

**Supplementary Table 11: results of the pathway analysis by the David tool on the proteins modulated in response to 10 micrometers polystyrene particles**

selection of clusters by a FDR cutoff value of 0.1

**Annotation Cluster 1** Enrichment Score: 36.65196702650441

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0098641~cadherin binding involved in cell-cell adhesion	84	7.56756756756757	3.52486769465201E-41	Q61510, Q70456, Q62448, P70460, Q9D8U8, P19096, Q9Z0P5, Q8BTM8, Q61792, Q62167, Q6PAR5, Q8CBW3, Q80U87, P42225, Q9JHJ0, O55131, Q91VX2, Q60902, P47753, Q5FWK3, P07356, P84228, Q8BH43, Q8BK64, P51432, P30999, Q62418, Q9CPV4, Q6NZJ6, Q8VDJ3, Q9QXS1, P54823, Q9DBG5, P42932, Q9CWK8, E9PVA8, O88844, Q9JLQ0, P05064, P47226, Q922Q8, P60229, Q9WVA4, Q8BVY0, Q9ERG0, Q9Z0N1, P26040, Q78PY7, P26043, Q62261, Q9JKF1, P59325, Q7TQH0, Q99K01, Q9DCL9, P42567, Q9CWXJ9, P63101, A2AGT5, Q8VDD5, Q9D8B3, O54988, P42208, Q8K298, Q2L4X1, P62259, Q80UG5, P26039, Q8R1F1, Q3UZ39, Q9CQV8, Q8CI51, P10107, Q9D8N0, Q9CZ30, Q9EQP2, P35700, P35821, Q62433, P17182, P22682, Q9WUA3, Q8CIN4, Q9D0I9	1.8364560689137E-38
GOTERM_CC_DIRECT	GO:0005913~cell-cell adherens junction	85	7.65765765765766	2.24156836315111E-40	Q61510, Q70456, Q62448, P70460, Q9D8U8, P19096, Q9Z0P5, Q8BTM8, Q61792, Q62167, Q6PAR5, Q8CBW3, Q80U87, P42225, Q9JHJ0, O55131, Q91VX2, Q60902, P47753, Q5FWK3, P07356, P84228, Q8BH43, Q8BK64, P51432, O08917, P30999, Q62418, Q9CPV4, Q6NZJ6, Q8VDJ3, Q9QXS1, P54823, Q9DBG5, P42932, Q9CWK8, E9PVA8, O88844, Q9JLQ0, P05064, P47226, Q922Q8, P60229, Q9WVA4, Q8BVY0, Q9ERG0, Q9Z0N1, P26040, Q78PY7, P26043, Q62261, Q9JKF1, P59325, Q7TQH0, Q99K01, Q9DCL9, P42567, Q9CWXJ9, P63101, A2AGT5, Q8VDD5, Q9D8B3, O54988, P42208, Q8K298, Q2L4X1, P62259, Q80UG5, P26039, Q8R1F1, Q3UZ39, Q9CQV8, Q8CI51, P10107, Q9D8N0, Q9CZ30, Q9EQP2, P35700, P35821, Q62433, P17182, P22682, Q9WUA3, Q8CIN4, Q9D0I9	3.18302707567457E-38
GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	59	5.31531531531532	1.4008902463901E-30	O70456, Q62448, P70460, Q9D8U8, Q9Z0P5, Q61792, Q6PAR5, Q8CBW3, Q80U87, P42225, Q91VX2, Q60902, P47753, Q5FWK3, P84228, Q8BH43, Q8BK64, P51432, Q62418, Q9CPV4, Q6NZJ6, Q8VDJ3, Q9QXS1, P54823, Q9DBG5, O88844, P05064, P47226, Q922Q8, P60229, Q9WVA4, Q9ERG0, Q9Z0N1, Q78PY7, P59325, Q7TQH0, Q99K01, Q9DCL9, P42567, Q9CWXJ9, P63101, A2AGT5, O54988, P42208, Q8K298, Q2L4X1, P26039, Q8R1F1, Q3UZ39, Q9CQV8, Q8CI51, Q9D8N0, Q9CZ30, Q9EQP2, P35700, Q62433, P17182, Q9WUA3, Q9D0I9	4.18305827572084E-27

**Annotation Cluster 2** Enrichment Score: 21.358089831146827

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Nucleotide-binding	183	16.4864864864865	4.36820872122404E-32	Q8K1R7, Q8CG48, Q6NZQ2, Q61316, O70133, Q62407, Q9WTP7, Q8K1J6, Q9DBL7, Q922B2, P11440, P68181, P12382, O55131, Q9EPU0, Q8BML9, Q9JLV6, P62196, Q6P9R2, P46664, Q8BU30, Q569Z6, P05213, Q9DBC7, Q9QXB9, Q03265, Q9ER72, P18654, Q02053, P84096, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q61655, Q6P9P6, Q91VR5, Q8BG51, Q2NL51, Q9R1T4, Q80X41, Q5SUR0, Q9DCL9, P61161, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, Q9QVP9, P04184, P26638, P23249, P42208, P27601, P56380, P47857, Q8CFI2, Q80UG5, Q7TSS2, Q9CZ30, P68372, Q3V1L4, P32233, Q6PA06, Q05144, Q9D2R0, Q3UDE2, P68369, O54950, P68368, Q61390, Q64261, Q04447, Q99LE6, Q8BH69, P43247, Q8CIN4, P54775, Q8BFR5, P97386, Q8C0C7, B2RQC6, Q922F4, P46471, Q61879, Q9D2Y4, Q8VE47, Q9CS42, Q62167, P63085, P61222, Q9JHR7, Q9Z1F9, Q3THS6, P46467, P05132, P41216, P49615, Q8R1Q8, Q8CFV9, Q9WV85, Q91WQ3, P97310, Q64518, P46460, P97311, Q3TRM8, Q9WTM5, O08638, Q9Z2A0, P70698, Q6NVF4, P54823, Q9JIK5, P42932, Q8R050, Q68FH4, P61750, Q8BP47, Q3UQ84, Q9Z2I9, Q9QXG4, Q91W86, Q8VCW8, Q61699, P28740, P54276, Q9Z0N1, Q91YL3, O70551, Q9R0N0, P35279, P11983, P50516, P59325, P70248, P31750, Q922D8, P62331, P49718, O54984, Q04899, Q9D6F9, Q03963, Q9QUJ7, O54988, Q8K4Z3, P62334, Q9D7H3, Q35626, P80315, P80314, Q9Z1Q9, Q9ESL4, Q9CQN1, P80313, A2BDX3, Q64737, Q61183, P97930, P51855, Q9EQP2, P62192, Q99M31, Q3THK7, Q3UM18, Q9DOR2, Q9WUA2, P84078, P35276, P51859, Q6URW6, Q9WUA3, P28867, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316, E9PVX6	2.97038193043235E-30

UP_KEYWORDS	ATP-binding	147	<p>Q8K1R7, Q8CG48, Q6NZQ2, Q61316, O70133, Q62407, Q8K1J6, Q9DBL7, Q922B2, P11440, P68181, P12382, Q9EPU0, Q8BML9, Q9JLV6, P62196, Q6P9R2, Q8BU30, Q569Z6, Q03265, Q9ER72, P18654, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q61655, Q6P9P6, Q91VR5, Q2NLS1, Q80X41, Q5SUR0, Q9DCL9, P61161, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, Q9QVP9, P04184, P26638, P23249, P47857, Q8CFI2, Q7TSS2, Q9CZ30, Q9D2R0, Q3UDE2, O54950, Q61390, Q64261, Q04447, Q99LE6, Q8BH69, P43247, Q8CIN4, P54775, P97386, Q8COC7, B2RQC6, P46471, Q61879, Q9D2Y4, Q8VE47, Q9CS42, Q62167, P63085, P61222, Q8CFV9, Q9WV85, Q91WQ3, P97310, Q64518, P46460, P97311, Q3TRM8, Q9WTM5, O08638, Q9Z2A0, P70698, Q6NVF4, P54823, Q9JIK5, P42932, Q68FH4, Q8BP47, Q3UQ84, Q9Z2I9, Q9QXG4, Q8VCW8, Q61699, P28740, P54276, Q91YL3, O70551, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, P49718, O54984, Q04899, Q03963, Q9QUJ7, O54988, P62334, Q9D7H3, P80315, P80314, Q9Z1Q9, Q9ESL4, Q9CQN1, P80313, A2BDX3, Q64737, Q61183, P97930, P51855, Q9EQP2, P62192, Q99M31, Q3THK7, Q9D0R2, Q9WUA2, Q6URW6, Q9WUA3, P28867, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316, E9PVX6</p> <p>Q8BL97, Q61316, O70133, Q62407, Q9WTP7, Q8K1J6, P11440, Q9JLV6, Q6P9R2, P46664, P05213, Q569Z6, Q9DBC7, P18654, O88569, Q8K183, O88685, P32921, Q6P9P6, Q61655, Q91VR5, Q921F4, Q80X41, Q99K48, Q9Z1D1, P61161, Q9CZD3, Q8BMJ2, P47857, P56380, Q8CFI2, Q9CZ30, P32233, P68372, Q6PA06, Q64012, Q05144, Q9D2R0, P68369, O08583, P68368, Q64261, Q8R4X3, Q99LE6, P43247, Q8CIN4, Q8BFR5, Q8COC7, B2RQC6, P46471, Q9D2Y4, Q8VE47, O35326, P63085, P61222, Q9JHR7, P46467, P05132, P41216, P49615, Q9Z204, Q64518, P97310, Q3TRM8, P46460, P97311, Q9JL8, Q9WTM5, O08638, Q9Z2A0, Q6A0A2, Q6NVF4, P54823, Q8R050, Q68FH4, Q8BP47, Q3UQ84, Q9QXG4, Q91W86, Q61699, P54276, Q9Z0N1, Q91YL3, O70551, Q9CY64, P31750, P62331, P49718, Q5SF07, O54984, Q03963, O54988, P62334, P80315, P80314, P80313, Q9Z1Q9, Q64737, Q9EQP2, Q3THK7, Q61464, Q3UM18, Q9D0R2, Q9WUA2, Q6URW6, P24547, Q9WUA3, P80318, P80317, Q8BGQ7, P80316, E9PVX6, P09405, Q8K1R7, Q8CG48, Q6NZQ2, Q9DBL7, Q922B2, P68181, P12382, O55131, Q9EPU0, P62196, Q8BU30, Q6NV83, Q9QXB9, Q03265, Q9ER72, Q02053, P84096, Q68FL6, Q9JHU4, Q8R4R6, Q9CX86, Q8BG51, Q9R1T4, Q2NLS1, Q6PFR5, Q5SUR0, Q9DCL9, Q8CGC7, Q8VDD5, Q91V92, Q9QVP9, P04184, P23249, P26638, P42208, P27601, O35309, Q80UG5, Q7TSS2, Q3V1L4, Q8BGD9, Q3UDE2, O54950, Q61390, Q04447, Q8BH69, P54775, P97386, Q922F4, Q61879, Q9CS42, Q62167, Q3THS6, Q9Z1F9, Q8R1Q8, Q8CFV9, Q9WV85, Q91WQ3, Q9CPN8, P70698, Q9JIK5, P42932, P61750, Q9Z2I9, Q8VCW8, P28740, Q9R0N0, P35279, P11983, P50516, P59325, P70248, Q922D8, Q04899, Q9D6F9, Q9QUJ7, Q8K4Z3, Q9D7H3, O35626, Q8VE97, Q9ESL4, Q9CQN1, A2BDX3, Q61183, P97930, P51855, P62192, Q99M31, P84078, P35276, P51859, P28867, Q6P542, Q9D0I9</p>	3.1181307975757E-25
GOTERM_MF_DIRECTGO:0000166~nucleotide binding		207	<p>18.6486486486487 3.37407760812277E-26</p>	1.17192962255464E-23

GOTERM_MF_DIRECTGO:0005524~ATP binding	154	13.8738738738739	2.33827200943817E-17	<p>Q8K1R7, Q8CG48, Q6NZQ2, Q61316, O70133, Q9Z0P5, Q62407, Q9WTP7, Q8K1J6, Q9DBL7, Q922B2, P11440, P68181, P12382, Q9EPU0, Q8BML9, Q9JLV6, P62196, Q6P9R2, Q8BU30, Q569Z6, Q03265, Q9ER72, P18654, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q9CXY6, Q61655, Q6P9P6, Q91VR5, Q2NL51, Q80X41, Q5SUR0, Q9DCL9, P61161, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, Q9QVP9, P04184, P26638, P23249, P62814, P47857, Q8CFI2, Q9JK91, Q7TSS2, Q9CZ30, Q9D2R0, Q3UDE2, O54950, Q61390, Q64261, Q04447, Q99LE6, Q8BH69, P43247, Q8CIN4, P54775, P97386, Q8C0C7, B2RQC6, P46471, Q61879, Q9D2Y4, Q8VE47, Q9CS42, Q62167, P63085, P61222, Q9JHR7, Q9Z1F9, Q3THS6, P46467, P05132, P41216, P49615, Q8R1Q8, Q8CFV9, Q9WV85, Q91WQ3, P97310, Q64518, P46460, P97311, Q3TRM8, Q9WVTM5, O08638, Q9Z2A0, P70698, Q6NVF4, P54823, Q9JIK5, P42932, Q68FH4, Q8BP47, Q3UQ84, Q9Z2I9, Q9QXG4, Q8VCW8, Q61699, P28740, P54276, Q91YL3, O70551, Q6P5D8, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, P49718, O54984, Q04899, Q03963, Q9QUJ7, P82343, O54988, P62334, Q9D7H3, P80315, P80314, Q9Z1Q9, Q9ESL4, Q9CQN1, P80313, A2BDX3, Q64737, Q61183, P97930, P51855, Q9EQP2, P62192, Q99M31, Q3THK7, Q9D0R2, Q9WUA2, Q6URW6, Q9WUA3, P28867, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316, E9PVX6</p> <p>P54775, Q8CG48, Q8K1R7, O70133, P46471, Q61879, Q62407, Q9DBL7, Q62167, Q9CS42, P11440, P68181, P12382, Q9EPU0, Q9JLV6, P63085, P62196, Q3THS6, Q9Z1F9, Q6P9R2, P46467, P05132, Q8R1Q8, P49615, Q569Z6, P97310, P46460, P97311, Q3TRM8, Q03265, Q9WVTM5, O08638, Q9Z2A0, P54823, P18654, Q9JIK5, Q02053, Q68FH4, Q8K183, O88685, Q9JHU4, Q8VCW8, Q6P9P6, Q61655, Q91VR5, P28740, P54276, Q91YL3, O70551, Q2NL51, Q80X41, Q9R0N0, P50516, P70248, P31750, Q5SUR0, Q922D8, P61161, P49718, Q8CGC7, Q8VDD5, Q9CZD3, O54984, Q91V92, Q03963, Q04899, Q9QVP9, O54988, P04184, P26638, P23249, P62334, P47857, Q9ESL4, Q64737, Q9CZ30, P97930, P51855, Q9EQP2, P62192, Q3THK7, Q64261, Q04447, Q6URW6, Q8BH69, Q9WUA3, P28867, P43247, Q8CIN4</p>	6.09119858458644E-15	
UP_SEQ_FEATURE nucleotide phosphate-binding region:ATP	89	8.01801801801802	8.2016632734935E-08	<p>P54775, Q8CG48, Q8K1R7, O70133, P46471, Q61879, Q62407, Q9DBL7, Q62167, Q9CS42, P11440, P68181, P12382, Q9EPU0, Q9JLV6, P63085, P62196, Q3THS6, Q9Z1F9, Q6P9R2, P46467, P05132, Q8R1Q8, P49615, Q569Z6, P97310, P46460, P97311, Q3TRM8, Q03265, Q9WVTM5, O08638, Q9Z2A0, P54823, P18654, Q9JIK5, Q02053, Q68FH4, Q8K183, O88685, Q9JHU4, Q8VCW8, Q6P9P6, Q61655, Q91VR5, P28740, P54276, Q91YL3, O70551, Q2NL51, Q80X41, Q9R0N0, P50516, P70248, P31750, Q5SUR0, Q922D8, P61161, P49718, Q8CGC7, Q8VDD5, Q9CZD3, O54984, Q91V92, Q03963, Q04899, Q9QVP9, O54988, P04184, P26638, P23249, P62334, P47857, Q9ESL4, Q64737, Q9CZ30, P97930, P51855, Q9EQP2, P62192, Q3THK7, Q64261, Q04447, Q6URW6, Q8BH69, Q9WUA3, P28867, P43247, Q8CIN4</p>	6.16765078166711E-05	
<b>Annotation Cluster 3</b> Enrichment Score: 14.342782284986528						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Protein transport	82	7.38738738738739	2.66653297424901E-22	<p>P98078, Q9D8U8, Q9DBH5, Q8BUK6, Q6P5F9, Q91YJ2, A2A5R2, O08547, P17427, P17426, Q8BKC5, Q6P8X1, Q91YE6, O35643, Q8CIE6, Q01405, O09044, P62075, Q64152, P22892, P46467, Q8R307, Q9CT10, Q9EPL8, P46460, Q8VDV3, Q9CR16, Q8BFY9, Q9CR95, Q8CI71, Q8V175, Q5DQR4, Q9CWK8, O54774, P61750, P57780, Q9QXK3, Q9D906, Q9Z1T1, Q920Q4, O70404, Q5XJY5, Q8R4R6, Q91W86, Q9ERK4, Q61655, Q9WU78, P61924, Q8C2E7, Q8BJ71, Q99MD9, P35279, P70168, Q9D662, Q8C0E2, P84091, Q64324, P42567, P62331, O35344, Q9D8B3, Q8BIJ7, Q8BPX9, P61967, Q9CWZ7, Q9EQH3, Q8R0H9, P26450, O35382, Q924C1, Q8BH60, Q9D2V7, Q3UM18, Q9QZ88, P35276, P84078, O88746, P60521, Q9CWU9, O89079, P40336, Q3UMB9</p> <p>P98078, Q9D8U8, Q9DBH5, Q8BUK6, Q6P5F9, Q91YJ2, A2A5R2, O08547, P17427, P17426, Q8BKC5, Q6P8X1, Q91YE6, O35643, Q8CIE6, Q01405, O09044, P62075, Q64152, P22892, O88531, P46467, Q8R307, Q9CT10, Q9EPL8, P46460, Q8VDV3, Q9CR16, Q8BFY9, Q9CR95, Q8CI71, Q8V175, Q5DQR4, Q9CWK8, O54774, P61750, P57780, Q9QXK3, Q9D906, Q9Z1T1, Q920Q4, O70404, Q5XJY5, Q91W86, P50396, Q9ERK4, Q61655, Q9WU78, P61924, Q8C2E7, Q8BJ71, Q99MD9, P35279, O35075, P70168, Q9D662, Q8C0E2, P84091, Q64324, P42567, P62331, Q8VDD5, O35344, Q9D8B3, Q8BIJ7, Q8BPX9, P61967, Q9CWZ7, Q9EQH3, Q8R0H9, P26450, O35382, Q924C1, Q8BH60, Q9D2V7, Q3UM18, Q9QZ88, P35276, P84078, O88746, P60521, Q9CWU9, O89079, P40336, Q3UMB9</p>	1.03613852713676E-20
GOTERM_BP_DIRECTGO:0015031~protein transport		85	7.65765765765766	9.2877597444201E-19	<p>P98078, Q9D8U8, Q9DBH5, Q8BUK6, Q6P5F9, Q91YJ2, A2A5R2, O08547, P17427, P17426, Q8BKC5, Q6P8X1, Q91YE6, O35643, Q8CIE6, Q01405, O09044, P62075, Q64152, P22892, O88531, P46467, Q8R307, Q9CT10, Q9EPL8, P46460, Q8VDV3, Q9CR16, Q8BFY9, Q9CR95, Q8CI71, Q8V175, Q5DQR4, Q9CWK8, O54774, P61750, P57780, Q9QXK3, Q9D906, Q9Z1T1, Q920Q4, O70404, Q5XJY5, Q91W86, P50396, Q9ERK4, Q61655, Q9WU78, P61924, Q8C2E7, Q8BJ71, Q99MD9, P35279, O35075, P70168, Q9D662, Q8C0E2, P84091, Q64324, P42567, P62331, Q8VDD5, O35344, Q9D8B3, Q8BIJ7, Q8BPX9, P61967, Q9CWZ7, Q9EQH3, Q8R0H9, P26450, O35382, Q924C1, Q8BH60, Q9D2V7, Q3UM18, Q9QZ88, P35276, P84078, O88746, P60521, Q9CWU9, O89079, P40336, Q3UMB9</p>	1.38666252984192E-15

Annotation Cluster	Enrichment Score: 13.097889438383417	Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006886~intracellular protein transport			44	3.96396396396396	4.48607236197578E-14	Q9ERK4, P61924, Q9D8U8, Q68FD5, P35279, O35075, P70168, Q6P5F9, Q8R5A6, P17427, Q8C0E2, Q9D662, P17426, P84091, Q8BKC5, Q6P8X1, Q9CXF4, Q91YE6, O35643, Q01405, Q8CIE6, P68510, P22892, Q8R307, P61967, P49615, Q9CWZ7, Q9EQH3, Q9EPL8, P46460, Q8R0H9, Q8BFY9, Q924C1, Q8V175, Q9QZ88, Q9CWXK8, O54774, O88746, Q9QXX3, O88447, Q9Z1T1, Q920Q4, P40336, Q91W86	3.34885301821492E-11
UP_KEYWORDS	Transport			142	12.7927927927928	5.3819453027416E-12	Q9CR68, Q8BL97, Q8BVE3, Q8BUC6, Q91YJ2, A2A5R2, O08547, Q61792, P51863, P17427, O08788, P17426, Q6P8X1, O35643, Q01405, P62075, Q64152, Q8R307, Q9CT10, Q9EPL8, Q8VDV3, Q62418, Q9ES97, Q9CR51, Q03265, Q8C171, P35922, P53811, Q8V175, Q9R0Q9, Q5DQR4, P62482, Q9QXX3, O88569, Q9D906, Q9Z1T1, Q9JHU4, O70404, Q5XJY5, Q8R4R6, Q8BTY2, Q61655, P56135, Q9CPQ8, Q8R2E9, P70168, Q8C0E2, P42567, P51807, Q8BIJ7, P56383, Q8BPX9, P62814, P61967, Q8R0H9, Q9D855, Q9CQZ6, O35382, Q8BH60, Q924C1, P31786, Q9QZ88, Q05816, O08583, P60521, Q9CWU9, O89079, Q9CQA1, P98078, P53564, Q9D8U8, Q9DBH5, Q6P5F9, Q8BKC5, Q62048, Q91YE6, Q8CIE6, Q8C0L0, O09044, P22892, Q9CQH3, P46467, Q8R1I1, Q8R1Q8, Q64518, Q9CPN8, P46460, Q9CR16, Q8BFY9, Q9CR95, Q8VDJ3, Q9CQX2, Q8R180, Q9Z1G3, Q9CQ75, Q9DBG5, Q9CWXK8, O54774, P61750, P57780, Q920Q4, Q91W86, Q9ERK4, P61924, Q9WU78, B2RXC1, Q8C2E7, Q8BJ71, P99028, Q99MD9, P35279, Q9QXX4, P50516, P31750, Q9D662, P84091, Q64324, P62331, O35344, Q5SF07, P50518, O54984, Q9D8B3, Q9WU81, Q9QYB1, Q8VBT6, Q6PB66, Q9CWZ7, Q9EQH3, P26450, Q8BMD8, Q61462, Q9D2V7, Q3UM18, Q91VD9, P84078, P35276, O88746, P62627, Q921H1, P40336, Q3UMB9	8.13271734636509E-11
GOTERM_BP_DIRECT	GO:0006810~transport			142	12.7927927927928	3.23165573553106E-08	Q9CR68, Q8BL97, Q8BVE3, Q8BUC6, Q91YJ2, A2A5R2, O08547, Q61792, P51863, P17427, O08788, P17426, Q6P8X1, O35643, Q01405, P62075, Q64152, Q8R307, Q9CT10, Q9EPL8, Q8VDV3, Q62418, Q9ES97, Q9CR51, Q03265, Q8C171, P35922, P53811, Q8V175, Q9R0Q9, Q5DQR4, P62482, Q9QXX3, O88569, Q9D906, Q9Z1T1, Q9JHU4, O70404, Q5XJY5, Q8BTY2, Q61655, P56135, Q9CPQ8, Q8R2E9, P70168, Q8C0E2, P42567, P51807, Q8BIJ7, P56383, Q8BPX9, P62814, P61967, Q8R0H9, Q9D855, Q9CQZ6, O35382, Q8BH60, Q924C1, P31786, Q9QZ88, Q05816, O08583, P60521, Q9CWU9, O89079, Q9CQA1, P98078, P53564, Q9D8U8, Q9DBH5, Q6P5F9, Q8BKC5, Q62048, Q91YE6, Q8CIE6, Q8C0L0, O09044, P22892, Q9CQH3, P46467, Q8R1I1, Q8R1Q8, Q64518, Q9CPN8, P46460, Q9CR16, Q8BFY9, Q9CR95, Q8VDJ3, Q9CQX2, Q8R180, Q9Z1G3, Q9CQ75, Q9DBG5, Q9CWXK8, O54774, P61750, P57780, Q920Q4, Q91W86, Q9ERK4, P61924, Q9WU78, B2RXC1, Q8C2E7, Q8BJ71, P99028, Q99MD9, P35279, Q9QXX4, P50516, P31750, Q9D662, P84091, Q64324, P62331, O35344, Q5SF07, P50518, O54984, Q9D8B3, Q9WU81, Q9QYB1, Q8VBT6, Q6PB66, Q9CWZ7, Q9EQH3, P26450, Q8BMD8, Q61462, Q9D2V7, Q3UM18, Q91VD9, P84078, P35276, O88746, P62627, Q921H1, P40336, Q3UMB9	6.43314935086384E-06
UP_KEYWORDS	Actin-binding			44	3.96396396396396	2.37361711784978E-15	O89053, Q7TPR4, Q9WV32, Q9ERG0, Q9QXZ0, P70460, Q3V0K9, Q61879, P26043, Q9Z0P5, Q62261, Q8BTM8, Q61792, P70248, P48193, P40124, P61161, Q9JHJ0, P21107, Q7TMB8, Q8VDD5, Q8R1S4, Q9CVB6, Q9JM76, P47753, P47754, Q8K298, Q99K51, Q8BH43, Q8VD75, O70200, Q62418, O08638, Q9WUM4, Q9D2V7, P59999, Q9QXS1, Q9JJ28, P57780, Q6URW6, Q6IRU2, Q9CQI6, O88342, P26645	4.61159897182243E-14
GOTERM_MF_DIRECT	GO:0003779~actin binding			55	4.95495495495496	6.58355266468474E-14	Q9WV32, Q9QXZ0, P70460, Q61879, Q9Z0P5, Q8BTM8, Q71LX4, Q61792, P40124, Q9JHJ0, Q7TMB8, Q9CVB6, Q9JM76, P47753, P47754, P61982, Q8R307, Q99K51, Q8BH43, O70200, Q62418, O08638, P59999, Q9QXS1, P57780, Q6IRU2, Q920Q4, O89053, Q7TPR4, Q9ERG0, P26041, P26040, Q3V0K9, P26043, Q62261, P70248, P48193, P61161, P21107, Q8VDD5, Q8R1S4, P68510, Q8K298, P26039, Q8C151, Q8VD75, Q9WUM4, Q9D2V7, P97814, P70315, Q9JJ28, Q6URW6, Q9CQI6, O88342, P26645	8.57507734575187E-12
GOTERM_MF_DIRECT	GO:0051015~actin filament binding			31	2.79279279279279	3.25432337394627E-12	O89053, Q7TPR4, Q9WV32, Q9ERG0, P26040, Q3V0K9, Q61879, Q8BTM8, Q71LX4, Q61792, P61161, Q7TMB8, Q8VDD5, Q8R1S4, Q9CVB6, Q9JM76, P47753, Q8C052, P26039, Q99K51, Q8VD75, O70200, Q62418, O08539, Q9WUM4, P59999, Q3UQ44, P57780, Q6URW6, Q920Q4, O88342	3.08273177786547E-10

Annotation Cluster 5		Enrichment Score: 10.49321123568879					
Category	Term	Count	%	PValue	Genes	FDR	
INTERPRO	IPR016040:NAD(P)-binding domain	41	3.69369369369369	1.25435870506383E-15	P50396, P23591, Q9R1T2, Q91YR9, P19096, Q9EQ06, Q9DBB8, Q9CY64, Q8VBW6, Q9DCD0, Q9CQ62, Q99L04, Q8BV14, Q8VE47, Q64105, Q62465, Q922D8, Q3ULJ0, Q8C0L6, Q8K0C9, Q00612, Q91V92, O88712, Q9Z1F9, Q8R127, Q8K2T1, Q91X52, P06801, A2BDX3, P28474, Q99KP3, Q99MZ7, P50247, Q02053, Q58NB6, Q2TPA8, Q9JHU9, P14152, Q68FL4, Q9Z2G9, Q9D906	2.2126887557326E-12	
UP_KEYWORDS	Oxidoreductase	66	5.94594594594595	2.47461187024199E-11	P23591, Q9CR68, Q91YR9, P19096, Q9JMH6, Q99L04, Q8BV14, Q9JLJ2, Q64105, Q8JZN5, Q8C0L6, Q9D7B6, P45376, P61982, P45377, Q9EPL9, Q00519, O70325, Q6PDY2, Q8R180, Q99MZ7, Q2TPA8, P62482, Q61171, O88844, O09131, Q922Q1, O08807, P99029, Q9EQ06, Q9DBB8, Q9CY64, Q9DCD0, Q8R2E9, Q9CQ62, Q62465, Q922D8, Q3ULJ0, P47738, Q9JLT4, Q00612, O88712, Q8R127, P45952, P62259, Q91X52, P21300, P06801, Q9CQV8, Q8BSY0, P28474, P24270, P51174, P68254, Q9JH6, Q99KP3, Q9D051, Q61462, P11352, P35700, Q58NB6, Q91VD9, P14152, Q9Z2G9, G3X982, P24547	3.54260225634642E-10	
UP_KEYWORDS	NADP	31	2.79279279279279	3.58954501597315E-11	P23591, Q91YR9, P19096, Q9EQ06, Q9DBB8, Q9CY64, Q9JMH6, Q9DCD0, Q9CQ62, Q8BV14, Q64105, Q922D8, Q8K0C9, Q9JLT4, Q00612, P45376, Q8K4Z3, P45377, Q8K2T1, P21300, Q91X52, P06801, P24270, Q9JH6, Q61462, Q99MZ7, Q58NB6, Q2TPA8, P62482, Q9Z2G9, O88844	4.64931544926047E-10	
GOTERM_BP_DIRECT	GO:0055114~oxidation-reduction process	73	6.57657657657658	5.73549770816044E-10	P23591, Q9CR68, Q91YR9, P19096, Q9JMH6, Q99L04, Q8BV14, Q9JLJ2, Q64105, Q8JZN5, Q8C0L6, Q9D7B6, Q8C0L0, P45376, Q9CQH3, P45377, Q9EPL9, Q8R111, Q00519, O70325, Q6PDY2, Q9CQX2, Q8R180, Q99MZ7, Q9CQ75, Q2TPA8, P62482, Q61171, O88844, O09131, Q922Q1, P50396, O08807, P99029, Q9EQ06, P99028, Q9DBB8, Q9CY64, Q9DCD0, Q8R2E9, Q9CQ62, Q62465, Q922D8, Q3ULJ0, P47738, Q9JLT4, Q00612, O88712, Q8R127, P45952, Q91X52, P21300, P06801, Q8BSY0, P28474, P24270, O70145, Q9D855, P51174, A2AAAY5, Q9CQZ6, Q9JH6, Q99KP3, Q9D051, Q61462, P11352, P35700, Q58NB6, Q91VD9, P14152, Q9Z2G9, G3X982, P24547	1.71261961565671E-07	
GOTERM_MF_DIRECT	GO:0016491~oxidoreductase activity	64	5.76576576576577	5.35062441540495E-08	P23591, Q9CR68, Q91YR9, P19096, Q9JMH6, Q99L04, Q8BV14, Q9JLJ2, Q64105, Q8JZN5, Q8C0L6, Q9D7B6, P45376, P45377, Q9EPL9, Q00519, O70325, Q6PDY2, Q8R180, Q99MZ7, Q2TPA8, P62482, Q61171, O88844, O09131, Q922Q1, P50396, O08807, P99029, Q9EQ06, Q9DBB8, Q9CY64, Q9DCD0, Q8R2E9, Q9CQ62, Q62465, Q922D8, Q3ULJ0, P47738, Q9JLT4, Q00612, O88712, Q8R127, P45952, Q91X52, P21300, P06801, Q8BSY0, P28352, P28474, P24270, P51174, Q9JH6, Q99KP3, Q9D051, Q61462, P11352, P35700, Q58NB6, Q91VD9, P14152, Q9Z2G9, G3X982, P24547	3.71690042723464E-06	
Annotation Cluster 6		Enrichment Score: 6.886068530340012					
Category	Term	Count	%	PValue	Genes	FDR	
KEGG_PATHWAY	mmu04142:Lysosome	31	2.79279279279279	3.5771768617316E-10	P31996, Q9Z0J0, Q8BVE3, Q68FD5, O70370, P51569, P18242, P51863, Q571E4, O35643, Q9QWR8, P22892, O88531, P61967, O89023, O35604, P10605, P23780, Q9Z0M5, P11438, Q61207, Q8R0H9, Q8K2I4, P17439, Q9WUU7, P70699, P12265, P17047, O54774, O89017, Q9Z1T1	2.77827402927821E-08	
UP_KEYWORDS	Lysosome	31	2.79279279279279	1.7115707245255E-07	P31996, Q9Z0J0, P28740, Q80TY0, O70370, P51569, P18242, Q571E4, Q9QWR8, Q8BPX9, O88531, Q8R307, O89023, O35604, P10605, P23780, Q9Z0M5, P11438, Q61207, Q8K2I4, P17439, Q9WUU7, P70699, P12265, P17047, Q8C1Y8, O89017, Q920Q4, Q3TCN2, O70404, Q91W86	1.79056629642667E-06	
GOTERM_CC_DIRECT	GO:0005764~lysosome	34	3.06306306306306	3.58805545411426E-05	P31996, Q9Z0J0, P28740, Q80TY0, O08529, O70370, P51569, P18242, Q571E4, Q9QWR8, Q8BPX9, O88531, Q8R307, O89023, O35604, P10605, P23780, Q9Z0M5, P11438, P24270, Q61207, Q8K2I4, P17439, Q9WUU7, P70699, P12265, P17047, Q8C1Y8, O89017, Q920Q4, Q3TCN2, O70404, P05201, Q91W86	0.000481867142708	
Annotation Cluster 7		Enrichment Score: 6.154872773091855					
Category	Term	Count	%	PValue	Genes	FDR	
GOTERM_CC_DIRECT	GO:0005832~chaperonin-containing T-complex	9	0.810810810810811	1.89254413585153E-10	P80315, P80314, P80313, P42932, Q61390, P11983, P80318, P80317, P80316	6.32332393625689E-09	

GOTERM_BP_DIRECT	GO:1904874~positive regulation of telomerase RNA localization to Cajal body	11	0.990990990990991	1.96848045735179E-10	P80315, P80314, P80313, P42932, P11983, Q9WTM5, Q9CRB2, P80318, P80317, P80316, Q9ESX5	6.53098071739161E-08	
INTERPRO	IPR027410:TCP-1-like chaperonin intermediate domain	9	0.810810810810811	7.09195088423539E-10	P80315, P80314, P80313, P42932, Q61390, P11983, P80318, P80317, P80316	2.50204027195825E-07	
INTERPRO	IPR002194:Chaperonin TCP-1, conserved site	9	0.810810810810811	7.09195088423539E-10	P80315, P80314, P80313, P42932, Q61390, P11983, P80318, P80317, P80316	2.50204027195825E-07	
INTERPRO	IPR017998:Chaperone tailless complex polypeptide 1 (TCP-1)	9	0.810810810810811	2.49673198450877E-09	P80315, P80314, P80313, P42932, Q61390, P11983, P80318, P80317, P80316	7.34039203445579E-07	
GOTERM_BP_DIRECT	GO:1904871~positive regulation of protein localization to Cajal body	8	0.720720720720721	5.36479421284757E-09	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	1.45629777450571E-06	
GOTERM_BP_DIRECT	GO:1904851~positive regulation of establishment of protein localization to telomere	8	0.720720720720721	2.31068099135559E-08	P80315, P80314, P80313, P42932, P11983, P80317, P80316, Q9ESX5	4.92835245727765E-06	
INTERPRO	IPR027409:GroEL-like apical domain	9	0.810810810810811	4.02253819094346E-08	P80315, P80314, P80313, P42932, Q61390, P11983, P80318, P80317, P80316	8.02029383393424E-06	
INTERPRO	IPR027413:GroEL-like equatorial domain	9	0.810810810810811	4.02253819094346E-08	P80315, P80314, P80313, P42932, Q61390, P11983, P80318, P80317, P80316	8.02029383393424E-06	
GOTERM_BP_DIRECT	GO:1901998~toxin transport	13	1.171171171171171	5.69235066486781E-08	P80315, P80314, P80313, P61924, P29452, Q8R0H9, P11983, P42932, Q61390, P80318, P80317, P80316, Q91W86	1.06233494283095E-05	
INTERPRO	IPR002423:Chaperonin Cpn60/TCP-1	9	0.810810810810811	8.27681832583954E-08	P80315, P80314, P80313, P42932, Q61390, P11983, P80318, P80317, P80316, Q8BYA0, P11983, Q9CR00, P61222, P62075, Q64152, P80315, P80314, Q8BK64, Q9CQN1, P80313, P61759, Q9CR16, P35564, Q8BJY1, Q99M31, Q9CQP0, P42932, O08583, Q9CYG7, Q61390, Q9CQI6, Q9QY13, P80318, P80317, Q9Z2X2, P80316	1.09360549821977E-06	
UP_KEYWORDS	Chaperone	27	2.43243243243243	1.00515211233435E-07	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	1.33292203543405E-05	
GOTERM_CC_DIRECT	GO:0002199~zona pellucida receptor complex	8	0.720720720720721	6.33607305576047E-07	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316, P80315, P80314, P80313, P03995, P26040, P11983, P35922, O55131, P42932, P51807, Q9QVP9, Q8K4Z3, P20152, O09131, Q91V12, P80318, O89110, P80317, P80316	2.1255996952692E-05	
GOTERM_CC_DIRECT	GO:0044297~cell body	19	1.71171171171171	1.04783083569608E-06	P80315, P80314, P80313, P42932, Q9JLV6, P63085, P11983, P80318, P80317, P80316, Q9ESX5	0.000292695709611	
GOTERM_BP_DIRECT	GO:0032212~positive regulation of telomere maintenance via telomerase	11	0.990990990990991	1.96045351380464E-06	P80315, P80314, P80313, P42932, Q9JLV6, P63085, P11983, P80318, P80317, P80316, Q9ESX5	0.000292695709611	
GOTERM_BP_DIRECT	GO:0006457~protein folding	21	1.89189189189189	4.57503101853134E-06	P80315, P80314, P80313, P42932, Q9CR16, P11983, P35564, Q8R180, P42932, Q8C0L0, Q61390, P24369, P80318, Q8BGQ7, P80317, P80316, P05213	0.000620956482788	
GOTERM_BP_DIRECT	GO:0007339~binding of sperm to zona pellucida	9	0.810810810810811	0.000301830177014	P80315, P80314, P80313, P42932, P11983, P80318, P80317, Q80X50, P80316	0.022531622714125	
GOTERM_MF_DIRECT	GO:0051082~unfolded protein binding	12	1.08108108108108	0.001419652321844	P80315, Q8BQM4, P80314, P80313, P42932, Q9CQN1, Q61390, P11983, P35564, P80318, P80317, P80316	0.035220898080037	
GOTERM_BP_DIRECT	GO:0050821~protein stabilization	16	1.44144144144144	0.00162735143942	P80315, P80314, P80313, P11438, Q8VD75, P26450, Q8BTM8, P11983, Q91YE6, P17047, P42932, Q80UM3, P24369, P80318, P80317, P80316	0.075926115595452	
<b>Annotation Cluster 8</b> Enrichment Score: 5.928300490483733							
Category	Term	Count	%	PValue	Genes	FDR	
UP_KEYWORDS	Proteasome	23	2.07207207207207	1.58970186093811E-16	Q9D8W5, P54775, Q3TXS7, P46471, Q9CX56, Q9JMA1, O35593, Q8VDM4, O08759, Q9WUP7, P62192, P54726, Q9CR00, P61290, Q99J14, Q6PD15, P62196, O88685, P26516, P62334, Q8R317, O35955, P97371	3.93089914704696E-15	
GOTERM_CC_DIRECT	GO:0000502~proteasome complex	25	2.25225225225225	8.70070365908302E-16	Q9D8W5, P54775, P46471, O35593, Q8VDM4, Q9WUP7, Q9CR00, P61290, Q6PD15, P62196, P26516, P62334, P97371, Q3TXS7, Q9CX56, Q9JMA1, O08759, P62192, P54726, Q99J14, Q922Y1, O88685, Q8R317, O35955, Q9Z2X2	4.94199967835915E-14	
GOTERM_CC_DIRECT	GO:0022624~proteasome accessory complex	13	1.17117117117117	4.98679353820123E-13	Q9D8W5, P54775, Q3TXS7, P46471, Q9CX56, O35593, Q8VDM4, P62192, Q8BJY1, Q99J14, P62196, O88685, P62334	2.36041560808191E-11	
GOTERM_CC_DIRECT	GO:0008540~proteasome regulatory particle, base subcomplex	11	0.990990990990991	1.18101650454771E-11	P54775, Q3TXS7, P46471, P62196, Q8VDM4, P62192, O88685, Q8BJY1, P62334, Q9CR00, Q9Z2X2	4.47211583055401E-10	
GOTERM_CC_DIRECT	GO:0031597~cytosolic proteasome complex	9	0.810810810810811	9.07346072004997E-10	P54775, Q9JHR7, P46471, P62196, O35593, Q9WUP7, P62192, O88685, P62334	2.71248720473073E-08	
KEGG_PATHWAY	mmu03050:Proteasome	16	1.44144144144144	1.32348254017374E-07	Q9D8W5, P54775, Q3TXS7, P46471, Q9CX56, O35593, Q8VDM4, P62192, P61290, Q99J14, P62196, O88685, P26516, P62334, O35955, P97371	5.13952386434136E-06	
GOTERM_CC_DIRECT	GO:0031595~nuclear proteasome complex	7	0.630630630630631	2.63289947249576E-07	Q9D8W5, P54775, P46471, P62196, P62192, O88685, P62334	5.98194760151037E-06	
INTERPRO	IPR005937:26S proteasome subunit P45	6	0.540540540540541	1.08508194662038E-06	P54775, P46471, P62196, P62192, O88685, P62334	0.000127605636923	
GOTERM_CC_DIRECT	GO:0005838~proteasome regulatory particle	7	0.630630630630631	1.82104389017393E-06	Q9D8W5, Q99J14, Q9CX56, P62196, Q8VDM4, P62192, P26516	3.336622353609E-05	
GOTERM_MF_DIRECT	GO:0036402~proteasome-activating ATPase activity	6	0.540540540540541	1.97533771913985E-06	P54775, P46471, P62196, P62192, O88685, P62334	9.80143763497011E-05	
GOTERM_BP_DIRECT	GO:0030163~protein catabolic process	11	0.990990990990991	8.02061042221958E-05	P54775, Q9D4H8, P46471, P62196, Q9JKB1, Q9D906, P18242, P62192, O88685, P62334, P31750	0.008726371327283	
GOTERM_MF_DIRECT	GO:0016887~ATPase activity	25	2.25225225225225	8.90459204778717E-05	P28740, P54276, Q9QXZ0, P56135, P46471, Q9CPQ8, Q62167, Q8VDD5, P61222, O54984, Q9JHR7, P62196, Q8R323, P46467, Q9JK91, P46460, Q9CZ30, Q9CR51, Q9WTM5, Q03265, Q99LE6, Q9JHU4, P43247, Q6P542, E9Q555	0.003225965208734	
INTERPRO	IPR003960:ATPase, AAA-type, conserved site	8	0.720720720720721	0.000152249541173	P54775, P46460, P46471, P62196, P62192, O88685, P46467, P62334	0.008952273020976	

GOTERM_BP_DIRECT	GO:0045899~positive regulation of RNA polymerase II transcriptional preinitiation	6	0.540540540540541	0.000171994786234	P54775, P46471, P62196, P62192, O88685, P62334	0.014266011991484
KEGG_PATHWAY	mmu05169:Epstein-Barr virus infection	20	1.8018018018018	0.002075155750007	Q9D8W5, P54775, Q3TXXS7, P46471, Q9CX56, P26450, P24063, Q35593, Q8VDM4, P62192, P31750, Q04207, Q99J14, Q03963, P62196, P01900, O88685, P20152, P01897, P01896, P26516, P62334	0.023024347131025
GOTERM_MF_DIRECT	GO:0017025~TBP-class protein binding	6	0.540540540540541	0.003525097357	P54775, P46471, P62196, P62192, O88685, P62334	0.072022577372438
SMART	SM00382:AAA	15	1.35135135135135	0.004955447364589	P54775, P46471, P46460, Q9WTM5, P62192, P61222, P62196, O88685, Q8R323, Q99LE6, P46467, Q9JHU4, P62334, Q6P542, E9Q555	0.088888337102314

**Annotation Cluster 9** Enrichment Score: 5.862162759669797

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006413~translational initiation	19	1.71171171171171	4.64328172582524E-11	Q62448, Q99JX4, Q9Z0N1, Q99LC8, Q9DCH4, O70194, Q9Z1D1, Q6NZJ6, P59325, Q8R1B4, Q62167, Q8BGD9, P61222, Q61749, P23116, Q8QZY1, P60229, Q80XI3, Q6P542	1.98069131904488E-08
UP_KEYWORDS	Initiation factor	17	1.53153153153153	5.03071021986964E-09	Q62448, Q99JX4, Q9Z0N1, Q99LC8, Q9DCH4, O70194, Q9Z1D1, Q6NZJ6, P59325, Q8R1B4, Q8BGD9, Q03963, Q61749, P23116, Q8QZY1, P60229, Q80XI3	5.9493616513241E-08
GOTERM_CC_DIRECT	GO:0005852~eukaryotic translation initiation factor 3 complex	10	0.900900090090091	8.62920920391487E-09	Q99JX4, P61222, Q9DCH4, O70194, P23116, Q9Z1D1, Q8QZY1, Q8R1B4, P60229, Q62167	2.45069541391182E-07
GOTERM_BP_DIRECT	GO:0001731~formation of translation preinitiation complex	11	0.990990990990991	1.36240673234538E-07	Q99JX4, Q9Z0N1, Q9DCH4, O70194, P23116, Q9Z1D1, Q8QZY1, Q8R1B4, P59325, P60229, Q8BGD9	2.39302735457842E-05
GOTERM_MF_DIRECT	GO:0003743~translation initiation factor activity	17	1.53153153153153	2.25447904681005E-07	Q62448, Q99JX4, Q9Z0N1, Q99LC8, Q9DCH4, O70194, Q9Z1D1, Q6NZJ6, P59325, Q8R1B4, Q8BGD9, Q03963, Q61749, P23116, Q8QZY1, P60229, Q80XI3	1.3234809468025E-05
GOTERM_BP_DIRECT	GO:0006446~regulation of translational initiation	12	1.08108108108108	2.8505330772724E-07	Q62448, Q99JX4, Q99LC8, Q9DCH4, O70194, P23116, Q9Z1D1, Q6NZJ6, Q8QZY1, Q8R1B4, P59325, P60229	4.72871764929744E-05
SMART	SM00088:PINT	8	0.720720720720721	1.58249338600579E-06	Q9D8W5, Q99J14, Q99JX4, O88544, P23116, P61202, Q8R1B4, P60229	0.000227087800892
UP_SEQ_FEATURE	domain:PCI	9	0.810810810810811	2.11992723040014E-06	Q9D8W5, Q8VVBV7, Q99J14, Q99JX4, O88544, P23116, P61202, Q8R1B4, P60229	0.000863203839619
GOTERM_CC_DIRECT	GO:0016282~eukaryotic 43S preinitiation complex	8	0.720720720720721	2.18798111817962E-06	Q99JX4, Q9DCH4, O70194, P23116, Q9Z1D1, Q8QZY1, Q8R1B4, P60229	3.76597962159401E-05
GOTERM_CC_DIRECT	GO:0033290~eukaryotic 48S preinitiation complex	8	0.720720720720721	2.18798111817962E-06	Q99JX4, Q9DCH4, O70194, P23116, Q9Z1D1, Q8QZY1, Q8R1B4, P60229	3.76597962159401E-05
INTERPRO	IPR000717:Proteasome component (PCI) domain	8	0.720720720720721	3.03676906612939E-06	Q9D8W5, Q99J14, Q99JX4, O88544, P23116, P61202, Q8R1B4, P60229	0.000297603368481
KEGG_PATHWAY	mmu03013:RNA transport	29	2.61261261261261	9.89214346656791E-06	Q62448, Q9Z0N1, Q8BJ71, O70194, Q9DCH4, Q8K1J6, Q9Z1D1, Q35691, P59325, P70168, Q6P5F9, Q80UU2, Q80Y81, Q9EPU0, Q7TMB8, Q80XI3, Q99LC8, Q6NZJ6, Q924C1, Q8R1B4, P35922, Q61584, Q8BGD9, O08583, Q61749, P23116, Q9CWU9, P60229, Q8R4R6	0.000209533584337
GOTERM_CC_DIRECT	GO:0071541~eukaryotic translation initiation factor 3 complex, eIF3m	5	0.450450450450451	0.000284157130072	Q99JX4, Q9DCH4, O70194, P23116, Q8R1B4	0.0028316008751
GOTERM_BP_DIRECT	GO:0075525~viral translational termination-reinitiation	4	0.36036036036036	0.001113761157637	O70194, P23116, Q9Z1D1, Q8QZY1	0.056954799581534

**Annotation Cluster 10** Enrichment Score: 5.516385413965608

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Aminoacyl-tRNA synthetase	19	1.71171171171171	1.73901419252907E-15	P32921, Q9Z1Q9, Q91WQ3, Q8C0C7, Q922B2, Q9ER72, Q9D0R2, Q68FL6, Q8CGC7, Q9WUA2, Q8BML9, Q8BP47, Q9CZD3, Q3UQ84, Q8BMJ2, P26638, Q8BU30, Q8BGQ7, Q9D0I9	3.63855277206082E-14
GOTERM_MF_DIRECT	GO:0004812~aminoacyl-tRNA ligase activity	18	1.62162162162162	1.66136066159981E-12	P32921, Q9Z1Q9, Q91WQ3, Q8C0C7, Q922B2, Q9ER72, Q9D0R2, Q68FL6, Q8CGC7, Q9WUA2, Q8BP47, Q9CZD3, Q3UQ84, Q8BMJ2, P26638, Q8BU30, Q8BGQ7, Q9D0I9	1.731137809387E-10
GOTERM_BP_DIRECT	GO:0006418~tRNA aminoacylation for protein translation	17	1.53153153153153	3.16171994008566E-12	P32921, Q9Z1Q9, Q91WQ3, P31230, Q922B2, Q9ER72, Q9D0R2, Q68FL6, Q8CGC7, Q8BML9, Q8BP47, Q9CZD3, Q3UQ84, Q8BMJ2, P26638, Q8BU30, Q9D0I9	1.88817914821916E-09
UP_KEYWORDS	Ligase	44	3.96396396396396	3.02863383174092E-11	P32921, Q61510, Q8VCW8, P97386, Q9R1T2, B2RQC6, Q8C0C7, Q922B2, A2AN08, Q5SURO, Q9DCL9, Q922D8, Q80V11, Q8CGC7, Q8BML9, Q9CZD3, Q8BMJ2, Q9Z1F9, Q9QUJ7, P26638, P46664, Q8BU30, Q9D7H3, P41216, Q9Z1Q9, Q91WQ3, Q64737, P51855, Q9ER72, Q3THK7, P70698, Q9D2R0, Q9D0R2, Q02053, Q68FL6, Q9WUA2, Q8BP47, Q9Z2I9, Q3UQ84, P22682, Q9QXG4, Q8BGQ7, Q9D0I9, E9Q555	4.11894201116765E-10

GOTERM_MF_DIRECT	GO:0016874~ligase activity	44	3.96396396396396	2.2862434781617E-07	P32921, Q61510, Q8VCW8, P97386, Q9R1T2, B2RQC6, Q8C0C7, Q922B2, A2AN08, Q5SURO, Q9DCL9, Q922D8, Q80V11, Q8CGC7, Q9CZD3, Q8BMJ2, Q9Z1F9, Q9QUJ7, P26638, P46664, Q8BU30, Q9D7H3, P41216, Q9Z1Q9, Q91WQ3, Q64737, P51855, O08759, Q9ER72, Q3THK7, P70698, Q9D2R0, Q9D0R2, Q02053, Q68FL6, Q9WUA2, Q8BP47, Q9Z219, Q3UQ84, P22682, Q9QXG4, Q8BGQ7, Q9D019, E9Q555	1.3234809468025E-05
KEGG_PATHWAY	mmu00970:Aminoacyl-tRNA biosynthesis	19	1.71171171171171	2.36684164511744E-07	P32921, Q9Z1Q9, Q91WQ3, Q8C0C7, Q922B2, Q9ER72, Q9D0R2, Q68FL6, Q8CGC7, Q9WUA2, Q8BML9, Q8BP47, Q9CZD3, Q3UQ84, Q8BMJ2, P26638, Q8BU30, Q8BGQ7, Q9D019	7.15715659737465E-06
UP_SEQ_FEATURE	short sequence motif:"HIGH" region	9	0.810810810810811	7.47593021619084E-07	P32921, Q68FL6, Q9Z1Q9, Q8CGC7, Q91WQ3, Q8BMJ2, Q8BU30, Q9ER72, Q9D019	0.000421642464193
INTERPRO	IPR001412:Aminoacyl-tRNA synthetase, class I, conserved site	8	0.720720720720721	1.7777251287985E-06	P32921, Q68FL6, Q9Z1Q9, Q8CGC7, Q8BML9, Q8BMJ2, Q8BU30, Q9D019	0.00019599419545
INTERPRO	IPR014729:Rossmann-like alpha/beta/alpha sandwich fold	12	1.08108108108108	2.98580226292338E-06	P32921, Q68FL6, Q9Z1Q9, Q8CGC7, Q8BML9, Q91WQ3, Q8BMJ2, Q9DBL7, Q8BU30, Q3THK7, Q9ER72, Q9D019	0.000297603368481
UP_SEQ_FEATURE	short sequence motif:"KMSKS" region	8	0.720720720720721	4.09207350095125E-06	P32921, Q68FL6, Q9Z1Q9, Q8CGC7, Q91WQ3, Q8BMJ2, Q8BU30, Q9ER72	0.001153964727268
INTERPRO	IPR009080:Aminoacyl-tRNA synthetase, class 1a, anticodon-binding	6	0.540540540540541	0.00017829883479	Q68FL6, Q9Z1Q9, Q8BMJ2, Q8BU30, Q9ER72, Q9D019	0.010145778857104
SMART	SM00991:SM00991	4	0.36036036036036	0.001594134357824	P32921, Q68FL6, Q8CGC7, Q9CZD3	0.041592414608683
INTERPRO	IPR000738:WHEP-TRS	4	0.36036036036036	0.001667151763658	P32921, Q68FL6, Q8CGC7, Q9CZD3	0.061267827314441
INTERPRO	IPR009068:S15/NS1, RNA-binding	4	0.36036036036036	0.002819479396033	P32921, Q68FL6, Q8CGC7, Q9CZD3	0.088813600975053

**Annotation Cluster 11** Enrichment Score: 5.4399320655692565

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Mitochondrion	87	7.83783783783784	1.7054420395373E-09	Q9CR68, Q8BFR5, Q9CXW2, Q99KB8, Q9DCB8, Q8BK72, Q9WTP7, Q8K1J6, Q9ER88, Q9DBL7, Q80Y81, Q62167, P11440, Q8JZN5, Q9D7B6, Q8BMP6, P61222, Q9CRB9, P62075, Q3TIU4, Q8BGH2, Q9CQH3, P05132, P41216, Q8R1I1, Q9CR59, O70325, Q9CPV4, Q03265, Q9JIK9, Q8CG72, Q9CQX2, Q8BMF4, Q02053, Q9CQ75, Q07813, Q9Z219, Q9CYG7, Q3UQ84, Q922Q1, Q8BP40, Q8VCW8, Q8K411, Q8BKZ9, Q8BG51, P56135, P99029, Q9D0G0, P99028, Q9CPQ8, Q9CQ62, Q9QXX4, Q9CPQ1, Q62465, P47738, Q9JLT4, Q9CZD3, Q9QYR9, Q9QUJ7, Q9EPB4, Q8K4Z3, P56383, Q924T2, Q9JIM9, P45952, Q8R404, Q9QYB1, P62908, Q6PB66, Q9CQN1, Q9CQR4, P28352, Q9D855, Q9D338, P51174, Q14C51, Q9CQZ6, Q91VM9, Q8BMD8, Q9D172, Q9D051, P39749, O35459, Q91VD9, Q9DC61, Q9JK81, Q9JIY5, Q8K411, Q8VCW8, Q9CR68, Q8BFR5, Q8BKZ9, Q9DCB8, P99029, Q99KB8, P99028, Q9CQ62, Q9ER88, Q8K1J6, Q80Y81, Q8JZN5, P47738, Q9D7B6, Q9JLT4, Q9QYR9, Q3TIU4, Q8K4Z3, P56383, Q9CQH3, P45952, Q6PB66, O70325, Q9CQN1, Q9D338, P51174, Q14C51, Q03265, Q91VM9, Q9D172, Q9D051, Q8CG72, Q8BMF4, O35459, Q91VD9, Q9Z219, Q3UQ84, Q9DC61, Q922Q1, Q9JK81, Q9JIY5, Q8BP40	2.10854652160976E-08
UP_KEYWORDS	Transit peptide	44	3.96396396396396	8.97848803963553E-06	Q922Q1, Q9JK81, Q9JIY5, Q8BP40	6.97756784794533E-05

**Annotation Cluster 12** Enrichment Score: 4.591898595765302

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Endosome	39	3.51351351351351	2.04434432678435E-05	P31996, Q8C2E7, Q9D8U8, Q6R5N8, P97369, Q91YJ2, A2A5R2, Q8C0E2, Q6PAR5, Q80U87, P42567, Q6P8X1, P62331, Q80TM9, Q6PDI5, Q9D8B3, Q8BIJ7, P46467, Q8R307, O35604, Q9EQH3, P11438, O08917, Q8R0H9, P10107, Q62418, Q8CI71, Q9EQP2, Q9DBG5, Q9QZ88, P17047, Q9CWK8, Q920Q4, O70404, P40336, Q8BL66, Q810B6, Q3UMB9, Q91W86, Q89053, Q8C2E7, P51863, Q8C0E2, Q80U87, P42567, P62331, Q80TM9, Q6PDI5, P63085, Q8R307, P07356, Q0P5W1, Q8BH43, Q9EQH3, O08917, Q62418, P35821, O88746, Q920Q4, Q921H1, O70404, P40336, Q8BL66, Q810B6, Q3UMB9, Q91W86	0.000129316664392
GOTERM_CC_DIRECT	GO:0005769~early endosome	27	2.43243243243243	2.13984843585888E-05	P31996, Q8C2E7, Q9D8U8, P26040, Q6R5N8, P97369, O35075, Q91YJ2, A2A5R2, Q8C0E2, Q6PAR5, Q80U87, P42567, Q6P8X1, P62331, Q80TM9, Q6PDI5, P50518, Q9CVB6, Q9D8B3, Q8BIJ7, P46467, Q8R307, P07356, O35604, Q9EQH3, P11438, O08917, Q8R0H9, P10107, Q62418, Q8CI71, O35382, Q9EQP2, Q61462, Q9DBG5, Q9QZ88, P17047, Q9CWK8, O88746, Q920Q4, Q921H1, O70404, P40336, Q8BL66, Q810B6, Q3UMB9, Q91W86	0.000296447295504
GOTERM_CC_DIRECT	GO:0005768~endosome	48	4.32432432432432	3.83148521192644E-05	P31996, Q8C2E7, Q9D8U8, P26040, Q6R5N8, P97369, O35075, Q91YJ2, A2A5R2, Q8C0E2, Q6PAR5, Q80U87, P42567, Q6P8X1, P62331, Q80TM9, Q6PDI5, P50518, Q9CVB6, Q9D8B3, Q8BIJ7, P46467, Q8R307, P07356, O35604, Q9EQH3, P11438, O08917, Q8R0H9, P10107, Q62418, Q8CI71, O35382, Q9EQP2, Q61462, Q9DBG5, Q9QZ88, P17047, Q9CWK8, O88746, Q920Q4, Q921H1, O70404, P40336, Q8BL66, Q810B6, Q3UMB9, Q91W86	0.000494609909176

**Annotation Cluster 13** Enrichment Score: 4.5379866480997535

Category	Term	Count	%	PValue	Genes	FDR
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UP_KEYWORDS	Purine biosynthesis	9	0.810810810811	9.04194337092221E-09	Q9CWJ9, Q64737, P24547, P46664, Q3THK7, Q5SUR0, P54822, Q922D8, Q9DCL9	1.02475358203785E-07
GOTERM_BP_DIRECT	GO:0006164~purine nucleotide biosynthetic process	9	0.810810810811	2.54041640730269E-06	Q9CWJ9, Q64737, P24547, P46664, Q3THK7, Q5SUR0, P54822, Q922D8, Q9DCL9	0.000361223018676
GOTERM_BP_DIRECT	GO:0006189~de novo IMP biosynthetic process	5	0.450450450450451	8.18279963710402E-05	Q9CWJ9, Q64737, Q5SUR0, P54822, Q9DCL9	0.008726371327283
KEGG_PATHWAY	mmu00670:One carbon pool by folate	3	0.27027027027027	0.374959877517886	Q9CWJ9, Q64737, Q922D8	0.873851301163352

**Annotation Cluster 14** Enrichment Score: 4.4212248408739425

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0004177~aminopeptidase activity	11	0.990990990990991	6.49437965581029E-07	Q64514, Q99KK7, Q11136, Q6P1B1, P24527, Q8BP48, Q6NSR8, Q8R016, P97449, Q9Z2W0, Q11011	3.38357180067716E-05
UP_KEYWORDS	Aminopeptidase	8	0.720720720720721	3.82651438477593E-05	Q64514, Q99KK7, Q6P1B1, Q8BP48, Q6NSR8, P97449, Q9Z2W0, Q11011	0.000216835815137
GOTERM_MF_DIRECT	GO:0070006~metalloaminopeptidase activity	6	0.540540540540541	0.002192726441027	Q6P1B1, P24527, Q8BP48, P97449, Q9Z2W0, Q11011	0.048613211735107

**Annotation Cluster 15** Enrichment Score: 4.3335477887930995

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Protease	47	4.23423423423423	3.75811255452679E-06	Q8K411, Q11136, Q6P1B1, P29452, P56399, Q9JKB1, Q8K2H2, O35593, Q9DCH4, P34960, O08529, O70370, Q9WUP7, P18242, P97449, Q8C0M9, Q99K23, P61290, Q80U87, Q9QUR6, Q9JHR7, P62196, Q8CDG3, Q9Z2W0, Q89001, O89023, Q64514, P10605, Q9JMA1, Q6NSR8, Q80W54, Q920A5, P35123, Q9WUU7, P70677, P46737, Q99KK7, P24527, Q8BP48, O89017, Q9DC61, Q8R016, Q9JIY5, Q9D1A2, Q11011, O89110, O35955	3.29744069300415E-05
UP_KEYWORDS	Thiol protease	19	1.71171171171171	1.09437261345234E-05	P10605, P29452, Q9JMA1, P56399, Q9JKB1, Q9DCH4, Q8K2H2, O08529, O70370, Q9WUP7, P35123, Q9WUU7, P70677, Q99K23, Q80U87, O89017, Q8CDG3, Q8R016, O89110	8.26859307941771E-05
GOTERM_MF_DIRECT	GO:0008233~peptidase activity	48	4.32432432432432	8.97821411259852E-05	Q8K411, Q11136, Q6P1B1, P29452, P56399, Q9JKB1, Q8K2H2, O35593, Q9DCH4, P34960, O08529, O70370, Q9WUP7, P18242, P97449, Q8C0M9, Q99K23, P61290, Q80U87, Q9QUR6, Q9JHR7, P62196, Q8CDG3, Q9Z2W0, O89001, O89023, Q64514, P10605, P57716, Q9JMA1, Q6NSR8, Q80W54, Q920A5, P35123, Q9WUU7, P70677, P46737, Q99KK7, P24527, Q8BP48, O89017, Q9DC61, Q8R016, Q9JIY5, Q9D1A2, Q11011, O89110, O35955	0.003225965208734
GOTERM_BP_DIRECT	GO:0006508~proteolysis	50	4.50450450450451	0.00019036618432	Q11136, Q6P1B1, P29452, P56399, Q8K2H2, P34960, O70370, P18242, Q99K23, Q80U87, Q9JHR7, O88456, Q8CDG3, O89023, Q64514, P10605, Q9CX56, Q920A5, P35123, P46737, P24527, Q8BP48, O89017, Q8R016, Q9D1A2, O35955, Q8K411, Q99JW2, Q9JKB1, O35593, Q9DCH4, O08529, Q9WUP7, P97449, Q8C0M9, Q9QUR6, Q9Z2W0, O89001, Q9JMA1, Q6NSR8, Q80W54, Q9WUU7, P70677, Q99KK7, Q9DC61, P22682, Q9JIY5, Q11011, O89110, Q6P069	0.015363065577851
GOTERM_MF_DIRECT	GO:0008234~cysteine-type peptidase activity	19	1.71171171171171	0.000305735798736	P10605, P29452, Q9JMA1, P56399, Q9JKB1, Q9DCH4, Q8K2H2, O08529, O70370, Q9WUP7, P35123, Q9WUU7, P70677, Q99K23, Q80U87, O89017, Q8CDG3, Q8R016, O89110	0.009653839463129

**Annotation Cluster 16** Enrichment Score: 4.312562776801149

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0016192~vesicle-mediated transport	37	3.33333333333333	8.36532246930984E-11	B2RXC1, P61924, Q80TY0, Q68FD5, P35279, A2A5R2, O08547, P17427, Q9D662, P17426, P84091, Q64324, P62331, O35643, Q01405, Q8CIE6, Q09044, P22892, Q8R307, P61967, Q9CWZ7, P46460, Q8R0H9, Q9ES97, Q5DQR4, Q58A65, O54774, P84078, P61750, Q9QXK3, Q8C1Y8, Q9Z1T1, O89079, O70404, Q9CQA1, Q5XJY5, Q91W86	3.1223566116699E-08
UP_KEYWORDS	ER-Golgi transport	16	1.44144144144144	3.06326973872796E-06	Q9CWZ7, B2RXC1, P61924, Q9ES97, P35279, O08547, Q9D662, P62331, Q01405, Q8CIE6, P84078, P61750, Q9QXK3, O89079, Q9CQA1, Q5XJY5	2.87313575494485E-05

**Annotation Cluster 17** Enrichment Score: 4.142697057063472

Category	Term	Count	%	PValue	Genes	FDR
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UP_KEYWORDS	Cell cycle	55	4.95495495495496	3.22710574271764E-07	Q64701, Q8CG48, Q8K1R7, P97386, Q8VBW6, A2A432, Q9Z0H3, P11440, Q80U87, O55131, Q9Z0Y1, P63085, Q1HFZ0, Q60749, P46467, Q8R1Q8, P49615, Q9CR59, P97310, P97311, Q9D2X5, P18654, Q8VE37, P46737, Q9JLQ0, Q9WVA3, Q6P9P6, Q9WU78, P28740, Q8BFT2, Q8R3C0, Q9R1T4, Q99MD9, Q80X41, Q68FD5, P61290, P62331, A2AGT5, P49718, P51807, Q8K2Z4, P42208, Q8K298, P62137, Q8CFI2, Q80UG5, Q9JK91, P62908, P27661, Q9ESL4, Q64261, Q9CWU9, P28867, P43247, E9PVX6	3.25101022970073E-06
UP_KEYWORDS	Cell division	35	3.15315315315315	1.50374181937327E-05	Q8CG48, Q6P9P6, Q8K1R7, Q9WU78, P97386, P28740, Q8BFT2, Q9R1T4, Q8R3C0, Q80X41, Q68FD5, P11440, P62331, P49718, O55131, A2AGT5, Q9Z0Y1, P51807, Q8K2Z4, Q1HFZ0, P46467, P42208, Q8K298, P62137, Q8R1Q8, P49615, Q80UG5, P62908, Q9D2X5, Q8VE37, P46737, Q9JLQ0, Q64261, Q9CWU9, Q9WVA3	0.000102254443717
GOTERM_BP_DIRECT	GO:0007049~cell cycle	53	4.77477477477478	0.000105714741287	Q64701, Q8CG48, Q8K1R7, P97386, Q8VBW6, A2A432, Q9Z0H3, P11440, Q80U87, O55131, Q9Z0Y1, P63085, Q1HFZ0, Q60749, P46467, Q8R1Q8, P49615, Q9CR59, P97310, P97311, Q9D2X5, P18654, Q8VE37, P46737, Q9JLQ0, Q9WVA3, Q6P9P6, Q9WU78, P28740, Q8BFT2, Q8R3C0, Q9R1T4, Q99MD9, Q80X41, P61290, P62331, A2AGT5, P49718, Q8K2Z4, P42208, Q8K298, P62137, Q8CFI2, Q80UG5, Q9JK91, P62908, P27661, Q9ESL4, Q64261, Q9CWU9, P28867, P43247, E9PVX6	0.010522140582803
UP_KEYWORDS	Mitosis	25	2.25225225225225	0.000211061239273	Q8CG48, Q6P9P6, Q8K1R7, P28740, Q8BFT2, Q8R3C0, Q80X41, Q68FD5, P11440, O55131, A2AGT5, Q9Z0Y1, P51807, Q8K2Z4, Q1HFZ0, P42208, Q8K298, Q8R1Q8, P62908, Q9D2X5, Q8VE37, P46737, Q9JLQ0, Q9CWU9, Q9WVA3	0.0010631232793
GOTERM_BP_DIRECT	GO:0051301~cell division	35	3.15315315315315	0.00046749781889	Q8CG48, Q6P9P6, Q8K1R7, Q9WU78, P97386, P28740, Q8BFT2, Q9R1T4, Q8R3C0, Q80X41, P11440, P62331, P49718, O55131, A2AGT5, Q9Z0Y1, P51807, Q8K2Z4, Q1HFZ0, P46467, P42208, P27546, Q8K298, P62137, Q8R1Q8, P49615, Q80UG5, P62908, Q9D2X5, Q8VE37, P46737, Q9JLQ0, Q64261, Q9CWU9, Q9WVA3	0.030346706243628

**Annotation Cluster 18** Enrichment Score: 4.016622417706746

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Glucose metabolism	8	0.720720720720721	2.02764448075805E-05	Q7TSV4, Q00612, P31230, Q9D051, Q8BMF4, Q9D0F9, P31750, Q91X52	0.000129316664392
UP_KEYWORDS	Carbohydrate metabolism	15	1.35135135135135	2.48817117597745E-05	Q7TSV4, Q2NL51, P31230, Q9R0N0, Q9D051, Q8BMF4, P31750, Q88958, Q00612, Q8VHI3, Q8CHP8, Q9CYR6, Q9D0F9, P62137, Q91X52	0.000150396124415
GOTERM_BP_DIRECT	GO:0006006~glucose metabolic process	11	0.990990990990991	0.001767098191091	Q05816, Q80TM9, Q7TSV4, Q00612, P26450, P31230, Q9D051, Q8BMF4, Q9D0F9, P31750, Q91X52	0.079947806039344

**Annotation Cluster 19** Enrichment Score: 3.9003086258494895

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0030117~membrane coat	12	1.08108108108108	5.22452704307475E-08	O35643, Q8CIE6, P61924, O54774, Q9QXK3, Q9D8B3, Q68FD5, Q9Z1T1, P22892, P61967, P17427, P17426	1.29023102628977E-06
INTERPRO	IPR002553:Clathrin/coatomer adaptor, adaptin-like, N-terminal	7	0.630630630630631	1.85659747086415E-05	O35643, O54774, Q9QXK3, Q9Z1T1, P22892, P17427, P17426	0.001364599141085
INTERPRO	IPR013041:Coatomer/clathrin adaptor appendage, Ig-like subdomain	6	0.540540540540541	0.000113965444189	O35643, Q8R0H9, Q9QXK3, P22892, P17427, P17426	0.007732117059583
GOTERM_CC_DIRECT	GO:0030131~clathrin adaptor complex	7	0.630630630630631	0.000163702888487	O35643, Q8R0H9, Q9Z1T1, P22892, P17427, P17426, P84091	0.001788139243478
SMART	SM00809:Alpha_adaptinC2	5	0.450450450450451	0.000411624976949	O35643, Q8R0H9, P22892, P17427, P17426	0.016876624054891
INTERPRO	IPR008152:Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdo	5	0.450450450450451	0.000437426883655	O35643, Q8R0H9, P22892, P17427, P17426	0.020946575222027
INTERPRO	IPR009028:Coatomer/calthrin adaptor appendage, C-terminal subdomain	4	0.36036036036036	0.001667151763658	O35643, Q9QXK3, P17427, P17426	0.061267827314441

**Annotation Cluster 20** Enrichment Score: 3.8728156493750774

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0008641~small protein activating enzyme activity	7	0.630630630630631	3.07051586663889E-06	Q9R1T2, A2BDX3, Q9Z1F9, Q8VBW6, Q9D906, Q8VE47, Q02053	0.000145430796956
INTERPRO	IPR000594:UBA/THIF-type NAD/FAD binding fold	7	0.630630630630631	3.21198601620739E-06	Q9R1T2, A2BDX3, Q9Z1F9, Q8VBW6, Q9D906, Q8VE47, Q02053	0.000298207543821

**Annotation Cluster 21** Enrichment Score: 3.678891887676058

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Annexin	7	0.630630630630631	3.71904057239333E-06	Q07076, P48036, P10107, P14824, P07356, O35639, P97429	3.29744069300415E-05
SMART	SM00335:ANX	7	0.630630630630631	5.60249692754415E-06	Q07076, P48036, P10107, P14824, P07356, O35639, P97429	0.000401979154551
INTERPRO	IPR001464:Annexin	7	0.630630630630631	6.17731125444524E-06	Q07076, P48036, P10107, P14824, P07356, O35639, P97429	0.000473772915341
INTERPRO	IPR018252:Annexin repeat, conserved site	7	0.630630630630631	6.17731125444524E-06	Q07076, P48036, P10107, P14824, P07356, O35639, P97429	0.000473772915341
INTERPRO	IPR018502:Annexin repeat	7	0.630630630630631	6.17731125444524E-06	Q07076, P48036, P10107, P14824, P07356, O35639, P97429	0.000473772915341

UP_KEYWORDS	Calcium/phospholipid-binding	7	0.630630630630631	6.66400442171409E-06	Q07076, P48036, P10107, P14824, P07356, O35639, P97429	5.49275515971586E-05
UP_SEQ_FEATURE	repeat:Annexin 1	7	0.630630630630631	3.77379786689777E-05	Q07076, P48036, P10107, P14824, P07356, O35639, P97429	0.004683203784201
UP_SEQ_FEATURE	repeat:Annexin 2	7	0.630630630630631	3.77379786689777E-05	Q07076, P48036, P10107, P14824, P07356, O35639, P97429	0.004683203784201
UP_SEQ_FEATURE	repeat:Annexin 3	7	0.630630630630631	3.77379786689777E-05	Q07076, P48036, P10107, P14824, P07356, O35639, P97429	0.004683203784201
UP_SEQ_FEATURE	repeat:Annexin 4	7	0.630630630630631	3.77379786689777E-05	Q07076, P48036, P10107, P14824, P07356, O35639, P97429	0.004683203784201

**Annotation Cluster 22** Enrichment Score: 3.3251549543423433

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Endocytosis	17	1.53153153153153	2.95666509726667E-05	P98078, Q9D8U8, Q8VD75, Q80TY0, Q62418, Q9Z0R6, Q9CR95, O08539, P17427, P97814, P17426, P84091, Q6PAR5, P42567, Q8BIJ7, Q60902, Q810B6	0.000174828892708
GOTERM_CC_DIRECT	GO:0005905~clathrin-coated pit	11	0.990990990990991	0.000422364254585	P42567, P98078, Q80TY0, Q9CR95, Q60902, Q68FD5, P61967, Q92111, P17427, P17426, P84091	0.004054201823124
UP_KEYWORDS	Coated pit	9	0.810810810810811	0.000841767965852	P42567, P98078, Q80TY0, Q60902, Q68FD5, P61967, P17427, P17426, P84091	0.003634299789073
GOTERM_CC_DIRECT	GO:0030132~clathrin coat of coated pit	4	0.36036036036036	0.004761003467172	P42567, P98078, Q60902, Q68FD5	0.030730113288108

**Annotation Cluster 23** Enrichment Score: 3.180019520584447

Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR001494:Importin-beta, N-terminal	9	0.810810810810811	2.88314766872362E-07	Q91YE6, Q9ERK4, Q9EPL8, Q8BFY9, Q924C1, P70168, Q6P5F9, Q8VI75, Q8BKC5	3.91220960586805E-05
SMART	SM00913:SM00913	8	0.720720720720721	2.70559181227696E-06	Q91YE6, Q9ERK4, Q9EPL8, Q8BFY9, Q924C1, P70168, Q6P5F9, Q8VI75	0.000258834950041
GOTERM_MF_DIRECT	GO:0008536~Ran GTPase binding	11	0.990990990990991	3.6275073811628E-06	Q91YE6, Q9ERK4, Q9CT10, Q9EPL8, Q8BFY9, Q924C1, P70168, Q6P5F9, Q6VN19, Q8VI75, Q8BKC5	0.000164341856138
UP_SEQ_FEATURE	domain:Importin N-terminal	8	0.720720720720721	4.09207350095125E-06	Q91YE6, Q9ERK4, Q9EPL8, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q8BKC5	0.001153964727268
UP_SEQ_FEATURE	repeat:HEAT 4	11	0.990990990990991	1.52735973100349E-05	Q8BYA0, A2AGT5, Q6PDI5, Q9QXK3, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q80X13, Q8BKC5, Q76MZ3	0.003445723553144
UP_SEQ_FEATURE	repeat:HEAT 5	10	0.900900900900901	1.71485308362884E-05	A2AGT5, Q6PDI5, Q9QXK3, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q80X13, Q8BKC5, Q76MZ3	0.003517007778788
UP_SEQ_FEATURE	repeat:HEAT 1	12	1.08108108108108	2.95170168243794E-05	Q8BYA0, Q8BQM4, A2AGT5, Q6PDI5, Q9QXK3, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q80X13, Q8BKC5, Q76MZ3	0.004683203784201
UP_SEQ_FEATURE	repeat:HEAT 2	12	1.08108108108108	2.95170168243794E-05	Q8BYA0, Q8BQM4, A2AGT5, Q6PDI5, Q9QXK3, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q80X13, Q8BKC5, Q76MZ3	0.004683203784201
UP_SEQ_FEATURE	repeat:HEAT 3	11	0.990990990990991	3.9441875842119E-05	Q8BYA0, A2AGT5, Q6PDI5, Q9QXK3, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q80X13, Q8BKC5, Q76MZ3	0.004683203784201
UP_SEQ_FEATURE	repeat:HEAT 6	9	0.810810810810811	4.31373129474195E-05	A2AGT5, Q6PDI5, Q9QXK3, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q8BKC5, Q76MZ3	0.00486588900469
GOTERM_CC_DIRECT	GO:0034399~nuclear periphery	7	0.630630630630631	0.000224664685043	Q8BJ71, Q8BFY9, Q9D903, P70168, Q8VI75, Q99JF8, Q8BKC5	0.002320173474628
GOTERM_BP_DIRECT	GO:0006610~ribosomal protein import into nucleus	5	0.450450450450451	0.000352530164211	Q91YE6, Q8BFY9, P70168, Q8VI75, Q8BKC5	0.025063215960323
GOTERM_BP_DIRECT	GO:0006607~NLS-bearing protein import into nucleus	6	0.540540540540541	0.001092932009275	O35344, Q8BFY9, P70168, Q8VI75, Q8R4R6, Q8BKC5	0.056954799581534
UP_SEQ_FEATURE	repeat:HEAT 8	6	0.540540540540541	0.001296409011383	A2AGT5, Q6PDI5, Q8BFY9, P70168, Q6P5F9, Q76MZ3	0.10832217517335
COG_ONTOLOGY	Intracellular trafficking and secretion	10	0.900900900900901	0.003512658354766	Q01405, O35344, Q9QXK3, Q8BFY9, P70168, O08547, Q8VI75, Q9D662, Q8BKC5, Q64324	0.054446204498873

**Annotation Cluster 24** Enrichment Score: 3.0654071850019777

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0017124~SH3 domain binding	18	1.62162162162162	0.000101612154788	Q9WU78, P70460, Q3UIA2, Q61462, P11352, Q09014, P70315, Q9ESS2, Q80U87, P42567, Q9JUU8, Q9JLQ0, Q5FWK3, Q60749, Q8BPU7, P55194, P22682, O89112	0.003529328842986
UP_KEYWORDS	SH3-binding	11	0.990990990990991	0.00016342993156	P42567, P70460, Q9JUU8, Q9JLQ0, Q3UIA2, Q5FWK3, Q60749, P55194, Q8BPU7, Q9ESS2, Q80U87	0.00085486425739

**Annotation Cluster 25** Enrichment Score: 2.9147257245086537

Category	Term	Count	%	PValue	Genes	FDR
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GOTERM_CC_DIRECT:GO:0030529~intracellular ribonucleoprotein complex	44	3.96396396396396	4.38966277175081E-10	Q9CX86, Q9CXY6, P35979, Q9EQK5, P09405, Q9CXW2, Q91VR5, Q9JKB3, O70133, Q9D0G0, Q921F4, Q8BK72, P19253, Q9ER88, Q80WS3, Q9JKF1, Q6P5F9, Q8BMA6, Q8CGC7, P35980, P62317, Q924T2, Q9CRB2, Q9Z204, Q6PB66, P62908, Q9D338, Q91WM3, Q9WTM5, Q9JIK9, Q64012, P35922, Q9ESX5, P62320, O55142, P62960, P57780, Q9D8E6, O88569, P62305, Q9D8M4, P27659, P49962, P62843	1.38518247464137E-08
UP_KEYWORDS Ribonucleoprotein	32	2.88288288288288	5.2965545031503E-06	Q9CX86, P35979, Q9EQK5, Q9CXW2, Q9D0G0, Q921F4, Q8BK72, P19253, Q9ER88, Q80WS3, Q8BMA6, P35980, P62317, Q924T2, Q9CRB2, Q9Z204, P62908, Q9D338, Q91WM3, Q9JIK9, Q64012, P35922, Q9ESX5, P62320, O55142, Q9D8E6, O88569, P62305, Q9D8M4, P27659, P49962, P62843	4.50207132767775E-05
GOTERM_CC_DIRECT:GO:0005840~ribosome	19	1.71171171171171	0.003140471461229	P62908, P35979, Q9CXW2, Q9D0G0, Q8BK72, Q9D338, P19253, Q9ER88, Q9JIK9, Q99M31, O55142, P35980, Q9D8E6, Q9D8M4, P27659, Q924T2, Q6P542, P62843	0.02175350963387E
UP_KEYWORDS Ribosomal protein	16	1.44144144144144	0.022266753550483	P62908, P35979, Q9CXW2, Q9D0G0, Q8BK72, Q9D338, P19253, Q9ER88, Q9JIK9, O55142, P35980, Q9D8E6, Q9D8M4, P27659, Q924T2, P62843	0.060565569657314

**Annotation Cluster 26** Enrichment Score: 2.811732458952932

Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR023409:14-3-3 protein, conserved site	7	0.630630630630631	5.69361091595197E-08	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	1.00435296557393E-05
SMART	SM00101:14_3_3	7	0.630630630630631	1.97951139771116E-07	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	5.68119771143103E-05
INTERPRO	IPR000308:14-3-3 protein	7	0.630630630630631	2.1897133371542E-07	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	3.21887860561668E-05
INTERPRO	IPR023410:14-3-3 domain	7	0.630630630630631	6.31628805403384E-07	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	7.95852294808263E-05
PIR_SUPERFAMILY	PIRSF000868:14-3-3 protein	7	0.630630630630631	3.8438086612351E-06	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	0.00056119606454
UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	7	0.630630630630631	6.63364189285118E-06	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	0.001662832901141
KEGG_PATHWAY	mmu04114:Oocyte meiosis	17	1.53153153153153	0.003626250559142	Q9CQV8, Q9WTX6, P68254, P11440, P18654, P68181, Q76MZ3, P63101, P68510, P63085, P63328, O54988, P61982, P62715, P05132, P62137, P62259	0.036735494794787

**Annotation Cluster 27** Enrichment Score: 2.7837093563551996

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	mRNA processing	31	2.79279279279279	1.32047694864338E-05	Q8BL97, Q91VR5, O70551, Q6PFR5, Q99K48, O35691, Q62384, O35326, P51908, Q9DAR7, P83870, Q3TIU4, P62317, Q60749, Q569Z6, Q9Z204, Q8VE97, Q9JL8, Q61183, Q64012, P35922, P62320, P62960, P16110, O08583, O88569, Q922U1, P62305, Q9R1C7, Q9CWK3, Q9DAW6	9.20948025720513E-05
UP_KEYWORDS	mRNA splicing	26	2.34234234234234	2.34043798287213E-05	Q8BL97, O70551, Q6PFR5, Q99K48, O35691, Q62384, O35326, Q9DAR7, P83870, P62317, Q569Z6, Q9Z204, Q8VE97, Q9JL8, Q64012, P35922, P62320, P62960, P16110, O08583, O88569, Q922U1, P62305, Q9R1C7, Q9CWK3, Q9DAW6	0.000144681620759
GOTERM_BP_DIRECT:GO:0006397~mRNA processing		33	2.97297297297297	0.000139562024458	Q8BL97, Q91VR5, O70551, Q921F4, Q6PFR5, Q99K48, O35691, Q62384, O35326, P51908, Q9DAR7, P83870, Q3TIU4, P62317, Q60749, P05132, Q569Z6, Q9Z204, Q8VE97, Q9JL8, Q61183, Q64012, P35922, P62320, P62960, P16110, O08583, O88569, Q922U1, P62305, Q9R1C7, Q9CWK3, Q9DAW6	0.01237807312573
GOTERM_BP_DIRECT:GO:0008380~RNA splicing		27	2.43243243243243	0.000157538507377	Q8BL97, O70551, Q6PFR5, Q99K48, O35691, Q62384, O35326, Q9DAR7, P83870, P62317, Q569Z6, Q9Z204, Q8VE97, Q9JL8, Q64012, P35922, Q61464, P62320, P62960, P16110, O08583, O88569, Q922U1, P62305, Q9R1C7, Q9CWK3, Q9DAW6	0.013440285229378
UP_KEYWORDS	Spliceosome	12	1.08108108108108	0.009354588216983	Q9Z204, P62320, O08583, P16110, P83870, O88569, Q922U1, P62305, P62317, O35691, Q64012, Q9DAW6	0.030291047559753
GOTERM_CC_DIRECT:GO:0016607~nuclear speck		18	1.62162162162162	0.015923432909108	Q8VE97, P28352, Q9JL8, Q99K48, O35691, Q7TQH0, Q62167, Q61464, O35326, O08583, P83870, Q922U1, Q9R1C7, Q9CY57, P05132, Q569Z6, Q9DAW6, Q9CWK3	0.082476396081683

**Annotation Cluster 28** Enrichment Score: 2.7723771214648423

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT:GO:0030904~retromer complex		9	0.810810810810811	5.73772864685427E-06	Q9QZ88, Q6P8X1, Q9CWK8, Q9EQH3, Q9D8U8, P40336, Q8C0E2, O08788, Q810B6	8.80818884165736E-05
GOTERM_CC_DIRECT:GO:0030906~retromer, cargo-selective complex		3	0.27027027027027	0.006329891187867	Q9QZ88, Q9EQH3, P40336	0.03908019776857

**Annotation Cluster 29** Enrichment Score: 2.691541502007118

Category	Term	Count	%	PValue	Genes	FDR
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KEGG_PATHWAY	mmu00030: Pentose phosphate pathway	13	1.17117117117117	2.45739282313293E-07	Q91YP3, Q7TSV4, Q9DCD0, Q93092, Q9CS42, P12382, P40142, Q00612, P05063, P05064, Q9WUA3, Q9D0F9, P47857	7.15715659737465E-06	
KEGG_PATHWAY	mmu00010: Glycolysis / Gluconeogenesis	16	1.44144144144144	2.70294451075637E-05	Q7TSV4, Q3TRM8, P28474, Q9J116, Q9D051, Q8BMF4, Q9JLJ2, P12382, P47738, P05063, P05064, P17182, Q9WUA3, Q9D0F9, Q9QXG4, P47857	0.000524821725839	
GOTERM_BP_DIRECT	GO:006002~fructose 6-phosphate metabolic process	6	0.54054054054054	3.09945802350111E-05	P12382, Q88958, Q9WUA3, P47856, P47857, Q93092	0.003856242357573	
KEGG_PATHWAY	mmu00051: Fructose and mannose metabolism	11	0.99099099099099	5.82889638168781E-05	P23591, P12382, Q8K0C9, Q3TRM8, P05063, P45376, P05064, P45377, Q9WUA3, P47857, P21300	0.000970094897809	
UP_KEYWORDS	Allosteric enzyme	9	0.81081081081081	0.000543388748795	P12382, P10518, B2RQC6, Q3TRM8, Q9JHR7, Q3V1L4, Q9WUA3, P47857, Q8CIN4	0.002548305856419	
GOTERM_BP_DIRECT	GO:0030388~fructose 1,6-bisphosphate metabolic process	5	0.45045045045045	0.000609758631396	P12382, P05063, P05064, Q9WUA3, P47857	0.037157944354025	
GOTERM_BP_DIRECT	GO:0061615~glycolytic process through fructose-6-phosphate	4	0.36036036036036	0.001113761157637	P12382, P05064, Q9WUA3, P47857	0.056954799581534	
UP_KEYWORDS	Glycolysis	7	0.63063063063063	0.002889871646276	P12382, Q3TRM8, P05063, P05064, P17182, Q9WUA3, P47857	0.010917292885932	
GOTERM_CC_DIRECT	GO:0005945~6-phosphofructokinase complex	3	0.27027027027027	0.006329891187867	P12382, Q9WUA3, P47857	0.03908019776857	
<b>Annotation Cluster 30</b> Enrichment Score: 2.6582678921511045							
Category	Term	Count	%	PValue	Genes	FDR	
INTERPRO	IPR024969: Rpn11/EIF3F C-terminal domain	4	0.36036036036036	0.000357108188197	Q9DCH4, O35593, O88545, P26516	0.017998252685127	
SMART	SM00232: JAB_MPN	5	0.45045045045045	0.001452835327088	P46737, Q9DCH4, O35593, O88545, P26516	0.041592414608683	
INTERPRO	IPR000555: JAB1/Mov34/MPN/PAD-1	5	0.45045045045045	0.002146367556833	P46737, Q9DCH4, O35593, O88545, P26516	0.07011467352322	
<b>Annotation Cluster 31</b> Enrichment Score: 2.6261048795905495							
Category	Term	Count	%	PValue	Genes	FDR	
UP_KEYWORDS	Lipid metabolism	33	2.97297297297297	0.000652601761562	Q8VCW8, Q9Z0J0, P19096, Q9EQ06, Q9CQ62, P97823, Q8BLF1, Q8BMP6, Q8K2C9, Q8BLN5, Q8JZK9, Q91V92, Q9QUJ7, Q9EPL9, P45952, P41216, O35405, O35604, Q8VBT6, P51432, Q9Z0M5, P51174, P17439, Q8VDJ3, Q99MZ7, Q9D2R0, O35459, O54950, Q9JHU9, Q9DB29, Q3TCN2, Q8BP40, Q8BG07	0.002909961953195	
UP_KEYWORDS	Fatty acid metabolism	14	1.26126126126126	0.001926794072233	Q8VCW8, P19096, P51174, Q9CQ62, P97823, Q99MZ7, Q9D2R0, O35459, O54950, Q8K2C9, Q9QUJ7, P45952, Q9EPL9, P41216	0.007381520952778	
GOTERM_BP_DIRECT	GO:0006629~lipid metabolic process	38	3.42342342342342	0.002388889482063	Q8VCW8, Q9Z0J0, P19096, Q9EQ06, Q9CQ62, P97823, Q8BLF1, Q8BMP6, Q8K2C9, Q8BLN5, Q8JZK9, Q91V92, Q9QUJ7, Q9EPL9, P45952, P41216, O35405, O35604, Q8VBT6, P51432, Q9Z0M5, Q61207, P51174, Q9JL16, Q03265, P17439, Q8VDJ3, P11352, Q99MZ7, Q9D2R0, O35459, Q05816, O54950, Q9JHU9, Q9DB29, Q3TCN2, Q8BP40, Q8BG07	0.103256125962112	
<b>Annotation Cluster 32</b> Enrichment Score: 2.5780058180796197							
Category	Term	Count	%	PValue	Genes	FDR	
INTERPRO	IPR006195: Aminoacyl-tRNA synthetase, class II	8	0.72072072072072	4.9606870757413E-06	Q8CGC7, Q8BP47, Q8C0C7, Q9CZD3, Q3UQ84, P26638, Q922B2, Q9D0R2	0.00043753260008	
INTERPRO	IPR002314: Aminoacyl-tRNA synthetase, class II (G/ H/ P/ S), conserved domain	5	0.45045045045045	0.000252046935701	Q8CGC7, Q9CZD3, Q3UQ84, P26638, Q9D0R2	0.013076788075771	
GOTERM_BP_DIRECT	GO:0043039~tRNA aminoacylation	5	0.45045045045045	0.00212639957517	Q8CGC7, Q8C0C7, Q3UQ84, Q8BGQ7, Q9D0R2	0.094767598976981	
<b>Annotation Cluster 33</b> Enrichment Score: 2.5725145209809							
Category	Term	Count	%	PValue	Genes	FDR	
SMART	SM00033: CH	13	1.17117117117117	2.94436960505277E-05	Q99K51, Q7TPR4, P27870, Q9QXZ0, Q3V0K9, Q62261, Q8BTM8, Q9JKF1, Q9QXS1, Q3UQ44, P57780, Q9ROC8, Q9WVA4	0.0016900681533	
INTERPRO	IPR001589: Actinin-type, actin-binding, conserved site	8	0.72072072072072	4.92542495855678E-05	Q99K51, Q7TPR4, Q9QXZ0, P57780, Q3V0K9, Q8BTM8, Q62261, Q9QXS1	0.003475379850758	
UP_SEQ_FEATURE	domain: CH 1	8	0.72072072072072	5.6367708140287E-05	Q99K51, Q7TPR4, Q9QXZ0, P57780, Q3V0K9, Q8BTM8, Q62261, Q9QXS1	0.005780252252931	
UP_SEQ_FEATURE	domain: CH 2	8	0.72072072072072	5.6367708140287E-05	Q99K51, Q7TPR4, Q9QXZ0, P57780, Q3V0K9, Q8BTM8, Q62261, Q9QXS1	0.005780252252931	
INTERPRO	IPR001715: Calponin homology domain	13	1.17117117117117	0.000147328074604	Q99K51, Q7TPR4, P27870, Q9QXZ0, Q3V0K9, Q62261, Q8BTM8, Q9JKF1, Q9QXS1, Q3UQ44, P57780, Q9ROC8, Q9WVA4	0.008952273020976	
UP_SEQ_FEATURE	domain: Actin-binding	6	0.54054054054054	0.000477026336457	Q7TPR4, Q9QXZ0, P57780, Q8BTM8, Q62261, Q9QXS1	0.046790061523764	
GOTERM_BP_DIRECT	GO:0051017~actin filament bundle assembly	8	0.72072072072072	0.001397441072317	Q99K51, Q9ERG0, Q7TPR4, P57780, Q3V0K9, P26040, O70200, Q62418	0.067384811746088	
<b>Annotation Cluster 34</b> Enrichment Score: 2.5637994619434257							
Category	Term	Count	%	PValue	Genes	FDR	
GOTERM_MF_DIRECT	GO:0005200~structural constituent of cytoskeleton	18	1.62162162162162	3.10777628432023E-07	P03995, Q9WV32, Q922F4, Q62261, Q71LX4, P68372, P59999, Q9QXS1, P48193, P61161, P68369, Q9CVB6, Q9JM76, P68368, Q9D6F9, P20152, P26039, P05213	1.70436994119036E-05	

GOTERM_BP_DIRECT	GO:0007017~microtubule-based process	10	0.90090009000901	0.000140942560708	Q8K1R7, P68369, P61759, Q9Z0Y1, P68368, Q922F4, Q9D6F9, P70188, P68372, P05213	0.01237807312573
SMART	SM00864:SM00864	6	0.540540540540541	0.001534711343066	P68369, P68368, Q922F4, Q9D6F9, P68372, P05213	0.041592414608683
SMART	SM00865:SM00865	6	0.540540540540541	0.001534711343066	P68369, P68368, Q922F4, Q9D6F9, P68372, P05213	0.041592414608683
INTERPRO	IPR017975:Tubulin, conserved site	6	0.540540540540541	0.001648975689858	P68369, P68368, Q922F4, Q9D6F9, P68372, P05213	0.061267827314441
INTERPRO	IPR018316:Tubulin/FtsZ, 2-layer sandwich domain	6	0.540540540540541	0.001648975689858	P68369, P68368, Q922F4, Q9D6F9, P68372, P05213	0.061267827314441
INTERPRO	IPR000217:Tubulin	6	0.540540540540541	0.002084460469524	P68369, P68368, Q922F4, Q9D6F9, P68372, P05213	0.069377137136625
INTERPRO	IPR008280:Tubulin/FtsZ, C-terminal	6	0.540540540540541	0.002084460469524	P68369, P68368, Q922F4, Q9D6F9, P68372, P05213	0.069377137136625
INTERPRO	IPR023123:Tubulin, C-terminal	6	0.540540540540541	0.002084460469524	P68369, P68368, Q922F4, Q9D6F9, P68372, P05213	0.069377137136625
INTERPRO	IPR003008:Tubulin/FtsZ, GTPase domain	6	0.540540540540541	0.002084460469524	P68369, P68368, Q922F4, Q9D6F9, P68372, P05213	0.069377137136625
<b>Annotation Cluster 35</b> Enrichment Score: 2.4694739997089603						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	GTP-binding	31	2.79279279279279	5.79095267886579E-05	Q8BFR5, Q9Z0N1, Q8BG51, Q922F4, Q9R1T4, Q9WTP7, P35279, P59325, P62331, O55131, Q9D6F9, P42208, P46664, P27601, P56380, Q80UG5, Q35626, P05213, Q9QXB9, P68372, Q6PA06, P32233, Q05144, Q3UM18, P84096, P68369, Q8R050, P84078, P61750, P35276, P68368	0.00031502782573
GOTERM_MF_DIRECT	GO:0005525~GTP binding	35	3.15315315315315	0.001262398159457	Q8BFR5, Q9Z0N1, Q8BG51, Q922F4, Q9R1T4, Q9WTP7, P35279, P59325, P62331, O55131, Q9D6F9, P42208, P46664, P27601, P56380, Q80UG5, Q35626, P05213, Q9QLC8, Q9CZ30, Q9QXB9, P14824, P68372, Q6PA06, P32233, Q9EQP2, Q05144, Q3UM18, P84096, P68369, Q8R050, P84078, P61750, P35276, P68368	0.032885472053857
<b>Annotation Cluster 36</b> Enrichment Score: 2.43839802553254						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	DNA replication	13	1.17117117117117	0.000553109503195	Q9CY94, P97386, P97310, P97311, Q8R3C0, Q99MD9, P39749, Q920B9, Q8VVE4, P49718, Q9D2L9, P17918, Q8R323	0.002549928557102
<b>Annotation Cluster 37</b> Enrichment Score: 2.376545878489653						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR017926:Glutamine amidotransferase	4	0.36036036036036	0.001667151763658	B2RQC6, Q3THK7, P70698, Q5SUR0	0.061267827314441
GOTERM_BP_DIRECT	GO:0006541~glutamine metabolic process	6	0.540540540540541	0.002420605766024	B2RQC6, Q3THK7, P47856, P70698, Q5SUR0, Q9JHW2	0.103256125962112
UP_KEYWORDS	Glutamine amidotransferase	4	0.36036036036036	0.003398194818803	Q3THK7, P47856, P70698, Q5SUR0	0.012208275684488
<b>Annotation Cluster 38</b> Enrichment Score: 2.278357354943106						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0046034~ATP metabolic process	9	0.810810810810811	0.000644019904765	Q91VD9, P56135, Q9CPQ8, Q9CZ30, Q9WTP7, Q03265, P50516, O08739, P62814	0.038460868712572
GOTERM_BP_DIRECT	GO:0015991~ATP hydrolysis coupled proton transport	8	0.720720720720721	0.000967438747444	P50518, Q8BVE3, Q03265, P56383, P50516, P62814, P51863, Q9Z1G3	0.054505133959742
<b>Annotation Cluster 39</b> Enrichment Score: 2.2360086346064105						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0045454~cell redox homeostasis	13	1.17117117117117	7.00008326300767E-05	P28352, O08807, P99029, Q9JMH6, Q8R2E9, P11352, Q8R180, P35700, Q8C0L0, Q9JLT4, Q61171, Q9CQM9, Q91VW3	0.008039326393593
UP_KEYWORDS	Peroxidase	7	0.630630630630631	0.000210240029655	O70325, O08807, P24270, P99029, Q61171, P11352, P35700	0.0010631232793
GOTERM_BP_DIRECT	GO:0042744~hydrogen peroxide catabolic process	6	0.540540540540541	0.000400207349998	P24270, P99029, Q61171, Q9JMH6, P11352, P35700	0.027791142955654
INTERPRO	IPR012336:Thioredoxin-like fold	17	1.53153153153153	0.00043935560273	P10649, O70325, O08807, Q9D8N0, P99029, P11352, P35700, Q9CQ75, Q8CGC7, Q8C0L0, Q9JJU8, Q61171, Q3TDN2, Q9CQM9, O09131, Q91VW3, Q9QYB1	0.020946575222027
UP_KEYWORDS	Redox-active center	9	0.810810810810811	0.000631373438787	Q8C0L0, Q9JLT4, O08807, P99029, Q61171, Q9JMH6, Q8R2E9, Q8R180, P35700	0.00286226255833
GOTERM_BP_DIRECT	GO:0006979~response to oxidative stress	16	1.44144144144144	0.002381251834053	P10518, P62908, O70325, P24270, P99029, Q9JMH6, P31750, P11352, P35700, Q9JLV6, Q00612, Q61171, O88844, Q6P9R2, P28867, Q99JF8	0.103256125962112
<b>Annotation Cluster 40</b> Enrichment Score: 2.225303263587286						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0008180~COP9 signalosome	7	0.630630630630631	0.003824326533221	Q8VBV7, Q8VDD5, O08917, O88544, Q03265, O88545, P61202	0.02555549965729
UP_KEYWORDS	Signalosome	4	0.36036036036036	0.006842645579295	Q8VBV7, O88544, O88545, P61202	0.022697556067906

<b>Annotation Cluster 41</b> Enrichment Score: 2.2013648150410914						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu05100:Bacterial invasion of epithelial cells	15	1.35135135135135	0.000692260657827	Q8BH43, Q9WV32, Q9R1T4, P26450, Q68FD5, P59999, P70315, P84096, Q9CVB6, Q9JM76, Q9JLQ0, Q8BPU7, P42208, P22682, Q80UG5	0.008064836663683
GOTERM_BP_DIRECT	GO:0034314~Arp2/3 complex-mediated actin nucleation	6	0.540540540540541	0.00080394778129	Q3UQ44, P61161, Q9WV32, Q9CVB6, Q9JM76, P59999	0.047070354410402
GOTERM_CC_DIRECT	GO:0005885~Arp2/3 protein complex	5	0.450450450450451	0.001196711823564	P61161, Q9WV32, Q9CVB6, Q9JM76, P59999	0.009996063467417
<b>Annotation Cluster 42</b> Enrichment Score: 2.0912103543341356						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Amino-acid biosynthesis	7	0.630630630630631	0.000448650350739	Q99K85, Q91Y10, Q8BGB7, Q8VCN5, P05201, Q9WVQ5, Q922D8	0.00221877991638
GOTERM_BP_DIRECT	GO:0008652~cellular amino acid biosynthetic process	7	0.630630630630631	0.001125362751276	Q99K85, Q91Y10, Q8BGB7, Q8VCN5, P05201, Q9WVQ5, Q922D8	0.056954799581534
UP_KEYWORDS	Methionine biosynthesis	3	0.27027027027027	0.040688922883113	Q8BGB7, Q9WVQ5, Q922D8	0.098151618205237
<b>Annotation Cluster 43</b> Enrichment Score: 2.0877824654812085						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	SH3 domain	20	1.8018018018018	0.001099616219704	P70290, P27870, Q9QXZ0, O70145, P26450, Q80TY0, A2AAY5, Q62418, Q9Z0R6, Q3UNDO, P97369, O08539, Q61792, P70248, P97814, Q8C3J5, Q09014, Q8CBW3, Q9JLQ0, Q9R0C8	0.004601470950145
SMART	SM00326:SH3	19	1.71171171171171	0.003064638686487	P70290, P27870, O70145, P26450, Q80TY0, A2AAY5, Q62418, Q9Z0R6, Q3UNDO, P97369, O08539, Q61792, P70248, P97814, Q8C3J5, Q09014, Q8CBW3, Q9JLQ0, Q9R0C8	0.067657792540142
<b>Annotation Cluster 44</b> Enrichment Score: 2.032899025060787						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Tricarboxylic acid cycle	6	0.540540540540541	0.003218244082614	Q9Z219, P14152, O88844, P28271, Q9D051, Q8BMF4	0.011829221492853
<b>Annotation Cluster 45</b> Enrichment Score: 2.0325529074081596						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	mRNA transport	12	1.08108108108108	0.000835633037227	Q6PB66, Q61655, Q8BL97, Q5SF07, O08583, Q9CPN8, Q8BJ71, O88569, Q6P5F9, Q9CWU9, P35922, Q8R4R6	0.003634299789073
<b>Annotation Cluster 46</b> Enrichment Score: 1.9999608282299022						
Category	Term	Count	%	PValue	Genes	FDR
UP_SEQ_FEATURE	domain:PX	9	0.810810810810811	0.001360174777651	Q6P8X1, Q9CWK8, Q80TM9, Q9D8U8, Q3TC93, A2AAY5, P97369, Q91YJ2, Q09014	0.10959122494216
INTERPRO	IPR001683:Phox homologous domain	9	0.810810810810811	0.001928161977935	Q6P8X1, Q9CWK8, Q80TM9, Q9D8U8, Q3TC93, A2AAY5, P97369, Q91YJ2, Q09014	0.069377137136625
<b>Annotation Cluster 47</b> Enrichment Score: 1.998582452290484						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0043171~peptide catabolic process	7	0.630630630630631	0.000538232659017	Q99JW2, P24527, Q9JHR7, P97449, Q11011, Q9D1A2, O89023	0.033482556663027
GOTERM_MF_DIRECT	GO:0070006~metalloaminopeptidase activity	6	0.540540540540541	0.002192726441027	Q6P1B1, P24527, Q8BP48, P97449, Q9Z2W0, Q11011	0.048613211735107
<b>Annotation Cluster 48</b> Enrichment Score: 1.9854443501796497						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Metalloprotease	16	1.44144144144144	0.000893334617017	Q8K411, Q11136, Q6P1B1, P34960, O35593, Q80W54, P97449, P46737, Q99KK7, P24527, Q9JHR7, Q9DC61, Q9Z2W0, Q9D1A2, Q11011, O89001	0.003796672122321
<b>Annotation Cluster 49</b> Enrichment Score: 1.9671926829835977						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0005777~peroxisome	17	1.53153153153153	0.000403906261093	P52760, P24270, P99029, Q99MZ7, O35459, Q8C0L6, P40142, Q2TPA8, Q9JHR7, O88844, Q9QUJ7, P20152, Q9EPB5, Q922Q1, Q9EPL9, P41216, Q00519	0.003955495798294
UP_KEYWORDS	Peroxisome	12	1.08108108108108	0.004837878578276	O35459, Q8C0L6, Q2TPA8, P24270, P99029, Q9QUJ7, Q9EPB5, Q922Q1, Q9EPL9, P41216, Q00519, Q99MZ7	0.016448787166138
GOTERM_CC_DIRECT	GO:0005782~peroxisomal matrix	5	0.450450450450451	0.006899793450854	Q8C0L6, Q9JHR7, P99029, Q9EPL9, P35700	0.04125350189563

Annotation Cluster 50		Enrichment Score: 1.9591284792285628					
Category	Term	Count	%	PValue	Genes	FDR	
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	22	1.98198198198198	0.000434256341412	Q9CR68, P56135, Q8BVE3, Q9CPQ8, Q9D855, P99028, Q9CR51, Q03265, Q9CQZ6, Q91VM9, P50516, P51863, Q9CPQ1, Q9Z1G3, Q9CQ75, Q91VD9, P50518, P56383, Q9CQH3, P62814, Q8R1I1, Q9D819	0.00562120708606	
UP_KEYWORDS	Electron transport	13	1.17117117117117	0.001596769293938	Q9CR68, Q9D855, P99028, Q8R2E9, Q9CQZ6, Q9CQX2, Q61462, Q8R180, Q9CQ75, Q91VD9, Q8CQO1, Q9CQH3, Q8R1I1	0.006482406685837	
KEGG_PATHWAY	mmu05010:Alzheimer's disease	22	1.98198198198198	0.008792721346468	Q9CR68, P51432, P57716, Q64518, Q8VBW6, Q9D855, P99028, O08529, Q03265, Q9CQZ6, P70677, Q9CPQ1, Q9CQ75, Q91VD9, P63085, Q9JHR7, P63328, P56383, Q9CQH3, Q8R1I1, O89110, P49615	0.07316800263311	
Annotation Cluster 51		Enrichment Score: 1.9173620357575265					
Category	Term	Count	%	PValue	Genes	FDR	
GOTERM_CC_DIRECT	GO:0005694~chromosome	30	2.7027027027027	0.001617414127565	Q8CG48, P54276, Q9R1T4, Q6P5D8, P15864, Q920B9, Q64522, O55131, Q9Z0Y1, Q8K2Z4, P43274, P43275, P42208, P43277, P62715, Q9WUB4, Q8R1Q8, Q9JK91, Q61686, P27661, P35922, Q6NVF4, Q76MZ3, Q3UM45, P0C0S6, Q9QZQ8, Q9CWU9, Q5DW34, Q9WVA3, E9PVX6	0.012584811293934	
UP_KEYWORDS	Chromosome	30	2.7027027027027	0.003642954308448	Q8CG48, P54276, Q9R1T4, Q6P5D8, P15864, Q920B9, Q64522, O55131, A2AGT5, Q9Z0Y1, Q8K2Z4, P43274, P43275, P42208, P43277, P62715, Q9WUB4, P84228, Q8R1Q8, Q61686, P27661, P35922, Q6NVF4, Q76MZ3, P0C0S6, Q9QZQ8, Q9CWU9, Q5DW34, Q9WVA3, E9PVX6	0.012868617816854	
UP_KEYWORDS	Centromere	13	1.17117117117117	0.00989560545328	Q61686, Q9R1T4, P35922, Q76MZ3, O55131, A2AGT5, Q9Z0Y1, Q9CWU9, P62715, P42208, Q9WUB4, Q9WVA3, Q8R1Q8	0.031083600471665	
GOTERM_CC_DIRECT	GO:000776~kinetochore	13	1.17117117117117	0.010353507104708	Q61686, Q9R1T4, Q6P5F9, O08788, O55131, A2AGT5, Q9Z0Y1, Q9CWU9, P42208, Q9WUB4, Q9WVA3, Q8R1Q8, Q6ZQL4	0.058225663717564	
GOTERM_CC_DIRECT	GO:000775~chromosome, centromeric region	14	1.26126126126126	0.014838801388392	Q61686, P23198, Q9R1T4, P35922, Q76MZ3, O55131, Q9Z0Y1, Q9CWU9, P62715, P42208, Q9WUB4, Q9WVA3, Q8R1Q8, E9PVX6	0.07944288243809	
UP_KEYWORDS	Kinetochore	9	0.81081081081081	0.043492175392883	O55131, A2AGT5, Q9Z0Y1, Q9R1T4, P42208, Q9CWU9, Q9WUB4, Q9WVA3, Q8R1Q8	0.102424539821265	
Annotation Cluster 52		Enrichment Score: 1.9104178018469977					
Category	Term	Count	%	PValue	Genes	FDR	
SMART	SM00515:eIF5C	5	0.450450450450451	0.000122837883937	Q62448, Q6NZJ6, P59325, Q80X13, Q2L4X1	0.00587545448337	
INTERPRO	IPR003307:W2 domain	5	0.450450450450451	0.000130714920465	Q62448, Q6NZJ6, P59325, Q80X13, Q2L4X1	0.008540041470368	
UP_SEQ_FEATURE	domain:W2	5	0.450450450450451	0.000704434374218	Q62448, Q6NZJ6, P59325, Q80X13, Q2L4X1	0.06150697964946	
Annotation Cluster 53		Enrichment Score: 1.9000720797270978					
Category	Term	Count	%	PValue	Genes	FDR	
UP_KEYWORDS	Hydrogen ion transport	11	0.990990990990991	1.21333361529685E-05	P50518, Q8BVE3, P56135, Q9CPQ8, Q9CR51, Q03265, P56383, P50516, P62814, P51863, Q9Z1G3	8.6849142989691E-05	
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	22	1.98198198198198	0.000434256341412	Q9CR68, P56135, Q8BVE3, Q9CPQ8, Q9D855, P99028, Q9CR51, Q03265, Q9CQZ6, Q91VM9, P50516, P51863, Q9CPQ1, Q9Z1G3, Q9CQ75, Q91VD9, P50518, P56383, Q9CQH3, P62814, Q8R1I1, Q9D819	0.00562120708606	
GOTERM_BP_DIRECT	GO:0015992~proton transport	11	0.990990990990991	0.000494515558861	P50518, Q8BVE3, P56135, Q9CPQ8, Q9CR51, Q03265, P56383, P50516, P62814, P51863, Q9Z1G3	0.031417520399158	
GOTERM_BP_DIRECT	GO:0015991~ATP hydrolysis coupled proton transport	8	0.720720720720721	0.000967438747444	P50518, Q8BVE3, Q03265, P56383, P50516, P62814, P51863, Q9Z1G3	0.054505133959742	
KEGG_PATHWAY	mmu04721:Synaptic vesicle cycle	12	1.08108108108108	0.002789873467061	P50518, P46460, Q8BVE3, Q9CR51, Q68FD5, P50516, P62814, P51863, P17427, P17426, P84091, Q9Z1G3	0.02954729626478	
GOTERM_MF_DIRECT	GO:0008553~hydrogen-exporting ATPase activity, phosphorylative mechanism	5	0.450450450450451	0.004481910421556	P50518, Q9CPQ8, Q9CR51, P51863, Q9Z1G3	0.083395547486807	
Annotation Cluster 54		Enrichment Score: 1.888121326960176					
Category	Term	Count	%	PValue	Genes	FDR	
UP_KEYWORDS	Actin capping	4	0.36036036036036	0.031257824186654	P26043, P47753, Q62261, P47754	0.080972649321617	
Annotation Cluster 55		Enrichment Score: 1.873168453696123					
Category	Term	Count	%	PValue	Genes	FDR	
GOTERM_MF_DIRECT	GO:0009055~electron carrier activity	11	0.990990990990991	0.000302114498358	Q91VD9, Q9D7B6, P51174, G3X982, Q9CQM9, Q91VW3, Q61462, P45952, Q9EPL9, Q8JZN5, Q00519	0.009653839463129	
GOTERM_MF_DIRECT	GO:000062~fatty-acyl-CoA binding	8	0.720720720720721	0.001694923130198	Q9D7B6, Q8BMP6, P51174, P45952, Q9EPL9, Q91V12, Q8JZN5, P31786	0.041072323294558	



UP_KEYWORDS	Flavoprotein	13	1.17117117117117	0.00785478121626	Q8CFV9, P51174, Q9JMH6, Q8R2E9, Q8R180, Q8JZN5, Q8COL6, Q9D7B6, Q9JLT4, G3X982, P45952, Q9EPL9, Q00519	0.025740969768948
UP_KEYWORDS	FAD	12	1.08108108108108	0.009942181033216	Q8COL6, Q9D7B6, Q9JLT4, P51174, Q9JMH6, Q8R2E9, G3X982, P45952, Q9EPL9, Q8R180, Q8JZN5, Q00519	0.031083600471665
<b>Annotation Cluster 56</b> Enrichment Score: 1.8510354542174643						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR011993:Pleckstrin homology-like domain	34	3.06306306306306	0.00102835762221	P27870, P98078, P26041, P70460, P26040, P26043, Q9Z0R6, Q69ZK0, Q62261, Q71LX4, Q9ERS5, P31750, P48193, Q61210, Q80YW0, Q8R5A3, Q9QVP9, Q5DU25, Q9JM90, Q8K298, P26039, Q8R1F1, P51432, Q9CT10, Q3UND0, Q9CR95, Q9Z2A0, Q9JHK5, P70315, Q8K1B8, Q8BYW1, Q9R0C8, Q8BPU7, Q8K124	0.042186577804165
<b>Annotation Cluster 57</b> Enrichment Score: 1.8265762565031798						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:2000643~positive regulation of early endosome to late endosome transport	5	0.450450450450451	0.000352530164211	P98078, P26041, P26040, P26043, Q91W86	0.025063215960323
GOTERM_BP_DIRECT	GO:1902115~regulation of organelle assembly	4	0.36036036036036	0.000462539102969	P26041, P26040, P26043, Q91W86	0.030346706243628
INTERPRO	IPR014352:FERM/acyl-CoA-binding protein, 3-helical bundle	10	0.900900900900901	0.000488037572199	Q8K1B8, P26041, Q8BMP6, P26040, P26043, Q9QVP9, Q71LX4, P48193, P31786, P26039	0.022655217825234
GOTERM_MF_DIRECT	GO:0008092~cytoskeletal protein binding	12	1.08108108108108	0.000614469200006	O89053, P61161, P26041, P26040, P26043, P05063, O08529, P05064, P07356, Q9QXS1, P48193, P49615	0.018293625897323
SMART	SM00295:B41	8	0.720720720720721	0.005682171174512	Q8K1B8, P26041, P26040, P26043, Q9QVP9, Q71LX4, P48193, P26039	0.095928419240283
GOTERM_CC_DIRECT	GO:0019898~extrinsic component of membrane	11	0.990990990990991	0.006162180608643	Q6P8X1, Q9CWK8, P26041, Q9D8U8, P10107, P26040, P26043, O70310, Q91YJ2, P48193, Q90914	0.03908019776857
<b>Annotation Cluster 58</b> Enrichment Score: 1.807128533453858						
Category	Term	Count	%	PValue	Genes	FDR
SMART	SM00182:CULLIN	4	0.36036036036036	0.002697606713293	Q9D4H8, Q9D5V5, Q9WTX6, A2A432	0.0645177605596
SMART	SM00884:SM00884	4	0.36036036036036	0.004173959091763	Q9D4H8, Q9D5V5, Q9WTX6, A2A432	0.079861750622394
<b>Annotation Cluster 59</b> Enrichment Score: 1.8045761338347768						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0046034~ATP metabolic process	9	0.810810810810811	0.000644019904765	Q91VD9, P56135, Q9CPQ8, Q9CZ30, Q9WTP7, Q03265, P50516, O08739, P62814	0.038460868712572
<b>Annotation Cluster 60</b> Enrichment Score: 1.7815641885608242						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0048027~mRNA 5'-UTR binding	5	0.450450450450451	0.001107695571189	Q5SF07, Q9CPN8, P28271, P35922, Q62167	0.029595353466122
SMART	SM00322:KH	7	0.630630630630631	0.006246783121819	Q9CPS7, Q5SF07, Q9CPN8, Q60749, Q8VDDJ3, P35922, Q61584	0.099601486442336
<b>Annotation Cluster 61</b> Enrichment Score: 1.7732107861348325						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Redox-active center	9	0.810810810810811	0.000631373438787	Q8COL0, Q9JLT4, O08807, P99029, Q61171, Q9JMH6, Q8R2E9, Q8R180, P35700	0.002862226255833
<b>Annotation Cluster 62</b> Enrichment Score: 1.702619066623082						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu00040:~Pentose and glucuronate interconversions	10	0.900900900900901	0.000259542407748	Q9DBB8, P45376, Q9JII6, Q99KP3, P45377, Q6ZQM8, P12265, Q91X52, Q91ZJ5, P21300	0.003557257706188
<b>Annotation Cluster 63</b> Enrichment Score: 1.6799066987171134						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	DNA repair	21	1.89189189189189	0.012603544734794	P62908, P27661, P97386, P28352, P54276, Q99K48, O35593, Q9WTM5, Q9WUP7, P11103, A2A432, P39749, P54726, Q920B9, P46737, Q8VEE4, Q9JLV6, Q8BP27, P17918, P43247, Q9JK91	0.038956410998453
UP_KEYWORDS	DNA damage	22	1.98198198198198	0.040933027448589	P62908, P27661, P97386, P28352, P54276, Q99K48, O35593, Q9WTM5, Q9WUP7, P11103, A2A432, P39749, P54726, P35922, Q920B9, P46737, Q8VEE4, Q9JLV6, Q8BP27, P17918, P43247, Q9JK91	0.098151618205237

<b>Annotation Cluster 64</b> Enrichment Score: 1.6595703915995288						
Category	Term	Count	%	PValue	Genes	FDR
SMART	SM00165:UBA	7	0.630630630630631	0.003536161194484	Q922Y1, Q91VX2, P56399, P22682, P54726, Q8R317, Q80X50	0.072491304486915
<b>Annotation Cluster 65</b> Enrichment Score: 1.602188643342761						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Citrullination	12	1.08108108108108	0.001748796296666	P03995, O08583, Q9D8E6, Q922K7, P43274, P19253, P43275, P43277, P15864, P84228, Q99JF8, Q64522	0.006795322752759
GOTERM_CC_DIRECT	GO:0005719~nuclear euchromatin	7	0.630630630630631	0.002309194927403	P23198, P0C0S6, P43275, Q9WTM5, P43277, P15864, P35700	0.017034061282664
GOTERM_MF_DIRECT	GO:0031490~chromatin DNA binding	10	0.900900900900901	0.005551855029641	Q04207, P28352, P57780, P0C0S6, P43274, Q9QZQ8, P43275, Q9WTM5, P43277, P15864	0.101491805980461
<b>Annotation Cluster 66</b> Enrichment Score: 1.5989759993741295						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Thiol protease	19	1.71171171171171	1.09437261345234E-05	P10605, P29452, Q9JMA1, P56399, Q9JKB1, Q9DCH4, Q8K2H2, O08529, O70370, Q9WUP7, P35123, Q9WUU7, P70677, Q99K23, Q80U87, O89017, Q8CDG3, Q8R016, O89110	8.26859307941771E-05
GOTERM_MF_DIRECT	GO:0008234~cysteine-type peptidase activity	19	1.71171171171171	0.000305735798736	P10605, P29452, Q9JMA1, P56399, Q9JKB1, Q9DCH4, Q8K2H2, O08529, O70370, Q9WUP7, P35123, Q9WUU7, P70677, Q99K23, Q80U87, O89017, Q8CDG3, Q8R016, O89110	0.009653839463129
<b>Annotation Cluster 67</b> Enrichment Score: 1.498910222000838						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0005868~cytoplasmic dynein complex	6	0.540540540540541	0.003656326083094	P51807, Q9JHU4, P62627, Q91YJ2, O08788, Q8R1Q8	0.024723278752347
UP_KEYWORDS	Dynein	5	0.450450450450451	0.037935022603142	P51807, Q9JHU4, P62627, O08788, Q8R1Q8	0.093802964982314
<b>Annotation Cluster 68</b> Enrichment Score: 1.4980844420165231						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0030123~AP-3 adaptor complex	5	0.450450450450451	0.001729050088609	O54774, Q9Z1T1, Q920Q4, Q8R307, Q91W86	0.013094672671069
GOTERM_CC_DIRECT	GO:0033263~CORVET complex	4	0.36036036036036	0.003082186090733	Q920Q4, Q8R307, Q0P5W1, Q91W86	0.021753509633876
GOTERM_CC_DIRECT	GO:0030136~clathrin-coated vesicle	8	0.720720720720721	0.019517787425873	P42567, P98078, Q8VD75, Q68FD5, P22892, Q920Q4, Q8R307, Q91W86	0.094587780037672
GOTERM_CC_DIRECT	GO:0030897~HOPS complex	4	0.36036036036036	0.02042009088115	Q8BUK6, Q920Q4, Q8R307, Q91W86	0.096655096837441
<b>Annotation Cluster 69</b> Enrichment Score: 1.347430938343867						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0008121~ubiquinol-cytochrome-c reductase activity	4	0.36036036036036	0.003979859556909	Q9CR68, P99028, Q9D855, Q8R1I1	0.07964664044084
GOTERM_CC_DIRECT	GO:0005750~mitochondrial respiratory chain complex III	4	0.36036036036036	0.009511449425718	Q9CR68, P99028, Q9D855, Q8R1I1	0.054078563885491
UP_KEYWORDS	Respiratory chain	8	0.720720720720721	0.013934084511917	Q91VD9, Q9CR68, P99028, Q9D855, Q9CQZ6, Q9CQH3, Q8R1I1, Q9CQ75	0.042585067272374
GOTERM_CC_DIRECT	GO:0070469~respiratory chain	8	0.720720720720721	0.017899653652635	Q91VD9, Q9CR68, P99028, Q9D855, Q9CQZ6, Q9CQH3, Q8R1I1, Q9CQ75	0.089973480307049
<b>Annotation Cluster 70</b> Enrichment Score: 1.3297000170879947						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0042555~MCM complex	4	0.36036036036036	0.006895215930491	P49718, P97310, P97311, Q8R3C0	0.04125350189563
<b>Annotation Cluster 71</b> Enrichment Score: 1.2602450157304304						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	WD repeat	19	1.71171171171171	0.020671634644234	O89053, Q9Z0H1, Q9WV32, Q7TMQ7, Q91WM3, Q7TNG5, Q9WUM4, Q8BX09, Q9D2V7, P58404, Q8CIE6, Q9CWU9, P27612, O88342, Q0P5W1, Q9WVA3, P61965, Q6ZQL4, Q9DAW6	0.057965820858058
<b>Annotation Cluster 72</b> Enrichment Score: 1.2413105630164416						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Calmodulin-binding	14	1.26126126126126	0.0051989854324	Q61879, Q62261, O08638, Q9JKF1, P70248, A2AN08, P58404, P48193, Q8VCN5, Q3UQ44, Q8VDD5, P63328, Q6URW6, P26645	0.017458321452009
GOTERM_CC_DIRECT	GO:0097513~myosin II filament	3	0.27027027027027	0.006329891187867	Q8VDD5, Q61879, Q6URW6	0.03908019776857
UP_KEYWORDS	Motor protein	12	1.08108108108108	0.017493596588581	Q6P9P6, P28740, Q8VDD5, P51807, O88447, Q61879, Q6URW6, O08638, Q9JHU4, P62627, P70248, Q8R1Q8	0.051126960201847
UP_KEYWORDS	Cell shape	5	0.450450450450451	0.021187584576258	Q8VDD5, Q7TMB8, P26040, Q61879, Q6URW6	0.058806357191246

<b>Annotation Cluster 73</b> Enrichment Score: 1.2401419545683408						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0031105~septin complex	4	0.36036036036036	0.000945073641715	O55131, Q9R1T4, P42208, Q80UG5	0.008387528570219
<b>Annotation Cluster 74</b> Enrichment Score: 1.2110416690147345						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0004553~hydrolase activity, hydrolyzing O-glycosyl compounds	8	0.720720720720721	0.002784896315863	Q9D6Y9, P23780, Q9QWR8, P51569, Q8K2I4, Q91W89, P70699, P12265	0.058631531417288
UP_KEYWORDS	Glycosidase	9	0.810810810810811	0.024544207637062	P23780, P08905, Q9QWR8, P51569, Q8K2I4, P17439, Q91W89, P70699, P12265	0.064815771624086
<b>Annotation Cluster 75</b> Enrichment Score: 1.139626837569982						
Category	Term	Count	%	PValue	Genes	FDR
SMART	SM00360:RRM	20	1.8018018018018	0.006781117563507	Q9CX86, Q8VE97, Q9Z204, P09405, Q8BL97, Q9CPN8, Q921F4, Q9JL18, Q99K48, Q6PFR5, Q9Z1D1, Q64012, Q8BGD9, Q61464, O35326, Q5SF07, O08583, O88569, Q8R4X3, Q6NV83	0.102430565301397
<b>Annotation Cluster 76</b> Enrichment Score: 1.1317616891423437						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR011990:Tetratricopeptide-like helical	20	1.8018018018018	0.002373697362788	Q9D2X5, Q99J14, Q9CYG7, O88447, Q80UM3, O88544, Q5SW19, Q9D706, P61202, Q9QY13, Q8QZY1, O89079	0.0761309481447
UP_KEYWORDS	TPR repeat	12	1.08108108108108	0.037423370348772	Q60864, Q8BSY0, Q9CYG7, O88447, O70145, Q80UM3, Q9CR16, Q99MD9, Q9D2X5, Q5SW19, Q9D706, Q9QY13	0.093461074663301
<b>Annotation Cluster 77</b> Enrichment Score: 1.0771279107332454						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR012675:Beta-grasp domain	6	0.540540540540541	0.000736888553314	Q91VD9, Q3UQ84, Q9CZ30, G3X982, Q9D0R2, Q00519	0.031704180684066
UP_KEYWORDS	Iron-sulfur	7	0.630630630630631	0.040142010312359	Q91VD9, Q9CR68, Q9DCB8, P28271, G3X982, Q9CQM9, Q00519	0.098151618205237
<b>Annotation Cluster 78</b> Enrichment Score: 1.0227578122344523						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Helicase	14	1.26126126126126	0.00293034772609	Q61655, Q91VR5, P97310, Q6NZQ2, P97311, O70133, Q9WTM5, Q62167, P54823, Q6NVF4, Q9JIK5, P49718, Q9EPU0, P23249	0.01091855591091
<b>Annotation Cluster 79</b> Enrichment Score: 0.9778497170775678						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Motor protein	12	1.08108108108108	0.017493596588581	Q6P9P6, P28740, Q8VDD5, P51807, O88447, Q61879, Q6URW6, O08638, Q9JHU4, P62627, P70248, Q8R1Q8	0.051126960201847
<b>Annotation Cluster 80</b> Enrichment Score: 0.9443242832063248						
Category	Term	Count	%	PValue	Genes	FDR
UP_SEQ_FEATURE	active site:Proton acceptor	58	5.22522522522523	0.000526183051914	Q8K1R7, Q62407, Q9JMH6, Q99L04, Q8BV14, Q62087, P11440, P68181, Q8JZN5, P12382, Q9D7B6, P63085, Q8BLN5, Q9JHR7, Q6P9R2, P05132, P49615, Q00519, Q9Z2A0, P54822, P18654, Q99MZ7, Q2TPA8, P05063, P05064, Q9D1A2, Q8K411, Q99JW2, O70551, Q2NL51, Q9EQ06, Q80X41, Q9CQ62, P31750, Q9CWJ9, Q3ULJ0, P47738, Q9JLT4, Q00612, Q03963, Q04899, Q9QVP9, O54988, P45952, P47857, Q91X52, P06801, Q9ESL4, P28352, Q58NB6, P14152, Q64261, Q9Z2G9, P17182, Q9WUA3, P28867, Q8CIN4, Q9JHW2	0.049461206879902
GOTERM_BP_DIRECT	GO:0018107~peptidyl-threonine phosphorylation	9	0.810810810810811	0.001065421197053	B2RQC6, P63085, Q6P9R2, Q9Z2A0, P05132, P28867, P31750, P11440, P49615	0.056954799581534

UP_KEYWORDS	Transferase	91	8.1981981981982	0.004771523339257	Q91YR5, Q9CWQ0, Q61510, Q9D6Y9, Q8K1R7, B2RQC6, P19096, Q62407, Q9WTP7, Q8K1J6, Q9DBL7, O35130, Q9CS42, P11440, P68181, P12382, Q9JLV6, P63085, Q8BY71, Q3THS6, Q6P9R2, Q1HFZ0, Q9JKX6, P05132, P49615, P10649, Q9WV85, Q8CFV9, Q9DBC7, Q3TRM8, Q91YQ5, Q9JL16, O08759, Q9Z2A0, Q8BMF4, Q64674, Q9DBG6, P18654, Q09200, Q68FH4, Q8VHI3, Q8K183, O09131, Q91WU5, P23492, Q99K85, Q91YL3, O70551, Q2NL51, O70310, Q80X41, P11103, Q9R0N0, Q80WS3, Q99KQ4, Q3TW96, P31750, Q93092, Q91ZJ5, Q9CWJ9, P40142, Q91V92, Q8JZK9, Q03963, Q04899, Q9QVP9, Q80VA0, O54988, P04184, Q6ZQM8, P47856, P47857, Q8CFI2, Q9ESL4, Q7TSS2, A2BDX3, Q64737, P26450, Q922K7, P97930, Q61183, Q8BWU5, Q64261, Q04447, P08030, Q5DW34, Q8BH69, Q9WUA3, P28867, Q8CIN4, P05201	0.016428536054152
UP_KEYWORDS	Kinase	42	3.78378378378378	0.018914653577931	Q8K1R7, Q91YL3, O70551, Q2NL51, Q62407, Q80X41, Q9WTP7, Q9R0N0, Q9DBL7, P31750, Q9CS42, P11440, P68181, P12382, Q9JLV6, P63085, Q03963, Q04899, Q9QVP9, Q6P9R2, O54988, P04184, P05132, P47857, P49615, Q9WV85, Q8CFV9, Q9DBC7, Q9ESL4, Q3TRM8, P26450, P97930, Q9Z2A0, P18654, Q68FH4, Q64261, Q04447, Q8K183, Q8BH69, Q9WUA3, P28867, Q8CIN4	0.053591518470804

**Annotation Cluster 81** Enrichment Score: 0.928923891773362

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Pyridoxal phosphate	7	0.630630630630631	0.037453151243749	Q99K85, P19096, Q9JL16, Q9Z2Y8, Q99K01, Q8VCN5, P05201	0.093461074663301

**Annotation Cluster 82** Enrichment Score: 0.7269971565574219

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Innate immunity	17	1.53153153153153	0.043681053747304	Q18PI6, Q61510, Q9D8Y7, Q9D8T2, P56477, Q6R5N8, P10107, P14106, P97814, Q62167, A2AIV8, Q80V11, P16110, Q62192, Q03963, Q921X6, Q9EPB4	0.102424539821265

**Annotation Cluster 83** Enrichment Score: 0.6711910709442734

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Metal-binding	166	14.954954954955	0.014459963770774	Q6P069, Q61510, Q11136, P97386, B2RQC6, P10711, Q9D967, P56399, Q99KB8, Q9DCB8, Q9DBH5, Q8VE47, Q9CS42, Q9JHR7, Q9Z1F9, Q3THS6, Q3TIU4, Q9JKX6, P62715, P60898, Q00519, Q8CFV9, Q9WV85, P97310, Q64518, P46460, O70200, O08759, P35564, Q8CG72, Q9CQX2, Q8BGB7, Q9WVQ5, P46737, Q8BP48, P57780, Q99N69, Q6IRU2, Q91W89, Q91W86, Q8K411, Q99JW2, Q7TPR4, Q0P678, Q9CY64, O08529, O35593, P11103, Q9QXX4, P29391, Q62384, Q9CPU0, Q571E4, Q6PGG2, O54984, Q8K4Z3, Q0P5W1, Q9D819, Q9ESL4, Q8BSY0, P28352, A2BDX3, P28474, P24270, Q64737, Q61183, P51855, Q80W54, Q91VM9, Q9EQP2, Q8BMD8, P39749, Q61462, Q61464, P53996, Q91VD9, Q3TIV5, Q8CHP8, Q9CQM9, P24547, P17182, P62748, Q92111, Q9WUA3, P28867, Q8BGQ7	0.043701223840561