E+07</td> <td>1.7333405</td>	E9Q6B6	C-Jun-amino-terminal kinase-interacting protein 3	Mapk8ip3	1.4	1.4	3.23E+07	1.86E+07	1.7333405
P20788 Vitronactin V/m 3.8 3.8 2.88-06 1.787226 005CV04 14.3 protein betringhen Viruhab 20.9 23.15 4.20E+07 1.7855641 P17807 Lyacoyme C-1 Lyz1 8.1 8.1 3.00E+06 2.18E+00 1.7755081 05303 Autroplint-1 Myr1 2.3 3.1 3.35E+06 1.98E+06 1.87E+07 1.87E+01 1.82E+07 1.87E+01 1.82E+07	Q8BIZ0	Protocadherin-20	Pcdh20	0.7	0.7	6.59E+05	3.79E+05	1.7368837
OBCCVM 14.3-3 protein betavlapha Yuehab 20.9 23.16 4.00e+07 2.38E-07 1.785908 P17897 Lyzzt 8.1 3.00E+06 1.98E+006 1.785908 P07333 Neuroplin-1 Nyp1 2.3 3.1 3.36E+06 1.99E+006 1.785908 P03280 Acin Acin Acya1 47.6 4.4.6 3.33E+06 1.94E+00 1.8022027 P03080 Acin Acin Acya2 C.1 2.1 7.19E+06 3.85E+06 1.8266545 P03082 Cullin-2 Cullin-2 Cullin-2 Sizet-06 1.8277042 Cullin-2 Sizet-06 1.8271042 Sizet-06	P29788	Vitronectin	Vtn	3.8	3.8	2.38E+06	1.35E+06	1.7573225
Pi7837 Lysoyme C-1 Lyst 8.1 8.1 3.00E-00 2.19E-06 1.795009 97333 Neuroplin-1 Np1 2.3 3.1 3.55E-00 1.39E-06 1.79E-07 9.72E+06 1.89E-06 1.89	Q9CQV8	14-3-3 protein beta/alpha	Ywhab	20.9	23.15	4.20E+07	2.38E+07	1.7635641
PP7333 Neurophin-1 Mpr 2.3 1.1 5.58F+06 1.98F+06 1.79F40 P83280 Actin Adyrd 5 6 1.79E+07 1.78E+06 1.88E+06 1.8028027 P83280 Actin Adyrd 7.8 4.65 3.53E+06 1.88E+06 1.88E+06 </td <td>P17897</td> <td>Lysozyme C-1</td> <td>Lvz1</td> <td>8.1</td> <td>8.1</td> <td>3.90E+06</td> <td>2.19E+06</td> <td>1,7755069</td>	P17897	Lysozyme C-1	Lvz1	8.1	8.1	3.90E+06	2.19E+06	1,7755069
GXX81A AyrREF S. 1 1.75E-07 9.73E-06 1.892490.2 P03260 Actin Actin Appr 2.1 2.1 7.19E-06 3.94E+06 1.892690.2 P03202 AGS ribosomal protein S7 Appr 2.1 2.1 7.19E-06 3.94E+06 1.892640.0 1.892640.0 1.892640.0 1.892640.0 1.892640.0 1.892640.0 1.892640.0 1.892640.0 1.892640.0 1.892640.0 1.892640.0 1.894240.0 1.894240.0 1.894240.0 1.894240.0 1.894240.0 1.894240.0 1.894240.0 1.894240.0 1.894240.0 1.895749.0	P97333	Neuropilin-1	Nrp1	2.3	3.1	3.55E+06	1.99E+06	1.7817533
PA3260 Actin Actin Actin Actin Actin Actin I 382-06	G3X9I4	Alv/REF export factor 2	Alvref2	5	5	1.75E+07	9.73E+06	1.8022802
Pacebase Als Current 7:15E-06 3.94E+06 1.8266542 VFMSS2 Cullin? Cullin? Cullin? State-06 1.8277042 OBR 1P1 Probaseme subunit beta type-3 Pamb2 E.8 3.4 6.66E+06 3.83E+06 1.8286+16 OBVEX3 Heterogeneous nuclear ribonucleoprotein U Hampu 4.65 4.65 S.36E+06 1.8257481 OSUEX3 Heterogeneous nuclear ribonucleoprotein U Hampu 4.65 4.95 S.36E+06 1.857483 OSUEX4 Meesin Arto 3.84E+06 1.87E+06 1.857483 OSUEX4 Meesin Arto 3.37E+06 1.3857432 1.3824643 OSUEX4 Meesin Arto 3.37E+06 1.857432 1.891742 OSUEX4 Meesin Arto 3.37E+06 1.3857432 1.891742 OSUEX4 Meesin Arto 3.37E+06 1.897042 1.891744 OSUEX4 Meesin Arto 1.381762 1.222 1.2347464 1.891646	P63260	Actin	Acta1	47.6	44.65	3.53E+06	1.94E+06	1.8262027
HTBX2 Cull 17.8 17.8 17.8 5.21E+06 2.85E+06 1.8277042 ORR P1 Protessome subunit beta type-3 Syne2 1.1 0.55 7.38E+06 1.8204916 F6WIR9 Nesprin-2 Syne2 1.1 0.55 7.38E+06 1.8057485 GAUKS3 Hettrogeneous nuclear ribourcleoproten U Horpput 4.65 4.65 5.36E+06 1.8657485 GAURS1 Protein degivase D.1 Part/ 9.1 7.7 7.71E+06 4.15E+06 1.8657495 GAURS1 Hexptoma-dimethylaminodylarioase 2 Daft/ 4.75 3.75E+06 1.91E+06 1.8695037 GAURS7 Hexptoma-dimethylaminodylarioase 2 Daft/ 4.75 3.75E+06 1.9817640 1.981777 D327E6 Maetion-advating factor acelyhylariolase B subunit gamma Arts 1.39 1.6.4 8.71E+06 1.897787 D327E6 Platele-advating factor acelyhylariolase B subunit gamma Path 18.2 9.2 2.82E+06 1.92E+06 1.92E+06 1.92E+166 1.99E+166 1.99E+166	P62082	40S ribosomal protein S7	Rns7	21	21	7 19E+06	3 94E+06	1 8266545
ORR 111 Protessore subunit beta ppe-3 Psm02 1.6 3.4 6.64E-06 1.6224916 PRWBR9 Neaprin-2 Sym2 1.1 0.55 7.38E+06 1.00E+06 1.843401 OaVEK3 Heterogeneous nuclear ribonucleoprotein U Harp 4.65 5.38E+06 0.08E+06 1.8872681 OSULTO Mich 4.75 4.77 1.771E+06 1.187E+06 1.8872681 OSULTO Mich 4.75 4.77 3.471E+06 1.8872681 OSULTO Michain Andre 4.75 4.77 5.71E+06 1.8872681 OSULTO Hegatoma-derived growth factor-related protein 3 Holg/rp33 8.2 8.2 2.53E+06 1.8814383 OSULTO Hateles-activating factor-activation growth factor-related protein 3 Holg/rp33 8.9 1.2.4 1.80E+07 7.38E+06 1.8872831 OSUMOR Raserlated protein activation activat	H7BX52	Cullin-2	Cul2	17.8	17.8	5 21E+06	2 85E+06	1 8277042
FRWBR0 Nespiral Sym2 1.1 0.55 7.38E+06 4.00E+06 1443401 020KPG Heterogeneous nuclear ribonucleoprotein U Hampu 4.65 6.58E+06 2.89E+06 1.8557485 020URD NIG,NiG-dimethylarginine dimethylaminohydrolase 2 Dafan 1.655 19.7 3.48E+06 1.87E+06 1.857485 020URD Nigonido-dimethylaminohydrolase 2 Dafan 4.75 4.75 3.57E+06 1.31E+66 1.8657085 020URD Hepatoma-derived growth factor-reliated protein 3 Marx 4.75	Q9R1P1	Proteasome subunit beta type-3	Psmb3	6.8	3.4	6.64E+06	3.63E+06	1.8284916
OaVER3 Heterogeneous nuclear ribonucleoprotein U Frampu 4.65 4.65 5.86±06 2.89±06 1.8557465 A2AB13 Protein deglycase D.1 Park7 9.1 7.7 7.71±06 4.15±06 1.8575405 P2604 Mossin Mosin 4.75 3.37±06 1.91±06 1.8555037 P2604 Mossin Aster-tool 1.34±06 1.8575301 1.8295037 D3ZTEC Platelet-activating factor accellyhydrolase IB subunit gamma Pafahr13 13.9 16.4 8.71±06 4.81±06 1.8297046 OS2TEC Platelet-activating factor accellyhydrolase IB subunit gamma Pafahr13 13.9 16.4 8.71±06 4.81±06 1.8214661 1.8214661 1.8214661 1.8214661 1.8214661 1.8214614 1.823451 Coatomer subunit opsilon Cope 7.3 9.9 1.54±06 2.82±06 2.1197271 7.85±06 1.8214614 O20204 Protein phosphataes 1 regulatory subunit 14B Ppp1r14b 17 17.3 8.45±06 1.18±06 2.448±016 2.448±016	F6W8R9	Nesprin-2	Svne2	1.1	0.55	7.38E+06	4.00E+06	1.843401
DATABIN Protein degresse DJ-1 Park7 0.1 7.7 7.71 7.73 8.91 1.5444001 7.7644001 2.21103271 026420 Antisting partin 10.21 Paghon1 8.5 8.5 2.46460 1.19877232 <td>Q8VEK3</td> <td>Heterogeneous nuclear ribonucleoprotein U</td> <td>Hnrnnu</td> <td>4 65</td> <td>4 65</td> <td>5.36E+06</td> <td>2 89E+06</td> <td>1 8557495</td>	Q8VEK3	Heterogeneous nuclear ribonucleoprotein U	Hnrnnu	4 65	4 65	5.36E+06	2 89E+06	1 8557495
C3U2700 NKG/NC/-dimethylarginine dimethylaminohydrolase 2 Data/2 16.55 19.7 3.48E+66 1.37E+66 1.3859537 P2804 Moesin 4.75 4.75 3.57E+66 1.34E+66 1.8491587 D327E6 Platelet-activating factor acetyhydrolase 18 subunit gamma Parlat/103 13.9 16.4 8.71E+06 4.61E+06 1.887394 D327E6 Platelet-activating factor acetyhydrolase 18 subunit gamma Parlat/103 13.9 16.4 8.71E+06 4.61E+06 1.887394 OSWW8 Ras-related protein Rab-1A Rab1 8.9 12.4 1.80E+07 9.3E44668 G4233 Plastel-6 7.75E+06 1.9872323 Plastel-6 7.75E+06 1.9872323 D26204 Protein phosphatases 1*regulatory subunit 14B Ppp1r14 17 17.35 8.34E+06 1.19E+06 2.217373 Q4C0B Gila maturation fador beta Fina 1 0.3 2.64E+06 1.19E+06 2.217373 Q4C0B Gila maturation fador beta Ginth 1.46 1.414+07 5.01E+06	A2A813	Protein deglycase D.I-1	Park7	91	77	7 71E+06	4 15E+06	1 8572581
P2604 Messin Ar5 5.75 5.75 5.75 6.11 1.91E+06 1.9841898 QBJMG7 Hepatoma-derived growth factor-related protein 3 Hdgfrp3 8.2 2.53E+06 1.34E+06 1.887787 DSZFE6 Plattelt-activating factor acetyhydrolase B subunit gamma Plath103 1.3.9 16.4 8.71E+06 4.61E+06 1.887094 QSW88 Ras-related protein Rab-1A Rab 8.9 12.4 1.80E+07 7.75E+06 1.924466 QS1233 Plastin-2 Lop1 9 6.45 1.52E+06 7.76E+05 1.987233 QS2044 Protein phosphatase 1r gulatory subuni 14B Poptr14b 17 17.35 8.34E+06 3.96E+06 2.1448012 QS1V42 Protein phosphatase 1r gulatory subuni 14B Poptr14b 17 17.35 8.34E+06 1.92E+06 2.1448012 QSQC03 Glia maturation factor beta Gmth 14.6 14.6 1.14E+07 5.01E+06 2.287431 QBC066 Caprin-1 Caprin1 3.3 3.3 2.74E	G3UZR0	N(G) N(G)-dimethylarginine dimethylaminohydrolase 2	Ddah2	16.55	197	3 48E+06	1.87E+06	1 8595037
GallMG7 Hepatoma-derived growth factor-related protein 3 Hdg/p3 8.2 2.53E+06 1.34E+06 1.8807377 D3Z7E6 Platelet-activating factor eaclyhlydrolase IB subunit gamma Plafn/b3 13.9 16.4 8.7TE+06 4.0E+06 1.887304 D3Z7E6 Platelet-activating factor acety/hlydrolase IB subunit gamma Plafn/b3 13.9 16.4 8.7TE+06 1.827406 1.827466 OSW08 Ras-related protein Rab-1A Rab 1 8.9 12.4 1.80E+07 9.98E+06 1.9274666 1.9274668 D32315 Coatomer subunit opsilon Cope 7.3 9.9 1.54E+06 2.52E+06 2.1103271 D62084 Protein phosphates 1 regulatory subunit 148 Pp1r1/40 17 7.3 8.34E+06 1.92E+06 2.1813008 B7FAV1 Filamin-A Fina 1 0.3 2.64E+06 1.19E+06 2.267761 G30422 Polyadenylate-binding protein 2 Pabpn1 8.5 8.5 2.46E+06 1.92E+06 2.1813008 B7AV1 Frilamin-A Grin1	P2604	Moesin	Msn	4.75	4.75	3.57E+06	1.91E+06	1.8641588
DB27E6 Platelet-activating factor acetylhydrolase IB subunit gamma Pafah1b3 13.9 16.4 8.71E+06 4.61E+06 1.927304 QSSW88 Ras-related protein Rab-1A Rab Rab 8.9 1.2.4 1.80E+07 7.75E+06 1.9274568 QG1233 Plastin-2 Lop1 9 6.45 1.52E+07 7.75E+06 1.9674168 D32515 Coatomer subunit epsilon Cope 7.3 9.9 1.54E+06 7.75E+06 1.9672323 D32545 Coatomer subunit opsilon inding protein 2 Papan1 8.5 8.5 2.45E+06 1.12E+06 2.1103271 Q62044 Protein phosphatase 1 regulatory subunit 14B Papan1 8.5 8.5 2.45E+06 1.12E+06 2.113730 Q62043 Gila maturation factor beta Gmb 1.46 1.46 1.46 1.46+07 5.01E+06 2.267461 YFEX03 Triosephosphate isomerase Tpi1 12.9 12.6 4.71E+06 2.318521 Q60865 Caprin1 S.26 Stosemal protein Sa 3.3	Q9JMG7	Hepatoma-derived growth factor-related protein 3	Hdafrp3	8.2	8.2	2.53E+06	1.34E+06	1.8807877
Action Rabit 8.9 12.4 1.80E+07 0.38E+06 1.9244680 Q61233 Plastin-2 L.QD1 9 6.45 1.52E+07 7.75E+06 1.9644182 Q52315 Coatomer subunit epsilon Cope 7.3 9.9 1.54E+06 7.76E+05 1.9872323 P26645 Myristoylated alanine-rich C-kinase substrate Marcks 16.2 8.1 5.31E+06 2.52E+06 2.1148012 Q62084 Protein phosphatase 1 regulatory subunit 14B <i>Ppp114</i> 140 17 17.35 8.34E+06 3.88E+06 2.217373 Q3CQ13 Glam anturation factor beta Gmfb 14.6 14.6 1.14E+07 5.01E+06 2.267461 H7BXC3 Triosephosphate isomerase Tp11 12.9 12.6 4.71E+06 2.07E+06 2.2687512 Q60865 Caprin-1 Caprin-1 3.3 3.3 2.74E+07 1.26E+07 2.3381521 P6VR6 Ubadisi Intermodifier-activating enzyme 5 Ubadis 16.2 8.1 5.5E+05 2.2381+05	D3Z7E6	Platelet-activating factor acetylhydrolase IB subunit gamma	Pafah1b3	13.9	16.4	8.71E+06	4.61E+06	1.8873094
Def 1233 Plastin-2 Lcp1 9 6.45 1.52E+07 7.75E+06 1.9644182 D32315 Coatomer subunit epsilon Cope 7.3 9.9 1.54E+06 7.76E+06 1.9873233 D32315 Coatomer subunit epsilon Cope 7.3 9.9 1.54E+06 7.76E+06 1.9873233 D42044 Protein phosphatase 1 regulatory subunit 14B <i>Ppp1114b</i> 17 17.35 8.34E+06 3.89E+06 2.1448012 G3UY42 Polyadenylate-inding protein 2 <i>Pabpn1</i> 8.5 8.5 2.46E+06 1.19E+06 2.217373 Q9CQ13 Glia maturation factor beta Gmth 14.6 1.46 1.4E+07 5.01E+06 2.2677461 H7BXC3 Trisesphesphate isomerase Tp11 12.9 12.6 4.71E+06 2.2877461 Q60265 Caprin-1 Caprin1 3.3 3.3 2.74E+07 1.20E+07 2.2897018 P60267 20S protease regulatory subunit 6A Psmc3 7.9 3.95 6.35E+05 2.38E+05 2.3875143	Q5SW88	Ras-related protein Rab-1A	Rah1	89	12.4	1 80E+07	9.38E+06	1 9214568
D32315 Coatomer subunit epsilon Cope 7.3 9.9 1.54E+06 7.76E+05 1.9872323 P26645 Myristoylated alanine-rich C-kinase substrate Marcks 8.1 5.31E+06 2.52E+06 2.1103271 G82094 Protein phosphatase 1 regulatory subunit 14B Pppfr14b 17 17.35 8.34E+06 1.19E+06 2.1448012 G3UY42 Polyadenylate-binding protein 2 Pabpn1 8.5 8.5 2.46E+06 1.19E+06 2.217373 Q8CQ13 Glia maluration factor beta Gmfb 14.6 14.6 1.14E+07 5.01E+06 2.267461 H7BXC3 Triosephosphate isomerase Tpi1 12.9 12.6 4.71E+06 2.23875143 G80865 Caprin-1 3.3 3.3 2.74E+07 1.20E+07 2.2881093 F6V2E3 285 protease regulatory subunit 6A Psmc3 7.9 3.95 6.35E+05 2.338521 F6VRI6 Ubiquitin-like modifier-activating enzyme 5 Ubiquitin-like modifier-activating enzyme 5 Ubiquitin-like modifier-activating enzyme 5 2.482 9.65<	Q61233	Plastin-2	l cn1	9	6.45	1.52E+07	7 75E+06	1.9644182
P26645 Myristoylated atanine-rich C-kinase substrate Marcks 16.2 8.1 5.31E+06 2.52E+06 2.1103271 Q62084 Protein phosphatase 1 regulatory subunit 14B Ppp1r14b 17 17.35 8.34E+06 3.99E+06 2.1448012 Q62044 Protein phosphatase 1 regulatory subunit 14B Pabpn1 8.5 8.5 2.45E+06 1.12E+06 2.217373 Q62013 Glia maturation factor beta Gmth 14.6 14.6 1.14E+07 5.01E+06 2.267461 H7EXC3 Triosephosphate isomerase Tpi1 12.9 12.6 4.71E+06 2.07E+06 2.2881761 Q60665 Caprin-1 Caprin-1 3.3 3.3 2.74E+07 1.20E+07 2.2891093 P60253 256 protease regulatory subunit 6A Psrac3 7.9 3.95 6.35E+05 2.331E>16 2.331E>16 2.331E>16 2.331E>16 2.331E>16 2.331E>16 2.333E>16 2.333E>16 2.333E>16 2.332E>16 2.332E>16 2.332E>16 2.331E>16 2.408667 1.42E+06 2.36E+07	D37315	Coatomer subunit ensilon	Cone	73	9.9	1.54E+06	7 76E+05	1.9872323
Q62084 Protein phosphatase 1 regulatory subunit 14B Pp1r14b 17 17.35 8.34E+06 3.89E+06 2.1448012 G3UY42 Polyadenylate-binding protein 2 Pabpn1 8.5 8.5 2.46E+06 1.19E+06 2.17373 Q3CQ13 Glia maturation factor beta Gmfb 14.6 14.6 1.14E+07 5.01E+06 2.267461 VBXC3 Triosephosphate isomerase Tp11 12.9 12.6 4.71E+06 2.07E+06 2.267461 VBXC3 Triosephosphate isomerase Tp11 13.3 3.3 2.74E+07 1.00E+07 2.2891093 F6Q2E3 265 protease regulatory subunit 6A Psmc3 7.9 3.95 6.35E+05 2.3318521 P60867 40S ribosomal protein S20 Rps20 14.25 9.65 1.46E+07 6.10E+06 2.3875143 Q14AA6 GTP-binding nuclear protein Ran Ran 9.7 14.8 5.11E+07 2.13E+07 2.3989767 Q2039 Hemoglobin subunit beta-2 Hob-b2 46.9 46.6 1.38E+06 7.37	P26645	Myristovlated alanine-rich C-kinase substrate	Marcks	16.2	8.1	5.31E+06	2.52E+06	2 1103271
G3UY42 Polyadenylate-binding protein 2 Pabpr1 8.5 2.45E+06 1.12E+06 2.1813408 B7FAV1 Filamin-A Fila 1 0.3 2.64E+06 1.19E+06 2.217373 Q9CQ13 Gila maturation factor beta Gm/b 14.6 14.6 1.14E+07 5.01E+06 2.287461 H7BXC3 Triosephosphate isomerase Tp/1 12.9 12.6 4.71E+06 2.07E+06 2.2887512 Q60685 Caprin-1 Caprin1 3.3 3.3 2.74E+07 1.20E+07 2.2891702 F6VR16 Ubigutin-like modifier-activating enzyme 5 Uba5 16.2 8.1 5.56E+05 2.33E+05 2.383202 P60867 40S ribosomal protein S20 Rps20 14.25 9.65 1.46E+07 6.10E+06 2.387143 Q14AA6 GTP-binding nuclear protein Ran Ran 9.7 14.8 5.11E+07 2.13E+07 2.4080667 P35700 Peroxiredoxin-1 Pridx1 17.75 20.15 6.77E+07 2.4657958 P02089<	Q62084	Protein phosphatase 1 regulatory subunit 14B	Ppp1r14b	17	17.35	8.34E+06	3.89E+06	2.1448012
B7FAV1 Filamin-A Fina 1 0.3 2.64E+06 1.19E+06 2.217373 QBCQ13 Glia maturation factor beta Gm/b 14.6 14.6 1.14E+07 5.01E+06 2.2877461 H7BXC3 Triosephosphate isomerase Tp/1 12.9 12.6 4.71E+06 2.2677461 Q60865 Caprin 1 3.3 3.3 2.74E+07 1.20E+07 2.2887512 Q60865 Caprin 1 3.3 3.3 2.74E+07 1.20E+07 2.2891093 F6Q2E3 26S protease regulatory subunit 6A Parnc3 7.9 3.95 6.35E+05 2.33E+05 2.383202 P60867 40S ribosomal protein S20 Rps20 14.25 9.65 1.46E+07 6.10E+06 2.3875143 Q14AA6 GTP-binding nuclear protein Ran Ran 9.7 14.8 5.11E+07 2.15E+07 2.5EE+07 2.4989767 P02089 Heroglobin subunit beta-2 Hbb-b2 46.9 46.6 1.84E+08 7.0E+05 2.487758 Q24750 DNA to	G3UY42	Polyadenylate-binding protein 2	Pabpn1	8.5	8.5	2.45E+06	1.12E+06	2.1813408
QCQ13 Glia maturation factor beta Gm/b 14.6 14.6 1.14E+07 5.01E+06 2.267461 H7EXC3 Trosephosphate isomerase Tpi1 12.9 12.6 4.71E+06 2.267461 QCQ23 26S protease regulatory subunit 6A Psmc3 7.9 3.95 6.35E+05 2.72E+05 2.3318521 F6VR16 Ubiquitin-like modifier-activating enzyme 5 Uba5 16.2 8.1 5.56E+05 2.338202 P60867 40S ribosomal protein S20 Rps20 14.25 9.65 1.46E+07 6.10E+06 2.3875143 Q14AA6 GTP-binding nuclear protein Ran Ran 9.7 14.8 5.11E+07 2.13E+07 2.3989767 P6813 Actin abs keletal muscle Acta1 26.4 23.45 8.55E+07 2.4108667 P68730 DNA topoisomerase 1 70p1 2.1 2.1 1.98E+06 7.37E+05 2.4867958 P02099 Hemoglobin subunit beta-2 Hibb-b2 46.9 46.6 1.84E+08 1.74E+08 2.804844	B7FAV1	Filamin-A	Fina	1	0.3	2.64E+06	1 19E+06	2 217373
H7BXC3 Triosephosphate isomerase Tpi1 12.9 12.6 4.71E+06 2.07E+06 2.2687512 Q60865 Caprin-1 3.3 3.3 2.74E+07 1.20E+07 2.2891093 G602E3 26S protease regulatory subunit 6A Psmc3 7.9 3.95 6.35E+05 2.328+05 2.388202 F602E3 26S protease regulatory subunit 6A Psmc3 7.9 3.95 6.35E+05 2.328+05 2.388202 P60867 40S ribosomal protein S20 Rps20 14.25 9.65 1.46E+07 6.10E+06 2.3875143 O14AA6 GTP-binding nuclear protein Ran Ran 9.7 14.8 5.11E+07 2.318+07 2.3890767 P68134 Actin, alpha skeletal muscle Acta1 26.4 23.45 8.55E+07 3.55E+07 2.4106667 P35700 Peroxiredoxin-1 Prdx1 17.75 20.15 6.77E+07 2.75E+07 2.487958 Q64750 DNA topoisomerase 1 Top1 2.1 2.1 9.8766 2.6873618 Q6	090013	Glia maturation factor beta	Gmfb	14.6	14.6	1 14F+07	5.01E+06	2 267461
Q60885 Caprin-1 Caprin 1 3.3 3.3 2.74E+07 1.20E+07 2.2891093 F602E3 265 protease regulatory subunit 6A Psmc3 7.9 3.95 6.35E+05 2.72E+05 2.3318521 F602E3 265 protease regulatory subunit 6A Psmc3 7.9 3.95 6.35E+05 2.3318521 F602E3 265 protease regulatory subunit 6A Psmc3 7.9 3.95 6.35E+05 2.338202 P60867 40S ribosomal protein S20 Rps20 14.25 9.65 1.46E+07 6.10E+06 2.389767 P68134 Actin, alpha skeletal muscle Acta1 26.4 23.45 8.55E+07 2.56E+07 2.4010667 P35700 Peroxiredoxin-1 Prdx1 17.75 20.15 6.77E+07 2.49119 Q04750 DNA topoisomerase 1 Top1 2.1 1.98E+06 7.37E+05 2.487318 Q643K9 Purine nucleoside phosphorylase Prp:Pnp2 6.6 3.3 7.72E+05 2.84E+05 2.704358 Q8CGP4 Histone HZA </td <td>H7BXC3</td> <td>Triosephosphate isomerase</td> <td>Tpi1</td> <td>12.9</td> <td>12.6</td> <td>4.71E+06</td> <td>2.07E+06</td> <td>2.2687512</td>	H7BXC3	Triosephosphate isomerase	Tpi1	12.9	12.6	4.71E+06	2.07E+06	2.2687512
Boole Dis Dis <thdis< th=""> <thdis< td="" th<=""><td>Q60865</td><td>Caprin-1</td><td>Caprin1</td><td>3.3</td><td>3.3</td><td>2 74F+07</td><td>1 20E+07</td><td>2 2891093</td></thdis<></thdis<>	Q60865	Caprin-1	Caprin1	3.3	3.3	2 74F+07	1 20E+07	2 2891093
Formation Database	E602E3	26S protease regulatory subunit 6A	Psmc3	7.9	3.95	6.35E+05	2 72E+05	2.3318521
Poil Poil< Poil< </td <td>F6VRI6</td> <td>Ubiquitin-like modifier-activating enzyme 5</td> <td>Uba5</td> <td>16.2</td> <td>8.1</td> <td>5.56E+05</td> <td>2.33E+05</td> <td>2.383202</td>	F6VRI6	Ubiquitin-like modifier-activating enzyme 5	Uba5	16.2	8.1	5.56E+05	2.33E+05	2.383202
Order Open Open <t< td=""><td>P60867</td><td>40S ribosomal protein S20</td><td>Rps20</td><td>14.25</td><td>9.65</td><td>1.46E+07</td><td>6.10E+06</td><td>2.3875143</td></t<>	P60867	40S ribosomal protein S20	Rps20	14.25	9.65	1.46E+07	6.10E+06	2.3875143
P68134 Actin, alpha skeletal muscle Acta 1 26.4 23.45 8.55E+07 3.55E+07 2.4108667 P35700 Peroxiredoxin-1 Prdx1 17.75 20.15 6.77E+07 2.75E+07 2.4657958 P02089 Hemoglobin subunit beta-2 Hbb-b2 46.9 46.6 1.84E+08 7.40E+07 2.4912119 Q04750 DNA topoisomerase 1 Top1 2.1 1.98E+06 7.37E+05 2.6873618 Q643K9 Purine nucleoside phosphorylase Pnp:Pnp2 6.6 3.3 7.72E+05 2.84E+06 2.7204358 Q8CGP4 Histone H2A Hist1h2aa 21.4 21.4 4.88E+08 1.74E+08 2.8048444 P83917 Chromobox protein homolog 1 Cbx1 9.2 7.55 1.22E+06 4.26E+05 2.8537753 Q32640 26S proteasome non-ATPase regulatory subunit 5 Cops5 14.3 14.3 4.69E+06 1.63E+06 3.0804593 P00015 Cytochrome c, testis-specific Cyct 24.3 17.65 1.89E+07 5.88E+06	Q14AA6	GTP-binding nuclear protein Ran	Ran	9.7	14.8	5.11E+07	2.13E+07	2.3989767
Pastron Person Pastron Pastron <th< td=""><td>P68134</td><td>Actin, alpha skeletal muscle</td><td>Acta1</td><td>26.4</td><td>23.45</td><td>8.55E+07</td><td>3.55E+07</td><td>2.4108667</td></th<>	P68134	Actin, alpha skeletal muscle	Acta1	26.4	23.45	8.55E+07	3.55E+07	2.4108667
Poolog Hemoglobin subunit beta-2 Hbb-b2 46.9 46.6 1.84±08 7.40±07 2.4912119 Q04750 DNA topoisomerase 1 Top 1 2.1 1.98±06 7.37±05 2.4812119 Q04750 DNA topoisomerase 1 Top 1 2.1 2.1 1.98±06 7.37±05 2.4873618 Q343K9 Purine nucleoside phosphorylase Pnp:Pnp2 6.6 3.3 7.72±05 2.84±05 2.7204358 Q8CGP4 Histone H2A Histh2aa 21.4 21.4 4.88±08 1.74±08 2.8048444 P83917 Chromobox protein homolog 1 Cbx1 9.2 7.55 1.22±06 4.26±05 2.8337753 Q35864 COP9 signalosome complex subunit 5 Cops5 14.3 14.3 4.69±06 1.63±06 3.0804593 Q9CR00 26S proteasome non-ATPase regulatory subunit 9 Psmd9 5.1 2.55 4.20±06 1.38±06 3.2051827 P28658 Ataxin-10 Abr 10 1.45 1.45 8.12±05 2.29±05 3.5437179	P35700	Peroxiredoxin-1	Prdx1	17 75	20.15	6 77E+07	2 75E+07	2 4657958
Oddr50 DNA topoisomerase 1 Top 1 2.1 2.1 1.05 <th1.05< th=""> <th1.05< th=""> 1.05<td>P02089</td><td>Hemoglobin subunit beta-2</td><td>Hbb-b2</td><td>46.9</td><td>46.6</td><td>1.84E+08</td><td>7.40E+07</td><td>2.4912119</td></th1.05<></th1.05<>	P02089	Hemoglobin subunit beta-2	Hbb-b2	46.9	46.6	1.84E+08	7.40E+07	2.4912119
QS43K9 Purine nucleoside phosphorylase Pnp:Pnp2 6.6 3.3 7.72E+05 2.84E+05 2.7204338 Q8CGP4 Histone H2A Hist1h2aa 21.4 21.4 4.88E+08 1.74E+08 2.8048444 P83917 Chromobox protein homolog 1 Cbx1 9.2 7.55 1.22E+06 4.26E+05 2.8307753 O35864 COP9 signalosome complex subunit 5 Cops5 14.3 14.3 4.69E+06 1.63E+06 2.8804678 O9CR00 26S proteasome non-ATPase regulatory subunit 9 Psmd9 5.1 2.55 4.20E+06 1.38E+06 3.0804593 P00015 Cytochrome c, testis-specific Cytct 24.3 17.65 1.89E+07 5.88E+06 3.2051827 P28658 Ataxin-10 Atxn10 1.45 1.45 8.12E+05 2.29E+05 3.5437179 P20357 Microtubule-associated protein 2 Map2 1.75 1.4 4.00E+06 1.13E+06 3.965426 P11087 Collagen alpha-1(l) chain Col1a1 6.15 3.95 1.68E+07 <td>Q04750</td> <td>DNA topoisomerase 1</td> <td>Top1</td> <td>21</td> <td>21</td> <td>1.98E+06</td> <td>7.37E+05</td> <td>2 6873618</td>	Q04750	DNA topoisomerase 1	Top1	21	21	1.98E+06	7.37E+05	2 6873618
Q8CGP4 Histone H2A HistifhZaa 21.4 4.88E+08 1.74E+08 2.8048444 P83917 Chromobox protein homolog 1 Cbx1 9.2 7.55 1.22E+06 4.26E+05 2.8537753 O35864 COP9 signalosome complex subunit 5 Cops5 14.3 14.3 4.69E+06 1.63E+06 2.8804678 Q9CR00 26S proteasome non-ATPase regulatory subunit 9 Psmd9 5.1 2.55 4.20E+06 1.36E+06 3.0804593 P00015 Cytochrome c, testis-specific Cyct 24.3 17.65 1.89E+07 5.88E+06 3.2051827 P28658 Ataxin-10 Atxn10 1.45 1.45 8.12E+05 2.29E+05 3.5437179 P20357 Microtubule-associated protein 2 Map2 1.75 1.4 4.00E+06 1.13E+06 3.95426 P11087 Collagen alpha-1(l) chain Col1a1 6.15 3.95 1.68E+07 4.21E+06 4.28950303 P97379 Ras GTPase-activating protein-binding protein 2 G3bp2 12 12 3.87E+06 <	Q543K9	Purine nucleoside phosphorylase	Pnp:Pnp2	6.6	3.3	7.72E+05	2.84E+05	2.7204358
Pasapir Chromobox protein homolog 1 Cbx1 P.1 Pasapir Pasapir <td>Q8CGP4</td> <td>Histone H2A</td> <td>Hist1h2aa</td> <td>21.4</td> <td>21.4</td> <td>4.88E+08</td> <td>1.74E+08</td> <td>2.8048444</td>	Q8CGP4	Histone H2A	Hist1h2aa	21.4	21.4	4.88E+08	1.74E+08	2.8048444
Ods Data Data <thdata< th=""> Data Data D</thdata<>	P83917	Chromobox protein homolog 1	Chx1	92	7.55	1.22E+06	4 26E+05	2 8537753
Operation Operation <t< td=""><td>O35864</td><td>COP9 signalosome complex subunit 5</td><td>Cops5</td><td>14.3</td><td>14.3</td><td>4.69E+06</td><td>1.63E+06</td><td>2.8804678</td></t<>	O35864	COP9 signalosome complex subunit 5	Cops5	14.3	14.3	4.69E+06	1.63E+06	2.8804678
Protect Protect <t< td=""><td>09CR00</td><td>26S proteasome pon-ATPase regulatory subunit 9</td><td>Psmd9</td><td>51</td><td>2 55</td><td>4 20E+06</td><td>1 36E+06</td><td>3 0804593</td></t<>	09CR00	26S proteasome pon-ATPase regulatory subunit 9	Psmd9	51	2 55	4 20E+06	1 36E+06	3 0804593
P26658 Ataxin-10 Abxn10 1.45 1.45 1.45 2.29E+05 3.5437179 P20357 Microtubule-associated protein 2 Map2 1.75 1.4 4.00E+06 1.13E+06 3.54397179 P20357 Microtubule-associated protein 2 Map2 1.75 1.4 4.00E+06 1.13E+06 3.5489953 P61750 ADP-ribosylation factor 4 Ar/4 11.7 11.7 9.87E+06 2.49E+06 3.955426 P11087 Collagen alpha-1(l) chain Col1a1 6.15 3.95 1.68E+07 4.21E+06 3.9850303 P97379 Ras GTPase-activating protein-binding protein 2 G3bp2 12 12 3.87E+06 9.04E+05 4.278474 D3Z7K0 Ubiquitin thioesterase OTUB1 Otub1 18.65 14.9 2.72E+07 5.13E+06 5.3105051 P27048 Small nuclear ribonucleoprotein-associated protein B Snrpb 8.25 3.25 1.68E+06 2.01E+05 8.3721104 P35396 Peroxisome proliferator-activated receptor delta Ppard 1.6	P00015	Cytochrome c. testis-specific	Cvct	24.3	17.65	1.89E+07	5.88E+06	3.2051827
P20357 Microtubule-associated protein 2 Map2 1.75 1.4 4.00E+06 1.13E+06 3.5489953 P61750 ADP-ribosylation factor 4 Ar/4 11.7 11.7 9.87E+06 2.49E+06 3.955426 P11087 Collagen alpha-1(l) chain Col1a1 6.15 3.95 1.68E+07 4.21E+06 3.9850303 P97379 Ras GTPase-activating protein-binding protein 2 G3bp2 12 12 3.87E+06 9.04E+05 4.278474 D3Z7K0 Ubiquitin thioesterase OTUB1 Otub1 18.65 14.9 2.72E+07 5.13E+06 5.3105051 P27048 Small nuclear ribonucleoprotein-associated protein B Snrpb 8.25 3.25 1.68E+06 2.01E+05 8.3721104 P35396 Peroxisome proliferator-activated receptor delta Ppard 1.6 1.39E+06 1.00E+07 13.877689 P07309 Transthyretin Ttr 11.9 5.1 7.35E+07 1.55E+06 47.408315	P28658	Ataxin-10	Atxn10	1.45	1.45	8.12E+05	2.29E+05	3.5437179
P61750 ADP-ribosylation factor 4 Ar/4 11.7 11.7 9.87E+06 2.49E+06 3.955426 P11087 Collagen alpha-1(l) chain Col1a1 6.15 3.95 1.68E+07 4.21E+06 3.9850303 P97379 Ras GTPase-activating protein-binding protein 2 G3bp2 12 12 3.87E+06 9.04E+05 4.278474 D3Z7K0 Ubiquitin thioesterase OTUB1 Otub1 18.65 14.9 2.72E+07 5.13E+06 5.3105051 P27048 Small nuclear ribonucleoprotein-associated protein B Snrpb 8.25 3.25 1.68E+06 2.01E+05 8.3721104 P35396 Peroxisome proliferator-activated receptor delta Ppard 1.6 1.39E+08 1.00E+07 13.877689 P07309 Transthyretin Ttr 11.9 5.1 7.35E+07 1.55E+06 47.408315	P20357	Microtubule-associated protein 2	Map2	1.75	1.4	4.00E+06	1.13E+06	3.5489953
P11087 Collagen alpha-1(l) chain Colla1 6.15 3.95 1.68E+07 4.21E+06 3.9850303 P97379 Ras GTPase-activating protein-binding protein 2 G3bp2 12 12 3.87E+06 9.04E+05 4.278474 D3Z7K0 Ubiquitin thioesterase OTUB1 Otub1 18.65 14.9 2.72E+07 5.13E+06 5.3105051 P27048 Small nuclear ribonucleoprotein-associated protein B Snrpb 8.25 3.25 1.68E+06 2.01E+05 8.3721104 P35396 Peroxisome proliferator-activated receptor delta Ppard 1.6 1.39E+08 1.00E+07 13.877689 P07309 Transthyretin Ttr 11.9 5.1 7.35E+07 1.55E+06 47.408315	P61750	ADB-ribosylation factor 4	Arf4	11.7	11.7	9.87E+06	2 49E+06	3 955426
P37379 Ras GTPase-activating protein-binding protein 2 G3bp2 12 12 3.87E+06 9.04E+05 4.278474 D3Z7K0 Ubiquitin thioesterase OTUB1 Otub1 18.65 14.9 2.72E+07 5.13E+06 5.3105051 P27048 Small nuclear ribonucleoprotein-associated protein B Snrpb 8.25 3.25 1.68E+06 2.01E+05 8.3721104 P35396 Peroxisome proliferator-activated receptor delta Ppard 1.6 1.39E+08 1.00E+07 15.877689 P07309 Transthyretin Ttr 11.9 5.1 7.35E+07 1.55E+06 47.408315			1	1		2.0.2.00		0.005120
D327K0 Ubiquitin thioesterase OTUB1 Otub1 18.65 14.9 2.72E+07 5.13E+06 5.3105051 P27048 Small nuclear ribonucleoprotein-associated protein B Snrpb 8.25 3.25 1.68E+06 2.01E+05 8.3721104 P35396 Peroxisome proliferator-activated receptor delta Ppard 1.6 1.39E+08 1.00E+07 13.877689 P07309 Transthyretin Ttr 11.9 5.1 7.35E+07 1.55E+06 47.408315	P11087	Collagen alpha-1(I) chain	Col1a1	6.15	3.95	1.68E+07	4.21E+06	3.9850303
P27048 Small nuclear ribonucleoprotein-associated protein B Snrpb 8.25 3.25 1.68E+06 2.01E+05 8.3721104 P35396 Peroxisome proliferator-activated receptor delta Ppard 1.6 1.39E+08 1.00E+07 13.877689 P07309 Transthyretin Ttr 11.9 5.1 7.35E+07 1.55E+06 47.408315	P11087 P97379	Collagen alpha-1(l) chain Ras GTPase-activating protein-binding protein 2	Col1a1 G3bp2	6.15 12	3.95 12	1.68E+07 3.87E+06	4.21E+06 9.04E+05	3.9850303
P35396 Peroxisome proliferator-activated receptor delta Ppard 1.6 1.6 1.39E+08 1.00E+07 13.877689 P07309 Transthyretin Ttr 11.9 5.1 7.35E+07 1.55E+06 47.408315	P11087 P97379 D3Z7K0	Collagen alpha-1(I) chain Ras GTPase-activating protein-binding protein 2 Ubioutin thioesterase OTUB1	Col1a1 G3bp2 Otub1	6.15 12 18.65	3.95 12 14.9	1.68E+07 3.87E+06 2.72E+07	4.21E+06 9.04E+05 5.13E+06	3.9850303 4.278474 5.3105051
Transferred Transferred Total 100 Total 100 <thtotal 100<="" th=""> <thtotal 100<="" th=""></thtotal></thtotal>	P11087 P97379 D3Z7K0 P27048	Collagen alpha-1(I) chain Ras GTPase-activating protein-binding protein 2 Ubiquitin thioesterase OTUB1 Small nuclear ribonucleoprotein-associated protein B	Col1a1 G3bp2 Otub1 Snrpb	6.15 12 18.65 8.25	3.95 12 14.9 3.25	1.68E+07 3.87E+06 2.72E+07 1.68E+06	4.21E+06 9.04E+05 5.13E+06 2.01E+05	3.9850303 4.278474 5.3105051 8.3721104
	P11087 P97379 D3Z7K0 P27048 P35396	Collagen alpha-1(I) chain Ras GTPase-activating protein-binding protein 2 Ubiquitin thioesterase OTUB1 Small nuclear ribonucleoprotein-associated protein B Peroxisome proliferator-activated receptor delta	Col1a1 G3bp2 Otub1 Snrpb Ppard	6.15 12 18.65 8.25 1.6	3.95 12 14.9 3.25 1.6	1.68E+07 3.87E+06 2.72E+07 1.68E+06 1.39E+08	4.21E+06 9.04E+05 5.13E+06 2.01E+05 1.00E+07	3.9850303 4.278474 5.3105051 8.3721104 13.877689