

Supplementary Table 3: results of the pathway analysis by the David tool on the proteins modulated in response to PLA beads

Annotation Cluster 1	Enrichment Score: 9.368300008141553	Count	%	PValue	Genes	FDR
Category	Term					
GOTERM_BP_DIRECT	GO:0006412~translation	31	8.7078652	1.75093E-16	P62918, Q9D7S7, P62717, O70194, Q9DC44, P19253, P62281, P14115, Q8K0D5, Q61035, P67984, P62751, P62274, Q9DIR9, Q8C0D5, P62270, Q8IZQ9, P63276, O55142, Q8BP47, P61255, P58252, Q9D8E6, P62900, P60229, Q9JHW4, Q99KK9, P47964, P41105, P60843, Q9CQE3	3.4090576E-13
GOTERM_BP_DIRECT	GO:0002181~cytoplasmic translation	19	5.3370787	1.30116E-15	P62918, Q9D7S7, P62717, Q9DIR9, P19253, P62281, P62270, P14115, P63276, O55142, P67984, P62751, P61255, Q9D8E6, P62274, P62900, Q9CQK7, P41105, P47964	1.266679E-12
GOTERM_CC_DIRECT	GO:0022626~cytosolic ribosome	16	4.494382	5.6014E-13	P62918, P62717, Q9DIR9, P19253, P62281, P62270, P14115, P63276, O55142, P67984, P62751, P61255, Q9D8E6, P62900, P41105, P47964	8.1220271E-11
GOTERM_CC_DIRECT	GO:0005840~ribosome	21	5.8988764	5.78761E-12	P62918, P11928, Q9D7S7, P62717, Q9DIR9, P19253, P35564, P62281, P62270, P14115, P63276, O55142, P67984, P62751, P61255, Q9D8E6, P62274, P62900, P41105, P47964, Q9CQE3	6.2940266E-10
GOTERM_CC_DIRECT	GO:0022625~cytosolic large ribosomal subunit	13	3.6516854	2.69666E-10	P62918, P62717, Q9DIR9, P19253, P14115, O55142, P67984, P62751, P61255, Q9D8E6, P62900, P41105, P47964	1.6757841E-08
GOTERM_MF_DIRECT	GO:0003735~structural constituent of ribosome	19	5.3370787	8.67998E-10	P62918, Q9D7S7, P62717, Q9DIR9, P19253, P62281, P62270, P14115, P63276, O55142, P67984, P62751, P61255, Q9D8E6, P62274, P62900, P41105, P47964, Q9CQE3	1.9124894E-07
KEGG_PATHWAY	mmu05171:Coronavirus disease - COVID-19	25	7.0224719	2.29093E-09	P62918, P11928, Q9D7S7, P62717, Q8BT19, P19253, P62281, P14115, P67984, P62751, P62274, P98086, P42227, Q8V193, Q9DIR9, P62270, P30993, P63276, O55142, P61255, Q61093, Q9D8E6, P62900, P47964, P41105	5.7044048E-07
UP_KW_MOLECULAR_FUNCTION	KW-0687~Ribonucleoprotein	24	6.741573	5.13169E-09	P62918, Q9D7S7, P62717, Q9DIR9, P19253, P62281, Q9D7A6, P62270, P14115, Q62376, Q3UEB3, P63276, O55142, P67984, P62751, P61255, Q9D8E6, P62274, P62900, Q9QXK7, Q9D0E1, P41105, P47964, Q9CQE3	2.6541449E-07
UP_KW_MOLECULAR_FUNCTION	KW-0689~Ribosomal protein	19	5.3370787	8.04286E-09	P62918, Q9D7S7, P62717, Q9DIR9, P19253, P62281, P62270, P14115, P63276, O55142, P67984, P62751, P61255, Q9D8E6, P62274, P62900, P41105, P47964, Q9CQE3	2.6541449E-07

KEGG_PATHWAY	mmu03010:Ribosome	19	5.3370787	1.11694E-07	P62918, Q9D7S7, P62717, Q9DIR9, P19253, P62281, P62270, P14115, P63276, O55142, P67984, P62751, P61255, Q9D8E6, P62274, P62900, P41105, P47964, Q9CQE3	9.2706324E-06
GOTERM_CC_DIRECT	GO:0098793~presynapse	18	5.0561798	6.35201E-07	P62918, Q9DIR9, P19253, Q9CR95, P35564, P62281, P14115, Q64324, O55142, P67984, P62751, P61255, O08992, Q9D8E6, P61028, P41105, P47964, P49615	2.7631264E-05
GOTERM_CC_DIRECT	GO:0045202~synapse	35	9.8314607	3.56897E-06	P62918, Q61235, P62717, Q5SSL4, O70194, Q9DCH4, P19253, P10852, P62281, P14115, P67984, O35864, P70704, P62751, P50518, O08992, G5E829, P49615, P98086, P57716, Q9DIR9, P35564, Q64430, P62270, Q81ZQ9, P63276, O55101, O55142, P61255, P58252, Q9D8E6, P62900, Q9D0E1, P47964, P41105	0.00011942339
GOTERM_CC_DIRECT	GO:0098794~postsynapse	17	4.7752809	3.93723E-06	P62918, Q9DIR9, P19253, P62281, P62270, P14115, P63276, O55142, P67984, P62751, P61255, Q9D8E6, P62900, P98086, P41105, P47964, P49615	0.00012233546
Annotation Cluster 2	Enrichment Score: 6.992234447958213					
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0000166~nucleotide binding	64	17.977528	5.94397E-11	Q8CG48, Q8BT19, O70133, P46471, P70388, P37913, P11440, Q8K0D5, Q61035, Q8VEH6, P70704, P61222, P61028, P09411, P48722, P61027, P56480, P49615, P28650, Q9WUK4, Q64430, P70698, P35601, Q8BP47, P09581, Q9WTT7, P06795, E9Q634, Q9JIY4, O70551, Q2NL51, Q9CY64, O08528, P50516, P70248, P36371, Q8VDD5, Q91V92, Q04899, P61087, P04184, G5E829, P62334, Q8C111, P80314, Q8V193, Q9CZ30, Q8C0D5, Q6ZQB6, Q04692, O35379, P58252, O09110, P24547, Q9EPE9, Q9Z110, Q9DIG2, P63038, Q9WUA3, P80318, Q9JHW4, Q99KK9, P60843, Q3UFY7	1.9644822E-08
GOTERM_MF_DIRECT	GO:0005524~ATP binding	53	14.88764	4.83696E-08	Q8CG48, P11928, Q8BT19, O70133, P46471, P70388, P37913, P11440, Q61035, P70704, P61222, P09411, P48722, P56480, P49615, Q9WUK4, Q64430, P70698, P35601, Q8BP47, P09581, Q9WTT7, P06795, E9Q634, Q9JIY4, O70551, Q2NL51, O08528, P50516, P70248, P36371, Q8VDD5, Q91V92, Q04899, P61087, P04184, G5E829, P62334, P80314, Q8V193, Q9CZ30, Q6ZQB6, Q04692, O35379, O09110, Q9EPE9, Q9Z110, Q9DIG2, P63038, Q9WUA3, P80318, Q99KK9, P60843	6.3944586E-06

Annotation Cluster 3	Enrichment Score: 5.913199641887708	Count	%	PValue	Genes	FDR
UP_KW_LIGAND	KW-0547~Nucleotide-binding	63	17.696629	2.08501E-07	Q8CG48, P11928, Q8BT19, O70133, P46471, P70388, P37913, P11440, Q8K0D5, Q61035, Q8VEH6, P70704, P61222, P61028, P09411, P48722, P61027, P56480, P49615, P28650, Q9WUK4, Q64430, P70698, P35601, Q8BP47, P09581, Q9WTT7, P06795, E9Q634, Q9JYY4, O70551, Q2NL51, O08528, P50516, P70248, P36371, Q8VDD5, Q91V92, Q04899, P61087, P04184, G5E829, P62334, Q8C111, P80314, Q8VI93, Q9CZ30, Q8C0D5, Q6ZQB6, Q04692, O35379, P58252, O09110, Q9EPE9, Q9Z110, Q9D1G2, P63038, Q9WUA3, P80318, Q9JHW4, Q99KK9, P60843, Q3UPLY7	4.5599432E-06
UP_KW_LIGAND	KW-0067~ATP-binding	53	14.88764	3.64795E-07	Q8CG48, P11928, Q8BT19, O70133, P46471, P70388, P37913, P11440, Q61035, P70704, P61222, P09411, P48722, P56480, P49615, Q9WUK4, Q64430, P70698, P35601, Q8BP47, P09581, Q9WTT7, P06795, E9Q634, Q9JYY4, O70551, Q2NL51, O08528, P50516, P70248, P36371, Q8VDD5, Q91V92, Q04899, P61087, P04184, G5E829, P62334, P80314, Q8VI93, Q9CZ30, Q6ZQB6, Q04692, O35379, O09110, Q9EPE9, Q9Z110, Q9D1G2, P63038, Q9WUA3, P80318, Q99KK9, P60843, P80314, Q8CG48, P46471, O70133, Q9CZ30, P70388, Q9WUK4, Q64430, P35601, Q04692, P70704, P48722, Q9EPE9, G5E829, P56480, P62334, P63038, P80318, E9Q634, Q9JYY4, P60843	4.5599432E-06
GOTERM_MF_DIRECT	GO:0016887~ATPase activity	21	5.8988764	1.0894E-06	Q8CG48, O70133, P46471, P50516, P70388, P70248, Q8K0D5, P36371, Q8VDD5, P61222, P61028, P04184, P61027, P62334, P56480, Q8C111, P28650, Q9CZ30, Q8C0D5, Q9WUK4, P70698, P35601, Q04692, O35379, P58252, Q9WTT7, Q9D1G2, P06795, Q9JYY4, Q9JHW4, E9Q634, P60843	0.00012001558
INTERPRO	IPR027417:P-loop containing nucleoside triphosphate hydrolase	33	9.2696629	4.67304E-06	Q8CG48, O70133, P46471, Q9JKF1, P50516, P70388, P70248, Q8K0D5, P36371, Q8VDD5, P61222, P61028, P04184, P61027, P62334, P56480, Q8C111, P28650, Q9CZ30, Q8C0D5, Q9WUK4, P70698, P35601, Q04692, O35379, P58252, Q9WTT7, Q9D1G2, P06795, Q9JYY4, Q9JHW4, E9Q634, P60843	0.00165425601
UP_KW_DOMAIN	KW-0809~Transit peptide	25	7.0224719	5.08189E-08	Q8K3J1, Q8K0D5, P42125, Q9CZB0, Q9CZ13, P56383, P45952, P56480, P08249, Q9DB77, Q9D6R2, Q9CYR0, P53395, Q8CG76, O08715, Q8BMF4, Q9JH15, Q8C0I1, P20108, Q9CQA3, O09111, Q99K10, P63038, Q99KK9, Q9CQE3	1.0671968E-06
UP_SEQ_FEATURE	TRANSIT:Mitochondrion	24	6.741573	5.09651E-07	Q9D6R2, Q8K3J1, Q9CYR0, P53395, Q8CG76, O08715, Q9JH15, Q8BMF4, Q8K0D5, P20108, P42125, Q9CQA3, O09111, Q9CZB0, Q99K10, Q9CZ13, P56383, P45952, P56480, P63038, P08249, Q9DB77, Q99KK9, Q9CQE3	0.00016376794

Annotation Cluster	Enrichment Score:	Count	%	PValue	Genes	FDR
UP_KW_CELLULAR_CO MPONENT	KW-0496~Mitochondrion	39	10.955056	7.03239E-05	P11928, Q8K3J1, O08528, P11440, Q8K0D5, P42125, P61222, Q9CZB0, Q9CZ13, Q9DCZ4, P56383, P45952, P56480, P08249, Q8R1I1, Q9DB77, P62897, Q9D6R2, Q921M7, Q9QZD8, Q9CZR0, P53395, Q8CG76, O08715, Q8BMF4, Q9JH15, O08734, P20108, Q8BGE6, Q9CQA3, O09111, Q07813, Q99K10, Q9Z110, P63038, P60603, Q99KK9, Q9CQE3, P00397	0.00093765164
Annotation Cluster 4	4.82314446763019905					
Category	Term					FDR
KEGG_PATHWAY	mmu01200:Carbon metabolism	16	4.494382	1.062E-07	Q9D6R2, P06801, P06745, Q9R0P3, O08528, Q8BMF4, P47968, Q9CQA3, P40142, Q9CZB0, Q99K10, P05063, P09411, Q9WUA3, P08249, P05201	9.2706324E-06
UP_KW_BIOLOGICAL_P ROCESS	KW-0816~Tricarboxylic acid cycle	6	1.6853933	4.609E-05	Q9D6R2, Q9CQA3, Q9CZB0, Q99K10, Q8BMF4, P08249	0.0013366095
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	7	1.9662921	7.72258E-05	Q9D6R2, Q9CQA3, Q91V92, Q9CZB0, Q99K10, Q8BMF4, P08249	0.00197905107
GOTERM_BP_DIRECT	GO:0006099~tricarboxylic acid cycle	6	1.6853933	0.000134874	Q9D6R2, Q9CQA3, Q9CZB0, Q99K10, Q8BMF4, P08249	0.0437664787
Annotation Cluster 5	Enrichment Score: 4.704741333913531					
Category	Term	Count	%	PValue	Genes	FDR
UP_SEQ_FEATURE	CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2)	36	10.11236	2.6101E-07	P62918, P09405, P62717, O70133, Q3U1J4, P14733, P10852, P97822, P11440, P62751, O35226, P40142, Q99JF8, P62996, Q8C1I1, Q9DBE9, P80314, Q60973, Q9DIR9, Q6PDM2, Q99020, P62270, Q62376, Q8CGZ0, Q91VE6, Q3UEB3, P35601, Q04692, P61255, Q9D8E6, P24547, Q9D0E1, P63038, P80318, P41105, P60843, P62918, P09405, Q8BL97, P62717, O70133, P46471, Q3U1J4, Q9JMH6, P97822, P11440, Q9QY76, Q80U87, Q9R0L6, P62751, P61222, P61027, A1L314, P84228, P62996, P06745, Q91YQ5, Q9DIR9, Q6PDM2, P35564, Q9CQ71, Q62376, P35601, P14685, Q61093, P09581, Q9QXK7, P14733, P10852, Q8VDD5, O35226, P40142, Q91V92, P61087, P17095, P04184, Q99JF8, Q8C1I1, Q9DBE9, P80314, Q60972, Q60973, Q921M7, Q99020, P36993, P62270, Q8CGZ0, Q91VE6, Q3UEB3, Q04692, P63276, Q8BGE6, P58252, P61255, Q9D8E6, P24547, Q9D0E1, P63038, P80318, P41105, P60843	0.00012580665
UP_KW_PTM	KW-0832~Ubl conjugation	73	20.505618	0.000159532		0.00066462281

UP_KW_PTM	KW-1017~Isopeptide bond	54	15.168539	0.000184617	P62918, P09405, Q8BL97, P62717, P62717, 070133, Q3U114, P97822, P11440, Q9QY76, P62751, P61027, P62996, Q91YQ5, Q9DIR9, Q6PDM2, Q9CQ71, Q62376, P35601, P14685, Q61093, Q9QXK7, P14733, P10852, Q35226, P40142, Q91V92, P61087, P17095, Q99JF8, Q8C111, Q9DBE9, P80314, Q60972, Q60973, Q921M7, Q99020, P36993, P62270, Q8CGZ0, Q91VE6, Q3UEB3, Q04692, P63276, Q8BGE6, P58252, P61255, Q9D8E6, P24547, Q9D0E1, P63038, P80318, P41105, P60843	0.00066462281
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Annotation Cluster 6	Enrichment Score: 4.24596503935281	Count	%	PValue	Genes	FDR
Category	Term				Q60664, P11928, Q9JLJ5, P14115, O08547, Q9QY76, O08795, P70704, O08992, P62274, P61027, Q9DCZ4, O88455, Q8BHN3, Q91YQ5, Q9DIR9, O08715, P35564, P17439, Q64430, Q8R180, Q9DB25, O54692, Q9JK23, Q07813, Q61093, Q9DBS1, Q9WV55, O70551, Q9CPU4, P36371, Q6ZWQ7, Q9JHP7, P35441, Q9WU81, Q9EQH2, P57716, Q8CGZ0, O08734, P97858, P35821, Q8VDP6, Q6P5E4, Q8BGE6, Q8R1V4, B9EJ86, Q9EPE9, O70503, P47964	

GOTERM_CC_DIRECT	GO:0005783~endoplasmic reticulum	49	13.764045	1.88325E-06	Q60664, P11928, Q9WV55, O70551, Q9JLJ5, O08547, Q9QY76, Q9CPU4, O08795, P36371, P70704, Q6ZWQ7, Q9JHP7, P35441, O08992, P62274, P61027, Q9DCZ4, Q9WU81, O88455, Q8BHN3, Q9EQH2, Q9DIR9, Q91YQ5, O08715, P35564, Q8CGZ0, P97858, Q8R180, P35821, Q8VDP6, Q6P5E4, Q8BGE6, Q9DB25, O54692, Q9JK23, Q91K23, Q8R1V4, B9EJ86, Q9EPE9, O70503, Q9DBS1, Q60664, Q9WV55, Q9JLJ5, O08547, Q9QY76, Q9CPU4, P36371, P40142, O08992, P61027, Q9DCZ4, Q9WU81, O88455, Q9EQH2, Q91YQ5, P35564, P97858, Q8R180, Q8VDP6, Q9DB25, O54692, Q07813, Q8R1V4, B9EJ86, Q9EPE9	0.00025280251
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UP_KW_CELLULAR_CO_MPONENT	KW-0256~Endoplasmic reticulum	41	11.516854	1.26401E-05	Q60664, P11928, Q9WV55, O70551, Q9JLJ5, O08547, Q9QY76, Q9CPU4, O08795, P36371, P70704, Q6ZWQ7, Q9JHP7, P35441, O08992, P62274, P61027, Q9DCZ4, Q9WU81, O88455, Q8BHN3, Q9EQH2, Q9DIR9, Q91YQ5, O08715, P35564, Q8CGZ0, P97858, Q8R180, P35821, Q8VDP6, Q6P5E4, Q8BGE6, Q9DB25, O54692, Q9JK23, Q8R1V4, B9EJ86, Q9EPE9, O70503, Q9DBS1, Q60664, Q9WV55, Q9JLJ5, O08547, Q9QY76, Q9CPU4, P36371, P40142, O08992, P61027, Q9DCZ4, Q9WU81, O88455, Q9EQH2, Q91YQ5, P35564, P97858, Q8R180, Q8VDP6, Q9DB25, O54692, Q07813, Q8R1V4, B9EJ86, Q9EPE9	0.00025280251
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GOTERM_CC_DIRECT	GO:0005789~endoplasmic reticulum membrane	25	7.0224719	0.007681496	Q60664, P11928, Q9WV55, O70551, Q9JLJ5, O08547, Q9QY76, Q9CPU4, O08795, P36371, P70704, Q6ZWQ7, Q9JHP7, P35441, O08992, P62274, P61027, Q9DCZ4, Q9WU81, O88455, Q8BHN3, Q9EQH2, Q9DIR9, Q91YQ5, O08715, P35564, Q8CGZ0, P97858, Q8R180, P35821, Q8VDP6, Q6P5E4, Q8BGE6, Q9DB25, O54692, Q9JK23, Q8R1V4, B9EJ86, Q9EPE9, O70503, Q9DBS1, Q60664, Q9WV55, Q9JLJ5, O08547, Q9QY76, Q9CPU4, P36371, P40142, O08992, P61027, Q9DCZ4, Q9WU81, O88455, Q9EQH2, Q91YQ5, P35564, P97858, Q8R180, Q8VDP6, Q9DB25, O54692, Q07813, Q8R1V4, B9EJ86, Q9EPE9	0.09030948567
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Annotation Cluster 7
Enrichment Score:
4.186778511904929

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0016491~oxidoreductase activity	27	7.5842697	4.68133E-06	Q8K3J1, Q9CY64, Q9JMH6, Q8CTK6, Q9ESY9, Q9CPU4, Q9CQF9, P45376, P45377, O88455, P45952, P08249, Q9D6R2, P06801, P08228, P47199, Q8CG76, Q9JH15, Q8R180, Q8C011, P20108, Q9CQA3, Q61093, Q9ZZG9, P24547, Q9Z110, O70503	0.00044205154

Category	Term	Count	%	PValue	Genes	FDR
UP_KW_MOLECULAR_FUNCTION	KW-0560~Oxidoreductase	27	7.5842697	8.63966E-05	Q8K3J1, Q9CXY64, Q9JMH6, Q8C7K6, Q9ESY9, Q9CPU4, Q9COF9, P45376, P45377, Q88455, P45952, P08249, Q9D6R2, P06801, P08228, P47199, Q8CG76, Q9JH15, Q8R180, P20108, Q9CQA3, Q61093, Q9Z2G9, P24547, Q9Z110, Q70503, P00397	0.00095036298
UP_KW_LIGAND	KW-0521~NADP	12	3.3707865	0.000680453	P06801, P47199, Q61093, Q9CXY64, Q8CG76, Q9Z2G9, Q9JMH6, P45376, Q88455, Q9Z110, P45377, Q70503	0.0056704419
Annotation Cluster 8	Enrichment Score: 3.7635340237459953					
GOTERM_MF_DIRECT	GO:0003723~RNA binding	49	13.764045	1.10561E-13	P62918, P09405, Q8BL97, Q9D757, Q6R5N8, O70133, O70194, P62281, Q35295, Q9JKP5, Q08795, P67984, P62751, P84104, Q9CSH3, P17095, P62996, Q8V193, Q60973, P47199, Q8C175, Q6PDM2, Q08715, Q99136, Q99020, Q9D7A6, P62270, Q62376, Q8CGZ0, Q9JH15, Q91VE6, Q3UEB3, Q991X7, Q9CQT2, Q8JZQ9, P70318, Q9CXX8, Q5U4D9, P58252, P61255, Q9D8E6, Q9QXK7, P24547, Q9D0E1, Q91VU7, Q9JY4, P60843, Q9CQE3, P62918, P11928, P09405, Q8BL97, Q6R5N8, O70133, O70194, P62281, Q9JKP5, P67984, P62751, Q9CSH3, P84104, P62996, Q8V193, P47199, Q8C175, Q6PDM2, Q08715, Q9D7A6, Q99020, P62270, Q62376, Q9JH15, Q91VE6, Q3UEB3, Q991X7, Q9CQT2, Q8JZQ9, P70318, Q9CXX8, Q5U4D9, P24547, Q9QXK7, Q9D0E1, P60843, Q9CQE3	7.3080929E-11
UP_KW_MOLECULAR_FUNCTION	KW-0694~RNA-binding	37	10.393258	1.67834E-08	P09405, Q8BL97, Q6PDM2, Q99020, Q62376, Q9JH15, Q91VE6, Q3UEB3, Q991X7, Q9CQT2, Q8JZQ9, P70318, P84104, Q9D0E1, P62996	3.6923401E-07
UP_SEQ_FEATURE	DOMAIN:RRM	15	4.2134831	2.78508E-06	P09405, Q8BL97, Q6PDM2, Q99020, Q62376, Q9JH15, P84104, Q9D0E1, P62996	0.00053696315
SMART	SM00360:RRM	14	3.9325843	9.46225E-06	P09405, Q8BL97, Q6PDM2, Q99020, Q62376, Q9JH15, Q91VE6, Q3UEB3, Q9CQT2, Q8JZQ9, P70318, P84104, Q9D0E1, P62996	0.00058665931
INTERPRO	IPR012677:Nucleotide-binding, alpha-beta plait	16	4.494382	1.18415E-05	P09405, Q8BL97, Q6PDM2, Q99020, Q62376, Q9JH15, P62751, P84104, Q9D0E1, P62996	0.00279458871
INTERPRO	IPR000504:RNA recognition motif domain	14	3.9325843	4.43036E-05	P09405, Q8BL97, Q6PDM2, Q99020, Q62376, Q9JH15, Q91VE6, Q3UEB3, Q9CQT2, Q8JZQ9, P70318, P84104, Q9D0E1, P62996	0.0072113923
GOTERM_MF_DIRECT	GO:0003676~nucleic acid binding	23	6.4606742	7.40358E-05	P09405, Q8BL97, Q70133, Q3U1J4, Q6PDM2, Q08715, P62270, Q99020, Q62376, Q8CGZ0, Q9JH15, Q91VE6, Q3UEB3, Q991X7, Q9CQT2, Q8JZQ9, P70318, Q8BP47, P84104, Q9D0E1, Q9JY4, P62996, P60843	0.00611720948

Annotation Cluster 9	Enrichment Score: 3.477831332166054	Count	%	PValue	Genes	FDR
Category	Term					
UP_SEQ_FEATURE	LIPID:N6-decanoyllysine	8	2.247191	1.78707E-10	P84228	1.7227368E-07
SMART	SM00428:H3	8	2.247191	6.17874E-10	P84228	7.6616402E-08
INTERPRO	IPR000164:Histone H3	8	2.247191	1.22785E-09	P84228	8.693177E-07
UP_KW_PTM	KW-0164~Citrullination	15	4.2134831	1.17666E-08	Q9DBE9, P62751, Q9D8E6, P19253, P62281, P84228, Q99JF8, Q91VE6	7.0599853E-08
GOTERM_BP_DIRECT	GO:0040029~regulation of gene expression, epigenetic	8	2.247191	2.12865E-06	P84228	0.00103612214
UP_SEQ_FEATURE	DOMAIN:Histone H2A/H2B/H3	8	2.247191	2.2727E-06	P84228	0.00053696315
GOTERM_BP_DIRECT	GO:0006334~nucleosome assembly	11	3.0898876	6.53341E-06	Q60972, Q78ZA7, Q9EST5, P84228	0.00254411153
INTERPRO	IPR007125:Histone core	8	2.247191	9.4574E-05	P84228	0.01115973651
GOTERM_CC_DIRECT	GO:0000785~chromatin	18	5.0561798	0.000206828	Q60972, Q8CG48, Q8BFQ4, O35864, Q78ZA7, O70551, P17095, P70388, P84228, P42227	0.00449850639
UP_KW_CELLULAR_COMPONENT	KW-0544~Nucleosome core	8	2.247191	0.000616416	P84228	0.00616416025
UP_KW_PTM	KW-0013~ADP-ribosylation	10	2.8089888	0.000654427	P17095, P84228	0.00196328195
UP_SEQ_FEATURE	LIPID:S-palmitoyl cysteine	12	3.3707865	0.000909053	P08228, P35564, P62281, P84228, Q9CPU4	0.08763272931
GOTERM_MF_DIRECT	GO:0046982~protein heterodimerization activity	16	4.494382	0.001136358	Q9WV55, Q9R1T2, Q07813, O08992, Q61093, Q6IRU2, O08734, P84228, Q9QY76	0.06259440522
UP_KW_PTM	KW-0379~Hydroxylation	12	3.3707865	0.001399025	P62918, P09411, P14115, P84228, P98086	0.00314780535
Annotation Cluster 10	Enrichment Score: 3.42643241519865	Count	%	PValue	Genes	FDR
Category	Term					
KEGG_PATHWAY	mmu05020:Prion disease	21	5.8988764	3.51395E-06	P08228, P46471, Q8BT19, Q8K311, P14685, Q99J14, Q9CQA3, O35226, O09111, Q07813, Q61093, Q9CZB0, Q9CZ13, P56383, P56480, P62334, Q8R111, Q9DB77, P98086, P62897, P00397	0.00021874329
UP_KW_BIOLOGICAL_PROCESS	KW-0249~Electron transport	11	3.0898876	1.16712E-05	Q9CQA3, O09111, Q61093, Q9CZB0, Q8K311, Q9CZ13, Q8R111, Q9DB77, Q8R180, P62897, P00397	0.00061912631
KEGG_PATHWAY	mmu05014:Amyotrophic lateral sclerosis	24	6.741573	1.31115E-05	P08228, Q8BL97, Q8R0G9, P46471, Q8K311, Q99JX7, P14685, Q9QY76, Q99J14, Q9CQA3, O35226, O09111, Q07813, O09110, Q9CZB0, P84104, Q9CZ13, P56383, P56480, P62334, Q8R111, Q9DB77, P62897, P00397	0.00065295464
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	13	3.6516854	6.3789E-05	Q8K311, P50516, Q9CQA3, O09111, P50518, Q9CZB0, Q9CZ13, P56383, P56480, Q8R111, Q9DB77, P62897, P00397	0.00197905107

KEGG_PATHWAY	mmu05010:Alzheimer disease	23	6.4606742	7.06135E-05	P57716, Q91ZX7, P46471, Q8BT19, Q8K3J1, Q9CR16, P14685, Q99J14, Q9CQA3, O35226, P11152, O09111, Q61093, Q9CZB0, Q9CZ13, P56383, P56480, P62334, Q8R111, Q9DB77, P62897, P49615, P00397	0.00197905107
KEGG_PATHWAY	mmu05012:Parkinson disease	18	5.0561798	0.000125524	P08228, P46471, Q8K3J1, P14685, Q99J14, Q9CQA3, O35226, O09111, Q07813, Q9CZB0, Q9CZ13, P56383, P56480, P62334, Q8R111, Q9DB77, P62897, P00397	0.00284141034
KEGG_PATHWAY	mmu05016:Huntington disease	19	5.3370787	0.000208078	P08228, P46471, Q8K3J1, P17426, P14685, Q99J14, Q9CQA3, O35226, O09111, Q07813, Q9CZB0, Q9CZ13, P56383, P56480, P62334, Q8R111, Q9DB77, P62897, P00397	0.00431762676
GOTERM_CC_DIRECT	GO:0070469~respiratory chain	7	1.9662921	0.000243472	O09111, Q8K3J1, Q9CZ13, Q8R111, Q9DB77, P62897, P00397	0.00504335103
KEGG_PATHWAY	mmu05022:Pathways of neurodegeneration - multiple diseases	24	6.741573	0.000525299	P08228, P46471, Q8K3J1, Q9CR16, O08734, P14685, Q9QY76, Q99J14, Q9CQA3, O35226, O09111, Q07813, O09110, Q61093, Q9CZB0, Q9CZ13, P56383, P56480, P62334, Q8R111, Q9DB77, P62897, P49615, P00397	0.01006149919
KEGG_PATHWAY	mmu05208:Chemical carcinogenesis - reactive oxygen species	15	4.2134831	0.000613365	Q60631, P08228, Q8BT19, Q8K3J1, P35821, Q9CPU4, Q9CQA3, O09111, Q9CZB0, Q9CZ13, P56383, P56480, Q8R111, Q9DB77, P00397	0.01090913552
UP_KW_BIOLOGICAL_P ROCESS	KW-0679~Respiratory chain	7	1.9662921	0.000616075	O09111, Q8K3J1, Q9CZ13, Q8R111, Q9DB77, P62897, P00397	0.01071970068
KEGG_PATHWAY	mmu04932:Non-alcoholic fatty liver disease	12	3.3707865	0.000951092	Q9CQA3, O09111, Q07813, Q8BT19, Q9CZB0, Q2NL51, Q8K3J1, Q9CZ13, Q8R111, Q9DB77, P62897, P00397	0.01480136181
GOTERM_CC_DIRECT	GO:0005743~mitochondrial inner membrane	18	5.0561798	0.001485937	Q9QZD8, Q8K3J1, P42125, Q9CQA3, O09111, Q9CZB0, Q9CZ13, Q9DCZ4, Q9Z110, P56480, P63038, P60603, P08249, Q8R111, Q9DB77, P42227, P00397, Q9CQE3	0.02394009673
UP_KW_CELLULAR_CO MPONENT	KW-0999~Mitochondrion inner membrane	13	3.6516854	0.005255569	Q9QZD8, Q8K3J1, Q9CQA3, O09111, Q9CZB0, Q9CZ13, Q9DCZ4, Q9Z110, P56480, P60603, Q8R111, Q9DB77, P00397	0.03003182093
Annotation Cluster 11		Enrichment Score: 3.082004013922556				
Category	Term	Count	%	PValue	Genes	FDR
UP_KW_BIOLOGICAL_P ROCESS	KW-0249~Electron transport	11	3.0898876	1.16712E-05	Q9CQA3, O09111, Q61093, Q9CZB0, Q8K3J1, Q9CZ13, Q8R111, Q9DB77, Q8R180, P62897, P00397	0.00061912631
GOTERM_CC_DIRECT	GO:0070469~respiratory chain	7	1.9662921	0.000243472	O09111, Q8K3J1, Q9CZ13, Q8R111, Q9DB77, P62897, P00397	0.00504335103
GOTERM_CC_DIRECT	GO:0005750~mitochondrial respiratory chain complex III	4	1.1235955	0.000564085	Q9CZ13, Q8R111, Q9DB77, P00397	0.01066855759
UP_KW_BIOLOGICAL_P ROCESS	KW-0679~Respiratory chain	7	1.9662921	0.000616075	O09111, Q8K3J1, Q9CZ13, Q8R111, Q9DB77, P62897, P00397	0.01071970068

Annotation Cluster 12		Enrichment Score: 2.64491711107640685							
Category	Term	Count	%	PValue	Genes	FDR			
UP_KW_BIOLOGICAL_P ROCESS	KW-0648~Protein biosynthesis	12	3.3707865	1.423228E-05	P58252, Q8BP47, Q9DCH4, O70194, Q8C0D5, P60229, Q8K0D5, Q9JHW4, P60843, Q99KK9, Q61035, Q8JZQ9	0.00061912631			
GOTERM_CC_DIRECT	GO:0033290~eukaryotic 48S preinitiation complex	4	1.1235955	0.001130424	Q9DCH4, O70194, P60229, Q8JZQ9	0.02048892849			
GOTERM_CC_DIRECT	GO:0005852~eukaryotic translation initiation factor 3 complex	4	1.1235955	0.001376767	Q9DCH4, O70194, P60229, Q8JZQ9	0.02394009673			
GOTERM_BP_DIRECT	GO:001732~formation of cytoplasmic translation initiation complex	4	1.1235955	0.001561436	Q9DCH4, O70194, P60229, Q8JZQ9	0.19318868947			
GOTERM_CC_DIRECT	GO:0016282~eukaryotic 43S preinitiation complex	4	1.1235955	0.001654348	Q9DCH4, O70194, P60229, Q8JZQ9	0.02570147671			
Annotation Cluster 13		Enrichment Score: 2.5479359384965816							
Category	Term	Count	%	PValue	Genes	FDR			
GOTERM_MF_DIRECT	GO:0017124~SH3 domain binding	9	2.5280899	0.001030467	Q60631, Q9WU78, P29351, Q8BJJ7, Q5FWK3, Q6P549, Q8BHL5, Q8BPJ7, Q80U87	0.06192171506			
Annotation Cluster 14		Enrichment Score: 2.420377273906477							
Category	Term	Count	%	PValue	Genes	FDR			
GOTERM_CC_DIRECT	GO:0022624~proteasome accessory complex	5	1.4044944	8.13869E-05	Q99JI4, O35226, P46471, P62334, P14685	0.00208254785			
UP_KW_CELLULAR_CO MPONENT	KW-0647~Proteasome	6	1.6853933	0.001433291	Q99JI4, O35226, P46471, P54728, P62334, P14685	0.01146632984			
GOTERM_CC_DIRECT	GO:0000502~proteasome complex	6	1.6853933	0.001850621	Q99JI4, O35226, P46471, P54728, P62334, P14685	0.02775930834			
Annotation Cluster 15		Enrichment Score: 2.1450240188303296							
Category	Term	Count	%	PValue	Genes	FDR			
UP_KW_BIOLOGICAL_P ROCESS	KW-0324~Glycolysis	5	1.4044944	0.0022224592	P06745, P05063, O08528, P09411, Q9WUA3	0.03225658557			
Annotation Cluster 16		Enrichment Score: 1.7525834387892805							
Category	Term	Count	%	PValue	Genes	FDR			

UP_KW_LIGAND	KW-0274~FAD	8	2.247191	0.009548578	Q8C0I1, Q9CQF9, Q61093, Q9JMH6, Q8C7K6, P45952, Q9JH15, Q8R180	0.05412698994
UP_KW_LIGAND	KW-0285~Flavoprotein	8	2.247191	0.010825398	Q8C0I1, Q9CQF9, Q61093, Q9JMH6, Q8C7K6, P45952, Q9JH15, Q8R180	0.05412698994
Annotation Cluster 17	Enrichment Score: 1.6746771580234787					
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR017900:4Fe-4S ferredoxin, iron-sulphur binding, conserved site	3	0.8426966	0.001217217	Q9CQA3, P61222, Q8K3I1	0.09631275432
Annotation Cluster 18	Enrichment Score: 1.6476167193215445					
Category	Term	Count	%	PValue	Genes	FDR
UP_KW_BIOLOGICAL_P ROCESS	KW-0509~mRNA transport	7	1.9662921	0.003806516	Q5U4D9, Q8BL97, Q8R0G9, O70133, Q6PPDM2, P84104, Q99JX7	0.04730955162
Annotation Cluster 19	Enrichment Score: 1.5583078211177934					
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0005764~lysosome	16	4.494382	0.003315368	P08228, P57716, P23780, Q9Z0M5, P11438, P10852, Q9ESY9, P50516, P17439, P70318, Q9CQF9, P24668, P45377, Q3TCN2, Q8VEB4, P05201	0.04652210261
Annotation Cluster 20	Enrichment Score: 1.5036738713049727					
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0015629~actin cytoskeleton	11	3.0898876	0.003808661	Q9JKF1, P59999, P70248, E9Q634, O70318, P13020, P21107, Q8VDD5, O70133, Q9WTT7, Q6IRU2,	0.05177398992
Annotation Cluster 21	Enrichment Score: 1.4497999795318788					
Category	Term	Count	%	PValue	Genes	FDR
UP_KW_BIOLOGICAL_P ROCESS	KW-0249~Electron transport	11	3.0898876	1.16712E-05	Q9CQA3, O09111, Q61093, Q9CZB0, Q8K3I1, Q9CZ13, Q8R1I1, Q9DB77, Q8R180, P62897, P00397	0.00061912631
Annotation Cluster 22	Enrichment Score: 1.4168460123066215					
Category	Term	Count	%	PValue	Genes	FDR

SMART	SM00382:AAA	9	2.5280899	0.00065347	P36371, O35379, P61222, P46471, Q9WUK4, P62334, P56480, P06795, P35601	0.02701010409
INTERPRO	IPR003593:AAA+ ATPase domain	9	2.5280899	0.001224315	P36371, O35379, P61222, P46471, Q9WUK4, P62334, P56480, P06795, P35601	0.09631275432
Annotation Cluster 23		Enrichment Score: 1.2694767495088586				
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu03430:Mismatch repair	5	1.4044944	0.001455378	Q9CYR0, Q9CQ71, P37913, Q9WUK4, P35601	0.02131701364
KEGG_PATHWAY	mmu03420:Nucleotide excision repair	6	1.6853933	0.0029459	Q3U1J4, P54728, Q9CQ71, P37913, Q9WUK4, P35601	0.04075161853
UP_KW_BIOLOGICAL_PROCESS	KW-0235~DNA replication	7	1.9662921	0.004466235	Q60972, Q60973, Q9CYR0, Q9CQ71, P37913, Q9WUK4, P35601	0.0485703026
KEGG_PATHWAY	mmu03030:DNA replication	5	1.4044944	0.008247428	Q9CYR0, Q9CQ71, P37913, Q9WUK4, P35601	0.0977909279