

Supplementary Table 9: results of the pathway analysis by the David tool on the proteins modulated in response to 0.1 µm polystyrene particles

selection of clusters by a FDR cutoff value of 0.1

Annotation Cluster 1 Enrichment Score: 33.88072958076219

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0098641~cadherin binding involved in cell-cell adhesion	73	8.17469204927212	8.25764313235833E-38	Q61510, O70456, Q62448, P19096, Q9Z0P5, Q8BTM8, P12970, Q62167, Q6PAR5, Q80U87, P42225, Q9JHJ0, Q91VX2, Q60902, Q5FWK3, P61027, P25444, P07356, P84228, Q6Y7W8, Q8BH43, Q8BK64, P51432, P30999, Q62418, Q9CPV4, Q6NZJ6, Q8VDJ3, P57776, Q9QXS1, P54823, Q9DBG5, P42932, E9PVA8, O88844, Q9JLQ0, Q922Q8, P60229, Q9WVA4, Q8BVY0, Q9Z0N1, Q6ZQ58, Q78PY7, Q62261, Q9JKF1, Q7TQH0, Q99K01, Q9CWJ9, P63101, A2AGT5, Q8VDD5, Q9QYJ3, O54988, Q8K298, Q2L4X1, P62259, Q80UG5, P26039, Q9Z0G0, Q3UZ39, Q9CQV8, Q8CI51, Q9D8N0, Q9CZ30, Q9EQP2, Q3UEB3, P60122, P58252, P17182, P22682, Q9WUA3, Q8CIN4, Q9D0I9	3.77787173305394E-35
					Q61510, O70456, Q62448, P19096, Q9Z0P5, Q8BTM8, P12970, Q62167, Q6PAR5, Q80U87, P42225, Q9JHJ0, Q91VX2, Q60902, Q5FWK3, P61027, P25444, P07356, P84228, Q6Y7W8, Q8BH43, Q8BK64, P51432, P30999, Q62418, Q9CPV4, Q6NZJ6, Q8VDJ3, P57776, Q9QXS1, P54823, Q9DBG5, P42932, E9PVA8, O88844, Q9JLQ0, Q922Q8, P60229, Q9WVA4, Q8BVY0, Q9Z0N1, Q6ZQ58, Q78PY7, Q62261, Q9JKF1, Q7TQH0, Q99K01, Q9CWJ9, P63101, A2AGT5, Q8VDD5, Q9QYJ3, O54988, Q8K298, Q2L4X1, P62259, Q80UG5, P26039, Q9Z0G0, Q3UZ39, Q9CQV8, Q8CI51, Q9D8N0, Q9CZ30, Q9EQP2, Q3UEB3, P60122, P58252, P17182, P22682, Q9WUA3, Q8CIN4, Q9D0I9	
					O70456, Q62448, Q9Z0P5, P12970, Q6PAR5, Q80U87, P42225, Q91VX2, Q60902, Q5FWK3, P61027, P25444, P84228, Q6Y7W8, Q8BH43, Q8BK64, P51432, Q62418, Q9CPV4, Q6NZJ6, Q8VDJ3, P57776, Q9QXS1, P54823, Q9DBG5, O88844, Q922Q8, P60229, Q9WVA4, Q9Z0N1, Q6ZQ58, Q78PY7, Q7TQH0, Q99K01, Q9CWJ9, P63101, A2AGT5, Q9QYJ3, O54988, Q8K298, Q2L4X1, P26039, Q9Z0G0, Q3UZ39, Q9CQV8, Q8CI51, Q9D8N0, Q9CZ30, Q9EQP2, Q3UEB3, P17182, Q9WUA3, Q9D0I9	
GOTERM_CC_DIRECT	GO:0005913~cell-cell adherens junction	73	8.17469204927212	2.26018500126768E-36	Q61510, O70456, Q62448, P19096, Q9Z0P5, Q8BTM8, P12970, Q62167, Q6PAR5, Q80U87, P42225, Q9JHJ0, Q91VX2, Q60902, Q5FWK3, P61027, P25444, P07356, P84228, Q6Y7W8, Q8BH43, Q8BK64, P51432, P30999, Q62418, Q9CPV4, Q6NZJ6, Q8VDJ3, P57776, Q9QXS1, P54823, Q9DBG5, P42932, E9PVA8, O88844, Q9JLQ0, Q922Q8, P60229, Q9WVA4, Q8BVY0, Q9Z0N1, Q6ZQ58, Q78PY7, Q62261, Q9JKF1, Q7TQH0, Q99K01, Q9CWJ9, P63101, A2AGT5, Q8VDD5, Q9QYJ3, O54988, Q8K298, Q2L4X1, P62259, Q80UG5, P26039, Q9Z0G0, Q3UZ39, Q9CQV8, Q8CI51, Q9D8N0, Q9CZ30, Q9EQP2, Q3UEB3, P60122, P58252, P17182, P22682, Q9WUA3, Q8CIN4, Q9D0I9	2.92128911413847E-34
					Q61510, O70456, Q62448, P19096, Q9Z0P5, Q8BTM8, P12970, Q62167, Q6PAR5, Q80U87, P42225, Q9JHJ0, Q91VX2, Q60902, Q5FWK3, P61027, P25444, P07356, P84228, Q6Y7W8, Q8BH43, Q8BK64, P51432, P30999, Q62418, Q9CPV4, Q6NZJ6, Q8VDJ3, P57776, Q9QXS1, P54823, Q9DBG5, O88844, Q922Q8, P60229, Q9WVA4, Q9Z0N1, Q6ZQ58, Q78PY7, Q7TQH0, Q99K01, Q9CWJ9, P63101, A2AGT5, Q9QYJ3, O54988, Q8K298, Q2L4X1, P26039, Q9Z0G0, Q3UZ39, Q9CQV8, Q8CI51, Q9D8N0, Q9CZ30, Q9EQP2, Q3UEB3, P17182, Q9WUA3, Q9D0I9	
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GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	53	5.93505039193729	1.22126850950545E-29	Q61510, O70456, Q62448, P19096, Q9Z0P5, Q8BTM8, P12970, Q62167, Q6PAR5, Q80U87, P42225, Q9JHJ0, Q91VX2, Q60902, Q5FWK3, P61027, P25444, P07356, P84228, Q6Y7W8, Q8BH43, Q8BK64, P51432, Q62418, Q9CPV4, Q6NZJ6, Q8VDJ3, P57776, Q9QXS1, P54823, Q9DBG5, O88844, Q922Q8, P60229, Q9WVA4, Q9Z0N1, Q6ZQ58, Q78PY7, Q7TQH0, Q99K01, Q9CWJ9, P63101, A2AGT5, Q9QYJ3, O54988, Q8K298, Q2L4X1, P26039, Q9Z0G0, Q3UZ39, Q9CQV8, Q8CI51, Q9D8N0, Q9CZ30, Q9EQP2, Q3UEB3, P17182, Q9WUA3, Q9D0I9	3.00798433891192E-26
					Q61510, O70456, Q62448, P19096, Q9Z0P5, Q8BTM8, P12970, Q62167, Q6PAR5, Q80U87, P42225, Q9JHJ0, Q91VX2, Q60902, Q5FWK3, P61027, P25444, P07356, P84228, Q6Y7W8, Q8BH43, Q8BK64, P51432, Q62418, Q9CPV4, Q6NZJ6, Q8VDJ3, P57776, Q9QXS1, P54823, Q9DBG5, O88844, Q922Q8, P60229, Q9WVA4, Q9Z0N1, Q6ZQ58, Q78PY7, Q7TQH0, Q99K01, Q9CWJ9, P63101, A2AGT5, Q9QYJ3, O54988, Q8K298, Q2L4X1, P26039, Q9Z0G0, Q3UZ39, Q9CQV8, Q8CI51, Q9D8N0, Q9CZ30, Q9EQP2, Q3UEB3, P17182, Q9WUA3, Q9D0I9	
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Annotation Cluster 2 Enrichment Score: 21.388455818116206

Category	Term	Count	%	PValue	Genes	FDR
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UP_KEYWORDS	Nucleotide-binding	161	18.0291153415454	5.43175311558991E-33	<p>Q9JMH9, Q8K1R7, Q8CG48, Q61316, Q5U3K5, Q9WTP7, Q8K1J6, Q9DBL7, Q922B2, P11440, Q61035, P68181, Q61036, P12382, Q9EPU0, Q8BML9, Q9JLV6, P62196, Q62095, Q05D44, Q6P9R2, P61027, P49138, P46664, Q8BU30, Q569Z6, Q9DBC7, Q9QXB9, P58389, Q03265, Q9WUK4, Q9ER72, P18654, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q61655, Q6P9P6, Q6P3D0, Q91VR5, Q61656, Q9Z255, Q2NL51, Q80X41, Q5SUR0, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, P04184, P26638, Q8CFI2, Q80UG5, Q9CZ30, Q3V1L4, P97855, P32233, Q6PA06, Q9D2R0, O54950, P60122, P33174, Q64261, Q04447, Q99LE6, Q9D1G2, Q8BH69, Q8CIN4, Q3UFY7, P07742, P54775, Q8BFR5, P97386, Q8C0C7, B2RQC6, P46471, Q61879, Q9D2Y4, P37913, Q8VE47, Q9CS42, Q62167, P63085, P61222, Q9Z1F9, Q3THS6, P46467, P05132, Q8R1Q8, Q9WV85, Q91WQ3, P97311, Q3TRM8, Q9WTM5, O08638, P61082, P70698, P54823, P35601, P42932, Q8R050, Q68FH4, P61750, Q8BP47, Q61699, P28740, P54276, Q9Z0N1, O70551, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, Q9JM14, P49718, O54984, Q04899, Q03963, P61087, Q9QUJ7, O54988, P62334, Q9D7H3, O35626, P80315, P97494, P80314, Q9Z1Q9, Q9ESL4, Q9CQN1, P80313, Q64737, Q61183, P97930, P51855, Q9EQP2, P62192, Q99M31, Q3THK7, O08810, Q3UM18, Q9D0R2, Q9WUA2, P47809, P58252, P84078, P51859, Q6URW6, Q9WUA3, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316</p>	3.82938594649088E-31
					<p>Q9JMH9, Q8K1R7, Q8CG48, Q61316, Q8K1J6, Q9DBL7, Q922B2, P11440, Q61035, P68181, Q61036, P12382, Q9EPU0, Q8BML9, Q9JLV6, P62196, Q62095, Q6P9R2, P49138, Q8BU30, Q569Z6, P58389, Q03265, Q9WUK4, Q9ER72, P18654, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q61655, Q6P9P6, Q91VR5, Q61656, Q9Z255, Q2NL51, Q80X41, Q5SUR0, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, P04184, P26638, Q8CFI2, Q9CZ30, P97855, Q9D2R0, O54950, P60122, P33174, Q64261, Q04447, Q99LE6, Q9D1G2, Q8BH69, Q8CIN4, P07742, P54775, P97386, Q8C0C7, B2RQC6, P46471, Q61879, Q9D2Y4, P37913, Q8VE47, Q9CS42, Q62167, P63085, P61222, Q9Z1F9, Q3THS6, P46467, P05132, Q8R1Q8, Q9WV85, Q91WQ3, P97311, Q3TRM8, Q9WTM5, O08638, P61082, P70698, P54823, P35601, P42932, Q68FH4, Q8BP47, Q61699, P28740, P54276, O70551, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, P49718, O54984, Q04899, Q03963, P61087, Q9QUJ7, O54988, P62334, Q9D7H3, P80315, P97494, P80314, Q9Z1Q9, Q9ESL4, Q9CQN1, P80313, Q64737, Q61183, P97930, P51855, Q9EQP2, P62192, Q99M31, Q3THK7, Q9D0R2, Q9WUA2, P47809, Q6URW6, Q9WUA3, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316</p>	
UP_KEYWORDS	ATP-binding	137	15.3415453527436	9.12062341842937E-32	<p>Q9JMH9, Q8K1R7, Q8CG48, Q61316, Q8K1J6, Q9DBL7, Q922B2, P11440, Q61035, P68181, Q61036, P12382, Q9EPU0, Q8BML9, Q9JLV6, P62196, Q62095, Q6P9R2, P49138, Q8BU30, Q569Z6, P58389, Q03265, Q9WUK4, Q9ER72, P18654, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q61655, Q6P9P6, Q91VR5, Q61656, Q9Z255, Q2NL51, Q80X41, Q5SUR0, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, P04184, P26638, Q8CFI2, Q9CZ30, P97855, Q9D2R0, O54950, P60122, P33174, Q64261, Q04447, Q99LE6, Q9D1G2, Q8BH69, Q8CIN4, P07742, P54775, P97386, Q8C0C7, B2RQC6, P46471, Q61879, Q9D2Y4, P37913, Q8VE47, Q9CS42, Q62167, P63085, P61222, Q9Z1F9, Q3THS6, P46467, P05132, Q8R1Q8, Q9WV85, Q91WQ3, P97311, Q3TRM8, Q9WTM5, O08638, P61082, P70698, P54823, P35601, P42932, Q68FH4, Q8BP47, Q61699, P28740, P54276, O70551, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, P49718, O54984, Q04899, Q03963, P61087, Q9QUJ7, O54988, P62334, Q9D7H3, P80315, P97494, P80314, Q9Z1Q9, Q9ESL4, Q9CQN1, P80313, Q64737, Q61183, P97930, P51855, Q9EQP2, P62192, Q99M31, Q3THK7, Q9D0R2, Q9WUA2, P47809, Q6URW6, Q9WUA3, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316</p>	5.14403160799416E-30
					<p>Q9JMH9, Q8K1R7, Q8CG48, Q61316, Q8K1J6, Q9DBL7, Q922B2, P11440, Q61035, P68181, Q61036, P12382, Q9EPU0, Q8BML9, Q9JLV6, P62196, Q62095, Q6P9R2, P49138, Q8BU30, Q569Z6, P58389, Q03265, Q9WUK4, Q9ER72, P18654, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q61655, Q6P9P6, Q91VR5, Q61656, Q9Z255, Q2NL51, Q80X41, Q5SUR0, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, P04184, P26638, Q8CFI2, Q9CZ30, P97855, Q9D2R0, O54950, P60122, P33174, Q64261, Q04447, Q99LE6, Q9D1G2, Q8BH69, Q8CIN4, P07742, P54775, P97386, Q8C0C7, B2RQC6, P46471, Q61879, Q9D2Y4, P37913, Q8VE47, Q9CS42, Q62167, P63085, P61222, Q9Z1F9, Q3THS6, P46467, P05132, Q8R1Q8, Q9WV85, Q91WQ3, P97311, Q3TRM8, Q9WTM5, O08638, P61082, P70698, P54823, P35601, P42932, Q68FH4, Q8BP47, Q61699, P28740, P54276, O70551, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, P49718, O54984, Q04899, Q03963, P61087, Q9QUJ7, O54988, P62334, Q9D7H3, P80315, P97494, P80314, Q9Z1Q9, Q9ESL4, Q9CQN1, P80313, Q64737, Q61183, P97930, P51855, Q9EQP2, P62192, Q99M31, Q3THK7, Q9D0R2, Q9WUA2, P47809, Q6URW6, Q9WUA3, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316</p>	

GOTERM_MF_DIRECTGO:0000166~nucleotide binding	178	19.93281075028	1.89087123323823E-26	<p>Q9JMH9, Q8K1R7, Q8CG48, Q61316, Q5U3K5, Q9WTP7, Q8K1J6, Q9DBL7, Q922B2, P11440, Q61035, P68181, Q61036, P12382, Q9EPU0, Q9JLV6, P62196, Q62095, Q05D44, Q6P9R2, P61027, P49138, P46664, Q8BU30, Q569Z6, Q9DBC7, Q9QXB9, P58389, Q03265, Q9WUK4, Q9ER72, P18654, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q61655, Q6P9P6, Q6P3D0, Q91VR5, Q61656, Q9Z255, Q2NL51, Q80X41, Q99K48, Q9Z1D1, Q62189, Q5SUR0, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, Q6NVF9, P04184, P26638, O35309, Q8CFI2, Q80UG5, Q9CZ30, Q3V1L4, P97855, P32233, Q6PA06, Q9D2R0, O54950, O08583, P60122, P33174, Q64261, Q04447, Q8R4X3, Q99LE6, Q9D1G2, Q8BH69, Q8CIN4, Q3UFY7, Q9CQI7, P07742, P54775, Q8BFR5, P97386, Q8C0C7, B2RQC6, P46471, Q61879, Q9D2Y4, P37913, Q8VE47, Q9CS42, Q62167, P63085, P61222, Q9Z1F9, Q3THS6, P46467, P05132, Q8R1Q8, Q9WV85, Q91WQ3, Q9CPN8, P97311, Q3TRM8, P29341, Q9JL18, Q6PDM2, Q9WTM5, O08638, Q6A0A2, P61082, P70698, P54823, P35601, P42932, Q8R050, Q68FH4, P61750, Q8BP47, Q61699, P28740, P54276, Q9Z0N1, O70551, Q8R3C6, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, Q9JM14, P49718, O54984, Q04899, Q03963, P61087, Q9QUJ7, O54988, P62334, Q9D7H3, O35626, P80315, P97494, P80314, Q9Z1Q9, Q9ESL4, Q9CQN1, P80313, Q64737, P97379, Q61183, P97930, P51855, Q9EQP2, P62192, Q99020, Q99M31, Q3THK7, Q3UEB3, O08810, Q3UM18, Q9D0R2, Q9WUA2, P47809, P58252, P84078, P51859, Q6URW6, P24547, Q9WUA3, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316</p>	5.76715726137661E-24
GOTERM_MF_DIRECTGO:0005524~ATP binding	143	16.013437849944	3.54161757023658E-22	<p>Q9JMH9, Q8K1R7, Q8CG48, Q61316, Q9Z0P5, Q9WTP7, Q8K1J6, Q9DBL7, Q922B2, P11440, Q61035, P68181, Q61036, P12382, Q9EPU0, Q8BML9, Q9JLV6, P62196, Q62095, Q6P9R2, P49138, Q8BU30, Q569Z6, P58389, Q03265, Q9WUK4, Q9ER72, P18654, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q9CXY6, Q61655, Q6P9P6, Q91VR5, Q61656, Q9Z255, Q2NL51, Q80X41, Q5SUR0, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, P04184, P26638, Q8CFI2, Q8BH61, Q9CZ30, P97855, Q9D2R0, O54950, P60122, P33174, Q64261, Q04447, Q9DBQ7, Q99LE6, Q9D1G2, Q8BH69, Q8CIN4, P07742, P54775, P97386, Q8C0C7, B2RQC6, P46471, Q61879, Q9D2Y4, P37913, Q8VE47, Q9CS42, Q62167, P63085, P61222, Q9Z1F9, Q3THS6, P46467, P05132, Q8R1Q8, Q9WV85, Q91WQ3, P97311, Q3TRM8, Q9WTM5, O08638, P61082, P70698, P54823, P35601, P42932, Q68FH4, Q8BP47, Q61699, P28740, P54276, O70551, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, P49718, O54984, Q04899, Q03963, P61087, Q9QYJ0, Q9QUJ7, O54988, P62334, Q9D7H3, P80315, P97494, P80314, Q9Z1Q9, Q9ESL4, Q9CQN1, P80313, Q64737, Q61183, P97930, P51855, Q9EQP2, P62192, Q99M31, Q3THK7, Q9D0R2, Q9WUA2, P47809, Q6URW6, Q9WUA3, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316</p>	6.48116015353294E-20

UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	85	9.51847704367301	5.19573859541068E-11	P54775, Q8CG48, Q9JMH9, Q8K1R7, P46471, Q61879, Q9DBL7, Q62167, Q9CS42, P11440, P68181, Q61036, P12382, Q9EPU0, Q9JLV6, P63085, P62196, Q62095, Q3THS6, Q9Z1F9, Q6P9R2, P49138, P46467, P05132, Q8R1Q8, Q569Z6, P97311, Q3TRM8, Q03265, Q9WTM5, O08638, Q9WUK4, P54823, P18654, P35601, Q02053, Q68FH4, Q8K183, O88685, Q9JHU4, Q6P9P6, Q61655, Q91VR5, Q61656, P28740, P54276, O70551, Q2NL51, Q80X41, Q9R0N0, P50516, P70248, P31750, Q5SUR0, Q922D8, P49718, Q8CGC7, Q8VDD5, Q9CZD3, O54984, Q91V92, Q03963, Q04899, O54988, P04184, P26638, P62334, Q9ESL4, Q64737, Q9CZ30, P97930, P51855, Q9EQP2, P62192, Q3THK7, P47809, P60122, P33174, Q64261, Q04447, Q6URW6, Q9D1G2, Q8BH69, Q9WUA3, Q8CIN4	1.02304092943636E-07
					P54775, Q8CG48, Q8BFR5, Q9JMH9, P46471, Q61879, Q5U3K5, Q9WTP7, Q9DBL7, Q62167, Q9EPU0, Q9JLV6, P61222, P62196, Q62095, Q05D44, P61027, P46467, P46664, Q8R1Q8, P97311, Q9QXB9, Q03265, Q9WTM5, O08638, Q9WUK4, P54823, P70698, P35601, Q8R050, P61750, O88685, Q9JHU4, Q6P9P6, Q61655, Q91VR5, Q61656, P28740, P54276, Q9Z0N1, Q9JKF1, P50516, P70248, Q922D8, P49718, Q8VDD5, O54984, P04184, P62334, Q00P19, Q80UG5, O35626, Q9CZ30, P97930, P32233, Q9EQP2, Q6PA06, P62192, O08810, Q3UM18, P60122, P33174, P58252, P84078, Q6URW6, Q99LE6, Q9D1G2, Q6P542	
INTERPRO	IPR027417:P-loop containing nucleoside triphosphate hydrolase	68	7.61478163493841	2.70887916785413E-08		4.42149277508635E-06
Annotation Cluster 3						
Category	Enrichment Score: 8.540858437494068 Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Protein biosynthesis	43	4.81522956326988	1.04429686114307E-27	P32921, Q8BFR5, Q62448, P10711, Q9Z0N1, Q8C0C7, O70194, P31230, Q9DCH4, Q9Z1D1, Q922B2, Q61035, Q8CGC7, Q8BML9, Q9CZD3, Q03963, Q8BMJ2, P63242, Q8BMJ3, Q05D44, P26638, Q8BU30, Q9Z1Q9, Q91WQ3, Q99JX4, Q9D8N0, Q99LC8, Q6NZJ6, Q8R1B4, Q9ER72, P57776, O08810, Q9D0R2, Q68FL6, Q9WUA2, Q8R050, Q8BP47, P58252, Q61749, P23116, P60229, Q8BGQ7, Q9D0I9	4.90819524737241E-26
UP_KEYWORDS	Aminoacyl-tRNA synthetase	19	2.12765957446808	3.50251491486403E-17	P32921, Q9Z1Q9, Q91WQ3, Q8C0C7, Q922B2, Q9ER72, Q61035, Q9D0R2, Q68FL6, Q8CGC7, Q9WUA2, Q8BML9, Q8BP47, Q9CZD3, Q8BMJ2, P26638, Q8BU30, Q8BGQ7, Q9D0I9	8.97917459992415E-16
GOTERM_MF_DIRECT	GO:0004812~aminoacyl-tRNA ligase activity	19	2.12765957446808	2.18751227150796E-15	P32921, Q9Z1Q9, Q91WQ3, Q8BH61, Q8C0C7, Q922B2, Q9ER72, Q61035, Q9D0R2, Q68FL6, Q8CGC7, Q9WUA2, Q8BP47, Q9CZD3, Q8BMJ2, P26638, Q8BU30, Q8BGQ7, Q9D0I9	2.85939104061398E-13
GOTERM_BP_DIRECT	GO:0006418~tRNA aminoacylation for protein translation	18	2.01567749160134	4.8898385307608E-15	P32921, Q9Z1Q9, Q91WQ3, Q8BH61, P31230, Q922B2, Q9ER72, Q61035, Q9D0R2, Q68FL6, Q8CGC7, Q8BML9, Q8BP47, Q9CZD3, Q8BMJ2, P26638, Q8BU30, Q9D0I9	4.01455743375462E-12
UP_KEYWORDS	Ligase	43	4.81522956326988	8.99331198749337E-14	P32921, Q61510, P97386, Q9R1T2, B2RQC6, Q8C0C7, Q922B2, P37913, A2AN08, Q61035, Q5SUR0, Q922D8, Q99PP7, Q8CGC7, Q8BML9, Q9CZD3, Q99KP6, Q8BMJ2, Q9Z1F9, Q9QUJ7, P26638, P46664, Q8BU30, Q9D7H3, P97494, Q9Z1Q9, Q91WQ3, Q62318, Q64737, P51855, Q9ER72, P61082, Q3THK7, P70698, Q9D2R0, Q9D0R2, Q02053, Q68FL6, Q9WUA2, Q8BP47, P22682, Q8BGQ7, Q9D0I9	1.81150998605224E-12
GOTERM_MF_DIRECT	GO:0016874~ligase activity	42	4.70324748040314	3.33506726117029E-09	P32921, Q61510, P97386, Q9R1T2, B2RQC6, Q8C0C7, Q922B2, P37913, A2AN08, Q61035, Q5SUR0, Q922D8, Q99PP7, Q8CGC7, Q9CZD3, Q99KP6, Q8BMJ2, Q9Z1F9, Q9QUJ7, P26638, P46664, Q8BU30, Q9D7H3, P97494, Q9Z1Q9, Q91WQ3, Q62318, Q64737, P51855, Q9ER72, P61082, Q3THK7, P70698, Q9D2R0, Q9D0R2, Q02053, Q68FL6, Q9WUA2, Q8BP47, P22682, Q8BGQ7, Q9D0I9	3.81448317996352E-07

KEGG_PATHWAY	mmu00970:Aminoacyl-tRNA biosynthesis	19	2.12765957446808	8.76919154725896E-09	P32921, Q9Z1Q9, Q91WQ3, Q8C0C7, Q922B2, Q9ER72, Q61035, Q9D0R2, Q68FL6, Q8CGC7, Q9WUA2, Q8BML9, Q8BP47, Q9CZD3, Q8BMJ2, P26638, Q8BU30, Q8BGQ7, Q9D0I9	9.64611070198486E-07
UP_SEQ_FEATURE	short sequence motif:"HIGH" region	9	1.00783874580067	1.41003448315905E-07	P32921, Q68FL6, Q9Z1Q9, Q8CGC7, Q91WQ3, Q8BMJ2, Q8BU30, Q9ER72, Q9D0I9	0.000137138020892
INTERPRO	IPR014729:Rossmann-like alpha/beta/alpha sandwich fold	12	1.3437849944009	3.36769827544882E-07	P32921, Q68FL6, Q9Z1Q9, Q8CGC7, Q8BML9, Q91WQ3, Q8BMJ2, Q9DBL7, Q8BU30, Q3THK7, Q9ER72, Q9D0I9	3.24173042085191E-05
INTERPRO	IPR001412:Aminoacyl-tRNA synthetase, class I, conserved site	8	0.895856662933931	3.9721679765374E-07	P32921, Q68FL6, Q9Z1Q9, Q8CGC7, Q8BML9, Q8BMJ2, Q8BU30, Q9D0I9	3.24173042085191E-05
UP_SEQ_FEATURE	short sequence motif:"KMSKS" region	8	0.895856662933931	9.51551211847182E-07	P32921, Q68FL6, Q9Z1Q9, Q8CGC7, Q91WQ3, Q8BMJ2, Q8BU30, Q9ER72	0.000374720867225
INTERPRO	IPR006195:Aminoacyl-tRNA synthetase, class II	8	0.895856662933931	1.12654918173837E-06	Q8CGC7, Q8BP47, Q8C0C7, Q9CZD3, P26638, Q922B2, Q61035, Q9D0R2	8.27450373986836E-05
INTERPRO	IPR009080:Aminoacyl-tRNA synthetase, class 1a, anticodon-binding	6	0.671892497200448	6.21542626048933E-05	Q68FL6, Q9Z1Q9, Q8BMJ2, Q8BU30, Q9ER72, Q9D0I9	0.003804358823608
Annotation Cluster 4	Enrichment Score: 7.16237599917099					
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Actin-binding	29	3.2474804031355	2.61002940668022E-08	O89053, Q7TPR4, Q61879, Q9Z0P5, Q62261, Q8BTM8, P70248, Q9JHJ0, P21107, Q8VDD5, Q9CVB6, Q9JM76, P47754, Q8K298, Q8BQ30, Q8BH43, P97376, Q8VD75, O70200, Q62418, O08638, Q9WUM4, Q9D2V7, Q9QXS1, P13020, P57780, Q6URW6, Q9CQI6, O88342	3.68014146341911E-07
GOTERM_MF_DIRECT	GO:0051015~actin filament binding	22	2.46360582306831	8.50716731441449E-08	O89053, Q9JMH9, Q7TPR4, P97376, Q8VD75, Q61879, O70200, Q62418, Q8BTM8, O08539, Q9WUM4, Q71LX4, Q3UQ44, Q8VDD5, Q9CVB6, Q9JM76, P58252, P57780, Q6URW6, O88342, Q8C052, P26039	5.70146351784828E-06
GOTERM_MF_DIRECT	GO:0003779~actin binding	37	4.14333706606943	1.46703889292032E-07	O89053, Q7TPR4, Q61879, Q9Z0P5, Q62261, Q8BTM8, Q71LX4, P70248, Q9JHJ0, P21107, Q8VDD5, Q9CVB6, P68510, Q9JM76, P47754, P61982, Q8K298, P26039, Q8BQ30, Q8BH43, Q9Z0G0, P97376, Q8C151, Q8VD75, O70200, Q62418, O08638, Q9WUM4, Q9D2V7, Q9QXS1, P97814, P70315, P13020, P57780, Q6URW6, Q9CQI6, O88342	8.94893724681394E-06
Annotation Cluster 5	Enrichment Score: 7.008903138754214					
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0030529~intracellular ribonucleoprotein complex	49	5.48712206047032	1.21322104090703E-16	P62918, Q9EQK5, P35979, Q9D7S7, P62082, Q6P5F9, P12970, P14115, Q61990, Q80ZK0, O09167, P62317, P25444, P62830, P29341, Q9WTM5, Q60591, Q9D7A6, P62320, P14131, P57780, P62889, P49962, P62843, Q9CXY6, Q91VR5, Q61656, P99027, Q80WS3, Q9JKF1, Q8BMA6, Q62189, P67984, Q8CGC7, Q6NVF9, Q924T2, P62852, P62908, Q9CQJ2, P97379, Q9D338, Q99020, Q3UEB3, Q9CQV5, P60122, P58252, Q9D8E6, P62702, Q9CQI7	7.84044097686166E-15
UP_KEYWORDS	Ribonucleoprotein	36	4.03135498320269	2.57268649762329E-10	P62918, P35979, Q9EQK5, P99027, Q9D7S7, Q9CQK8, P62082, Q80WS3, Q8BMA6, P14115, Q61990, P12970, Q62189, Q80ZK0, P67984, P63323, O09167, P62317, Q924T2, P25444, P62852, P62830, P62908, Q9D338, Q9D7A6, Q99020, Q3UEB3, Q9CQV5, P62320, P14131, Q9D8E6, P62702, P62889, P49962, P62843, Q9CQI7	4.53435995206105E-09
GOTERM_CC_DIRECT	GO:0005840~ribosome	25	2.79955207166853	1.47531169955735E-07	P62918, P35979, P99027, Q9D7S7, P62082, P14115, P12970, Q80ZK0, P67984, O09167, Q924T2, P25444, P62852, P62830, P62908, Q9D338, P35564, Q99M31, Q9CQV5, P14131, Q9D8E6, P62702, P62889, Q6P542, P62843	3.81368074335574E-06
UP_KEYWORDS	Ribosomal protein	23	2.57558790593505	1.22690622346629E-06	P62918, P62908, P35979, P99027, Q9D7S7, Q9D338, P62082, P12970, P14115, Q9CQV5, Q80ZK0, P14131, P67984, P63323, Q9D8E6, O09167, P62702, P62889, Q924T2, P25444, P62852, P62830, P62843	1.3307213654519E-05

KEGG_PATHWAY	mmu03010:Ribosome	22	2.46360582306831	3.95788466244988E-05	P62918, P62908, P35979, P99027, Q9D7S7, Q9D338, P62082, P12970, P14115, Q80ZK0, P14131, P67984, P63323, Q9D8E6, O09167, P62702, P62889, Q924T2, P25444, P62852, P62830, P62843	0.001741469251478
GOTERM_CC_DIRECT	GO:0022625~cytosolic large ribosomal subunit	13	1.45576707726764	0.000139807490362	P62918, P35979, P99027, Q9D7S7, P12970, P14115, P67984, P63323, Q9D8E6, O09167, P62889, P62830, Q8BVY0	0.002190317349007
GOTERM_MF_DIRECT	GO:0003735~structural constituent of ribosome	22	2.46360582306831	0.002771165718843	P62918, P62908, P35979, P99027, Q9D7S7, Q9D338, P62082, P14115, Q9CQV5, Q80ZK0, P14131, P67984, P63323, Q9D8E6, O09167, P62702, P62889, Q924T2, P25444, P62852, P62830, P62843	0.06037182458908
Annotation Cluster 6 Enrichment Score: 6.874711952375081						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0000502~proteasome complex	29	3.2474804031355	5.15257484483323E-23	Q9D8W5, P54775, P46471, O35593, Q9WUP7, Q9R1P4, Q9CR00, P61290, Q9CZH3, O35226, P62196, Q9Z2U1, P26516, P62334, O09061, P97371, P97372, Q3TXS7, Q9JMA1, P70195, Q9EST4, P62192, P54726, Q99J14, Q922Y1, Q9QUM9, O88685, Q8R317, Q9Z2X2	3.80554456396968E-21
UP_KEYWORDS	Proteasome	25	2.79955207166853	3.54509365545851E-21	Q9D8W5, P54775, P46471, O35593, Q9WUP7, Q9R1P4, Q9CR00, P61290, O35226, P62196, Q9Z2U1, P26516, P62334, O09061, P97371, P97372, Q3TXS7, Q9JMA1, P70195, P62192, P54726, Q99J14, Q9QUM9, O88685, Q8R317	1.11079601204367E-19
KEGG_PATHWAY	mmu03050:Proteasome	20	2.23964165733483	5.08170507165565E-13	P97372, Q9D8W5, P54775, Q3TXS7, P70195, P46471, O35593, Q9R1P4, P62192, P61290, Q99J14, O35226, P62196, Q9Z2U1, Q9QUM9, O88685, P26516, P62334, O09061, P97371	1.11797511576424E-10
GOTERM_CC_DIRECT	GO:0008540~proteasome regulatory particle, base subcomplex	11	1.23180291153415	1.26193618905255E-12	P54775, O35226, Q3TXS7, P46471, P62196, P62192, O88685, Q8BJY1, P62334, Q9CR00, Q9Z2X2	6.52421009740169E-11
GOTERM_CC_DIRECT	GO:0022624~proteasome accessory complex	12	1.3437849944009	1.81161688214238E-12	Q9D8W5, P54775, Q99J14, O35226, Q3TXS7, P46471, P62196, O35593, P62192, O88685, Q8BJY1, P62334	8.51459934606918E-11
GOTERM_CC_DIRECT	GO:0031597~cytosolic proteasome complex	8	0.895856662933931	1.05856209854079E-08	P54775, P46471, P62196, O35593, Q9WUP7, P62192, O88685, P62334	3.42047878090994E-07
GOTERM_CC_DIRECT	GO:0031595~nuclear proteasome complex	7	0.783874580067189	6.90977952254155E-08	Q9D8W5, P54775, P46471, P62196, P62192, O88685, P62334	1.98464222952999E-06
INTERPRO	IPR005937:26S proteasome subunit P45	6	0.671892497200448	3.58339590976844E-07	P54775, P46471, P62196, P62192, O88685, P62334	3.24173042085191E-05
GOTERM_MF_DIRECT	GO:0036402~proteasome-activating ATPase activity	6	0.671892497200448	6.43050340315827E-07	P54775, P46471, P62196, P62192, O88685, P62334	3.26883922993879E-05
GOTERM_BP_DIRECT	GO:0045899~positive regulation of RNA polymerase II transcriptional preinit	6	0.671892497200448	5.94830119781498E-05	P54775, P46471, P62196, P62192, O88685, P62334	0.007234431634192
INTERPRO	IPR003959:ATPase, AAA-type, core	9	1.00783874580067	0.000298409142106	P54775, P46471, P62196, P62192, O88685, P46467, Q9WUK4, P62334, P35601	0.015655822491194
INTERPRO	IPR003960:ATPase, AAA-type, conserved site	7	0.783874580067189	0.000341453589796	P54775, P46471, P62196, P62192, O88685, P46467, P62334	0.017296390462439
GOTERM_BP_DIRECT	GO:0030163~protein catabolic process	9	1.00783874580067	0.000456295850684	P54775, Q9D4H8, P46471, P62196, Q9D906, P62192, O88685, P62334, P31750	0.034056263037421
INTERPRO	IPR003593:AAA+ ATPase domain	15	1.67973124300112	0.00075693763269	P54775, P46471, Q9WTM5, P62192, Q9WUK4, P35601, P61222, P60122, P62196, O88685, Q99LE6, P46467, Q9JHU4, P62334, Q6P542	0.030052469795193
SMART	SM00382:AAA	15	1.67973124300112	0.000890808836471	P54775, P46471, Q9WTM5, P62192, Q9WUK4, P35601, P61222, P60122, P62196, O88685, Q99LE6, P46467, Q9JHU4, P62334, Q6P542	0.024843668661584
KEGG_PATHWAY	mmu05169:Epstein-Barr virus infection	18	2.01567749160134	0.001209630829409	Q9D8W5, P54775, Q3TXS7, P46471, O35593, P62192, P31750, Q04207, Q99J14, O35226, P47809, Q03963, P62196, P25799, O88685, P26516, P62334, P42227	0.017741252164662
GOTERM_MF_DIRECT	GO:0017025~TBP-class protein binding	6	0.671892497200448	0.001308829305995	P54775, P46471, P62196, P62192, O88685, P62334	0.032366994999614
Annotation Cluster 7 Enrichment Score: 6.562235809367333						
Category	Term	Count	%	PValue	Genes	FDR

UP_KEYWORDS	Chaperone	36	4.03135498320269	1.28671271825218E-16	Q99L47, P11983, Q9CR00, Q9CZH3, P61222, Q61081, P62075, Q64152, Q9QYJ0, Q9QYJ3, P0C7N9, P80315, P80314, Q8BK64, Q9CQN1, P80313, P54103, P61759, Q9CR16, Q9WU28, Q9EST4, P35564, Q8BJY1, Q99M31, Q64378, O08997, P42932, O08583, Q9CYG7, Q9CQI6, Q9CWM4, Q9QYI3, P80318, P80317, Q9Z2X2, P80316	3.02377488789263E-15
GOTERM_BP_DIRECT	GO:1904874~positive regulation of telomerase RNA localization to Cajal body	10	1.11982082866741	8.9804718117527E-10	P80315, P80314, P80313, P42932, P60122, P11983, Q9WTM5, P80318, P80317, P80316	4.42378041446938E-07
GOTERM_BP_DIRECT	GO:1904871~positive regulation of protein localization to Cajal body	8	0.895856662933931	1.12413926123429E-09	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	4.61459166736675E-07
GOTERM_CC_DIRECT	GO:0005832~chaperonin-containing T-complex	8	0.895856662933931	3.28164587534659E-09	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	1.13107394503612E-07
GOTERM_BP_DIRECT	GO:0006457~protein folding	23	2.57558790593505	5.56277961063175E-09	P80315, P80314, Q8BK64, Q9CQN1, P80313, P61759, Q9CR16, Q9WU28, Q99L47, P11983, P35564, Q64378, Q8R180, P42932, Q61081, Q9QYJ0, Q9QYJ3, Q9CWM4, P80318, Q8BGQ7, P80317, P80316, Q8R1N4	1.95730374014086E-06
GOTERM_MF_DIRECT	GO:0051082~unfolded protein binding	18	2.01567749160134	6.33263421101452E-09	P80315, P80314, Q9CQN1, P80313, Q9WU28, Q99L47, P11983, P35564, Q8BQM4, P42932, Q61081, Q9QYJ0, Q9QYJ3, Q9CWM4, P80318, P80317, P80316, Q8R1N4	6.43817811453142E-07
INTERPRO	IPR027410:TCP-1-like chaperonin intermediate domain	8	0.895856662933931	8.68541583576768E-09	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	3.18971896568568E-06
INTERPRO	IPR002194:Chaperonin TCP-1, conserved site	8	0.895856662933931	8.68541583576768E-09	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	3.18971896568568E-06
INTERPRO	IPR017998:Chaperone tailless complex polypeptide 1 (TCP-1)	8	0.895856662933931	2.31357521551534E-08	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	4.24830248949004E-06
GOTERM_CC_DIRECT	GO:0002199~zona pellucida receptor complex	8	0.895856662933931	1.37193317232973E-07	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	3.73310236891826E-06
INTERPRO	IPR027409:GroEL-like apical domain	8	0.895856662933931	2.18694916472059E-07	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	2.47125255613427E-05
INTERPRO	IPR027413:GroEL-like equatorial domain	8	0.895856662933931	2.18694916472059E-07	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	2.47125255613427E-05
GOTERM_BP_DIRECT	GO:1904851~positive regulation of establishment of protein localization to tel	7	0.783874580067189	2.81670370336046E-07	P80315, P80314, P80313, P42932, P11983, P80317, P80316	7.70837913486311E-05
INTERPRO	IPR002423:Chaperonin Cpn60/TCP-1	8	0.895856662933931	3.9721679765374E-07	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	3.24173042085191E-05
GOTERM_BP_DIRECT	GO:1901998~toxin transport	11	1.23180291153415	6.48242126646055E-07	P80315, P80314, P80313, P42932, P61924, P29452, Q8R0H9, P11983, P80318, P80317, P80316	0.000145147305266
GOTERM_BP_DIRECT	GO:0032212~positive regulation of telomere maintenance via telomerase	10	1.11982082866741	2.74917944464889E-06	P80315, P80314, P80313, P42932, Q9JLV6, P63085, P11983, P80318, P80317, P80316	0.00052086376709
GOTERM_BP_DIRECT	GO:0007339~binding of sperm to zona pellucida	9	1.00783874580067	6.43944412919921E-05	P80315, P80314, P80313, P42932, P11983, P80318, P80317, Q80X50, P80316	0.007234431634192
GOTERM_BP_DIRECT	GO:0050821~protein stabilization	16	1.79171332586786	0.000160561181118	P80315, P80314, P80313, P11438, Q8VD75, Q8BTM8, P11983, Q9QUR7, Q91YE6, P17047, P42932, Q61081, Q80UM3, P80318, P80317, P80316	0.0146467477442
GOTERM_CC_DIRECT	GO:0044297~cell body	13	1.45576707726764	0.000412563429801	P80315, P80314, Q9CXW3, P80313, P03995, P11983, P42932, P51807, O09131, Q91V12, P80318, P80317, P80316	0.005469110082235

Annotation Cluster 8 Enrichment Score: 5.773752457285372

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006413~translational initiation	19	2.12765957446808	1.12627335718676E-12	Q62448, Q99JX4, Q6ZQ58, Q9Z0N1, Q99LC8, Q9DCH4, O70194, Q9Z1D1, Q6NZJ6, Q8R1B4, Q62167, P61222, Q62095, Q8BMJ3, Q61749, Q05D44, P23116, P60229, Q6P542	6.93502819687747E-10
UP_KEYWORDS	Initiation factor	15	1.67973124300112	1.83219510915517E-08	Q62448, Q99JX4, Q9Z0N1, Q99LC8, Q9DCH4, O70194, Q9Z1D1, Q6NZJ6, Q8R1B4, Q03963, Q8BMJ3, Q61749, Q05D44, P23116, P60229	2.71936326727241E-07
GOTERM_CC_DIRECT	GO:0005852~eukaryotic translation initiation factor 3 complex	9	1.00783874580067	3.54557556111695E-08	Q99JX4, P61222, Q9DCH4, O70194, P23116, Q9Z1D1, Q8R1B4, P60229, Q62167	1.07827209711616E-06
GOTERM_BP_DIRECT	GO:0006446~regulation of translational initiation	11	1.23180291153415	3.51118540957044E-07	Q62448, Q99JX4, Q99LC8, Q9DCH4, Q05D44, O70194, P23116, Q9Z1D1, Q6NZJ6, Q8R1B4, P60229	8.648049663772E-05

UP_SEQ_FEATURE	domain:PCI	9	1.00783874580067	4.07279173049243E-07	Q9D8W5, Q8VBV7, Q8BV13, Q99JI4, Q99JX4, Q9CZ04, P23116, Q8R1B4, P60229	0.000200483172933
SMART	SM00088:PINT	8	0.895856662933931	4.49805112513618E-07	Q9D8W5, Q8BV13, Q99JI4, Q99JX4, Q9CZ04, P23116, Q8R1B4, P60229	3.76336944136393E-05
GOTERM_MF_DIRECT	GO:0003743~translation initiation factor activity	15	1.67973124300112	4.90661852804581E-07	Q62448, Q99JX4, Q9Z0N1, Q99LC8, Q9DCH4, O70194, Q9Z1D1, Q6NZJ6, Q8R1B4, Q03963, Q8BMJ3, Q61749, Q05D44, P23116, P60229	2.8059724707262E-05
INTERPRO	IPR000717:Proteasome component (PCI) domain	8	0.895856662933931	6.84068614579653E-07	Q9D8W5, Q8BV13, Q99JI4, Q99JX4, Q9CZ04, P23116, Q8R1B4, P60229	5.28893049903953E-05
GOTERM_BP_DIRECT	GO:0001731~formation of translation preinitiation complex	9	1.00783874580067	3.38240967748298E-06	Q99JX4, Q9Z0N1, Q9DCH4, O70194, P23116, Q9Z1D1, Q8R1B4, P25444, P60229	0.000595062502546
GOTERM_CC_DIRECT	GO:0033290~eukaryotic 48S preinitiation complex	7	0.783874580067189	9.86494551033019E-06	Q99JX4, Q9DCH4, O70194, P23116, Q9Z1D1, Q8R1B4, P60229	0.000196160647263
GOTERM_CC_DIRECT	GO:0016282~eukaryotic 43S preinitiation complex	7	0.783874580067189	9.86494551033019E-06	Q99JX4, Q9DCH4, O70194, P23116, Q9Z1D1, Q8R1B4, P60229	0.000196160647263
GOTERM_CC_DIRECT	GO:0071541~eukaryotic translation initiation factor 3 complex, eIF3m	5	0.559910414333707	0.000118947780283	Q99JX4, Q9DCH4, O70194, P23116, Q8R1B4	0.001983742013103
KEGG_PATHWAY	mmu03013:RNA transport	23	2.57558790593505	0.000146149345697	Q62448, Q9Z0N1, Q99LC8, P29341, Q9DCH4, O70194, Q9Z1D1, Q8K1J6, Q6NZJ6, Q924C1, P70168, Q6P5F9, Q8R1B4, Q61584, Q9EPU0, Q8CIG8, O08583, Q8BMJ3, Q61749, Q05D44, P23116, Q9CWU9, P60229	0.003451321689556

Annotation Cluster 9 Enrichment Score: 4.9469867867081865

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Protein transport	50	5.59910414333707	2.17527578609148E-09	P98078, Q6P5F9, O08547, P17427, P17426, Q8BKC5, Q6P8X1, Q91YE6, O35643, Q8CIE6, Q01405, P62075, Q64152, P63242, P61027, P46467, Q9CT10, Q9CR16, Q8BFY9, Q9CR95, P61750, P57780, Q9QXK3, Q9D906, P52293, Q5XJY5, Q91ZR2, Q9ERK4, Q61655, Q9WU78, P61924, Q99MD9, P70168, Q9D662, Q8C0E2, P84091, O35344, O35343, Q8BPX9, Q8R0H9, Q924C1, Q9D2V7, Q3UM18, Q9QZ88, Q6PGL7, P84078, O88746, P60521, Q9CWU9, Q3UMB9	3.40793206487665E-08
GOTERM_BP_DIRECT	GO:0015031~protein transport	52	5.82306830907055	1.48775137696149E-07	P98078, Q6P5F9, O08547, P17427, P17426, Q8BKC5, Q6P8X1, Q91YE6, O35643, Q8CIE6, Q01405, P62075, Q64152, P63242, P61027, O88531, P46467, Q9CT10, Q9CR16, Q8BFY9, Q9CR95, P61750, P57780, Q9QXK3, Q9D906, Q5XJY5, P50396, Q91ZR2, Q9ERK4, Q61655, Q9WU78, P61924, Q99MD9, P70168, Q9D662, Q8C0E2, P84091, Q8VDD5, O35344, O35343, Q8BPX9, Q8R0H9, Q924C1, Q9D2V7, Q3UM18, Q9QZ88, Q6PGL7, P84078, O88746, P60521, Q9CWU9, Q3UMB9	4.5804145518202E-05
UP_KEYWORDS	Transport	88	9.85442329227324	0.001417733693606	P98078, P53564, Q8BVE3, Q3UBX0, Q6P5F9, O08547, P17427, P17426, Q8BKC5, Q62048, Q6P8X1, Q91YE6, P63168, O35643, Q8CIE6, Q01405, P62075, Q64152, P63242, P61027, Q9CQH3, P46467, Q8R1Q8, Q9CT10, Q9CPN8, Q9CR16, Q8BFY9, Q62418, Q9CR95, Q6PDM2, Q03265, Q8VDJ3, Q9CQX2, P53811, O08997, Q8R180, Q9Z1G3, Q9CQ75, Q9DBG5, P61750, P57780, Q9QXK3, P62482, Q9D906, P52293, Q9JHU4, Q5XJY5, Q91ZR2, Q9ERK4, Q61655, Q9WU78, B2RXC1, P61924, Q99MD9, Q8R2E9, P50516, P70168, P31750, Q9D662, Q8C0E2, P84091, O35344, P50518, O54984, P51807, O35343, Q8BPX9, P56383, Q9QYB1, Q91YT0, Q8VBT6, Q8R0H9, P97379, P97855, Q924C1, Q9D2V7, Q3UM18, Q9QZ88, Q6PGL7, Q91VD9, Q05816, O08583, P84078, O88746, Q3U0V1, P60521, Q9CWU9, Q3UMB9	0.007543413237679

Annotation Cluster 10 Enrichment Score: 4.863316553080941

Category	Term	Count	%	PValue	Genes	FDR
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UP_KEYWORDS	Cell division	33	3.69540873460246	1.03752616323386E-06	Q91ZR2, Q8CG48, Q6P9P6, Q8K1R7, Q9WU78, P97386, P28740, Q8BFT2, Q8R3C0, Q80X41, Q68FD5, P37913, P11440, P49718, A2AGT5, P51807, Q8K2Z4, Q1HFZ0, P46467, Q8K298, P25322, Q8R1Q8, Q80UG5, P62908, Q8CI75, Q9D2X5, Q99P69, P60122, Q9JLQ0, Q64261, Q9CWU9, Q9WVA3, Q8BK67 Q64701, Q91ZR2, Q8CG48, Q6P9P6, Q8K1R7, Q9WU78, P97386, P28740, Q8BFT2, Q8R3C0, Q8VBW6, Q99MD9, Q80X41, Q68FD5, Q61074, P37913, P11440, P61290, Q80U87, Q9QUR7, P49718, A2AGT5, P63085, P51807, Q8K2Z4, Q1HFZ0, Q60749, P46467, Q8K298, P25322, Q8R1Q8, Q8CFI2, Q80UG5, P62908, Q9ESL4, P97311, Q8CI75, Q9D2X5, P18654, Q99P69, P60122, Q9JLQ0, Q64261, Q9CWU9, Q9WVA3, Q8BK67	1.21909324179979E-05
UP_KEYWORDS	Cell cycle	46	5.1511758118701	1.18511975800538E-06	Q91ZR2, Q8CG48, Q6P9P6, Q8K1R7, P28740, Q8BFT2, Q8R3C0, Q80X41, Q68FD5, P11440, A2AGT5, P51807, Q8K2Z4, Q1HFZ0, Q8K298, Q8R1Q8, P62908, Q8CI75, Q9D2X5, Q99P69, P60122, Q9JLQ0, Q9CWU9, Q9WVA3, Q8BK67	1.3307213654519E-05
UP_KEYWORDS	Mitosis	25	2.79955207166853	6.55225765650144E-06	Q91ZR2, Q8CG48, Q6P9P6, Q8K1R7, P28740, Q8BFT2, Q8R3C0, Q80X41, Q68FD5, P11440, A2AGT5, P51807, Q8K2Z4, Q1HFZ0, Q8K298, Q8R1Q8, P62908, Q8CI75, Q9D2X5, Q99P69, P60122, Q9JLQ0, Q9CWU9, Q9WVA3, Q8BK67	6.15912219711135E-05
GOTERM_BP_DIRECT	GO:0051301~cell division	33	3.69540873460246	3.67266014935758E-05	Q91ZR2, Q8CG48, Q6P9P6, Q8K1R7, Q9WU78, P97386, P28740, Q8BFT2, Q8R3C0, Q80X41, P37913, P11440, P49718, A2AGT5, P51807, Q8K2Z4, Q1HFZ0, P46467, P27546, Q8K298, P25322, Q8R1Q8, Q80UG5, P62908, Q8CI75, Q9D2X5, Q99P69, P60122, Q9JLQ0, Q64261, Q9CWU9, Q9WVA3, Q8BK67	0.004760927340983
GOTERM_BP_DIRECT	GO:0007067~mitotic nuclear division	26	2.91153415453527	0.00010865419601	Q91ZR2, Q8CG48, Q6P9P6, Q8K1R7, P28740, Q8BFT2, Q8R3C0, Q80X41, Q68FD5, P11440, Q9DBR7, A2AGT5, P51807, Q8K2Z4, Q1HFZ0, Q8K298, Q8R1Q8, P62908, Q8CI75, Q9D2X5, Q99P69, P60122, Q9JLQ0, Q9CWU9, Q9WVA3, Q8BK67	0.010292895568159
GOTERM_BP_DIRECT	GO:0007049~cell cycle	44	4.92721164613662	0.000205551747639	Q64701, Q91ZR2, Q8CG48, Q6P9P6, Q8K1R7, Q9WU78, P97386, P28740, Q8BFT2, Q8R3C0, Q8VBW6, Q99MD9, Q80X41, Q61074, P37913, P11440, P61290, Q80U87, Q9QUR7, P49718, A2AGT5, P63085, Q8K2Z4, Q1HFZ0, Q60749, P46467, Q8K298, P25322, Q8R1Q8, Q8CFI2, Q80UG5, P62908, Q9ESL4, P97311, Q8CI75, Q9D2X5, P18654, Q99P69, P60122, Q9JLQ0, Q64261, Q9CWU9, Q9WVA3, Q8BK67	0.017881220420622

Annotation Cluster 11 Enrichment Score: 4.497162829121329

Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR000738:WHEP-TRS	6	0.671892497200448	3.58339590976844E-07	P32921, Q68FL6, Q8CGC7, Q8BH61, Q9CZD3, Q61035	3.24173042085191E-05
SMART	SM00991:SM00991	6	0.671892497200448	3.94811793585588E-07	P32921, Q68FL6, Q8CGC7, Q8BH61, Q9CZD3, Q61035	3.76336944136393E-05
INTERPRO	IPR009068:S15/NS1, RNA-binding	5	0.559910414333707	5.47799197704691E-05	P32921, Q68FL6, Q8CGC7, Q9CZD3, Q61035	0.003498769658383
UP_SEQ_FEATURE	domain:WHEP-TRS	4	0.447928331466965	0.000271058365123	P32921, Q68FL6, Q9CZD3, Q61035	0.048519447356932

Annotation Cluster 12 Enrichment Score: 4.063436394191277

Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu01130:Biosynthesis of antibiotics	33	3.69540873460246	1.7865004115296E-07	Q99K85, Q99JW2, Q9DCD0, Q9WTP7, Q9CQ60, Q9R1J0, Q3TW96, Q93092, Q9CS42, Q5SUR0, Q8CAY6, Q9CWJ9, P12382, P58044, Q8JZK9, Q91V92, Q9Z0S1, Q9D0F9, P47856, Q9WV85, Q91Y10, Q3TRM8, Q64737, Q08739, Q8VCN5, P54822, Q8VEE0, Q9JHU9, O88844, Q8CHP8, P17182, Q9WUA3, P05201	1.31010030178837E-05
KEGG_PATHWAY	mmu01230:Biosynthesis of amino acids	13	1.45576707726764	0.000820170702319	Q99K85, Q99JW2, Q91Y10, Q93092, Q9CS42, Q8VCN5, P12382, Q8VEE0, Q3THS6, O88844, P17182, Q9WUA3, P05201	0.016403414046382
KEGG_PATHWAY	mmu01200:Carbon metabolism	15	1.67973124300112	0.004403352418593	Q99K85, Q3TRM8, Q9DCD0, Q9R0P3, Q9CQ60, Q93092, Q9CS42, Q8CAY6, P12382, Q8VEE0, O88844, Q8CHP8, P17182, Q9WUA3, P05201	0.048436876604523

Annotation Cluster 13 Enrichment Score: 4.043509348525895

Category	Term	Count	%	PValue	Genes	FDR
UP_SEQ_FEATURE	nucleotide phosphate-binding region:NADP	15	1.67973124300112	2.08945689526069E-07	P23591, Q91YR9, Q8BVI4, Q64105, Q99MZ7, Q922D8, P62482, O88844, P45377, Q8K2T1, Q91Z53, P48758, Q91X52, P00375, P21300	0.000137138020892
UP_KEYWORDS	NADP	20	2.23964165733483	6.27338543170864E-06	P23591, Q91YR9, P19096, Q9JMH6, Q9DCD0, Q8BVI4, Q64105, Q99MZ7, Q922D8, Q8K0C9, Q9JLT4, P62482, O88844, P45377, Q8K2T1, Q91Z53, P48758, Q91X52, P00375, P21300	6.10032652324771E-05
UP_SEQ_FEATURE	binding site:NADP	8	0.895856662933931	4.95118584634787E-05	Q8K0C9, Q91YR9, P62482, O88844, Q8K2T1, Q91Z53, Q64105, Q922D8	0.011921138533456
UP_KEYWORDS	Oxidoreductase	40	4.47928331466965	0.000214008286471	P23591, P09528, Q91YR9, O08807, P19096, P99029, Q9JMH6, Q9DCD0, Q8R2E9, Q8BVI4, Q9R1J0, Q64105, Q62465, Q922D8, Q8C0L6, Q9JLT4, P61982, P45377, Q91Z53, P62259, Q91YT0, P21300, Q00519, Q91X52, O70325, Q9CQV8, Q8BSY0, P68254, Q8R180, Q99MZ7, P20108, Q91VD9, Q9Z0X1, P62482, O88844, O09131, P24547, P48758, P07742, P00375	0.001471959433775
Annotation Cluster 14 Enrichment Score: 3.8190555663749297						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Purine biosynthesis	8	0.895856662933931	6.29139679100756E-08	Q9CWXJ9, Q64737, P24547, P46664, Q3THK7, Q5SUR0, P54822, Q922D8	8.448447119353E-07
GOTERM_BP_DIRECT	GO:0006164~purine nucleotide biosynthetic process	8	0.895856662933931	7.18266001293964E-06	Q9CWXJ9, Q64737, P24547, P46664, Q3THK7, Q5SUR0, P54822, Q922D8	0.001179392774125
GOTERM_BP_DIRECT	GO:0006189~de novo IMP biosynthetic process	4	0.447928331466965	0.001121247956221	Q9CWXJ9, Q64737, Q5SUR0, P54822	0.070811120927489
Annotation Cluster 15 Enrichment Score: 3.5114946149023094						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0008641~small protein activating enzyme activity	6	0.671892497200448	2.35520201600397E-05	Q9R1T2, Q9Z1F9, Q8VBW6, Q9D906, Q8VE47, Q02053	0.000936960802019
INTERPRO	IPR000594:UBA/THIF-type NAD/FAD binding fold	6	0.671892497200448	2.37046626033684E-05	Q9R1T2, Q9Z1F9, Q8VBW6, Q9D906, Q8VE47, Q02053	0.001582824971107
Annotation Cluster 16 Enrichment Score: 3.464097031686257						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR006195:Aminoacyl-tRNA synthetase, class II	8	0.895856662933931	1.12654918173837E-06	Q8CGC7, Q8BP47, Q8C0C7, Q9CZD3, P26638, Q922B2, Q61035, Q9D0R2	8.27450373986836E-05
INTERPRO	IPR002314:Aminoacyl-tRNA synthetase, class II (G/ H/ P/ S), conserved doma	4	0.447928331466965	0.002312820943201	Q8CGC7, Q9CZD3, P26638, Q9D0R2	0.070781957615872
Annotation Cluster 17 Enrichment Score: 3.2927390997003294						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	DNA replication	14	1.56774916013438	1.54883782818429E-05	P97386, P97311, Q8R3C0, Q99MD9, Q9WUK4, P39749, P37913, Q9CQ71, P35601, Q8VEE4, P49718, O35654, P17918, P07742	0.000140894279854
KEGG_PATHWAY	mmu03030:DNA replication	10	1.11982082866741	8.29077370649117E-05	Q8VEE4, P49718, O35654, P97311, P17918, P37913, Q9CQ71, Q9WUK4, P39749, P35601	0.003039950359047
GOTERM_BP_DIRECT	GO:0006260~DNA replication	16	1.79171332586786	0.000102179000032	P54103, P97386, P97311, Q8R3C0, Q99MD9, Q9WUK4, P39749, P37913, Q9CQ71, P35601, Q8VEE4, P49718, Q9EPU0, O35654, P17918, P07742	0.010115370053237
KEGG_PATHWAY	mmu03430:Mismatch repair	8	0.895856662933931	0.000120035765666	Q8VEE4, O35654, P54276, P17918, P37913, Q9CQ71, Q9WUK4, P35601	0.003451321689556
KEGG_PATHWAY	mmu03420:Nucleotide excision repair	9	1.00783874580067	0.002414218476252	Q8VEE4, O35654, Q3U1J4, P17918, P37913, Q9CQ71, Q9WUK4, P54726, P35601	0.027954108672389
Annotation Cluster 18 Enrichment Score: 3.2455611193619545						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	mRNA processing	29	3.2474804031355	1.56037341188773E-06	Q91VR5, Q61656, O70551, Q9CQQ8, Q99K48, Q62384, Q62189, Q9JKP5, Q9DAR7, Q99KP6, Q6NVF9, Q3TIU4, P62317, Q60749, Q9DBR1, Q569Z6, Q0VGB7, P97376, Q9JLI8, P29341, Q6PDM2, Q61183, O08810, Q3UEB3, P62320, P16110, O08583, Q3U0V1, Q9CQI7	1.62972334130496E-05

UP_KEYWORDS	mRNA splicing	23	2.57558790593505	1.85998967566938E-05	Q0VGB7, Q61656, P97376, O70551, Q9CQQ8, Q9JLI8, P29341, Q99K48, Q6PDM2, Q62384, Q62189, O08810, Q3UEB3, Q9JKP5, P62320, Q9DAR7, O08583, P16110, Q99KP6, Q3U0V1, P62317, Q569Z6, Q9CQI7	0.000163911590168
GOTERM_BP_DIRECT	GO:0006397~mRNA processing	29	3.2474804031355	8.29247722434613E-05	Q91VR5, Q61656, O70551, Q99K48, Q62384, Q62189, Q9JKP5, Q9DAR7, Q99KP6, Q6NVF9, Q3TIU4, P62317, Q60749, P05132, Q9DBR1, Q569Z6, Q0VGB7, P97376, Q9JLI8, P29341, Q6PDM2, Q61183, O08810, Q3UEB3, P62320, P16110, O08583, Q3U0V1, Q9CQI7	0.008880161479811
UP_KEYWORDS	Spliceosome	13	1.45576707726764	0.000527217655643	Q61656, P97376, Q9CQQ8, P29341, Q6PDM2, Q62189, O08810, P62320, O08583, P16110, Q99KP6, P62317, Q9CQI7	0.003303897308697
GOTERM_BP_DIRECT	GO:0008380~RNA splicing	22	2.46360582306831	0.000603078061376	Q0VGB7, Q61656, P97376, O70551, Q9JLI8, P29341, Q99K48, Q6PDM2, Q62384, Q62189, O08810, Q3UEB3, Q9JKP5, P62320, Q9DAR7, O08583, P16110, Q99KP6, Q3U0V1, P62317, Q569Z6, Q9CQI7	0.042762870924881
GOTERM_CC_DIRECT	GO:0071013~catalytic step 2 spliceosome	10	1.11982082866741	0.009583378702083	P62320, Q61656, P97376, Q99KP6, Q9CQQ8, P29341, Q6PDM2, P62317, O08810, Q9CQI7	0.072861864543776
GOTERM_CC_DIRECT	GO:0005681~spliceosomal complex	12	1.3437849944009	0.012944475226979	P62320, Q61656, O08583, P16110, P97376, Q99KP6, P29341, Q6PDM2, P62317, O08810, Q62189, Q9CQI7	0.091675256059566
Annotation Cluster 19 Enrichment Score: 3.216174223679425						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR024969:Rpn11/EIF3F C-terminal domain	4	0.447928331466965	0.00018426972214	Q9DCH4, O35593, O88545, P26516	0.010411239300921
SMART	SM00232:JAB_MPN	5	0.559910414333707	0.000723032576984	Q76N33, Q9DCH4, O35593, O88545, P26516	0.022685147102862
INTERPRO	IPR000555:JAB1/Mov34/MPN/PAD-1	5	0.559910414333707	0.000940047780329	Q76N33, Q9DCH4, O35593, O88545, P26516	0.034523254732585
UP_SEQ_FEATURE	domain:MPN	5	0.559910414333707	0.001090288247402	Q76N33, Q9DCH4, O35593, O88545, P26516	0.119265419951889
Annotation Cluster 20 Enrichment Score: 3.215399339830062						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR023409:14-3-3 protein, conserved site	7	0.783874580067189	1.50334513332797E-08	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	3.8624607819365E-06
INTERPRO	IPR000308:14-3-3 protein	7	0.783874580067189	5.828232065999E-08	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	8.56167290495253E-06
SMART	SM00101:14_3_3	7	0.783874580067189	6.52100186603694E-08	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	1.63677146837527E-05
INTERPRO	IPR023410:14-3-3 domain	7	0.783874580067189	1.69466887644541E-07	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	2.26315325408937E-05
PIR_SUPERFAMILY	PIRSF000868:14-3-3 protein	7	0.783874580067189	4.79320149114403E-07	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	5.03286156570123E-05
UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	7	0.783874580067189	1.86782798650331E-06	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259	0.000525393329346
KEGG_PATHWAY	mmu04114:Oocyte meiosis	16	1.79171332586786	0.001144501115447	Q9CQV8, P68254, P11440, P18654, P68181, Q76MZ3, P63101, P68510, P63085, P63328, P0DP26, O54988, P61982, P62715, P05132, P62259	0.017741252164662
KEGG_PATHWAY	mmu04110:Cell cycle	15	1.67973124300112	0.007942823413915	Q64701, O70456, Q9CQV8, P97311, P68254, P11440, P63101, P49718, P68510, Q64261, P17918, P61982, Q9WVA3, P25322, P62259	0.072809214627559
Annotation Cluster 21 Enrichment Score: 3.168653057469934						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu00030:Pentose phosphate pathway	9	1.00783874580067	0.000156878258616	Q91YP3, P12382, Q8VEE0, Q9DCD0, Q9CQ60, Q9WUA3, Q9D0F9, Q93092, Q9CS42	0.003451321689556
GOTERM_MF_DIRECT	GO:0048029~monosaccharide binding	6	0.671892497200448	0.000332780516517	P12382, P16110, Q8VEE0, Q8CGY8, Q9CQ60, Q93092	0.010499799055629
Annotation Cluster 22 Enrichment Score: 2.9038329971221266						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Elongation factor	7	0.783874580067189	8.2284948590384E-05	Q8BFR5, P10711, P58252, Q9D8N0, P63242, P57776, O08810	0.00062714474331
GOTERM_MF_DIRECT	GO:0003746~translation elongation factor activity	7	0.783874580067189	0.000637259352399	Q8BFR5, P10711, P58252, Q9D8N0, P63242, P57776, O08810	0.017755455761237
Annotation Cluster 23 Enrichment Score: 2.8600012085370294						
Category	Term	Count	%	PValue	Genes	FDR

UP_KEYWORDS	Endocytosis	15	1.67973124300112	3.81629618512232E-05	Q91ZR2, Q91ZX7, P98078, Q8VD75, Q80TY0, Q62418, Q9Z0R6, Q9CR95, O08539, P17427, P97814, P17426, P84091, Q6PAR5, Q60902	0.000316528095354
GOTERM_BP_DIRECT	GO:0006897~endocytosis	20	2.23964165733483	0.000102673264852	Q8BH43, Q91ZR2, Q91ZX7, P98078, Q8BVE3, Q8VD75, Q80TY0, Q62418, Q9Z0R6, Q9CR95, O08539, P17427, P97814, P17426, P84091, Q6PAR5, Q6P8X1, O08553, Q60902, Q8BL66	0.010115370053237
UP_KEYWORDS	Coated pit	8	0.895856662933931	0.001111682854171	Q91ZX7, P98078, Q80TY0, Q60902, Q68FD5, P17427, P17426, P84091	0.006397848262782
GOTERM_CC_DIRECT	GO:0005905~clathrin-coated pit	9	1.00783874580067	0.001656136203265	Q91ZX7, P98078, Q80TY0, Q9CR95, Q60902, Q68FD5, P17427, P17426, P84091	0.016373601413773
Annotation Cluster 24 Enrichment Score: 2.664318982756836						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR017926:Glutamine amidotransferase	4	0.447928331466965	0.00087228730895	B2RQC6, Q3THK7, P70698, Q5SUR0	0.032856155303782
GOTERM_BP_DIRECT	GO:0006541~glutamine metabolic process	6	0.671892497200448	0.000895017093113	B2RQC6, Q3THK7, P47856, P70698, Q5SUR0, Q9JHW2	0.058011239482539
UP_KEYWORDS	Glutamine amidotransferase	4	0.447928331466965	0.001808295894618	Q3THK7, P47856, P70698, Q5SUR0	0.00927162623316
Annotation Cluster 25 Enrichment Score: 2.5790777804976757						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR013041:Coatomer/clathrin adaptor appendage, Ig-like subdomain	5	0.559910414333707	0.000669926697959	O35643, Q8R0H9, Q9QXK3, P17427, P17426	0.027336731091705
GOTERM_CC_DIRECT	GO:0030117~membrane coat	7	0.783874580067189	0.000725676155433	O35643, Q8CIE6, P61924, Q9QXK3, Q68FD5, P17427, P17426	0.008932727913309
INTERPRO	IPR009028:Coatomer/clathrin adaptor appendage, C-terminal subdomain	4	0.447928331466965	0.00087228730895	O35643, Q9QXK3, P17427, P17426	0.032856155303782
INTERPRO	IPR008152:Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like su	4	0.447928331466965	0.003376207682554	O35643, Q8R0H9, P17427, P17426	0.095377867032156
SMART	SM00809:Alpha_adaptinC2	4	0.447928331466965	0.003581500675026	O35643, Q8R0H9, P17427, P17426	0.0691505130332
GOTERM_CC_DIRECT	GO:0030131~clathrin adaptor complex	5	0.559910414333707	0.004747227331017	O35643, Q8R0H9, P17427, P17426, P84091	0.042315802243725
Annotation Cluster 26 Enrichment Score: 2.569620879648123						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0008180~COP9 signalosome	7	0.783874580067189	0.001230991473026	Q8VBV7, Q8BV13, P63168, Q8VDD5, Q9CZ04, Q03265, O88545	0.013450572740493
UP_KEYWORDS	Signalosome	4	0.447928331466965	0.003686560310303	Q8VBV7, Q8BV13, Q9CZ04, O88545	0.016501746150881
Annotation Cluster 27 Enrichment Score: 2.445688237855775						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR004161:Translation elongation factor EFTu/EF1A, domain 2	6	0.671892497200448	9.38046678400298E-05	Q8BFR5, Q8R050, Q9Z0N1, P58252, Q05D44, O08810	0.00551196228228
INTERPRO	IPR009000:Translation elongation/initiation factor/Ribosomal, beta-barrel	7	0.783874580067189	0.000515169003137	Q8BFR5, Q8R050, Q9Z0N1, P58252, Q05D44, O08810, Q8BGQ7	0.023649477050261
INTERPRO	IPR000795:Elongation factor, GTP-binding domain	6	0.671892497200448	0.000606268748722	Q8BFR5, Q8R050, Q9Z0N1, P58252, Q05D44, O08810	0.026988145208267
Annotation Cluster 28 Enrichment Score: 2.3747755673357						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0030117~membrane coat	7	0.783874580067189	0.000725676155433	O35643, Q8CIE6, P61924, Q9QXK3, Q68FD5, P17427, P17426	0.008932727913309
GOTERM_CC_DIRECT	GO:0030126~COPI vesicle coat	4	0.447928331466965	0.008822437760591	Q8CIE6, P61924, Q9QXK3, Q5XJY5	0.068077616749634
Annotation Cluster 29 Enrichment Score: 2.3642976995714995						
Category	Term	Count	%	PValue	Genes	FDR
SMART	SM00165:UBA	8	0.895856662933931	0.000204381089233	Q922Y1, Q91VX2, P56399, P61087, P22682, P54726, Q8R317, Q80X50	0.008836527267224
INTERPRO	IPR009060:UBA-like	9	1.00783874580067	0.001103257714486	Q922Y1, Q91VX2, P56399, P61087, P22682, P54726, Q8R317, Q80X50, Q6P5G6	0.039528916648289
INTERPRO	IPR015940:Ubiquitin-associated/translation elongation factor EF1B, N-termina	8	0.895856662933931	0.002047584129957	Q922Y1, Q91VX2, P56399, P61087, P22682, P54726, Q8R317, Q80X50	0.066842246375716
Annotation Cluster 30 Enrichment Score: 2.3630367821479115						
Category	Term	Count	%	PValue	Genes	FDR

UP_KEYWORDS	DNA recombination	9	1.00783874580067	0.002204085773633	Q8VEE4, P97386, P28352, P60122, Q99K48, Q9WTM5, Q9WUP7, P37913, Q9CQ71	0.010904424353763
UP_KEYWORDS	DNA repair	20	2.23964165733483	0.002640147463894	P62908, P97386, P28352, P54276, Q9Z255, Q3U1J4, Q99K48, O35593, Q9WTM5, Q9WUP7, P11103, P39749, P37913, Q9CQ71, P54726, Q8VEE4, Q9JLV6, P60122, Q99KP6, P17918	0.012408693080302
UP_KEYWORDS	DNA damage	21	2.35162374020157	0.009096418905288	P62908, P97386, P28352, P54276, Q9Z255, Q3U1J4, Q99K48, O35593, Q9WTM5, Q9WUP7, P11103, P39749, P37913, Q9CQ71, P54726, Q8VEE4, Q9JLV6, P60122, Q99KP6, P17918, P49138	0.036645573304159
Annotation Cluster 31 Enrichment Score: 2.3623257815888565						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	TPR repeat	15	1.67973124300112	0.000326240676303	Q60864, Q8BSY0, O70145, Q99MD9, Q8CGY8, Q9CR16, Q9D2X5, Q99L47, Q64378, Q9CYG7, O88447, Q80UM3, Q5SW19, Q9D706, Q9QYI3	0.002190473112318
SMART	SM00028:TPR	14	1.56774916013438	0.000446907748807	Q60864, Q8BSY0, O70145, Q99MD9, Q8CGY8, Q9CR16, Q9D2X5, Q99L47, Q64378, Q9CYG7, O88447, Q80UM3, Q9D706, Q9QYI3	0.016024834992922
UP_SEQ_FEATURE	repeat:TPR 3	15	1.67973124300112	0.000647795050102	Q60864, Q8BSY0, O70145, Q99MD9, Q8CGY8, Q9CR16, Q9D2X5, Q99L47, Q64378, Q9CYG7, O88447, Q80UM3, Q5SW19, Q9D706, Q9QYI3	0.100309912461739
INTERPRO	IPR019734:Tetratricopeptide repeat	14	1.56774916013438	0.000660753306421	Q60864, Q8BSY0, O70145, Q99MD9, Q8CGY8, Q9CR16, Q9D2X5, Q99L47, Q64378, Q9CYG7, O88447, Q80UM3, Q9D706, Q9QYI3	0.027336731091705
INTERPRO	IPR001440:Tetratricopeptide TPR-1	6	0.671892497200448	0.001202514508142	Q60864, Q9CYG7, O70145, Q8CGY8, Q9D706, Q64378	0.042059376487158
INTERPRO	IPR011990:Tetratricopeptide-like helical	18	2.01567749160134	0.001261035274539	Q60864, Q8BSY0, O70145, Q9JLI8, Q99MD9, Q8CGY8, Q9CR16, Q68FD5, Q9D2X5, Q99L47, Q64378, Q99J14, Q9CYG7, O88447, Q80UM3, Q5SW19, Q9D706, Q9QYI3	0.043080484146449
INTERPRO	IPR013026:Tetratricopeptide repeat-containing domain	13	1.45576707726764	0.001381214692085	Q60864, Q8BSY0, O70145, Q99MD9, Q8CGY8, Q9CR16, Q99L47, Q64378, Q9CYG7, O88447, Q80UM3, Q9D706, Q9QYI3	0.046113735969838
Annotation Cluster 32 Enrichment Score: 2.3542239936537666						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0015935~small ribosomal subunit	7	0.783874580067189	0.000599238169022	P62908, P14131, P62702, Q924T2, P25444, P62852, P62843	0.007745153334615
GOTERM_CC_DIRECT	GO:0022627~cytosolic small ribosomal subunit	9	1.00783874580067	0.000720875786436	P62908, P14131, P63323, P62702, P62082, P25444, P62852, Q62167, P62843	0.008932727913309
Annotation Cluster 33 Enrichment Score: 2.346081648361987						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR001494:Importin-beta, N-terminal	7	0.783874580067189	1.94588343630614E-05	Q91YE6, Q9ERK4, Q8BFY9, Q924C1, P70168, Q6P5F9, Q8BKC5	0.001361191794254
SMART	SM00913:SM00913	6	0.671892497200448	0.000211231727503	Q91YE6, Q9ERK4, Q8BFY9, Q924C1, P70168, Q6P5F9	0.008836527267224
UP_SEQ_FEATURE	domain:Importin N-terminal	6	0.671892497200448	0.000250515489755	Q91YE6, Q9ERK4, Q8BFY9, P70168, Q6P5F9, Q8BKC5	0.048519447356932
GOTERM_MF_DIRECT	GO:0008536~Ran GTPase binding	8	0.895856662933931	0.00030643682235	Q91YE6, Q9ERK4, Q9CT10, Q8BFY9, Q924C1, P70168, Q6P5F9, Q8BKC5	0.010013917587499
UP_SEQ_FEATURE	repeat:HEAT 6	7	0.783874580067189	0.000679498877226	A2AGT5, Q9QXK3, Q8BFY9, P70168, Q6P5F9, Q8BKC5, Q76MZ3	0.100309912461739
UP_SEQ_FEATURE	repeat:HEAT 2	9	1.00783874580067	0.000812541579811	Q8BQM4, A2AGT5, Q9QXK3, Q9DBQ7, Q8BFY9, P70168, Q6P5F9, Q8BKC5, Q76MZ3	0.100309912461739
UP_SEQ_FEATURE	repeat:HEAT 1	9	1.00783874580067	0.000812541579811	Q8BQM4, A2AGT5, Q9QXK3, Q9DBQ7, Q8BFY9, P70168, Q6P5F9, Q8BKC5, Q76MZ3	0.100309912461739
UP_SEQ_FEATURE	repeat:HEAT 4	8	0.895856662933931	0.000815113559872	A2AGT5, Q9QXK3, Q9DBQ7, Q8BFY9, P70168, Q6P5F9, Q8BKC5, Q76MZ3	0.100309912461739
Annotation Cluster 34 Enrichment Score: 2.2985441125723307						
Category	Term	Count	%	PValue	Genes	FDR

UP_KEYWORDS	SH3-binding	9	1.00783874580067	0.000798446177658	Q9JJU8, Q9JLQ0, Q3UIA2, Q5FWK3, Q60749, Q8BPU7, Q61036, Q9ESS2, Q80U87	0.004894822219555
GOTERM_MF_DIRECT	GO:0017124~SH3 domain binding	13	1.45576707726764	0.003153260407963	Q9WU78, P29351, Q3UIA2, P70315, Q9ESS2, Q61036, Q80U87, Q9JJU8, Q9JLQ0, Q5FWK3, Q60749, Q8BPU7, P22682	0.067098448215957
Annotation Cluster 35 Enrichment Score: 2.2824731423621722						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0004177~aminopeptidase activity	7	0.783874580067189	0.000783398107006	Q64514, Q99KK7, O08663, Q6P1B1, Q6NSR8, Q8R016, Q11011	0.021082625526779
UP_KEYWORDS	Aminopeptidase	6	0.671892497200448	0.001006574242508	Q64514, Q99KK7, O08663, Q6P1B1, Q6NSR8, Q11011	0.005913623674736
Annotation Cluster 36 Enrichment Score: 2.2331888578166095						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0061136~regulation of proteasomal protein catabolic process	7	0.783874580067189	3.1618284308173E-05	P97372, Q9JMA1, O35593, Q9WUP7, P05132, P61290, P97371	0.004326435236168
GOTERM_MF_DIRECT	GO:0061133~endopeptidase activator activity	4	0.447928331466965	0.00470875539517	P97372, O35593, P61290, P97371	0.094494024502219
GOTERM_CC_DIRECT	GO:0008537~proteasome activator complex	3	0.335946248600224	0.007920738658179	P97372, P61290, P97371	0.064126464678606
Annotation Cluster 37 Enrichment Score: 2.21044117980303						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Protease	33	3.69540873460246	0.001330649885822	Q6P1B1, P29452, B2RRE7, P56399, Q8K2H2, O35593, Q9DCH4, Q9WUP7, Q9R1P4, Q8C0M9, P61290, Q80U87, P62196, Q9Z2U1, O09061, O89023, Q64514, Q8R5H1, P10605, Q9JMA1, P70195, Q6NSR8, Q76N33, Q920A5, P35123, P70677, Q99KK7, O08663, Q9QUM9, Q8R016, Q8BHG1, Q9D1A2, Q11011	0.007216216688497
UP_KEYWORDS	Thiol protease	13	1.45576707726764	0.001740594126442	P10605, Q8R5H1, P29452, B2RRE7, Q9JMA1, P56399, Q9DCH4, Q8K2H2, Q9WUP7, P35123, P70677, Q80U87, Q8R016	0.009089769326976
Annotation Cluster 38 Enrichment Score: 2.0514495825981833						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Redox-active center	9	1.00783874580067	0.000143373794576	P20108, Q9JLT4, O08807, Q9CQM5, P99029, Q80Y14, Q9JMH6, Q8R2E9, Q8R180	0.001010785251761
Annotation Cluster 39 Enrichment Score: 1.9602095445402905						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR004087:K Homology domain	7	0.783874580067189	0.002270938168644	Q9CPS7, Q9CPN8, Q3U0V1, Q60749, Q8VDJ3, Q61990, Q61584	0.070781957615872
SMART	SM00322:KH	7	0.783874580067189	0.002504740781806	Q9CPS7, Q9CPN8, Q3U0V1, Q60749, Q8VDJ3, Q61990, Q61584	0.062868993623321
Annotation Cluster 40 Enrichment Score: 1.8461163831498977						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu03420:Nucleotide excision repair	9	1.00783874580067	0.002414218476252	Q8VEE4, O35654, Q3UIJ4, P17918, P37913, Q9CQ71, Q9WUK4, P54726, P35601	0.027954108672389
Annotation Cluster 41 Enrichment Score: 1.8413090281197508						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0005903~brush border	12	1.3437849944009	0.000127312798568	Q9JMH9, Q9Z0G0, Q7TPR4, Q8VDD5, P57780, Q61879, Q8BTM8, Q6URW6, P47754, O08638, Q9QXS1, Q91XS2	0.002056897401865
UP_KEYWORDS	Motor protein	14	1.56774916013438	0.000345117921759	Q6P9P6, Q9JMH9, P28740, Q61879, O08638, P70248, P63168, Q8VDD5, P33174, P51807, O88447, Q6URW6, Q9JHU4, Q8R1Q8	0.002263331486888
INTERPRO	IPR027401:Myosin-like IQ motif-containing domain	6	0.671892497200448	0.000355821194791	Q9JMH9, Q8VDD5, Q61879, Q6URW6, O08638, Q9JKF1	0.017423377838263
GOTERM_CC_DIRECT	GO:0001725~stress fiber	10	1.11982082866741	0.000817870652367	P21107, Q7TPR4, Q8VDD5, P57780, Q61879, Q6URW6, O08638, P07356, P97814, Q80UG5	0.009833468076131
GOTERM_MF_DIRECT	GO:0003774~motor activity	11	1.23180291153415	0.001348715236776	Q9QUR7, P63168, Q9JMH9, Q8VDD5, P51807, Q61879, Q6URW6, O08638, Q9JHU4, P70248, Q8R1Q8	0.032475643201315
GOTERM_CC_DIRECT	GO:0097513~myosin II filament	3	0.335946248600224	0.004060710455295	Q8VDD5, Q61879, Q6URW6	0.036831356234872

GOTERM_CC_DIRECT	GO:0042641~actomyosin	4	0.447928331466965	0.006803402650435	Q9JMH9, Q8VDD5, Q61879, Q6URW6	0.057661625742212
UP_KEYWORDS	Calmodulin-binding	11	1.23180291153415	0.017856042544492	Q3UQ44, Q8VDD5, Q61879, Q62261, Q6URW6, P63328, O08638, Q9JKF1, P70248, A2AN08, Q8VCN5	0.06713871996729
UP_KEYWORDS	Myosin	6	0.671892497200448	0.021119713236213	Q9JMH9, Q8VDD5, Q61879, Q6URW6, O08638, P70248	0.073542218741895
Annotation Cluster 42 Enrichment Score: 1.8274588188480465						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0030863~cortical cytoskeleton	8	0.895856662933931	0.000116897087311	P21107, Q7TPR4, Q8VDD5, P57780, Q8BTM8, Q62261, P47754, Q9ES52	0.001983742013103
SMART	SM00033:CH	9	1.00783874580067	0.002883586712278	Q3UQ44, P27870, Q7TPR4, P57780, Q8BTM8, Q62261, Q9JKF1, Q9QXS1, Q9WVA4	0.06579820588925
Annotation Cluster 43 Enrichment Score: 1.8079701248952593						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Nucleotide metabolism	6	0.671892497200448	0.000819088433107	Q9WV85, Q9JM14, Q6P3D0, Q3V1L4, O08739, Q3UFY7	0.004914530598641
Annotation Cluster 44 Enrichment Score: 1.77418682420174						
Category	Term	Count	%	PValue	Genes	FDR
SMART	SM00185:ARM	9	1.00783874580067	0.000128325693458	O35643, Q8BNU0, O35344, P30999, E9PVA8, O35343, P70188, P52293, P70168	0.008052437264504
INTERPRO	IPR000225:Armadillo	9	1.00783874580067	0.000256723105174	O35643, Q8BNU0, O35344, P30999, E9PVA8, O35343, P70188, P52293, P70168	0.013967638574108
GOTERM_BP_DIRECT	GO:0006607~NLS-bearing protein import into nucleus	6	0.671892497200448	0.000394170478476	O35344, O35343, Q8BFY9, P52293, P70168, Q8BKC5	0.030338809015172
COG_ONTOLOGY	Intracellular trafficking and secretion	10	1.11982082866741	0.000666035065785	Q01405, O35344, Q9QXK3, O35343, Q8BFY9, P52293, P70168, O08547, Q9D662, Q8BKC5	0.009324490920996
GOTERM_MF_DIRECT	GO:0008139~nuclear localization sequence binding	6	0.671892497200448	0.002470816138548	O35344, O35343, Q8BFY9, P52293, P70168, Q8BKC5	0.055141384555407
Annotation Cluster 45 Enrichment Score: 1.740919079615381						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Citrullination	11	1.23180291153415	0.001135118976629	P03995, O08583, Q62318, Q9D8E6, P43274, P43275, P43277, P25444, P15864, P84228, Q99JF8	0.00640207102819
GOTERM_MF_DIRECT	GO:0031490~chromatin DNA binding	9	1.00783874580067	0.004750519264592	Q04207, P28352, P57780, P43274, P43275, Q9WTM5, P43277, P15864, P42227	0.094494024502219
Annotation Cluster 46 Enrichment Score: 1.699769025784726						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Threonine protease	5	0.559910414333707	0.005497897342676	P70195, Q9Z2U1, Q9QUM9, Q9R1P4, O09061	0.023852416163608
GOTERM_CC_DIRECT	GO:0005839~proteasome core complex	5	0.559910414333707	0.005761400535585	P70195, Q9Z2U1, Q9QUM9, Q9R1P4, O09061	0.049644067948293
Annotation Cluster 47 Enrichment Score: 1.6459982135692277						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu00480:Glutathione metabolism	9	1.00783874580067	0.009793831553797	P97494, O70325, O88844, Q9DCD0, O09172, P51855, O09131, Q64674, P07742	0.082870882378281
UP_KEYWORDS	Glutathione biosynthesis	3	0.335946248600224	0.020742051400234	P97494, O09172, P51855	0.073542218741895
Annotation Cluster 48 Enrichment Score: 1.638906603236534						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0097255~R2TP complex	4	0.447928331466965	0.001613827983022	P60122, Q9CQJ2, Q9WTM5, Q9D706	0.016359785631815
Annotation Cluster 49 Enrichment Score: 1.5982722223370445						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Amino-acid biosynthesis	6	0.671892497200448	0.001224119349834	Q99K85, Q91YI0, Q8VCN5, P05201, Q9WVQ5, Q922D8	0.006768659934379
Annotation Cluster 50 Enrichment Score: 1.4517064727056772						
Category	Term	Count	%	PValue	Genes	FDR

UP_KEYWORDS	Redox-active center	9	1.00783874580067	0.000143373794576	P20108, Q9JLT4, O08807, Q9CQM5, P99029, Q80Y14, Q9JMH6, Q8R2E9, Q8R180	0.001010785251761
Annotation Cluster 51 Enrichment Score: 1.3858343533266806						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Transferase	86	9.63045912653975	3.99522763552965E-05	Q91YR5, Q9CWQ0, Q61510, Q8K1R7, B2RQC6, P19096, Q8CGY8, Q9WTP7, Q8K1J6, Q9DBL7, Q9CS42, P11440, P68181, Q61036, Q8CAY6, P12382, Q9JLV6, P63085, Q8BY71, Q3THS6, Q9Z120, Q6P9R2, Q1HFEZ0, Q9JKX6, P49138, P05132, Q3TX08, Q9WV85, Q9DBC7, Q3TRM8, Q6PGB6, P13439, Q91YQ5, Q9JLI6, P22907, Q64674, Q9DBG6, P18654, Q09200, Q68FH4, Q9D270, Q8VHI3, Q8K183, O09131, Q91WU5, Q99K85, Q9Z255, O70551, Q2NL51, Q80X41, P11103, Q9R0N0, Q80WS3, Q99KQ4, Q3TW96, P31750, Q93092, Q9CQ65, Q9CWJ9, Q80TE0, Q8CIG8, Q91V92, Q8JZK9, Q03963, Q04899, P61087, O54988, P04184, P47856, Q8CFI2, Q8VE10, Q9ESL4, Q8BH61, Q64737, P97930, Q61183, O35654, P47809, Q64261, Q04447, P08030, Q9D1G2, Q8BH69, Q9WUA3, Q8CIN4, P05201	0.000321901198063
GOTERM_MF_DIRECT:GO:0016740-transferase activity		86	9.63045912653975	0.000640360699586	Q91YR5, Q9CWQ0, Q61510, Q8K1R7, B2RQC6, P19096, Q8CGY8, Q9WTP7, Q8K1J6, Q9DBL7, Q9CS42, P11440, P68181, Q61036, Q8CAY6, P12382, Q9JLV6, P63085, Q8BY71, Q3THS6, Q9Z120, Q6P9R2, Q1HFEZ0, Q9JKX6, P49138, P05132, Q3TX08, Q9WV85, Q3TRM8, Q6PGB6, P13439, Q91YQ5, Q9JLI6, P22907, Q64674, Q9DBG6, P18654, Q09200, Q68FH4, Q9D270, Q8VHI3, Q8K183, O09131, Q91WU5, Q99K85, Q9Z255, O70551, Q2NL51, Q80X41, P11103, Q9R0N0, Q80WS3, Q99KQ4, Q3TW96, P31750, Q93092, Q9CQ65, Q9CWJ9, Q80TE0, Q8CIG8, Q91V92, Q8JZK9, Q03963, Q04899, P61087, O54988, P04184, P47856, Q8CFI2, Q8VE10, Q9ESL4, Q8BH61, Q64737, P97930, Q61183, O35654, P47809, Q64261, Q04447, P08030, Q9D1G2, Q8BH69, Q9WUA3, Q8CIN4, P05201	0.017755455761237
Annotation Cluster 52 Enrichment Score: 1.3829206920248907						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	mRNA transport	9	1.00783874580067	0.007811048090155	Q61655, O08583, Q9CPN8, Q3U0V1, P63242, P97379, Q6PDM2, Q6P5F9, Q9CWU9	0.03239287590329
Annotation Cluster 53 Enrichment Score: 1.36593875031153						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Thiol protease	13	1.45576707726764	0.001740594126442	P10605, Q8R5H1, P29452, B2RRE7, Q9JMA1, P56399, Q9DCH4, Q8K2H2, Q9WUP7, P35123, P70677, Q80U87, Q8R016	0.009089769326976
Annotation Cluster 54 Enrichment Score: 1.343885102196996						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu03410:Base excision repair	7	0.783874580067189	0.011133068575857	O35654, P97386, P28352, P11103, P17918, P37913, P39749	0.090713892099577
Annotation Cluster 55 Enrichment Score: 1.2096845686327968						
Category	Term	Count	%	PValue	Genes	FDR

UP_KEYWORDS	Mitochondrion	53	5.93505039193729	0.003164710399439	Q8BFR5, Q9DCB8, Q9WTP7, Q8K1J6, Q9DBL7, Q62167, P11440, P63168, Q80ZK0, Q8BMP6, P61222, Q9CRB9, P62075, Q3TIU4, Q9CQH3, P05132, Q3U5F4, O70325, Q2YDW2, Q9CPV4, Q03265, Q9CQX2, Q02053, Q9CQ75, Q07813, Q9CYG7, Q8BP40, Q8BKZ9, P97287, P99029, Q62465, Q9JLT4, Q9CZD3, Q9QUJ7, Q9EPB4, P56383, Q924T2, Q9QYB1, Q91YT0, P62908, Q9CQN1, Q9CQR4, P28352, Q9D338, Q8WTY4, Q9D172, P39749, Q9CQV5, P20108, Q91VD9, Q9Z0X1, Q80Y14, Q9JK81	0.014630300535111
Annotation Cluster 56 Enrichment Score: 1.1967759216316445						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Signal recognition particle	3	0.335946248600224	0.020742051400234	Q9D7A6, P49962, Q8BMA6	0.073542218741895
Annotation Cluster 57 Enrichment Score: 1.1466822540494708						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Iron-sulfur	7	0.783874580067189	0.015602084078854	Q91VD9, Q9DCB8, Q80Y14, Q9CQM9, Q8WTY4, Q00519, Q91YT0	0.060271064523791
UP_KEYWORDS	2Fe-2S	4	0.447928331466965	0.031163664750255	Q91VD9, Q80Y14, Q8WTY4, Q00519	0.104620874518714
Annotation Cluster 58 Enrichment Score: 1.1200593042378628						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Helicase	12	1.3437849944009	0.004126336626741	Q61655, P49718, Q9EPU0, Q91VR5, Q61656, P60122, P97311, Q62095, Q9WTM5, P97855, Q62167, P54823	0.018181670761577
Annotation Cluster 59 Enrichment Score: 1.0877418023605847						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu00052:Galactose metabolism	7	0.783874580067189	0.007140747601959	P12382, Q3TRM8, Q9R0N0, P45377, Q9WUA3, Q9D0F9, P21300	0.068302803149174
KEGG_PATHWAY	mmu00051:Fructose and mannose metabolism	7	0.783874580067189	0.009660722173136	P23591, P12382, Q8K0C9, Q3TRM8, P45377, Q9WUA3, P21300	0.082870882378281
Annotation Cluster 60 Enrichment Score: 1.037098471235627						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Porphyrin biosynthesis	3	0.335946248600224	0.027053303235536	P10518, P70697, P22907	0.092996936179125
Annotation Cluster 61 Enrichment Score: 0.9624449823963407						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Cholesterol biosynthesis	4	0.447928331466965	0.02737143866265	P58044, Q8JZK9, Q9D1G2, Q9R1J0	0.092996936179125
Annotation Cluster 62 Enrichment Score: 0.8929607605814427						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Exonuclease	6	0.671892497200448	0.021119713236213	Q91VR5, P28352, Q8CI75, Q3TIU4, P39749, Q9DBR1	0.073542218741895