

**Supplementary Table 10: results of the pathway analysis by the David tool on the proteins modulated in response to 1 micrometer polystyrene particles**

selection of clusters by a FDR cutoff value of 0.1

**Annotation Cluster 1** Enrichment Score: 46.56191116100873

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0098641~cadherin binding involved in cell-c	94	8.49141824751581	2.16863644141276E-51	Q61510, O70456, Q62448, P70460, O08709, P19096, Q9Z0P5, Q8BTM8, Q61792, Q62167, Q6PAR5, Q8CBW3, Q80U87, P42225, Q9JHJ0, Q91VX2, Q60902, P47753, Q5FWK3, P61027, P25444, P07356, P84228, Q6Y7W8, Q9Z0U1, Q8BH43, Q8BK64, P51432, P24452, P30999, Q99LX0, Q62418, Q9CPV4, P11499, Q6NZJ6, Q8VDJ3, P57776, Q9QXS1, Q61166, P54823, Q9DBG5, P42932, Q9CWK8, E9PVA8, O88844, Q9JLQ0, P05064, P47226, Q922Q8, P60229, P62962, Q9WVA4, Q8BVY0, Q9Z0N1, Q6ZQ58, Q78PY7, Q62261, Q9JKF1, P59325, Q7TQH0, Q99K01, P42567, Q9CWJ9, P63101, A2AGT5, Q8VDD5, P68433, P62855, O54988, P42208, Q8K298, Q2L4X1, P62259, Q80UG5, P26039, Q8R1F1, Q9Z0G0, Q3UZ39, Q9CQV8, Q8CI51, Q9D8N0, Q9CZ30, Q9EQP2, O08579, Q3UEB3, P35700, Q62433, P60122, P58252, P17182, P22682, Q9WUA3, Q8CIN4, Q9D0I9	1.12010072198969E-48
GOTERM_CC_DIRECT	GO:0005913~cell-cell adherens junction	95	8.58175248419151	1.74539240811561E-50	Q62523, Q61510, O70456, Q62448, P70460, O08709, P19096, Q9Z0P5, Q8BTM8, Q61792, Q62167, Q6PAR5, Q8CBW3, Q80U87, P42225, Q9JHJ0, Q91VX2, Q60902, P47753, Q5FWK3, P61027, P25444, P07356, P84228, Q6Y7W8, Q9Z0U1, Q8BH43, Q8BK64, P51432, P24452, P30999, Q99LX0, Q62418, Q9CPV4, P11499, Q6NZJ6, Q8VDJ3, P57776, Q9QXS1, Q61166, P54823, Q9DBG5, P42932, Q9CWK8, E9PVA8, O88844, Q9JLQ0, P05064, P47226, Q922Q8, P60229, P62962, Q9WVA4, Q8BVY0, Q9Z0N1, Q6ZQ58, Q78PY7, Q62261, Q9JKF1, P59325, Q7TQH0, Q99K01, P42567, Q9CWJ9, P63101, A2AGT5, Q8VDD5, P68433, P62855, O54988, P42208, Q8K298, Q2L4X1, P62259, Q80UG5, P26039, Q8R1F1, Q9Z0G0, Q3UZ39, Q9CQV8, Q8CI51, Q9D8N0, Q9CZ30, Q9EQP2, O08579, Q3UEB3, P35700, Q62433, P60122, P58252, P17182, P22682, Q9WUA3, Q8CIN4, Q9D0I9	2.4260954472807E-48
GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	68	6.14272809394761	5.44736759603533E-40	O70456, Q62448, P70460, O08709, Q9Z0P5, Q61792, Q6PAR5, Q8CBW3, Q80U87, P42225, Q91VX2, Q60902, P47753, Q5FWK3, P61027, P25444, P84228, Q6Y7W8, Q8BH43, Q8BK64, P51432, P24452, Q62418, Q9CPV4, Q6NZJ6, Q8VDJ3, P57776, Q9QXS1, P54823, Q9DBG5, O88844, P05064, P47226, Q922Q8, P60229, Q9WVA4, Q9Z0N1, Q6ZQ58, Q78PY7, P59325, Q7TQH0, Q99K01, P42567, Q9CWJ9, P63101, A2AGT5, P68433, P62855, O54988, P42208, Q8K298, Q2L4X1, P26039, Q8R1F1, Q9Z0G0, Q3UZ39, Q9CQV8, Q8CI51, Q9D8N0, Q9CZ30, Q9EQP2, O08579, Q3UEB3, P35700, Q62433, P17182, Q9WUA3, Q9D0I9	1.52144976957267E-36

**Annotation Cluster 2** Enrichment Score: 27.280182377808515

Category	Term	Count	%	PValue	Genes	FDR
----------	------	-------	---	--------	-------	-----

UP_KEYWORDS	Nucleotide-binding	195	17.6151761517615	6.04867185025301E-39	<p>Q9JMH9, Q61316, Q62407, Q9CZW4, Q9WTP7, P11440, Q8BML9, Q9JLV6, P16460, Q6P9R2, P61027, P49138, P46664, P56480, P47758, Q569Z6, Q9DBC7, P18654, Q91VC3, Q8K183, O88685, P32921, Q6P9P6, Q61655, Q6P3D0, Q91VR5, Q9Z255, Q80X41, P62254, P61161, Q9CZD3, Q8BMJ2, P47857, Q8CFI2, Q9CZ30, P32233, Q9D2R0, Q64261, Q99LE6, Q8CIN4, P07742, Q8C0C7, B2RQC6, P46471, Q9D2Y4, Q8VE47, P61222, Q9JHR7, P46467, P05132, P41216, P49615, P97310, Q3TRM8, P97311, P70296, P11499, Q9WTM5, O08638, Q9Z2A0, Q6NVF4, P54823, Q8R050, Q68FH4, Q8BP47, Q9QXG4, Q61699, Q9Z0N1, Q91YL3, O70551, P31750, P49718, P49717, Q9QZL0, O54984, Q03963, O54988, P62334, P53994, P80315, P80314, P80313, Q9Z1Q9, Q60931, Q64737, Q9EQP2, Q3THK7, Q3UM18, Q9D0R2, Q9WUA2, Q6URW6, Q9WUA3, P80318, P80317, Q8BGQ7, P80316, Q8K1R7, Q8CG48, Q6NZQ2, Q5U3K5, Q9DBL7, Q922B2, Q61035, P68181, Q61036, Q8C878, P12382, Q9EPU0, P62196, Q05D44, P25206, P09411, Q8BU30, Q9QXB9, Q03265, Q9WUK4, Q9ER72, Q02053, P84096, Q68FL6, Q9JHU4, Q9R1T4, Q5SUR0, Q8CGC7, Q8VDD5, Q91V92, Q9JJ78, P04184, P26638, P42208, Q80UG5, Q7TSS2, Q3V1L4, P97855, Q3V300, Q3UDE2, O54950, P60122, P33174, Q04447, Q9D1G2, Q8BH69, Q3UFY7, P54775, P97386, Q922F4, Q69ZS7, Q61879, Q07832, P30285, P37913, Q9CS42, Q62167, Q3THS6, Q9Z1F9, P62835, Q8R1Q8, Q8CFV9, Q9WV85, Q91WQ3, P61082, P70698, Q61881, P70218, P42932, P61750, P28740, Q9R0N0, P11983, P50516, P59325, P70248, Q922D8, Q9JM14, Q04899, P61087, Q9QUJ7, Q9D7H3, O35626, P36916, P97494, Q9ESL4, A2BDX3, E9Q4Z2, P97930, P51855, P63280, P62192, Q99M31, O08810, Q9D892, P58252, P51859, Q6P542, Q9D0I9</p> <p>Q9JMH9, Q8K1R7, Q8CG48, Q6NZQ2, Q61316, Q62407, Q9CZW4, Q9DBL7, Q922B2, P11440, Q61035, P68181, Q61036, Q8C878, P12382, Q9EPU0, Q8BML9, Q9JLV6, P16460, P62196, P25206, Q6P9R2, P09411, P49138, Q8BU30, P56480, Q569Z6, Q03265, Q9WUK4, Q9ER72, P18654, Q91VC3, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q61655, Q6P9P6, Q91VR5, Q9Z255, Q80X41, Q5SUR0, P62254, P61161, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, Q9JJ78, P04184, P26638, P47857, Q8CFI2, Q7TSS2, Q9CZ30, P97855, Q9D2R0, Q3V300, Q3UDE2, O54950, P60122, P33174, Q64261, Q04447, Q99LE6, Q9D1G2, Q8BH69, Q8CIN4, P07742, P54775, P97386, Q8C0C7, B2RQC6, P46471, Q9Z1F9, Q3THS6, P46467, P05132, P41216, P49615, Q8R1Q8, Q8CFV9, Q9WV85, Q91WQ3, P97310, P97311, Q3TRM8, P70296, P11499, Q9WTM5, O08638, Q9Z2A0, P61082, Q61881, P70698, Q6NVF4, P54823, P70218, P42932, Q68FH4, Q8BP47, Q9QXG4, Q61699, P28740, Q91YL3, O70551, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, P49718, P49717, Q9QZL0, O54984, Q04899, Q03963, P61087, Q9QUJ7, O54988, P62334, Q9D7H3, P80315, P97494, P80314, Q9Z1Q9, Q9ESL4, P80313, A2BDX3, Q64737, E9Q4Z2, P97930, P51855, P63280, Q9EQP2, P62192, Q99M31, Q3THK7, Q9D0R2, Q9WUA2, Q6URW6, Q9WUA3, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316</p>	3.87114998416193E-37
UP_KEYWORDS	ATP-binding	162	14.6341463414634	2.05120488701444E-35	<p>Q9JMH9, Q61316, Q62407, Q9CZW4, Q9WTP7, P11440, Q8BML9, Q9JLV6, P16460, Q6P9R2, P61027, P49138, P46664, P56480, P47758, Q569Z6, Q9DBC7, P18654, Q91VC3, Q8K183, O88685, P32921, Q6P9P6, Q61655, Q6P3D0, Q91VR5, Q9Z255, Q80X41, P62254, P61161, Q9CZD3, Q8BMJ2, P47857, Q8CFI2, Q9CZ30, P32233, Q9D2R0, Q64261, Q99LE6, Q8CIN4, P07742, Q8C0C7, B2RQC6, P46471, Q9D2Y4, Q8VE47, P61222, Q9JHR7, P46467, P05132, P41216, P49615, P97310, Q3TRM8, P97311, P70296, P11499, Q9WTM5, O08638, Q9Z2A0, Q6NVF4, P54823, Q8R050, Q68FH4, Q8BP47, Q9QXG4, Q61699, Q9Z0N1, Q91YL3, O70551, P31750, P49718, P49717, Q9QZL0, O54984, Q03963, O54988, P62334, P53994, P80315, P80314, P80313, Q9Z1Q9, Q60931, Q64737, Q9EQP2, Q3THK7, Q3UM18, Q9D0R2, Q9WUA2, Q6URW6, Q9WUA3, P80318, P80317, Q8BGQ7, P80316, Q8K1R7, Q8CG48, Q6NZQ2, Q5U3K5, Q9DBL7, Q922B2, Q61035, P68181, Q61036, Q8C878, P12382, Q9EPU0, P62196, Q05D44, P25206, P09411, Q8BU30, Q9QXB9, Q03265, Q9WUK4, Q9ER72, Q02053, P84096, Q68FL6, Q9JHU4, Q9R1T4, Q5SUR0, Q8CGC7, Q8VDD5, Q91V92, Q9JJ78, P04184, P26638, P42208, Q80UG5, Q7TSS2, Q3V1L4, P97855, Q3V300, Q3UDE2, O54950, P60122, P33174, Q04447, Q9D1G2, Q8BH69, Q3UFY7, P54775, P97386, Q922F4, Q69ZS7, Q61879, Q07832, P30285, P37913, Q9CS42, Q62167, Q3THS6, Q9Z1F9, P62835, Q8R1Q8, Q8CFV9, Q9WV85, Q91WQ3, P61082, P70698, Q61881, P70218, P42932, P61750, P28740, Q9R0N0, P11983, P50516, P59325, P70248, Q922D8, Q9JM14, Q04899, P61087, Q9QUJ7, Q9D7H3, O35626, P36916, P97494, Q9ESL4, A2BDX3, E9Q4Z2, P97930, P51855, P63280, P62192, Q99M31, O08810, Q9D892, P58252, P51859, Q6P542, Q9D0I9</p> <p>Q9JMH9, Q8K1R7, Q8CG48, Q6NZQ2, Q61316, Q62407, Q9CZW4, Q9DBL7, Q922B2, P11440, Q61035, P68181, Q61036, Q8C878, P12382, Q9EPU0, Q8BML9, Q9JLV6, P16460, P62196, P25206, Q6P9R2, P09411, P49138, Q8BU30, P56480, Q569Z6, Q03265, Q9WUK4, Q9ER72, P18654, Q91VC3, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q61655, Q6P9P6, Q91VR5, Q9Z255, Q80X41, Q5SUR0, P62254, P61161, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, Q9JJ78, P04184, P26638, P47857, Q8CFI2, Q7TSS2, Q9CZ30, P97855, Q9D2R0, Q3V300, Q3UDE2, O54950, P60122, P33174, Q64261, Q04447, Q99LE6, Q9D1G2, Q8BH69, Q8CIN4, P07742, P54775, P97386, Q8C0C7, B2RQC6, P46471, Q9Z1F9, Q3THS6, P46467, P05132, P41216, P49615, Q8R1Q8, Q8CFV9, Q9WV85, Q91WQ3, P97310, P97311, Q3TRM8, P70296, P11499, Q9WTM5, O08638, Q9Z2A0, P61082, Q61881, P70698, Q6NVF4, P54823, P70218, P42932, Q68FH4, Q8BP47, Q9QXG4, Q61699, P28740, Q91YL3, O70551, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, P49718, P49717, Q9QZL0, O54984, Q04899, Q03963, P61087, Q9QUJ7, O54988, P62334, Q9D7H3, P80315, P97494, P80314, Q9Z1Q9, Q9ESL4, P80313, A2BDX3, Q64737, E9Q4Z2, P97930, P51855, P63280, Q9EQP2, P62192, Q99M31, Q3THK7, Q9D0R2, Q9WUA2, Q6URW6, Q9WUA3, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316</p>	1.05021690215139E-33

GOTERM_MF_DIRECTGO:0000166~nucleotide binding	215	19.4218608852755	2.19856190045985E-30	<p>Q9JMH9, Q61316, Q62407, Q9CZW4, Q9WTP7, P11440, Q9JLV6, P16460, Q6P9R2, P61027, P49138, P46664, P56480, P47758, Q569Z6, Q9DBC7, P18654, Q8K183, O88685, P32921, Q91WT8, Q6P9P6, Q61655, Q6P3D0, Q91VR5, Q9Z255, Q80X41, Q99K48, Q9Z1D1, Q62189, P62254, P61161, Q9CZD3, Q8BMJ2, P47857, Q8CFI2, Q9CZ30, P32233, Q9D2R0, O08583, Q64261, Q8R4X3, Q99LE6, Q8CIN4, P07742, Q8C0C7, B2RQC6, P46471, Q9D2Y4, P32067, Q8VE47, P61222, Q9JHR7, P46467, P05132, P41216, P49615, P97310, Q3TRM8, P97311, P29341, Q9JLH8, P70296, P11499, Q9WTM5, O08638, Q9Z2A0, Q6A0A2, Q6NVF4, P54823, Q8R050, Q68FH4, Q8BP47, Q9QXG4, Q61699, Q9Z0N1, Q91YL3, O70551, Q9CY64, P31750, P49718, P49717, Q8VIJ6, Q9QZL0, O54984, Q03963, O54988, P62334, P53994, P80315, P80314, P80313, Q9Z1Q9, Q60931, Q64737, Q9EQP2, Q3THK7, Q3UEB3, Q3UM18, Q9D0R2, Q9WUA2, Q6URW6, P24547, Q9WUA3, P80318, P80317, Q8BGQ7, P80316, Q8K1R7, Q8CG48, Q6NZQ2, Q5U3K5, Q9DBL7, Q922B2, Q9D883, Q61035, P68181, Q61036, Q8C878, P12382, Q9EPU0, P62196, Q05D44, P25206, Q8BU30, Q9QXB9, Q03265, Q9WUK4, Q9ER72, Q02053, P84096, Q68FL6, Q9JHU4, Q9CX86, Q9R1T4, Q5SUR0, Q8CGC7, Q8VDD5, Q91V92, Q6NVF9, Q9JJ78, P04184, P26638, P42208, O35309, Q80UG5, Q7TSS2, Q3V1L4, P97855, Q8BGD9, Q3V300, Q3UDE2, O54950, P60122, P33174, Q04447, Q8C166, Q9D1G2, Q8BH69, Q3UFY7, Q9CQI7, P54775, P97386, Q922F4, Q69ZS7, Q61879, Q07832, P30285, P37913, Q9CS42, Q62167, Q3THS6, Q9Z1F9, P62835, Q8R1Q8, Q8CFV9, Q9WV85, Q91WQ3, Q9CPN8, P61082, P70698, Q61881, P70218, P42932, P61750, P28740, Q9R0N0, P11983, P50516, P59325, P70248, Q922D8, Q9JM14, Q04899, P61087, Q9QUJ7, Q9D7H3, O35626, P36916, P97494, Q9ESL4, A2BDX3, P97379, E9Q4Z2, P97930, P51855, P63280, P62192, Q99M31, O08810, Q9D892, P58252, P51859, Q6P542, Q9D0I9</p> <p>Q9JMH9, Q8K1R7, Q8CG48, Q6NZQ2, Q61316, Q9Z0P5, Q62407, Q9CZW4, Q9WTP7, Q9DBL7, Q922B2, P11440, Q61035, P68181, Q61036, Q8C878, P12382, Q9EPU0, Q8BML9, Q9JLV6, P16460, P62196, P25206, Q6P9R2, P09411, P49138, Q8BU30, P56480, Q569Z6, Q03265, Q9WUK4, Q9ER72, P18654, Q91VC3, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q9CXY6, Q61655, Q6P9P6, Q91VR5, Q9Z255, Q80X41, Q5SUR0, P62254, P61161, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, Q9JJ78, P04184, P26638, P62814, P47857, Q8CFI2, Q7TSS2, Q9CZ30, P97855, Q9D2R0, Q3V300, Q3UDE2, O54950, P60122, P33174, Q64261, Q04447, Q9DBQ7, Q99LE6, Q9D1G2, Q8BH69, Q8CIN4, P07742, P54775, P97386, Q8C0C7, B2RQC6, P46471, Q61879, Q07832, P30285, Q9D2Y4, P37913, Q8VE47, Q9CS42, Q62167, P61222, Q9JHR7, Q9Z1F9, Q3THS6, P46467, P05132, P41216, P49615, Q8R1Q8, Q8CFV9, Q9WV85, Q91WQ3, P97310, P97311, Q3TRM8, P70296, P11499, Q9WTM5, O08638, Q9Z2A0, P61082, Q61881, P70698, Q6NVF4, P54823, P70218, P42932, Q68FH4, Q8BP47, Q9QXG4, Q61699, P28740, Q91YL3, O70551, Q9ERS2, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, P49718, P49717, Q9QZL0, O54984, Q04899, Q03963, P61087, Q9QUJ7, P82343, O54988, P62334, Q9D7H3, P80315, P97494, P80314, Q9Z1Q9, Q9ESL4, P80313, A2BDX3, Q64737, E9Q4Z2, P97930, P51855, P63280, Q9EQP2, P62192, Q99M31, Q3THK7, Q9D0R2, Q9WUA2, Q6URW6, Q9WUA3, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316</p>	7.57038147725007E-28
GOTERM_MF_DIRECTGO:0005524~ATP binding	169	15.2664859981933	6.83623506904534E-24	<p>Q9JMH9, Q8K1R7, Q8CG48, Q6NZQ2, Q61316, Q9Z0P5, Q62407, Q9CZW4, Q9WTP7, Q9DBL7, Q922B2, P11440, Q61035, P68181, Q61036, Q8C878, P12382, Q9EPU0, Q8BML9, Q9JLV6, P16460, P62196, P25206, Q6P9R2, P09411, P49138, Q8BU30, P56480, Q569Z6, Q03265, Q9WUK4, Q9ER72, P18654, Q91VC3, Q02053, Q68FL6, Q8K183, O88685, Q9JHU4, P32921, Q9CXY6, Q61655, Q6P9P6, Q91VR5, Q9Z255, Q80X41, Q5SUR0, P62254, P61161, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, Q9JJ78, P04184, P26638, P62814, P47857, Q8CFI2, Q7TSS2, Q9CZ30, P97855, Q9D2R0, Q3V300, Q3UDE2, O54950, P60122, P33174, Q64261, Q04447, Q9DBQ7, Q99LE6, Q9D1G2, Q8BH69, Q8CIN4, P07742, P54775, P97386, Q8C0C7, B2RQC6, P46471, Q61879, Q07832, P30285, Q9D2Y4, P37913, Q8VE47, Q9CS42, Q62167, P61222, Q9JHR7, Q9Z1F9, Q3THS6, P46467, P05132, P41216, P49615, Q8R1Q8, Q8CFV9, Q9WV85, Q91WQ3, P97310, P97311, Q3TRM8, P70296, P11499, Q9WTM5, O08638, Q9Z2A0, P61082, Q61881, P70698, Q6NVF4, P54823, P70218, P42932, Q68FH4, Q8BP47, Q9QXG4, Q61699, P28740, Q91YL3, O70551, Q9ERS2, Q9R0N0, P11983, P50516, P70248, P31750, Q922D8, P49718, P49717, Q9QZL0, O54984, Q04899, Q03963, P61087, Q9QUJ7, P82343, O54988, P62334, Q9D7H3, P80315, P97494, P80314, Q9Z1Q9, Q9ESL4, P80313, A2BDX3, Q64737, E9Q4Z2, P97930, P51855, P63280, Q9EQP2, P62192, Q99M31, Q3THK7, Q9D0R2, Q9WUA2, Q6URW6, Q9WUA3, P80318, P80317, Q6P542, Q8BGQ7, Q9D0I9, P80316</p> <p>Q9JMH9, Q8K1R7, Q8CG48, Q62407, Q9DBL7, P11440, P68181, Q61036, Q8C878, P12382, Q9EPU0, Q9JLV6, P16460, P62196, P25206, Q6P9R2, P09411, P49138, P56480, Q569Z6, Q03265, Q9WUK4, P18654, Q91VC3, Q02053, Q8K183, O88685, Q9JHU4, Q61655, Q6P9P6, Q91VR5, Q80X41, Q5SUR0, P61161, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q8BMJ2, Q9JJ78, P04184, P26638, P47857, Q9CZ30, Q3V300, P60122, P33174, Q64261, Q04447, Q9D1G2, Q8BH69, Q8CIN4, P54775, P46471, Q61879, Q07832, P30285, Q9CS42, Q62167, Q9Z1F9, Q3THS6, P46467, P05132, P49615, Q8R1Q8, P97310, P97311, Q3TRM8, Q9WTM5, O08638, Q9Z2A0, Q61881, P54823, P70218, Q68FH4, P28740, Q91YL3, O70551, Q9R0N0, P50516, P70248, P31750, Q922D8, P49718, P49717, Q9QZL0, O54984, Q04899, Q03963, O54988, P62334, Q9ESL4, Q64737, P97930, P51855, Q9EQP2, P62192, Q3THK7, Q6URW6, Q9WUA3</p>	1.76545770658096E-21
UP_SEQ_FEATURE nucleotide phosphate-binding region:ATP	99	8.94308943089431	2.13041081869451E-11	<p>Q9JMH9, Q8K1R7, Q8CG48, Q62407, Q9DBL7, P11440, P68181, Q61036, Q8C878, P12382, Q9EPU0, Q9JLV6, P16460, P62196, P25206, Q6P9R2, P09411, P49138, P56480, Q569Z6, Q03265, Q9WUK4, P18654, Q91VC3, Q02053, Q8K183, O88685, Q9JHU4, Q61655, Q6P9P6, Q91VR5, Q80X41, Q5SUR0, P61161, Q8CGC7, Q8VDD5, Q9CZD3, Q91V92, Q9JJ78, P04184, P26638, P47857, Q9CZ30, Q3V300, P60122, P33174, Q64261, Q04447, Q9D1G2, Q8BH69, Q8CIN4, P54775, P46471, Q61879, Q07832, P30285, Q9CS42, Q62167, Q9Z1F9, Q3THS6, P46467, P05132, P49615, Q8R1Q8, P97310, P97311, Q3TRM8, Q9WTM5, O08638, Q9Z2A0, Q61881, P54823, P70218, Q68FH4, P28740, Q91YL3, O70551, Q9R0N0, P50516, P70248, P31750, Q922D8, P49718, P49717, Q9QZL0, O54984, Q04899, Q03963, O54988, P62334, Q9ESL4, Q64737, P97930, P51855, Q9EQP2, P62192, Q3THK7, Q6URW6, Q9WUA3</p>	4.82325009352436E-08

**Annotation Cluster 3** Enrichment Score: 16.29908469535427  
Category Term

Count % PValue Genes

FDR

UP_KEYWORDS	Proteasome	30	2.710027100271	9.27817869827467E-20	Q9D8W5, P54775, P46471, O35593, Q9R1P1, Q9WUP7, P28063, Q9R1P4, Q9CR00, P61290, O35522, O35226, P62196, Q9Z2U1, P26516, P62334, Q9Z2U0, O09061, P97371, P97372, Q3TXS7, Q9CX56, Q9JMA1, P70195, P62192, P54726, Q99JI4, Q9QUM9, O88685, Q8R317	2.96901718344789E-24
GOTERM_CC_DIRECTGO:000502~proteasome complex		33	2.9810298102981	1.30445454817763E-23	Q9D8W5, P54775, P46471, O35593, Q9R1P1, Q9WUP7, P28063, Q9R1P4, Q9CR00, P61290, Q9CZH3, O35522, O35226, P62196, Q9Z2U1, P26516, P62334, Q9Z2U0, O09061, P97371, P97372, Q3TXS7, Q9CX56, Q9JMA1, P70195, P62192, P54726, Q99JI4, Q9QUM9, O88685, Q8R317, Q9Z2X2	1.20879454797794E-23
KEGG_PATHWAY	mmu03050:Proteasome	25	2.2583559168925	6.90935237846467E-17	Q9D8W5, P54775, P46471, O35593, Q9R1P1, P28063, Q9R1P4, P61290, O35522, O35226, P62196, Q9Z2U1, P26516, P62334, Q9Z2U0, O09061, P97371, P97372, Q3TXS7, Q9CX56, P70195, P62192, Q99JI4, Q9QUM9, O88685	1.55460428515455E-14
GOTERM_CC_DIRECTGO:0022624~proteasome accessory complex		13	1.1743450767841	4.04868445696203E-13	Q9D8W5, P54775, Q3TXS7, P46471, Q9CX56, O35593, P62192, Q8BJY1, Q99JI4, O35226, P62196, O88685, P62334	1.73159119851607E-11
KEGG_PATHWAY	mmu05169:Epstein-Barr virus infection	21	1.8970189701897	0.000943916475104	Q9D8W5, P54775, Q3TXS7, P46471, Q9CX56, P26450, P24063, O35593, P62192, P31750, Q04207, Q99JI4, O35226, P01902, Q03963, P62196, O88685, P20152, P26516, P62334, P42227	0.013273825431148

**Annotation Cluster 4** Enrichment Score: 10.521792819915726

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Actin-binding	41	3.7037037037037	1.82813309497347E-13	O89053, Q7TPR4, P70460, Q61879, Q9Z0P5, Q62261, Q8BTM8, Q61792, P70248, P40124, P61161, Q9JHJ0, P21107, Q7TMB8, Q8VDD5, Q8R1S4, Q9CVB6, Q9JM76, P47753, P47754, Q8K298, Q8BQ30, Q99K51, Q8BH43, P24452, Q8VD75, O70200, Q62418, O08638, Q9WUM4, Q9D2V7, Q9QXS1, O08579, Q9JJ28, P13020, P57780, Q6URW6, Q6IRU2, Q9CQI6, O88342, P62962	3.12001381542139E-12
GOTERM_MF_DIRECTGO:0003779~actin binding		49	4.42637759710931	7.83340968413688E-11	P70460, Q61879, Q9Z0P5, Q8BTM8, Q71LX4, Q61792, P40124, Q9JHJ0, Q7TMB8, Q9CVB6, Q9JM76, P47753, P47754, P61982, Q8BQ30, Q99K51, Q8BH43, P24452, O70200, Q62418, O08638, Q9QXS1, P57780, Q6IRU2, P62962, O89053, Q7TPR4, Q62261, P70248, P61161, P21107, Q8VDD5, Q8R1S4, P68510, Q8K298, P26039, Q9Z0G0, Q8CI51, Q8VD75, Q9WUM4, Q9D2V7, P97814, O08579, P70315, Q9JJ28, P13020, Q6URW6, Q9CQI6, O88342	8.93647143160808E-09
GOTERM_MF_DIRECTGO:0051015~actin filament binding		27	2.4390243902439	1.89960318408924E-09	O89053, Q9JMH9, Q7TPR4, Q61879, Q8BTM8, Q71LX4, Q61792, P61161, Q7TMB8, Q8VDD5, Q8R1S4, Q9CVB6, Q9JM76, P47753, Q8C052, P26039, Q99K51, Q8VD75, O70200, Q62418, O08539, Q9WUM4, Q3UQ44, P58252, P57780, Q6URW6, O88342	1.22643130572762E-07

**Annotation Cluster 5** Enrichment Score: 9.416796097645266

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Chaperone	40	3.613369467028	5.35455798797958E-17	Q8BYA0, Q99L47, P11983, P97822, Q9CR00, Q9CZH3, P61222, Q61081, P62075, Q64152, P0C7N9, P80315, P80314, Q8BK64, P80313, P54103, P61759, Q99LX0, Q9CR16, Q9WU28, P11499, Q9EST4, P35564, Q9EST5, Q8BJY1, Q99M31, Q64378, O08997, P42932, Q9JK23, O08583, Q9CYG7, Q9CQI6, Q9CWM4, Q9QYI3, Q9D1E6, P80318, P80317, Q9Z2X2, P80316	1.14230570410231E-15
GOTERM_BP_DIRECTGO:0006457~protein folding		24	2.1680216802168	5.32659974076987E-08	Q8BYA0, Q62446, P80315, P80314, P10639, Q8BK64, P80313, P61759, Q9CR16, Q9WU28, Q99L47, P11983, P11499, P35564, Q64378, Q8R180, P42932, Q61081, Q9CWM4, Q8VBT0, P80318, Q8BGQ7, P80317, P80316	1.06265664828359E-05
GOTERM_MF_DIRECTGO:0051082~unfolded protein binding		15	1.3550135501355	1.96987204599351E-05	P80315, P80314, P80313, Q9WU28, Q99L47, P11983, P11499, P35564, Q8BQM4, P42932, Q61081, Q9CWM4, P80318, P80317, P80316	0.000701682008107

**Annotation Cluster 6** Enrichment Score: 7.55458736277143

Category	Term	Count	%	PValue	Genes	FDR
----------	------	-------	---	--------	-------	-----

UP_KEYWORDS	Protein transport	64	5.78139114724481	1.46840068019253E-12	P98078, Q8BUK6, Q9CR60, Q6P5F9, A2A5R2, P17427, P17426, Q8BKC5, Q6P8X1, Q91YE6, O35643, Q8CIE6, Q01405, P62075, Q64152, P63242, P61027, P22892, P46467, Q9CT10, Q9EPL8, Q9CR16, Q8BFY9, Q9CR95, Q8CI71, Q8V175, Q9CRA5, Q9CWK8, P61750, P57780, Q9QXK3, Q9D906, P52293, Q5XJY5, Q9ERK4, Q61655, Q9WU78, P61924, Q8C2E7, Q99MD9, P70168, Q9D662, P84091, Q64324, P42567, O35344, Q8BIJ7, P53994, Q9CWZ7, Q9EQH3, Q8R0H9, P26450, Q924C1, Q8BH60, P35585, Q9D2V7, Q3UM18, Q9QZ88, Q6PGL7, O88746, P60521, Q9CWU9, P40336, Q3UMB9	2.21123867134876E-11
GOTERM_BP_DIRECTGO:0015031~	protein transport	67	6.05239385727191	2.84822070015513E-10	P98078, Q8BUK6, Q9CR60, Q6P5F9, A2A5R2, P17427, P17426, Q8BKC5, Q6P8X1, Q91YE6, O35643, Q8CIE6, Q01405, P62075, Q64152, P63242, P61027, P62835, P22892, O88531, P46467, Q9CT10, Q9EPL8, Q9CR16, Q8BFY9, Q9CR95, Q8CI71, Q8V175, Q9CRA5, Q9CWK8, P61750, P57780, Q9QXK3, Q9D906, Q5XJY5, P50396, Q9ERK4, Q61655, Q9WU78, P61924, Q8C2E7, Q99MD9, P70168, Q9D662, P84091, Q64324, P42567, Q8VDD5, O35344, Q8BIJ7, P53994, Q9CWZ7, Q9EQH3, Q8R0H9, P26450, Q924C1, Q8BH60, P35585, Q9D2V7, Q3UM18, Q9QZ88, Q6PGL7, O88746, P60521, Q9CWU9, P40336, Q3UMB9	1.31896289996603E-07
UP_KEYWORDS	Transport	120	10.840108401084	1.86855313294063E-06	P10639, Q8BVE3, Q3UBX0, Q8BUK6, Q9CR60, A2A5R2, Q61792, P17427, O08788, P17426, Q6P8X1, P63168, O35643, Q01405, P62075, Q64152, P61027, P48962, P56480, Q9CT10, Q9EPL8, Q62418, Q03265, Q8CI71, P53811, Q8V175, Q91VC3, P62482, Q9QXK3, Q9D906, P52293, Q9JHU4, Q5XJY5, P51881, Q61655, Q8R2E9, P70168, Q91WD5, P42567, P51807, Q8BIJ7, P56383, P62814, Q91VR2, Q8R0H9, P97855, Q8BH60, Q924C1, P35585, P31786, Q9QZ88, Q6PGL7, Q05816, O08583, Q3U0V1, P60521, Q9CWU9, Q9CQA1, P98078, P53564, Q6P5F9, Q8BKC5, Q62048, Q91YE6, Q8CIE6, P63242, Q9CZ13, P22892, P46467, Q9DB77, Q8R1Q8, Q9CPN8, Q9CR16, Q8BFY9, Q9CR95, Q8VVDJ3, Q9CQX2, Q8R180, O08997, Q9Z1G3, Q9CQ75, Q9DBG5, Q9CRA5, Q9CWK8, P61750, P57780, Q99LC3, Q9ERK4, P61924, Q9WU78, B2RXC1, Q8C2E7, Q99MD9, Q9ERS2, P50516, P31750, Q9D662, P84091, Q64324, O35344, P50518, O54984, Q9QYB1, Q91YT0, P53994, Q8VBT6, Q9CWZ7, Q9EQH3, Q60931, P26450, P97379, Q9D2V7, Q3UM18, Q9DC69, Q91VD9, O88746, Q8VBT0, P62627, P40336, Q3UMB9	1.49484250635251E-05
GOTERM_BP_DIRECTGO:0006810~	transport	119	10.7497741644083	0.000773974908973	P10639, Q8BVE3, Q3UBX0, Q8BUK6, Q9CR60, A2A5R2, Q61792, P17427, O08788, P17426, Q6P8X1, P63168, O35643, Q01405, P62075, Q64152, P61027, P48962, P56480, Q9CT10, Q9EPL8, Q62418, Q03265, Q8CI71, P53811, Q8V175, P62482, Q9QXK3, Q9D906, Q9JHU4, Q5XJY5, P51881, Q61655, Q8R2E9, P70168, Q91WD5, P42567, P51807, Q8BIJ7, P56383, P62814, Q91VR2, Q8R0H9, P97855, Q8BH60, Q924C1, P35585, P31786, Q9QZ88, Q6PGL7, Q05816, O08583, Q3U0V1, P60521, Q9CWU9, Q9CQA1, P98078, P53564, Q6P5F9, Q8BKC5, Q62048, Q91YE6, Q8CIE6, Q8BMP6, P63242, Q9CZ13, P22892, P46467, Q9DB77, Q8R1Q8, Q9CPN8, Q9CR16, Q8BFY9, Q9CR95, Q8VVDJ3, Q9CQX2, Q8R180, O08997, Q9Z1G3, Q9CQ75, Q9DBG5, Q9CRA5, Q9CWK8, P61750, P57780, Q99LC3, Q9ERK4, P61924, Q9WU78, B2RXC1, Q8C2E7, Q99MD9, P50516, P31750, Q9D662, P84091, Q64324, O35344, P50518, O54984, Q9QYB1, Q91YT0, P53994, Q8VBT6, Q9CWZ7, Q9EQH3, Q60931, P26450, P97379, Q9D2V7, Q3UM18, Q9DC69, Q91VD9, O09117, O88746, Q8VBT0, P62627, P40336, Q3UMB9	0.036028532012693
<b>Annotation Cluster 7</b> Enrichment Score: 7.073032244597856						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECTGO:0006413~	translational initiation	23	2.0776874435411	1.87090046386024E-15	Q62448, Q99JX4, Q6ZQ58, Q9Z0N1, Q99LC8, Q9DCH4, O70194, Q9Z1D1, Q99L45, Q6NZJ6, P59325, Q8R1B4, Q62167, Q8BGD9, P61222, Q8BMJ3, Q61749, Q05D44, P23116, Q8QZY1, P60229, Q80XI3, Q6P542	1.74180833185389E-12
UP_KEYWORDS	Initiation factor	20	1.806684733514	5.48662868294961E-12	Q62448, Q99JX4, Q9Z0N1, Q99LC8, Q9DCH4, O70194, Q9Z1D1, Q99L45, Q6NZJ6, P59325, Q8R1B4, Q8BGD9, Q03963, Q8BMJ3, Q61749, Q05D44, P23116, Q8QZY1, P60229, Q80XI3	7.80320523797277E-11
GOTERM_MF_DIRECTGO:0003743~	translation initiation factor activity	20	1.806684733514	5.97628309007059E-10	Q62448, Q99JX4, Q9Z0N1, Q99LC8, Q9DCH4, O70194, Q9Z1D1, Q99L45, Q6NZJ6, P59325, Q8R1B4, Q8BGD9, Q03963, Q8BMJ3, Q61749, Q05D44, P23116, Q8QZY1, P60229, Q80XI3	4.74884648618686E-08
GOTERM_CC_DIRECTGO:0005852~	eukaryotic translation initiation fa	10	0.903342366757	7.40046438617221E-09	Q99JX4, P61222, Q9DCH4, O70194, P23116, Q9Z1D1, Q8QZY1, Q8R1B4, P60229, Q62167	2.28592122150653E-07

GOTERM_BP_DIRECTGO:0001731~formation of translation preinitiation	12	1.0840108401084	8.30654457223654E-09	Q99JX4, Q9Z0N1, Q9DCH4, O70194, P23116, Q9Z1D1, Q8QZY1, Q8R1B4, P59325, P25444, P60229, Q8BGD9	2.32001789902567E-06	
GOTERM_BP_DIRECTGO:0006446~regulation of translational initiation	13	1.1743450767841	2.31212299155308E-08	Q62448, Q99JX4, Q99LC8, Q9DCH4, O70194, Q9Z1D1, Q6NZJ6, P59325, Q8R1B4, Q05D44, P23116, Q8QZY1, P60229	5.3814662628398E-06	
GOTERM_CC_DIRECTGO:0016282~eukaryotic 43S preinitiation complex	8	0.7226738934056	1.94526837063305E-06	Q99JX4, Q9DCH4, O70194, P23116, Q9Z1D1, Q8QZY1, Q8R1B4, P60229	3.8627471931142E-05	
GOTERM_CC_DIRECTGO:0033290~eukaryotic 48S preinitiation complex	8	0.7226738934056	1.94526837063305E-06	Q99JX4, Q9DCH4, O70194, P23116, Q9Z1D1, Q8QZY1, Q8R1B4, P60229	3.8627471931142E-05	
KEGG_PATHWAY mmu03013:RNA transport	30	2.710027100271	4.0454306634531E-06	Q62448, Q9Z0N1, O70194, Q9DCH4, Q9Z1D1, Q99L45, P59325, P70168, Q6P5F9, Q9EPU0, Q7TMB8, Q8CIG8, Q99JH1, Q8BMJ3, Q05D44, Q80XI3, Q99LC8, P29341, P63280, Q6NZJ6, Q924C1, Q8R1B4, Q61584, Q8BGD9, Q91VC3, O08583, Q61749, P23116, Q9CWU9, P60229	9.10221899276947E-05	
GOTERM_CC_DIRECTGO:0071541~eukaryotic translation initiation factor	5	0.4516711833785	0.000265541335547	Q99JX4, Q9DCH4, O70194, P23116, Q8R1B4	0.002870849473813	
GOTERM_BP_DIRECTGO:0075525~viral translational termination-reinitiation	4	0.3613369467028	0.001074077458913	O70194, P23116, Q9Z1D1, Q8QZY1	0.045453005193108	
<b>Annotation Cluster 8</b>	Enrichment Score: 7.0132568558682165					
Category	Term	Count	%	PValue	Genes	FDR
SMART	SM00088:PINT	9	0.8130081300813	5.30010575803517E-08	Q9D8W5, Q8BV13, Q99J14, Q99JX4, Q9CZ04, P23116, Q8R1B4, O88543, P60229	1.44162876618557E-05
UP_SEQ_FEATURE	domain:PCI	10	0.903342366757	1.22722798860304E-07	Q9D8W5, Q8VBV7, Q8BV13, Q99J14, Q99JX4, Q9CZ04, P23116, Q8R1B4, O88543, P60229	6.94611041549318E-05
INTERPRO	IPR000717:Proteasome component (PCI) domain	9	0.8130081300813	1.4028771626421E-07	Q9D8W5, Q8BV13, Q99J14, Q99JX4, Q9CZ04, P23116, Q8R1B4, O88543, P60229	2.10273635344812E-05
<b>Annotation Cluster 9</b>	Enrichment Score: 6.839604670278965					
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Ligase	51	4.6070460704607	1.12186499603661E-15	Q61510, P97386, Q8C0C7, B2RQC6, Q9CZW4, Q922B2, P37913, Q61035, Q99PP7, Q8C878, Q8BML9, P16460, Q9Z1F9, P46664, Q8BU30, P41216, Q91WQ3, Q9ER72, P61082, P70698, Q02053, Q68FL6, Q8BP47, Q9QXG4, E9Q555, P32921, Q9R1T2, A2AN08, Q5SUR0, Q922D8, Q80V11, Q8CGC7, Q9CZD3, Q8BMJ2, Q9QUJ7, P26638, Q9D7H3, P97494, Q9Z1Q9, Q62318, Q64737, E9Q4Z2, P51855, P63280, Q3THK7, Q9D2R0, Q9D0R2, Q9WUA2, P22682, Q8BGQ7, Q9D0I9	2.20921106911825E-14
UP_KEYWORDS	Aminoacyl-tRNA synthetase	19	1.7163504968383	1.43897259880912E-15	P32921, Q9Z1Q9, Q91WQ3, Q8C0C7, Q922B2, Q9ER72, Q61035, Q9D0R2, Q68FL6, Q8CGC7, Q9WUA2, Q8BML9, Q8BP47, Q9CZD3, Q8BMJ2, P26638, Q8BU30, Q8BGQ7, Q9D0I9	2.63126418067953E-14
GOTERM_MF_DIRECTGO:0004812~aminoacyl-tRNA ligase activity		18	1.6260162601626	1.36113034452581E-12	P32921, Q9Z1Q9, Q91WQ3, Q8C0C7, Q922B2, Q9ER72, Q61035, Q9D0R2, Q68FL6, Q8CGC7, Q9WUA2, Q8BP47, Q9CZD3, Q8BMJ2, P26638, Q8BU30, Q8BGQ7, Q9D0I9	1.75755955736895E-10
GOTERM_BP_DIRECTGO:0006418~tRNA aminoacylation for protein synthesis		17	1.5356820234869	2.61973382794464E-12	P32921, Q9Z1Q9, Q91WQ3, P31230, Q922B2, Q9ER72, Q61035, Q9D0R2, Q68FL6, Q8CGC7, Q8BML9, Q8BP47, Q9CZD3, Q8BMJ2, P26638, Q8BU30, Q9D0I9	1.82922914536235E-09
GOTERM_MF_DIRECTGO:0016874~ligase activity		51	4.6070460704607	8.65098880116949E-11	Q61510, P97386, Q8C0C7, B2RQC6, Q9CZW4, Q922B2, P37913, Q61035, Q99PP7, Q8C878, O88738, P16460, Q9Z1F9, P46664, Q8BU30, P41216, Q91WQ3, Q9ER72, P61082, P70698, Q02053, Q68FL6, Q8BP47, Q9QXG4, E9Q555, P32921, Q9R1T2, A2AN08, Q5SUR0, Q922D8, Q80V11, Q8CGC7, Q9CZD3, Q8BMJ2, Q9QUJ7, P26638, Q9D7H3, P97494, Q9Z1Q9, Q62318, Q64737, E9Q4Z2, P51855, P63280, Q3THK7, Q9D2R0, Q9D0R2, Q9WUA2, P22682, Q8BGQ7, Q9D0I9	8.93647143160808E-09
KEGG_PATHWAY mmu00970:Aminoacyl-tRNA biosynthesis		19	1.7163504968383	2.72904169997737E-07	P32921, Q9Z1Q9, Q91WQ3, Q8C0C7, Q922B2, Q9ER72, Q61035, Q9D0R2, Q68FL6, Q8CGC7, Q9WUA2, Q8BML9, Q8BP47, Q9CZD3, Q8BMJ2, P26638, Q8BU30, Q8BGQ7, Q9D0I9	1.02339063749151E-05
INTERPRO	IPR014729:Rossmann-like alpha/beta/alpha sandwich	13	1.1743450767841	3.19017657056931E-07	P32921, Q9Z1Q9, Q91WQ3, Q9DBL7, Q9ER72, Q3THK7, Q68FL6, Q8CGC7, Q8BML9, Q8BMJ2, P16460, Q8BU30, Q9D0I9	3.60277274036294E-05
UP_SEQ_FEATURE	short sequence motif:"HIGH" region	9	0.8130081300813	6.76841469022575E-07	P32921, Q68FL6, Q9Z1Q9, Q8CGC7, Q91WQ3, Q8BMJ2, Q8BU30, Q9ER72, Q9D0I9	0.000306473817173
INTERPRO	IPR001412:Aminoacyl-tRNA synthetase, class I,	8	0.7226738934056	1.59467425289947E-06	P32921, Q68FL6, Q9Z1Q9, Q8CGC7, Q8BML9, Q8BMJ2, Q8BU30, Q9D0I9	0.000122789917473
UP_SEQ_FEATURE	short sequence motif:"KMSKS" region	8	0.7226738934056	3.75129909973642E-06	P32921, Q68FL6, Q9Z1Q9, Q8CGC7, Q91WQ3, Q8BMJ2, Q8BU30, Q9ER72	0.001061617645225
INTERPRO	IPR006195:Aminoacyl-tRNA synthetase, class II	8	0.7226738934056	4.45572951333441E-06	Q8CGC7, Q8BP47, Q8C0C7, Q9CZD3, P26638, Q922B2, Q61035, Q9D0R2	0.000314500241483
INTERPRO	IPR009080:Aminoacyl-tRNA synthetase, class I,	6	0.5420054200542	0.000165200882193	Q68FL6, Q9Z1Q9, Q8BMJ2, Q8BU30, Q9ER72, Q9D0I9	0.008230891012782

**Annotation Cluster 10** Enrichment Score: 6.515229921475024

Category	Term	Count	%	PValue	Genes	FDR
UP_SEQ_FEATURE	nucleotide phosphate-binding region:NADP	17	1.5356820234869	6.3638536752724E-08	P23591, P06801, Q91YR9, Q8BVI4, Q9JII6, Q64105, Q99MZ7, Q922D8, P62482, O88844, P45376, P45377, Q8K2T1, Q91Z53, P48758, Q91X52, P21300	4.80258824027224E-05
UP_KEYWORDS	NADP	25	2.2583559168925	2.17094473793469E-07	P23591, Q91YR9, P19096, Q9CY64, Q9JMH6, Q9DCD0, Q8BVI4, Q64105, Q922D8, Q8K0C9, Q9JLT4, Q00612, P45376, P45377, Q8K2T1, Q91Z53, P21300, Q91X52, P06801, Q9JII6, Q99MZ7, Q2TPA8, P62482, O88844, P48758	2.13754558812031E-06
UP_SEQ_FEATURE	binding site:NADP	10	0.903342366757	2.0603513272553E-06	Q8K0C9, P06801, Q91YR9, Q00612, P62482, O88844, Q8K2T1, Q91Z53, Q64105, Q922D8	0.000777439234151
<b>Annotation Cluster 11</b> Enrichment Score: 5.75421132622884						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu01130:Biosynthesis of antibiotics	45	4.0650406504065	2.44752055970672E-11	Q99K85, Q99JW2, Q9DCD0, Q9WTP7, Q9CQ60, Q3TW96, Q9JLJ2, Q93092, P17751, Q9CS42, Q5SUR0, Q91ZJ5, Q8CAY6, Q9CWJ9, P12382, Q8JZK9, Q00612, Q91V92, P16460, Q9Z0S1, Q9CYR6, P09411, Q9D0F9, P47856, P47857, Q9WV85, P06745, Q91YI0, Q3TRM8, P28474, Q64737, Q9JII6, O08739, Q8VCN5, P54822, Q8VEE0, Q9JHU9, O88844, P05063, Q8CHP8, P05064, P17182, Q9WUA3, Q9QXG4, P05201	2.75346062967006E-09
KEGG_PATHWAY	mmu01200:Carbon metabolism	25	2.2583559168925	8.29126545833159E-07	Q99K85, Q9DCD0, Q9R0P3, Q9CQ60, Q93092, P17751, Q9CS42, Q8CAY6, P12382, Q00612, P09411, P47857, P06801, P06745, Q3TRM8, P28474, Q8VEE0, O88844, P05063, Q8CHP8, P05064, P17182, Q9WUA3, Q9QXG4, P05201	2.66504961160658E-05
KEGG_PATHWAY	mmu00051:Fructose and mannose metabolism	13	1.1743450767841	1.33913601508977E-06	P23591, Q3TRM8, P17751, P12382, Q8K0C9, P05063, P45376, P05064, Q8BZA9, P45377, Q9WUA3, P47857, P21300	3.76632004243997E-05
KEGG_PATHWAY	mmu01230:Biosynthesis of amino acids	19	1.7163504968383	2.61106421664957E-06	Q99K85, Q99JW2, Q91YI0, Q93092, P17751, Q9CS42, Q8VCN5, P12382, Q8VEE0, P16460, Q3THS6, O88844, P05063, P05064, P09411, P17182, Q9WUA3, P47857, P05201	6.52766054162392E-05
UP_KEYWORDS	Glycolysis	10	0.903342366757	8.43001605555818E-06	P12382, P06745, Q3TRM8, P05063, P05064, P09411, P17182, Q9WUA3, P47857, P17751	5.30079909507032E-05
GOTERM_BP_DIRECTGO:0030388--fructose 1,6-bisphosphate metaboli		6	0.5420054200542	2.91894123584364E-05	P12382, P05063, P05064, Q8BZA9, Q9WUA3, P47857	0.002625224225874
GOTERM_BP_DIRECTGO:0006096--glycolytic process		10	0.903342366757	4.29253220955281E-05	P12382, P06745, Q3TRM8, P05063, P05064, P09411, P17182, Q9WUA3, P47857, P17751	0.003330289572578
KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	15	1.3550135501355	0.000123467502122	P06745, Q3TRM8, P28474, Q9JII6, Q9JLJ2, P17751, P12382, P05063, P05064, P09411, P17182, Q9WUA3, Q9D0F9, Q9QXG4, P47857	0.00231501566479
<b>Annotation Cluster 12</b> Enrichment Score: 5.709414818966231						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	NADP	25	2.2583559168925	2.17094473793469E-07	P23591, Q91YR9, P19096, Q9CY64, Q9JMH6, Q9DCD0, Q8BVI4, Q64105, Q922D8, Q8K0C9, Q9JLT4, Q00612, P45376, P45377, Q8K2T1, Q91Z53, P21300, Q91X52, P06801, Q9JII6, Q99MZ7, Q2TPA8, P62482, O88844, P48758	2.13754558812031E-06
UP_KEYWORDS	Oxidoreductase	55	4.96838301716351	4.35375757011856E-07	P23591, P09528, Q91YR9, O08709, P19096, Q9JMH6, Q8BVI4, Q9JLJ2, Q64105, Q9DCN2, Q8COL6, P45376, P61982, P45377, Q00519, O70325, Q6PDY2, Q9JHI5, Q8R180, Q99MZ7, Q2TPA8, P62482, Q61171, O88844, Q9DCD0, Q8R2E9, Q91WD5, Q64521, Q62465, Q922D8, Q9JLT4, Q00612, Q91Z53, P62259, Q91X52, Q91YT0, P21300, P06801, Q9CQV8, P28474, P68254, Q9JII6, Q99KP3, P11352, P35700, P20108, Q91VD9, Q9Z0X1, P24547, P07742	3.84331702741501E-06
GOTERM_BP_DIRECTGO:0055114--oxidation-reduction process		63	5.69105691056911	1.30833783351878E-06	P23591, P09528, P10639, Q91YR9, O08709, P19096, Q9JMH6, Q8BVI4, Q9JLJ2, Q64105, Q9DCN2, Q8COL6, P45376, Q9CZ13, P45377, Q9DB77, Q00519, O70325, Q6PDY2, Q9CQX2, Q9JHI5, Q8R180, Q99MZ7, Q9CQ75, Q2TPA8, P62482, Q61171, O88844, O09131, P48758, Q99LC3, P50396, O08807, P99029, Q9CY64, Q9DCD0, Q8R2E9, Q91WD5, Q64521, Q62465, Q922D8, Q9JLT4, Q00612, Q91Z53, Q91X52, Q91YT0, P21300, P06801, P28474, O70145, A2AAAY5, Q9JII6, Q99KP3, P11352, P35700, Q9DC69, P20108, Q91VD9, Q9Z0X1, Q3U9G9, Q8VBT0, P24547, P07742	0.000243612504601
GOTERM_MF_DIRECTGO:0016491--oxidoreductase activity		53	4.78771454381211	0.000117518925747	P23591, P09528, Q91YR9, O08709, P19096, Q9JMH6, Q8BVI4, Q9JLJ2, Q64105, Q9DCN2, Q8COL6, P45376, P45377, Q00519, O70325, Q6PDY2, Q9JHI5, Q8R180, Q99MZ7, Q2TPA8, P62482, Q61171, O88844, O09131, P48758, P50396, O08807, P99029, Q9CY64, Q9DCD0, Q8R2E9, Q91WD5, Q64521, Q62465, Q922D8, Q9JLT4, Q00612, Q91Z53, Q91X52, Q91YT0, P21300, P06801, P28352, P28474, Q9JII6, Q99KP3, P11352, P35700, P20108, Q91VD9, Q9Z0X1, P24547, P07742	0.003468487151334

**Annotation Cluster 13** Enrichment Score: 5.598416617399601

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Cell division	40	3.613369467028	8.47725570639675E-08	Q8CG48, Q6P9P6, Q8K1R7, Q9WU78, P97386, P28740, Q8BFT2, Q9R1T4, Q8R3C0, Q80X41, Q68FD5, Q07832, P30285, P37913, P11440, P49718, A2AGT5, Q9Z0Y1, O88738, P51807, Q8K2Z4, Q1HFZ0, P46467, P42208, Q8K298, P62137, Q8R1Q8, P49615, Q80UG5, P62908, P63280, Q61166, Q99P69, P60122, Q3TCJ1, Q9JLQ0, Q64261, Q9CWU9, Q9WVA3, Q8BK67	9.43555417755465E-07
UP_KEYWORDS	Cell cycle	56	5.05871725383921	9.45767187125908E-08	Q64701, Q8CG48, Q8K1R7, P97386, Q8VBW6, Q61074, Q07832, P30285, P37913, P11440, Q80U87, Q8C878, O88738, Q9Z0Y1, P25206, Q1HFZ0, P46467, Q8R1Q8, P49615, P97310, P97311, Q61166, Q61881, P18654, Q99P69, Q9JLQ0, Q9WVA3, Q8BK67, Q6P9P6, Q9WU78, P28740, Q8BFT2, Q8R3C0, Q9R1T4, Q99MD9, Q80X41, Q68FD5, P61290, Q9QUR7, A2AGT5, P49718, P49717, P51807, Q8K2Z4, P42208, Q8K298, P62137, Q8CFI2, Q80UG5, P62908, Q9ESL4, P63280, P60122, Q3TCJ1, Q64261, Q9CWU9	1.0088183329343E-06
UP_KEYWORDS	Mitosis	29	2.6196928635953	3.061523563023E-06	Q8CG48, Q6P9P6, Q8K1R7, P28740, Q8BFT2, Q8R3C0, Q80X41, Q68FD5, Q07832, P11440, A2AGT5, Q9Z0Y1, O88738, P51807, Q8K2Z4, Q1HFZ0, P42208, Q8K298, Q8R1Q8, P62908, P63280, Q61166, Q99P69, P60122, Q3TCJ1, Q9JLQ0, Q9CWU9, Q9WVA3, Q8BK67	2.17708342259413E-05
GOTERM_BP_DIRECTGO:0051301	~cell division	40	3.613369467028	6.75937901403081E-06	Q8CG48, Q6P9P6, Q8K1R7, Q9WU78, P97386, P28740, Q8BFT2, Q9R1T4, Q8R3C0, Q80X41, Q07832, P30285, P37913, P11440, P49718, A2AGT5, Q9Z0Y1, O88738, P51807, Q8K2Z4, Q1HFZ0, P46467, P42208, P27546, Q8K298, P62137, Q8R1Q8, P49615, Q80UG5, P62908, P63280, Q61166, Q99P69, P60122, Q3TCJ1, Q9JLQ0, Q64261, Q9CWU9, Q9WVA3, Q8BK67	0.001015767892489
GOTERM_BP_DIRECTGO:0007067	~mitotic nuclear division	31	2.8003613369467	3.77164588252871E-05	Q8CG48, Q6P9P6, Q8K1R7, P28740, Q8BFT2, Q8R3C0, Q80X41, Q68FD5, Q07832, P11440, Q9DBR7, A2AGT5, Q9Z0Y1, O88738, P51807, Q8K2Z4, Q1HFZ0, Q8CDG3, P42208, Q8K298, Q8R1Q8, P62908, P63280, Q61166, Q99P69, P60122, Q3TCJ1, Q9JLQ0, Q9CWU9, Q9WVA3, Q8BK67	0.003116784797489
GOTERM_BP_DIRECTGO:0007049	~cell cycle	54	4.87804878048781	4.10284825006226E-05	Q64701, Q8CG48, Q8K1R7, P97386, Q8VBW6, Q61074, Q07832, P30285, P37913, P11440, Q80U87, Q8C878, O88738, Q9Z0Y1, P25206, Q1HFZ0, P46467, Q8R1Q8, P49615, P97310, P97311, Q61166, Q61881, P18654, Q99P69, Q9JLQ0, Q9WVA3, Q8BK67, Q6P9P6, Q9WU78, P28740, Q8BFT2, Q8R3C0, Q9R1T4, Q99MD9, Q80X41, P61290, Q9QUR7, A2AGT5, P49718, P49717, Q8K2Z4, P42208, Q8K298, P62137, Q8CFI2, Q80UG5, P62908, Q9ESL4, P63280, P60122, Q3TCJ1, Q64261, Q9CWU9	0.00327407290355

**Annotation Cluster 14** Enrichment Score: 5.571235894008052

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECTGO:1904874	~positive regulation of telomerase R	11	0.9936766034327	1.74294034537538E-10	P80315, P80314, P80313, P42932, P60122, P11983, Q9WTM5, P80318, P80317, P80316, Q9ESX5	9.73606476926685E-08
GOTERM_BP_DIRECTGO:1904871	~positive regulation of protein local	8	0.7226738934056	4.92024246862343E-09	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	1.52691524609614E-06
GOTERM_CC_DIRECTGO:0005832	~chaperonin-containing T-complex	8	0.7226738934056	1.38796317441281E-08	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	3.8585376248676E-07
GOTERM_BP_DIRECTGO:1904851	~positive regulation of establishmen	8	0.7226738934056	2.1203846527325E-08	P80315, P80314, P80313, P42932, P11983, P80317, P80316, Q9ESX5	5.3814662628398E-06
INTERPRO	IPR002194:Chaperonin TCP-1, conserved site	8	0.7226738934056	3.61987981752303E-08	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	8.76010915840574E-06
INTERPRO	IPR027410:TCP-1-like chaperonin intermediate	8	0.7226738934056	3.61987981752303E-08	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	8.76010915840574E-06
INTERPRO	IPR017998:Chaperone tailless complex polypept	8	0.7226738934056	9.57034283731048E-08	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	1.6212160766404E-05
GOTERM_CC_DIRECTGO:0002199	~zona pellucida receptor complex	8	0.7226738934056	5.62493257267272E-07	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	1.30310937933585E-05
INTERPRO	IPR027409:GroEL-like apical domain	8	0.7226738934056	8.84559372316474E-07	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	8.32468653724504E-05
INTERPRO	IPR027413:GroEL-like equatorial domain	8	0.7226738934056	8.84559372316474E-07	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	8.32468653724504E-05
INTERPRO	IPR002423:Chaperonin Cpn60/TCP-1	8	0.7226738934056	1.59467425289947E-06	P80315, P80314, P80313, P42932, P11983, P80318, P80317, P80316	0.000122789917473
GOTERM_BP_DIRECTGO:1901998	~toxin transport	11	0.9936766034327	4.364886757582E-06	P80315, P80314, P80313, P42932, P61924, P29452, Q8R0H9, P11983, P80318, P80317, P80316	0.000717125218466
GOTERM_BP_DIRECTGO:0032212	~positive regulation of telomere mai	10	0.903342366757	1.52469321825152E-05	P80315, P80314, P80313, P42932, Q9JLV6, P11983, P80318, P80317, P80316, Q9ESX5	0.001860295020895
GOTERM_MF_DIRECTGO:0051082	~unfolded protein binding	15	1.3550135501355	1.96987204599351E-05	P80315, P80314, P80313, Q9WU28, Q99L47, P11983, P11499, P35564, Q8BQM4, P42932, Q61081, Q9CWM4, P80318, P80317, P80316	0.000701682008107

GOTERM_BP_DIRECTGO:0050821~protein stabilization	19	1.7163504968383	4.92513178252076E-05	P80315, P80314, P80313, Q99LX0, Q8VD75, P26450, Q8BTM8, P11983, Q9QUR7, O35129, P67778, Q91YE6, P42932, Q61081, Q80UM3, P80318, P62962, P80317, P80316	0.003619971860153
GOTERM_CC_DIRECTGO:0044297~cell body	16	1.4453477868112	6.2331942579609E-05	P80315, P80314, Q9CXW3, P80313, P03995, Q99LX0, P11983, P42932, P51807, P20152, O09131, Q91V12, P80318, O89110, P80317, P80316	0.000805966513355
GOTERM_BP_DIRECTGO:0007339~binding of sperm to zona pellucida	9	0.8130081300813	0.00027751651684	P80315, P80314, P80313, P42932, P11983, P80318, P80317, Q80X50, P80316	0.01685007894638

**Annotation Cluster 15** Enrichment Score: 4.921934063329559

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECTGO:0022624~proteasome accessory complex		13	1.1743450767841	4.04868445696203E-13	Q9D8W5, P54775, Q3TXS7, P46471, Q9CX56, O35593, P62192, Q8BJY1, Q99JI4, O35226, P62196, O88685, P62334	1.73159119851607E-11
GOTERM_CC_DIRECTGO:0008540~proteasome regulatory particle, ba		11	0.9936766034327	9.92021719679901E-12	P54775, O35226, Q3TXS7, P46471, P62196, P62192, O88685, Q8BJY1, P62334, Q9CR00, Q9Z2X2	3.67709384094683E-10
GOTERM_CC_DIRECTGO:0031597~cytosolic proteasome complex		9	0.8130081300813	7.89046285610099E-10	P54775, Q9JHR7, P46471, P62196, O35593, Q9WUP7, P62192, O88685, P62334	2.58064549881891E-08
GOTERM_CC_DIRECTGO:0031595~nuclear proteasome complex		7	0.6323396567299	2.37203656908744E-07	Q9D8W5, P54775, P46471, P62196, P62192, O88685, P62334	5.73414057570703E-06
INTERPRO	IPR005937:26S proteasome subunit P45	6	0.5420054200542	1.00098378767082E-06	P54775, P46471, P62196, P62192, O88685, P62334	8.47833268157186E-05
GOTERM_MF_DIRECTGO:0036402~proteasome-activating ATPase acti		6	0.5420054200542	1.85713443969E-06	P54775, P46471, P62196, P62192, O88685, P62334	0.000100969467168
GOTERM_BP_DIRECTGO:0030163~protein catabolic process		11	0.9936766034327	7.23207914555294E-05	P54775, Q9D4H8, P46471, P62196, Q9JKB1, Q9D906, Q9R1P1, P62192, O88685, P62334, P31750	0.00492663342769
SMART	SM00382:AAA	18	1.6260162601626	0.00014045749284	P54775, P46471, Q9WTM5, P62192, Q9WUK4, Q61881, P61222, P60122, P62196, P25206, O88685, Q99LE6, P46467, Q9JHU4, P56480, P62334, Q6P542, E9Q555	0.005457776864649
GOTERM_BP_DIRECTGO:0045899~positive regulation of RNA polym		6	0.5420054200542	0.000162231360871	P54775, P46471, P62196, P62192, O88685, P62334	0.010537492811919
INTERPRO	IPR003593:AAA+ ATPase domain	18	1.6260162601626	0.000234241229209	P54775, P46471, Q9WTM5, P62192, Q9WUK4, Q61881, P61222, P60122, P62196, P25206, O88685, Q99LE6, P46467, Q9JHU4, P56480, P62334, Q6P542, E9Q555	0.011022351174457
INTERPRO	IPR003960:ATPase, AAA-type, conserved site	7	0.6323396567299	0.001015270969872	P54775, P46471, P62196, P62192, O88685, P46467, P62334	0.037388457020955
GOTERM_MF_DIRECTGO:0017025~TBP-class protein binding		6	0.5420054200542	0.003340943583598	P54775, P46471, P62196, P62192, O88685, P62334	0.056576962653388
GOTERM_MF_DIRECTGO:0016887~ATPase activity		20	1.806684733514	0.006081332737621	P28740, P46471, Q9CZ30, Q03265, Q9WTM5, Q62167, Q3V300, Q8VDD5, P61222, P60122, O54984, Q9JHR7, P62196, Q99LE6, P46467, Q9JHU4, P56480, Q6P542, Q91VR2, E9Q555	0.090857798751736

**Annotation Cluster 16** Enrichment Score: 4.690226041523324

Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR012340:Nucleic acid-binding, OB-fold	21	1.8970189701897	2.02712045110056E-09	P62918, Q91WQ3, P97386, P97310, Q9JKB3, Q9CPN8, P97311, P31230, Q922B2, P37913, Q9CQ71, Q61881, Q8VEE4, P49718, P49717, Q8BP47, P60122, P63242, Q8BMJ3, P25206, Q91W50	6.86788408832871E-07
KEGG_PATHWAY	mmu03030:DNA replication	14	1.2646793134598	2.41066311231235E-07	P97310, P97311, Q9WUK4, P39749, P37913, Q9CQ71, Q61881, P33610, Q8VEE4, P49718, O35654, P49717, P25206, P17918	1.02339063749151E-05
UP_KEYWORDS	DNA replication	18	1.6260162601626	2.82024272930346E-07	P97386, P97310, P97311, Q8R3C0, Q99MD9, Q9WUK4, P39749, P37913, Q9CQ71, Q61881, P33610, Q8VEE4, P49718, O35654, P49717, P25206, P17918, P07742	2.5785076382203E-06
GOTERM_CC_DIRECTGO:0042555~MCM complex		7	0.6323396567299	6.838517071339E-07	P49718, P49717, P97310, P97311, Q8R3C0, P25206, Q61881	1.52088619666579E-05
INTERPRO	IPR018525:Mini-chromosome maintenance, con:	6	0.5420054200542	1.00098378767082E-06	P49718, P49717, P97310, P97311, P25206, Q61881	8.47833268157186E-05
GOTERM_BP_DIRECTGO:0006260~DNA replication		21	1.8970189701897	2.01573169475565E-06	P54103, P97386, P97310, P97311, Q8R3C0, Q99MD9, Q9WUK4, P39749, P37913, Q9CQ71, Q61881, Q6NVF4, P33610, Q8VEE4, P49718, Q9EPU0, O35654, P49717, P25206, P17918, P07742	0.000351871163966
SMART	SM00350:MCM	6	0.5420054200542	1.5479968898661E-05	P49718, P49717, P97310, P97311, P25206, Q61881	0.001052637885109
GOTERM_MF_DIRECTGO:0003678~DNA helicase activity		8	0.7226738934056	1.58189698254336E-05	P49718, P49717, P97310, P60122, P97311, P25206, Q9WTM5, Q61881	0.000583606993917
UP_SEQ_FEATURE	domain:MCM	6	0.5420054200542	1.62190010538753E-05	P49718, P49717, P97310, P97311, P25206, Q61881	0.003059984865498
INTERPRO	IPR001208:Mini-chromosome maintenance, DN,	6	0.5420054200542	1.87823021619794E-05	P49718, P49717, P97310, P97311, P25206, Q61881	0.001272688794496
UP_KEYWORDS	Helicase	17	1.5356820234869	8.47286965413036E-05	Q61655, Q91VR5, P97310, Q6NZQ2, P97311, Q9WTM5, P97855, Q61881, Q62167, P54823, Q6NVF4, Q91VC3, P49718, Q9EPU0, P49717, P60122, P25206	0.000433810926291
GOTERM_MF_DIRECTGO:0004386~helicase activity		16	1.4453477868112	0.002155823400252	Q61655, Q91VR5, P97310, Q6NZQ2, P97311, Q9WTM5, P97855, Q61881, Q62167, P54823, Q6NVF4, P49718, Q9EPU0, P49717, P60122, P25206	0.039767242365354

**Annotation Cluster 17** Enrichment Score: 4.577030748491163

Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu03050:Proteasome	25	2.2583559168925	6.90935237846467E-17	Q9D8W5, P54775, P46471, O35593, Q9R1P1, P28063, Q9R1P4, P61290, O35522, O35226, P62196, Q9Z2U1, P26516, P62334, Q9Z2U0, O09061, P97371, P97372, Q3TXS7, Q9CX56, P70195, P62192, Q99J14, Q9QUM9, O88685	1.55460428515455E-14
GOTERM_CC_DIRECTIGO:0005839~proteasome core complex		9	0.8130081300813	1.46385509574046E-06	O35522, P70195, P28063, Q9Z2U1, Q9QUM9, Q9R1P1, Q9R1P4, O09061, Q9Z2U0	3.1303978201219E-05
UP_KEYWORDS	Threonine protease	9	0.8130081300813	1.4732361480893E-06	O35522, P70195, P28063, Q9Z2U1, Q9QUM9, Q9R1P1, Q9R1P4, O09061, Q9Z2U0	1.2571615130362E-05
INTERPRO	IPR001353:Proteasome, subunit alpha/beta	9	0.8130081300813	1.81745985557013E-06	O35522, P70195, P28063, Q9Z2U1, Q9QUM9, Q9R1P1, Q9R1P4, O09061, Q9Z2U0	0.000133859869362
GOTERM_BP_DIRECTIGO:0002479~antigen processing and presentatio		10	0.903342366757	8.49280323618038E-06	O35522, P70195, P01902, P28063, Q9Z2U1, Q9QUM9, Q9R1P1, Q9R1P4, O09061, Q9Z2U0	0.001129542830412
GOTERM_MF_DIRECTIGO:0004298~threonine-type endopeptidase activ		9	0.8130081300813	1.01059830273001E-05	O35522, P70195, P28063, Q9Z2U1, Q9QUM9, Q9R1P1, Q9R1P4, O09061, Q9Z2U0	0.000401518479508
GOTERM_BP_DIRECTIGO:0051603~proteolysis involved in cellular pro		13	1.1743450767841	1.56236363533631E-05	P10605, P70195, Q9R1P1, P28063, Q920A5, Q9R1P4, O35522, Q9JHR7, Q9Z2U1, Q9QUM9, O09061, Q9Z2U0, O89110	0.001860295020895
GOTERM_MF_DIRECTIGO:0004175~endopeptidase activity		18	1.6260162601626	4.46047193206668E-05	P10605, P57716, Q3TXS7, P29452, P70195, O35593, Q9R1P1, P28063, Q9R1P4, Q9QUR6, O35522, Q8C166, Q9Z2U1, Q9QUM9, O09061, Q9Z2U0, O89110, O89023	0.001486344356718
INTERPRO	IPR023333:Proteasome B-type subunit	5	0.4516711833785	0.001450749810729	O35522, P70195, P28063, Q9R1P1, O09061	0.05228872722076
INTERPRO	IPR016050:Proteasome, beta-type subunit, conse	5	0.4516711833785	0.002022104889989	O35522, P70195, P28063, Q9R1P1, O09061	0.063434179326705
SMART	SM00948:SM00948	4	0.3613369467028	0.005420287402438	Q9Z2U1, Q9QUM9, Q9R1P4, Q9Z2U0	0.09828787823088
GOTERM_CC_DIRECTIGO:0019773~proteasome core complex, alpha-st		4	0.3613369467028	0.006565098904081	Q9Z2U1, Q9QUM9, Q9R1P4, Q9Z2U0	0.043706969658558

**Annotation Cluster 18** Enrichment Score: 4.371647785596221

Category	Term	Count	%	PValue	Genes	FDR
UP_SEQ_FEATURE	domain:PCI	10	0.903342366757	1.22722798860304E-07	Q9D8W5, Q8V8V7, Q8BV13, Q99J14, Q99JX4, Q9CZ04, P23116, Q8R1B4, O88543, P60229	6.94611041549318E-05
GOTERM_CC_DIRECTIGO:0008180~COP9 signalosome		9	0.8130081300813	9.48276808252698E-05	Q8V8V7, Q8BV13, P63168, Q8VDD5, Q9CZ04, Q03265, P11499, O88545, O88543	0.001171648678641
UP_KEYWORDS	Signalosome	5	0.4516711833785	0.000481799368738	Q8V8V7, Q8BV13, Q9CZ04, O88545, O88543	0.002021977678638
GOTERM_BP_DIRECTIGO:0010388~cullin deneddylation		5	0.4516711833785	0.00058167748022	Q8V8V7, Q8BV13, Q9CZ04, O88545, O88543	0.029608909445711

**Annotation Cluster 19** Enrichment Score: 3.9916148083197127

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECTIGO:0005874~microtubule		39	3.5230352303523	1.45399405903289E-07	Q8BYA0, Q61699, Q6P9P6, Q8VC03, P28740, Q8BFT2, Q922F4, P11983, Q8B8K6, Q9JKF1, O08788, O08553, P63168, P27546, Q8C052, Q8R1Q8, Q80UG5, P80315, P80314, P80313, O08539, Q61166, O08579, Q62433, Q3V300, P42932, P33174, O88447, Q3TCJ1, P62482, Q3UMY5, P23116, Q9JHU4, P62627, Q9D1E6, P80318, Q8BK67, P80317, P80316, Q6P9P6, Q8VC03, P28740, Q8BFT2, Q922F4, Q8B8K6, O08788, Q61166, O08579, Q62433, Q3V300, P63168, P33174, Q3TCJ1, P51807, O88447, Q3UMY5, Q9JHU4, P62627, P27546, Q9D1E6, Q8BK67, Q8C052, Q8R1Q8	3.6746395310104E-06
UP_KEYWORDS	Microtubule	24	2.1680216802168	0.000576549330224	Q62433, Q3V300, P63168, P33174, Q3TCJ1, P51807, O88447, Q3UMY5, Q9JHU4, P62627, P27546, Q9D1E6, Q8BK67, Q8C052, Q8R1Q8	0.002380590782862

**Annotation Cluster 20** Enrichment Score: 3.9831356513955614

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECTIGO:0030529~intracellular ribonucleoprotein con		49	4.42637759710931	3.97598666905622E-13	P62918, Q9EQK5, P35979, Q6P5F9, P32067, Q9D883, O09167, P62317, P25444, P29341, Q9WTM5, Q60591, Q9JIK9, Q9D7A6, Q91VC3, P62320, P14131, P57780, P62889, P49962, P62843, Q9CX86, Q9CXY6, Q91VR5, Q9JKB3, P99027, Q80WS3, Q9JKF1, Q8BMA6, Q8BGA5, Q62189, P67984, Q8CGC7, Q6NVF9, Q924T2, P62852, O35900, P62908, P97379, Q9D338, Q3UEB3, Q9ESX5, P60122, P58252, Q9D8E6, Q9D8M4, P62702, P27659, Q9CQI7	1.73159119851607E-11
UP_KEYWORDS	Ribonucleoprotein	36	3.2520325203252	5.404367417618E-08	Q9CX86, P62918, P35979, Q9EQK5, P99027, Q9CQO8, Q80WS3, Q8BMA6, Q9D883, Q8BGA5, Q62189, P67984, P63323, O09167, P62855, P62317, Q924T2, P25444, P62852, O35900, P62908, Q9D338, Q9JIK9, Q9D7A6, Q3UEB3, Q9ESX5, P62320, P14131, Q9D8E6, Q9D8M4, P62702, P62889, P27659, P49962, P62843, Q9CQI7	6.28871844959185E-07

GOTERM_CC_DIRECTGO:0005840~ribosome	23	2.0776874435411	5.37613835418256E-05	P62918, P05555, P62908, P35979, P99027, Q9D338, P35564, Q9JIK9, Q99M31, P14131, P67984, Q9D8E6, O09167, P62855, Q9D8M4, P62702, P62889, P27659, Q924T2, P25444, P62852, Q6P542, P62843	0.000711698315458
GOTERM_CC_DIRECTGO:0015935~small ribosomal subunit	8	0.7226738934056	0.000268496713378	P62908, P14131, P62855, P62702, Q924T2, P25444, P62852, P62843	0.002870849473813
UP_KEYWORDS Ribosomal protein	20	1.806684733514	0.00071486289065	P62918, P62908, P35979, P99027, Q9D338, Q9JIK9, P14131, P67984, P63323, Q9D8E6, O09167, P62855, Q9D8M4, P62702, P62889, P27659, Q924T2, P25444, P62852, P62843	0.002904839682641
GOTERM_CC_DIRECTGO:0022627~cytosolic small ribosomal subunit	9	0.8130081300813	0.002694334817559	P62908, P14131, P63323, P62855, P62702, P25444, P62852, Q62167, P62843	0.022358957590489
GOTERM_CC_DIRECTGO:0022625~cytosolic large ribosomal subunit	12	1.0840108401084	0.002955330739545	P62918, P35979, P67984, P63323, P99027, Q9D8E6, O09167, Q9D8M4, P62889, P27659, Q8BVY0, Q91VY9	0.023813969437492

**Annotation Cluster 21** Enrichment Score: 3.8992458243096575

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECTGO:0045454~cell redox homeostasis		19	1.7163504968383	1.17115470648871E-09	P97494, P10639, O08709, P28352, O08807, P99029, Q9JMH6, Q8R2E9, P11352, Q8R180, P35700, P20108, Q9Z0X1, Q9JLT4, Q61171, Q80Y14, Q9CQM9, Q8VBT0, Q91VW3	4.08879386902872E-07
UP_KEYWORDS Redox-active center		14	1.2646793134598	3.24181515915869E-08	P10639, O08709, O08807, Q9CQM5, P99029, Q9JMH6, Q8R2E9, Q8R180, P35700, P20108, Q9JLT4, Q61171, Q80Y14, Q8VBT0	3.95192705116487E-07
INTERPRO IPR012336:Thioredoxin-like fold		23	2.0776874435411	1.48954169075428E-07	P10649, P54731, P10639, O70325, O08709, O08807, Q9D8N0, Q9CQM5, P99029, P11352, P35700, Q9CQ75, Q6P5G6, P20108, Q8CGC7, Q9JJU8, Q61171, Q80Y14, Q9CQM9, Q8VBT0, O09131, Q91VW3, Q9QYB1	2.10273635344812E-05
GOTERM_MF_DIRECTGO:0051920~peroxiredoxin activity		7	0.6323396567299	2.85580228428756E-06	P20108, O08709, O08807, Q99LX0, P99029, Q61171, P35700	0.00014047827427
UP_SEQ_FEATURE active site:Cysteine sulfenic acid (-SOH) interme		6	0.5420054200542	6.34793119054766E-06	P20108, O08709, O08807, P99029, P35700	0.00143717162154
UP_KEYWORDS Peroxidase		8	0.7226738934056	1.87903449804007E-05	P20108, O70325, O08709, O08807, P99029, Q61171, P11352, P35700	0.000106896184777
GOTERM_BP_DIRECTGO:0042744~hydrogen peroxide catabolic proce		7	0.6323396567299	2.83727407720762E-05	P20108, O08709, P99029, Q61171, Q9JMH6, P11352, P35700	0.002625224225874
INTERPRO IPR019479:Peroxiredoxin, C-terminal		5	0.4516711833785	5.45179099985276E-05	P20108, O08709, O08807, Q61171, P35700	0.003420494056945
UP_SEQ_FEATURE domain:Thioredoxin		10	0.903342366757	7.24838184871329E-05	P10639, P20108, O08709, O08807, Q9CQM5, P99029, Q61171, Q9CQM9, Q8VBT0, P35700	0.009116853614159
GOTERM_MF_DIRECTGO:0004601~peroxidase activity		9	0.8130081300813	0.00011346147661	P20108, O70325, O08709, O08807, Q9CQM5, P99029, Q61171, P11352, P35700	0.003447226627601
INTERPRO IPR000866:Alkyl hydroperoxide reductase subur		5	0.4516711833785	0.000122709447029	P20108, O08709, O08807, Q61171, P35700	0.006299084947469
UP_KEYWORDS Antioxidant		6	0.5420054200542	0.000242976766998	P20108, O08709, O08807, P99029, Q61171, P35700	0.001151889858359
INTERPRO IPR013766:Thioredoxin domain		9	0.8130081300813	0.000323769363595	P10639, P20108, O08709, O08807, P99029, Q61171, Q9CQM9, Q8VBT0, P35700	0.014823386538632
GOTERM_MF_DIRECTGO:0008379~thioredoxin peroxidase activity		4	0.3613369467028	0.003841593201985	P20108, P99029, Q61171, P35700	0.064005899639523
GOTERM_MF_DIRECTGO:0016209~antioxidant activity		6	0.5420054200542	0.006156869228094	P20108, O08709, O08807, P99029, Q61171, P35700	0.090857798751736
GOTERM_CC_DIRECTGO:0005623~cell		19	1.7163504968383	0.020252718627447	O08709, Q3TRM8, O08807, P99029, Q9Z0P5, Q9JMH6, Q8CCP0, P29391, Q8BMA6, P35700, Q3UM18, Q9D2R0, Q9Z0X1, Q9JLT4, Q61171, Q80Y14, Q8VBT0, P17918, P22892	0.108274149585199

**Annotation Cluster 22** Enrichment Score: 3.6630809249995626

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS Aminopeptidase		9	0.8130081300813	3.14968859322976E-06	Q64514, Q99KK7, O08663, Q6P1B1, Q8BP48, Q6NSR8, Q8VCT3, Q9Z2W0, Q11011	2.17924399964005E-05
GOTERM_MF_DIRECTGO:0004177~aminopeptidase activity		10	0.903342366757	5.88072204697869E-06	Q64514, Q99KK7, O08663, Q6P1B1, Q8BP48, Q6NSR8, Q8VCT3, Q8R016, Q9Z2W0, Q11011	0.00027612663066
GOTERM_MF_DIRECTGO:0070006~metalloaminopeptidase activity		6	0.5420054200542	0.002075990378736	O08663, Q6P1B1, Q8BP48, Q8VCT3, Q9Z2W0, Q11011	0.038990873840631

**Annotation Cluster 23** Enrichment Score: 3.475915846037723

Category	Term	Count	%	PValue	Genes	FDR
SMART SM00991:SM00991		5	0.4516711833785	4.67079059614364E-05	P32921, Q68FL6, Q8CGC7, Q9CZD3, Q61035	0.002540910084302
INTERPRO IPR000738:WHEP-TRS		5	0.4516711833785	5.45179099985276E-05	P32921, Q68FL6, Q8CGC7, Q9CZD3, Q61035	0.003420494056945
INTERPRO IPR009068:S15/NS1, RNA-binding		5	0.4516711833785	0.000122709447029	P32921, Q68FL6, Q8CGC7, Q9CZD3, Q61035	0.006299084947469
UP_SEQ_FEATURE domain:WHEP-TRS		4	0.3613369467028	0.000498013556639	P32921, Q68FL6, Q9CZD3, Q61035	0.051250122374116

**Annotation Cluster 24** Enrichment Score: 3.338525426816872

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECTGO:0008565	protein transporter activity	20	1.806684733514	1.33884052064582E-09	Q9EQH3, Q9EPL8, Q8BFY9, Q924C1, P70168, Q6P5F9, P17427, Q8VI75, P17426, Q8BKC5, Q9QZ88, Q91YE6, O35643, O35344, P62075, Q8BIJ7, P52293, P62835, P22892, P40336	9.22014838551423E-08
INTERPRO	IPR001494:Importin-beta, N-terminal	9	0.8130081300813	2.54627021275708E-07	Q91YE6, Q9ERK4, Q9EPL8, Q8BFY9, Q924C1, P70168, Q6P5F9, Q8VI75, Q8BKC5	3.08098695743607E-05
SMART	SM00913:SM00913	8	0.7226738934056	2.07757731150367E-06	Q91YE6, Q9ERK4, Q9EPL8, Q8BFY9, Q924C1, P70168, Q6P5F9, Q8VI75	0.000188367009576
UP_SEQ_FEATURE	domain:Importin N-terminal	8	0.7226738934056	3.75129909973642E-06	Q91YE6, Q9ERK4, Q9EPL8, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q8BKC5	0.001061617645225
UP_SEQ_FEATURE	repeat:HEAT 4	11	0.9936766034327	1.36308418793343E-05	Q8BYA0, A2AGT5, Q9QXK3, Q9DBQ7, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q80XI3, Q8BKC5, Q76MZ3	0.002805475092256
GOTERM_MF_DIRECTGO:0008536	Ran GTPase binding	10	0.903342366757	2.61497863008311E-05	Q91YE6, Q9ERK4, Q9CT10, Q9EPL8, Q8BFY9, Q924C1, P70168, Q6P5F9, Q8VI75, Q8BKC5	0.000900424308292
UP_SEQ_FEATURE	repeat:HEAT 1	12	1.0840108401084	2.61642467713422E-05	Q8BYA0, Q8BQM4, A2AGT5, Q9QXK3, Q9DBQ7, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q80XI3, Q8BKC5, Q76MZ3	0.003949056979355
UP_SEQ_FEATURE	repeat:HEAT 2	12	1.0840108401084	2.61642467713422E-05	Q8BYA0, Q8BQM4, A2AGT5, Q9QXK3, Q9DBQ7, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q80XI3, Q8BKC5, Q76MZ3	0.003949056979355
UP_SEQ_FEATURE	repeat:HEAT 3	11	0.9936766034327	3.52867969170832E-05	Q8BYA0, A2AGT5, Q9QXK3, Q9DBQ7, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q80XI3, Q8BKC5, Q76MZ3	0.004814104641534
UP_SEQ_FEATURE	repeat:HEAT 5	9	0.8130081300813	0.000116576088095	A2AGT5, Q9QXK3, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q80XI3, Q8BKC5, Q76MZ3	0.013890961234008
UP_SEQ_FEATURE	repeat:HEAT 6	8	0.7226738934056	0.000303386884803	A2AGT5, Q9QXK3, Q8BFY9, P70168, Q6P5F9, Q8VI75, Q8BKC5, Q76MZ3	0.034343395359755
GOTERM_BP_DIRECTGO:0006610	ribosomal protein import into nucl	5	0.4516711833785	0.000336127227841	Q91YE6, Q8BFY9, P70168, Q8VI75, Q8BKC5	0.019558403070002
GOTERM_MF_DIRECTGO:0008139	nuclear localization sequence bind	7	0.6323396567299	0.000995994256855	O35344, Q3U9G9, Q8BFY9, P52293, P70168, Q8VI75, Q8BKC5	0.020997185047584
GOTERM_BP_DIRECTGO:0006607	NLS-bearing protein import into nu	6	0.5420054200542	0.001033554830294	O35344, Q8BFY9, P52293, P70168, Q8VI75, Q8BKC5	0.045453005193108
GOTERM_CC_DIRECTGO:0034399	nuclear periphery	6	0.5420054200542	0.00175068538554	Q8BFY9, Q9D903, P70168, Q8VI75, Q99JF8, Q8BKC5	0.014975093451699
COG_ONTOLOGY	Intracellular trafficking and secretion	10	0.903342366757	0.002396064899822	Q01405, O35344, Q9QXK3, Q8BFY9, P52293, P70168, Q8VI75, Q9D662, Q8BKC5, Q64324	0.034742941047422

**Annotation Cluster 25** Enrichment Score: 3.3381065897438136

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Purine biosynthesis	8	0.7226738934056	2.6146432397322E-07	Q9CWJ9, Q64737, P24547, P46664, Q3THK7, Q5SUR0, P54822, Q922D8	2.47906914582016E-06
GOTERM_BP_DIRECTGO:0006164	purine nucleotide biosynthetic proc	8	0.7226738934056	2.84286693688031E-05	Q9CWJ9, Q64737, P24547, P46664, Q3THK7, Q5SUR0, P54822, Q922D8	0.002625224225874
GOTERM_BP_DIRECTGO:0006189	'de novo' IMP biosynthetic process	4	0.3613369467028	0.002070212624037	Q9CWJ9, Q64737, Q5SUR0, P54822	0.081438082520214

**Annotation Cluster 26** Enrichment Score: 3.289136531311033

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Amino-acid biosynthesis	9	0.8130081300813	4.46584813890632E-06	Q99K85, Q91YI0, P16460, Q9CQT1, Q8BGB7, Q8VCN5, P05201, Q9WVQ5, Q922D8	3.00857137778952E-05
GOTERM_BP_DIRECTGO:0008652	cellular amino acid biosynthetic pr	9	0.8130081300813	1.59853492665521E-05	Q99K85, Q91YI0, P16460, Q9CQT1, Q8BGB7, Q8VCN5, P05201, Q9WVQ5, Q922D8	0.001860295020895
GOTERM_BP_DIRECTGO:0019509	L-methionine biosynthetic process	4	0.3613369467028	0.001074077458913	Q9CQT1, Q8BGB7, Q9CQ65, Q9WVQ5	0.045453005193108
UP_KEYWORDS	Methionine biosynthesis	4	0.3613369467028	0.003286270986793	Q9CQT1, Q8BGB7, Q9WVQ5, Q922D8	0.011524457159164
KEGG_PATHWAY	mmu00270:Cysteine and methionine metabolism	9	0.8130081300813	0.005140099894247	Q3THS6, Q68FL4, Q9CQT1, Q64674, Q8BGB7, Q9CQ65, Q8VCN5, P05201, Q9WVQ5	0.042834165785395

**Annotation Cluster 27** Enrichment Score: 3.2596231130199516

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Endocytosis	18	1.6260162601626	6.35630540109906E-06	Q91ZX7, P98078, Q8VD75, Q80TY0, Q62418, Q9Z0R6, Q9CR95, O08539, Q62351, P17427, P97814, P17426, P84091, Q6PAR5, P42567, Q8BIJ7, Q60902, Q810B6	4.17234405815733E-05
GOTERM_BP_DIRECTGO:0006897	endocytosis	24	2.1680216802168	2.51871911972172E-05	O08539, Q62351, P17427, P97814, P17426, P84091, Q6PAR5, P42567, Q6P8X1, O08553, Q9CWK8, Q8BIJ7, Q60902, Q8BL66, Q810B6	0.002605475000512
GOTERM_CC_DIRECTGO:0005905	clathrin-coated pit	11	0.9936766034327	0.00036759870237	P42567, Q91ZX7, P98078, Q80TY0, Q9CR95, Q60902, Q68FD5, Q62351, P17427, P17426, P84091	0.003716088700324
UP_KEYWORDS	Coated pit	9	0.8130081300813	0.000779723347993	P42567, Q91ZX7, P98078, Q80TY0, Q60902, Q68FD5, P17427, P17426, P84091	0.003118893391972
GOTERM_CC_DIRECTGO:0030132	clathrin coat of coated pit	4	0.3613369467028	0.004530271179089	P42567, P98078, Q60902, Q68FD5	0.034504531172236

Annotation Cluster 28		Enrichment Score: 3.189944474104752							
Category	Term	Count	%	PValue	Genes			FDR	
INTERPRO	IPR023409:14-3-3 protein, conserved site	7	0.6323396567299	5.16744107154937E-08	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259			1.09420564690058E-05	
SMART	SM00101:14_3_3	7	0.6323396567299	1.56477290647094E-07	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259			2.12809115280048E-05	
INTERPRO	IPR000308:14-3-3 protein	7	0.6323396567299	1.98864167985819E-07	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259			2.59135308129214E-05	
INTERPRO	IPR023410:14-3-3 domain	7	0.6323396567299	5.74000470603175E-07	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259			6.07722998251111E-05	
PIR_SUPERFAMILY	PIRSF000868:14-3-3 protein	7	0.6323396567299	2.19033325089968E-06	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259			0.000284743322617	
UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting	7	0.6323396567299	6.15017890566757E-06	P63101, O70456, Q9CQV8, P68510, P68254, P61982, P62259			0.00143717162154	
KEGG_PATHWAY	mmu04110:Cell cycle	20	1.806684733514	0.00075564848454	Q64701, O70456, Q9CQV8, P97310, P97311, Q07832, P68254, P30285, Q61881, P11440, P63101, P49718, P49717, P68510, Q64261, P25206, P17918, P61982, Q9WVA3, P62259			0.011334727268105	
Annotation Cluster 29		Enrichment Score: 3.1784830696638124							
Category	Term	Count	%	PValue	Genes			FDR	
INTERPRO	IPR013041:Coatmer/clathrin adaptor appendage	6	0.5420054200542	0.000105527987192	O35643, Q8R0H9, Q9QXK3, P22892, P17427, P17426			0.006164290010437	
GOTERM_CC_DIRECTGO:0030131~clathrin adaptor complex		7	0.6323396567299	0.000148651527658	O35643, Q8R0H9, P22892, P35585, P17427, P17426, P84091			0.001796744551696	
GOTERM_CC_DIRECTGO:0030117~membrane coat		8	0.7226738934056	0.000336464079261	O35643, Q8CIE6, P61924, Q9QXK3, Q68FD5, P22892, P17427, P17426			0.00346433385313	
SMART	SM00809:Alpha_adaptinC2	5	0.4516711833785	0.000353820203019	O35643, Q8R0H9, P22892, P17427, P17426			0.012029886902638	
INTERPRO	IPR008152:Clathrin adaptor, alpha/beta/gamma-	5	0.4516711833785	0.000411128325354	O35643, Q8R0H9, P22892, P17427, P17426			0.01785727773063	
INTERPRO	IPR009028:Coatmer/calthrin adaptor appendage	4	0.3613369467028	0.001590543472708	O35643, Q9QXK3, P17427, P17426			0.053887612855343	
INTERPRO	IPR002553:Clathrin/coatmer adaptor, adaptin-li	5	0.4516711833785	0.002731916619757	O35643, Q9QXK3, P22892, P17427, P17426			0.075866668096212	
Annotation Cluster 30		Enrichment Score: 3.101058536539847							
Category	Term	Count	%	PValue	Genes			FDR	
INTERPRO	IPR006195:Aminoacyl-tRNA synthetase, class II	8	0.7226738934056	4.45572951333441E-06	Q8CGC7, Q8BP47, Q8C0C7, Q9CZD3, P26638, Q922B2, Q61035, Q9D0R2			0.000314500241483	
INTERPRO	IPR002314:Aminoacyl-tRNA synthetase, class II	4	0.3613369467028	0.004164218998097	Q8CGC7, Q9CZD3, P26638, Q9D0R2			0.105286372877264	
Annotation Cluster 31		Enrichment Score: 2.9377271179136666							
Category	Term	Count	%	PValue	Genes			FDR	
UP_KEYWORDS	SH3-binding	11	0.9936766034327	0.000148502587789	P42567, P70460, Q9JJU8, Q9JLQ0, P97797, Q3UIA2, Q5FWK3, Q8BPU7, Q61036, Q9ES52, Q80U87			0.000717295518379	
GOTERM_MF_DIRECTGO:0017124~SH3 domain binding		17	1.5356820234869	0.000285185222649	Q9WU78, P70460, P29351, P97797, Q3UIA2, P11352, Q62422, P70315, Q9ES52, Q61036, Q80U87, P42567, Q9JJU8, Q9JLQ0, Q5FWK3, Q8BPU7, P22682			0.007553752179383	
Annotation Cluster 32		Enrichment Score: 2.92413243672798							
Category	Term	Count	%	PValue	Genes			FDR	
INTERPRO	IPR024969:Rpn11/EIF3F C-terminal domain	4	0.3613369467028	0.000340316252043	Q9DCH4, O35593, O88545, P26516			0.015170940288457	
SMART	SM00232:JAB_MPN	5	0.4516711833785	0.001254086565924	Q76N33, Q9DCH4, O35593, O88545, P26516			0.037901282881256	
INTERPRO	IPR000555:JAB1/Mov34/MPN/PAD-1	5	0.4516711833785	0.002022104889989	Q76N33, Q9DCH4, O35593, O88545, P26516			0.063434179326705	
Annotation Cluster 33		Enrichment Score: 2.781194453945648							
Category	Term	Count	%	PValue	Genes			FDR	
GOTERM_BP_DIRECTGO:0051016~barbed-end actin filament capping		6	0.5420054200542	0.000759880538255	P13020, P24452, Q9Z0P5, Q62418, P47753, P47754			0.035971971921114	
GOTERM_BP_DIRECTGO:0051693~actin filament capping		6	0.5420054200542	0.001374062541526	P13020, P24452, Q8VDD5, P47753, Q62261, P47754			0.057279950425094	
UP_KEYWORDS	Actin capping	5	0.4516711833785	0.004341750030965	P13020, P24452, P47753, Q62261, P47754			0.014411270758299	
Annotation Cluster 34		Enrichment Score: 2.682329097428867							
Category	Term	Count	%	PValue	Genes			FDR	
UP_KEYWORDS	mRNA processing	31	2.8003613369467	1.0573774809287E-05	Q8BMZ5, Q91VR5, O70551, Q9CQQ8, Q99K48, Q62384, Q9D883, Q62189, Q9JKP5, Q9DAR7, Q8VIJ6, Q6NVF9, P83870, Q5SUF2, Q3TIU4, P62317, Q9DBR1, O35900, Q569Z6, Q0VGB7, Q9JL18, P29341, O08810, Q3UEB3, Q91VC3, P62320, P16110, O08583, Q3U0V1, Q9CQ17, Q9DAW6			6.44496750280353E-05	

UP_KEYWORDS	mRNA splicing	26	2.3486901535682	1.93085157493175E-05	O70551, Q9CQQ8, Q99K48, Q62384, Q9D883, Q62189, Q9JKP5, Q9DAR7, Q8VIJ6, P83870, Q5SUF2, P62317, O35900, Q569Z6, Q0VGB7, Q9JL18, P29341, O08810, Q3UEB3, Q91VC3, P62320, P16110, O08583, Q3U0V1, Q9CQI7, Q9DAW6	0.000107456087648
GOTERM_BP_DIRECT	GO:006397~mRNA processing	31	2.8003613369467	0.000534460803259	Q8BMZ5, Q91VR5, O70551, Q99K48, Q62384, Q9D883, Q62189, Q9JKP5, Q9DAR7, Q8VIJ6, Q6NVF9, P83870, Q5SUF2, Q3TIU4, P62317, P05132, Q9DBR1, O35900, Q569Z6, Q0VGB7, Q9JL18, P29341, O08810, Q3UEB3, Q91VC3, P62320, P16110, O08583, Q3U0V1, Q9CQI7, Q9DAW6	0.029608909445711
GOTERM_BP_DIRECT	GO:008380~RNA splicing	25	2.2583559168925	0.000745614285095	O70551, Q99K48, Q62384, Q9D883, Q62189, Q9JKP5, Q9DAR7, Q8VIJ6, P83870, Q5SUF2, P62317, O35900, Q569Z6, Q0VGB7, Q9JL18, P29341, O08810, Q3UEB3, Q91VC3, P62320, P16110, O08583, Q3U0V1, Q9CQI7, Q9DAW6	0.03590518445293
UP_KEYWORDS	Spliceosome	14	1.2646793134598	0.001017953008215	Q9CQQ8, P29341, Q9D883, Q62189, O08810, Q91VC3, P62320, O08583, P16110, P83870, P62317, O35900, Q9DAW6, Q9CQI7	0.003948423789441
GOTERM_CC_DIRECT	GO:005681~spliceosomal complex	14	1.2646793134598	0.009778249637941	P29341, Q9D883, Q62189, O08810, Q6NVF4, P62320, O35841, O08583, P16110, P83870, P62317, O35900, Q9DAW6, Q9CQI7	0.061086593243766

**Annotation Cluster 35** Enrichment Score: 2.5526310887031296

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Protease	47	4.2457091237579	2.80002753556564E-06	Q6PIB1, P29452, B2RRE7, P56399, Q9JKB1, Q8K2H2, O35593, Q9DCH4, Q9R1P1, Q9WUP7, P28063, Q9R1P4, Q8C0M9, Q99K23, P61290, Q80U87, Q9QUR6, O35522, Q9JHR7, P62196, Q9Z2U1, Q8CDG3, Q9Z2W0, Q9Z2U0, O09061, O89023, Q64514, Q8R5H1, P10605, Q9JMA1, Q99LX0, P70195, Q6NSR8, Q8VCT3, Q76N33, Q920A5, P35123, P70677, Q99KK7, O08663, Q8BP48, Q9QUM9, Q8R016, Q8BHG1, Q9D1A2, Q11011, O89110	2.04802014029944E-05
GOTERM_BP_DIRECT	GO:006508~proteolysis	52	4.69738030713641	3.7941526356827E-05	Q6PIB1, P29452, B2RRE7, P56399, Q9JKB1, Q8K2H2, Q99K23, Q80U87, O35522, Q9JHR7, O88456, Q8CDG3, Q9Z2U1, Q8R146, Q9DB77, Q9Z2U0, O89023, Q64514, Q8R5H1, P10605, Q9CX56, Q99LX0, Q8VCT3, Q920A5, P35123, Q8BP48, Q9QUM9, Q8R016, Q9D1A2, Q99JW2, Q9JKB1, O35593, Q9DCH4, Q9WUP7, P28063, Q9R1P1, Q9R1P4, Q8C0M9, Q9QUR6, Q9Z2W0, O09061, Q9JMA1, P70195, Q6NSR8, Q76N33, P70677, Q99KK7, O08663, Q8C166, Q8BHG1, P22682, Q11011, O89110	0.003116784797489
GOTERM_MF_DIRECT	GO:008233~peptidase activity	48	4.3360433604336	6.39820605540555E-05	Q6PIB1, P29452, B2RRE7, P56399, Q9JKB1, Q8K2H2, O35593, Q9DCH4, Q9R1P1, Q9WUP7, P28063, Q9R1P4, Q8C0M9, Q99K23, P61290, Q80U87, Q9QUR6, O35522, Q9JHR7, P62196, Q9Z2U1, Q8CDG3, Q9Z2W0, Q9Z2U0, O09061, O89023, Q64514, Q8R5H1, P10605, P57716, Q9JMA1, Q99LX0, P70195, Q6NSR8, Q8VCT3, Q76N33, Q920A5, P35123, P70677, Q99KK7, O08663, Q8BP48, Q9QUM9, Q8R016, Q8BHG1, Q9D1A2, Q11011, O89110	0.002002832380374
UP_KEYWORDS	Thiol protease	17	1.5356820234869	0.000121767139894	P10605, Q8R5H1, P29452, B2RRE7, Q9JMA1, P56399, Q9JKB1, Q9DCH4, Q8K2H2, Q9WUP7, P35123, P70677, Q99K23, Q80U87, Q8CDG3, Q8R016, O89110	0.000600668549165
GOTERM_MF_DIRECT	GO:008234~cysteine-type peptidase activity	17	1.5356820234869	0.002011879779301	P10605, Q8R5H1, P29452, B2RRE7, Q9JMA1, P56399, Q9JKB1, Q9DCH4, Q8K2H2, Q9WUP7, P35123, P70677, Q99K23, Q80U87, Q8CDG3, Q8R016, O89110	0.03848651503736
GOTERM_MF_DIRECT	GO:0036459~thiol-dependent ubiquitinyl hydrol	11	0.9936766034327	0.00518629450554	Q8R5H1, B2RRE7, Q9JMA1, P56399, Q9JKB1, Q9DCH4, Q8K2H2, Q8CDG3, Q9WUP7, P35123, Q80U87	0.081173367033685

**Annotation Cluster 36** Enrichment Score: 2.5265650857574364

Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR009000:Translation elongation/initiation fact	8	0.7226738934056	0.000223803964378	Q8R050, Q9Z0N1, P58252, Q69ZS7, Q05D44, P27659, O08810, Q8BGQ7	0.01083211187591
INTERPRO	IPR000795:Elongation factor, GTP-binding dom	6	0.5420054200542	0.0015344215208	Q8R050, Q9Z0N1, P58252, Q69ZS7, Q05D44, O08810	0.053887612855343
INTERPRO	IPR004161:Translation elongation factor EFTu/	5	0.4516711833785	0.002731916619757	Q8R050, Q9Z0N1, P58252, Q05D44, O08810	0.075866668096212

**Annotation Cluster 37** Enrichment Score: 2.471552700394736

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Elongation factor	7	0.6323396567299	0.000257610190846	P10711, P58252, Q9D8N0, Q69ZS7, P63242, P57776, O08810	0.001177646586726
GOTERM_MF_DIRECT	GO:0003746~translation elongation factor activit	7	0.6323396567299	0.001924837216249	P10711, P58252, Q9D8N0, Q69ZS7, P63242, P57776, O08810	0.03751616687519

**Annotation Cluster 38** Enrichment Score: 2.4566978174276994

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECTGO:0030904~retromer complex		8	0.7226738934056	5.36628269431775E-05	Q9QZ88, Q6P8X1, Q6PGL7, Q9CWK8, Q9EQH3, P40336, O08788, Q810B6	0.000711698315458
GOTERM_CC_DIRECTGO:0030906~retromer, cargo-selective complex		3	0.2710027100271	0.006114467923801	Q9QZ88, Q9EQH3, P40336	0.043033470451055

**Annotation Cluster 39** Enrichment Score: 2.4489385342962664

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECTGO:0030388~fructose 1,6-bisphosphate metabolism		6	0.5420054200542	2.91894123584364E-05	P12382, P05063, P05064, Q8BZA9, Q9WUA3, P47857	0.002625224225874
UP_SEQ_FEATURE	metal ion-binding site:Magnesium	8	0.722673893405601			3.61483122376666E-05
GOTERM_BP_DIRECTGO:0006002~fructose 6-phosphate metabolic process	via carb	5	0.4516711833785	0.00058167748022	P12382, Q9WUA3, P47856, P47857, Q93092	0.029608909445711
GOTERM_BP_DIRECTGO:0061615~glycolytic process through fructose		4	0.3613369467028	0.001074077458913	P12382, P05064, Q9WUA3, P47857	0.045453005193108
GOTERM_CC_DIRECTGO:0005945~6-phosphofructokinase complex		3	0.2710027100271	0.006114467923801	P12382, Q9WUA3, P47857	0.043033470451055
GOTERM_MF_DIRECTGO:0003872~6-phosphofructokinase activity		3	0.2710027100271	0.007368907513844	P12382, Q9WUA3, P47857	0.104275088517816

**Annotation Cluster 40** Enrichment Score: 2.3936440983155554

Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR017926:Glutamine amidotransferase	4	0.3613369467028	0.001590543472708	B2RQC6, Q3THK7, P70698, Q5SUR0	0.053887612855343
GOTERM_BP_DIRECTGO:0006541~glutamine metabolic process		6	0.5420054200542	0.002292604665817	B2RQC6, Q3THK7, P47856, P70698, Q5SUR0, Q9JHW2	0.088933955994832
UP_KEYWORDS	Glutamine amidotransferase	4	0.3613369467028	0.003286270986793	Q3THK7, P47856, P70698, Q5SUR0	0.011524457159164

**Annotation Cluster 41** Enrichment Score: 2.20720226785467

Category	Term	Count	%	PValue	Genes	FDR
UP_SEQ_FEATURE	metal ion-binding site:Magnesium	8	0.722673893405601			3.61483122376666E-05
UP_KEYWORDS	Nucleotide metabolism	7	0.6323396567299	0.000257610190846	Q9WV85, Q9JMJ4, Q6P3D0, Q3V1L4, O08739, Q9D892, Q3UFY7	0.001177646586726
GOTERM_BP_DIRECTGO:0009117~nucleotide metabolic process		7	0.6323396567299	0.001622677905164	Q9WV85, Q9JMJ4, Q6P3D0, Q3V1L4, O08739, Q9D892, Q3UFY7	0.065683179552513

**Annotation Cluster 42** Enrichment Score: 2.105246875802888

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Citrullination	13	1.1743450767841	0.000451899363529	P03995, Q62318, P15864, O08583, P68433, Q9D8E6, P43274, P43275, P43277, P25444, P84228, Q99JF8, P02301	0.001960783679039

**Annotation Cluster 43** Enrichment Score: 2.0888501721558557

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_MF_DIRECTGO:0003774~motor activity		14	1.2646793134598	0.000150002191255	Q9JMH9, Q61879, O08638, P70248, O08788, Q9QUR7, P63168, Q8VDD5, P51807, Q60605, Q6URW6, Q9JHU4, P62627, Q8R1Q8	0.004304229543519
GOTERM_CC_DIRECTGO:0005868~cytoplasmic dynein complex		6	0.5420054200542	0.003389828395156	P63168, P51807, Q9JHU4, P62627, O08788, Q8R1Q8	0.026924922681525
UP_KEYWORDS	Dynein	6	0.5420054200542	0.007990593971891	P63168, P51807, Q9JHU4, P62627, O08788, Q8R1Q8	0.024946244595172

**Annotation Cluster 44** Enrichment Score: 2.0773377590514213

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_BP_DIRECTGO:0061136~regulation of proteasomal protein catabolism		8	0.7226738934056	8.11290871701881E-06	P97372, Q9JMA1, O35593, Q9WUP7, P05132, P11352, P61290, P97371	0.001129542830412
GOTERM_CC_DIRECTGO:0008537~proteasome activator complex		3	0.2710027100271	0.011857177713275	P97372, P61290, P97371	0.072760689079764

**Annotation Cluster 45** Enrichment Score: 2.0492185372620626

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECTGO:0030665~clathrin-coated vesicle membrane		6	0.5420054200542	0.000189978384741	O35643, P98078, Q8VD75, Q62418, P22892, P35585	0.00224740387055

**Annotation Cluster 46** Enrichment Score: 1.9146194557192486

Category	Term	Count	%	PValue	Genes	FDR
SMART	SM00515:eIF5C	5	0.4516711833785	0.000105289049493	Q62448, Q6NZJ6, P59325, Q80XI3, Q2L4X1	0.004773103577

INTERPRO	IPR003307:W2 domain	5	0.4516711833785	0.000122709447029	Q62448, Q6NZJ6, P59325, Q80XI3, Q2L4X1	0.006299084947469
UP_SEQ_FEATURE	domain:W2	5	0.4516711833785	0.000670335976629	Q62448, Q6NZJ6, P59325, Q80XI3, Q2L4X1	0.06598437613424

**Annotation Cluster 47** Enrichment Score: 1.879500882094488

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0030863--cortical cytoskeleton	10	0.903342366757	6.99676893605065E-06	P21107, Q7TPR4, Q8VDD5, P57780, Q8BTM8, P47753, Q62261, Q6IRU2, P47754, Q9ESS2	0.000125490436401
SMART	SM00033:CH	10	0.903342366757	0.001903399551459	Q99K51, Q3UQ44, P27870, Q7TPR4, P57780, Q8BTM8, Q62261, Q9JKF1, Q9QXS1, Q9WVA4	0.047065879817901
INTERPRO	IPR001715:Calponin homology domain	11	0.9936766034327	0.00193884952245	Q99K51, Q3UQ44, P27870, Q7TPR4, P57780, Q8BTM8, Q62261, Q9JKF1, Q9QXS1, Q61166, Q9WVA4	0.063161751750597
INTERPRO	IPR001589:Actinin-type, actin-binding, conserve	6	0.5420054200542	0.002981015689982	Q99K51, Q7TPR4, P57780, Q8BTM8, Q62261, Q9QXS1	0.080156199663952

**Annotation Cluster 48** Enrichment Score: 1.8535421934588352

Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu05012:Parkinson's disease	22	1.9873532068654	0.001242876869027	P51881, Q60931, Q99LX0, Q9ERS2, Q03265, P70677, Q91WD5, P68181, Q9CQ75, Q02053, P62254, Q9DC69, Q91VD9, Q9CZ13, P56383, P05132, P48962, P56480, Q99LC3, Q9DB77, Q91VR2, Q91YT0	0.014255251366974
UP_KEYWORDS	Mitochondrion inner membrane	21	1.8970189701897	0.004166948610113	P51881, Q8CAQ8, P62908, Q8BGA9, Q9ERS2, Q03265, Q64521, Q91WD5, Q9CQ75, Q35129, P67778, Q91VD9, Q9Z0X1, Q9CRB9, P62075, Q9CZ13, P48962, P56480, Q9DB77, Q91VR2, Q91YT0	0.014036037423539
GOTERM_CC_DIRECT	GO:005743--mitochondrial inner membrane	29	2.6196928635953	0.011977126899161	P51881, Q8CAQ8, Q8BGA9, Q9ERS2, Q91WD5, Q64521, Q9DCN2, Q35129, Q9CRB9, P62075, Q9CZ13, Q91W50, P48962, P56480, Q9DB77, Q91VR2, P42227, Q91YT0, P62908, Q70325, Q60931, Q03265, Q9CQX2, Q9CQ75, P67778, Q9DC69, Q91VD9, Q9Z0X1, P16110	0.072760689079764

**Annotation Cluster 49** Enrichment Score: 1.8489716436322232

Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR011237:Peptidase M16 domain	4	0.3613369467028	0.002691418991987	Q9JHR7, Q9CZ13, Q8BHG1, Q9DB77	0.075866668096212
INTERPRO	IPR011249:Metalloenzyme, LuxS/M16 peptidase	4	0.3613369467028	0.002691418991987	Q9JHR7, Q9CZ13, Q8BHG1, Q9DB77	0.075866668096212
INTERPRO	IPR007863:Peptidase M16, C-terminal domain	4	0.3613369467028	0.002691418991987	Q9JHR7, Q9CZ13, Q8BHG1, Q9DB77	0.075866668096212
INTERPRO	IPR011765:Peptidase M16, N-terminal	4	0.3613369467028	0.002691418991987	Q9JHR7, Q9CZ13, Q8BHG1, Q9DB77	0.075866668096212

**Annotation Cluster 50** Enrichment Score: 1.834905897686386

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:005685-U1 snRNP	6	0.5420054200542	0.001364052277053	P62320, Q9CY14, Q7TNC4, Q5SUF2, P62317, Q62189	0.012232468807124

**Annotation Cluster 51** Enrichment Score: 1.8311105898226887

Category	Term	Count	%	PValue	Genes	FDR
SMART	SM00165:UBA	7	0.6323396567299	0.002906361699344	Q91VX2, P56399, P61087, P22682, P54726, Q8R317, Q80X50	0.06587753185179
INTERPRO	IPR009060:UBA-like	9	0.8130081300813	0.003989009528657	Q91VX2, P56399, P61087, P22682, P54726, Q9QZ73, Q8R317, Q80X50, Q6P5G6	0.103959725254541

**Annotation Cluster 52** Enrichment Score: 1.819771644049073

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:005903--brush border	15	1.3550135501355	9.36623957643872E-06	Q9JMH9, Q7TPR4, Q9Z0G0, Q61879, Q8BTM8, O08638, Q9QXS1, Q9JJ28, Q8VDD5, P57780, Q60605, P47753, Q6URW6, P47754, Q91X52	0.000162738412641
UP_KEYWORDS	Motor protein	17	1.5356820234869	7.02325944876648E-05	Q6P9P6, Q9JMH9, P28740, Q61879, O08638, P70248, Q3V300, P63168, Q8VDD5, P33174, P51807, O88447, Q60605, Q6URW6, Q9JHU4, P62627, Q8R1Q8	0.000366929473242
GOTERM_MF_DIRECT	GO:0003774--motor activity	14	1.2646793134598	0.000150002191255	Q9JMH9, Q61879, O08638, P70248, O08788, Q9QUR7, P63168, Q8VDD5, P51807, Q60605, Q6URW6, Q9JHU4, P62627, Q8R1Q8	0.004304229543519
GOTERM_CC_DIRECT	GO:001725--stress fiber	12	1.0840108401084	0.00021724266865	Q62523, P21107, Q7TPR4, Q8VDD5, P57780, Q61879, Q6URW6, Q6IRU2, O08638, P07356, P97814, Q80UG5	0.002465039260597

INTERPRO	IPR027401:Myosin-like IQ motif-containing domain	6	0.5420054200542	0.000913169063329	Q9JMH9, Q8VDD5, Q61879, Q6URW6, O08638, Q9JKF1	0.034375742072857
GOTERM_CC_DIRECTIGO:0097513~myosin II filament		3	0.2710027100271	0.006114467923801	Q8VDD5, Q61879, Q6URW6	0.043033470451055
GOTERM_CC_DIRECTIGO:0042641~actomyosin		4	0.3613369467028	0.012039538480824	Q9JMH9, Q8VDD5, Q61879, Q6URW6	0.072760689079764
UP_KEYWORDS	Myosin	7	0.6323396567299	0.013159248530889	Q9JMH9, Q8VDD5, Q61879, Q60605, Q6URW6, O08638, P70248	0.038721466941468
UP_KEYWORDS	Calmodulin-binding	12	1.0840108401084	0.027872516350975	Q3UQ44, Q8VDD5, Q61879, Q62261, Q6URW6, P63328, O08638, Q9JKF1, P70248, A2AN08, P58404, Q8VVCN5	0.072809838631119

**Annotation Cluster 53** Enrichment Score: 1.7880504824279126

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECTIGO:0005826~actomyosin contractile ring		4	0.3613369467028	0.001733905341856	Q8VDD5, P42208, P97814, Q8K298	0.014975093451699

**Annotation Cluster 54** Enrichment Score: 1.784243550797122

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Hydrogen ion transport	9	0.8130081300813	0.000430534054592	P50518, Q8BVE3, Q03265, P56383, P50516, P62814, P56480, Q91VR2, Q9Z1G3	0.001911493330035
GOTERM_BP_DIRECTIGO:0046034~ATP metabolic process		9	0.8130081300813	0.000593429485518	Q91VD9, Q9CZ30, Q9WTP7, Q03265, P50516, O08739, P62814, P56480, Q91VR2	0.029608909445711
INTERPRO	IPR020003:ATPase, alpha/beta subunit, nucleotide	4	0.3613369467028	0.000822530691339	Q03265, P50516, P62814, P56480	0.032403883514611
INTERPRO	IPR000194:ATPase, F1/V1/A1 complex, alpha/beta	4	0.3613369467028	0.000822530691339	Q03265, P50516, P62814, P56480	0.032403883514611
INTERPRO	IPR004100:ATPase, alpha/beta subunit, N-terminal	4	0.3613369467028	0.000822530691339	Q03265, P50516, P62814, P56480	0.032403883514611
GOTERM_BP_DIRECTIGO:0015991~ATP hydrolysis coupled proton transport		8	0.7226738934056	0.000899440896117	P50518, Q8BVE3, Q03265, P56383, P50516, P62814, P56480, Q9Z1G3	0.041182597095998
GOTERM_MF_DIRECTIGO:0046961~proton-transporting ATPase activity		7	0.6323396567299	0.000995994256855	P50518, Q8BVE3, Q03265, P50516, P56480, Q91VR2, Q9Z1G3	0.020997185047584
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	19	1.7163504968383	0.006718490920628	Q8BVE3, Q9ERS2, Q03265, P50516, Q91WD5, Q9Z1G3, Q9CQ75, Q9DC69, Q91VD9, P50518, Q9CZ13, P56383, P62814, P56480, Q99LC3, Q9DB77, Q91VR2, Q91YT0, Q9D819	0.050388681904711
UP_KEYWORDS	CF(1)	3	0.2710027100271	0.015432129600318	Q03265, P56480, Q91VR2	0.044273073300363
GOTERM_CC_DIRECTIGO:0000275~mitochondrial proton-transporting ATPase activity		3	0.2710027100271	0.01916356698515	Q03265, P56480, Q91VR2	0.103446050910132
GOTERM_CC_DIRECTIGO:0045261~proton-transporting ATP synthase		3	0.2710027100271	0.01916356698515	Q03265, P56480, Q91VR2	0.103446050910132

**Annotation Cluster 55** Enrichment Score: 1.7417696772809872

Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECTIGO:0005719~nuclear euchromatin		7	0.6323396567299	0.002113116610488	P23198, Q62318, P43275, Q9WTM5, P43277, P15864, P35700	0.017801406597447
GOTERM_MF_DIRECTIGO:0031490~chromatin DNA binding		10	0.903342366757	0.005124582139399	Q04207, P28352, P57780, P43274, Q9QZQ8, P43275, Q9WTM5, P43277, P15864, P42227	0.081173367033685

**Annotation Cluster 56** Enrichment Score: 1.7138615683588552

Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Electron transport	14	1.2646793134598	0.000433072707586	P10639, Q9ERS2, Q8R2E9, Q9CQX2, Q91WD5, Q8R180, Q9CQ75, Q9DC69, Q91VD9, Q8VBT0, Q9CZ13, Q99LC3, Q9DB77, Q91YT0	0.001911493330035
KEGG_PATHWAY	mmu05012:Parkinson's disease	22	1.9873532068654	0.001242876869027	P51881, Q60931, Q99LX0, Q9ERS2, Q03265, P70677, Q91WD5, P68181, Q9CQ75, Q02053, P62254, Q9DC69, Q91VD9, Q9CZ13, P56383, P05132, P48962, P56480, Q99LC3, Q9DB77, Q91VR2, Q91YT0	0.014255251366974
KEGG_PATHWAY	mmu05016:Huntington's disease	26	2.3486901535682	0.002203163948225	P51881, Q68FD5, Q9ERS2, Q91WD5, P17427, O08788, P17426, P84091, Q9CZ13, P56383, P48962, P56480, Q9DB77, Q91VR2, Q91YT0, P51432, Q60931, Q8VD75, Q03265, P70677, Q9CQ75, Q9DC69, Q91VD9, Q07813, Q99LC3, O89110	0.022532358561391
GOTERM_MF_DIRECTIGO:0003954~NADH dehydrogenase activity		5	0.4516711833785	0.003187755727024	Q9DC69, Q91VD9, Q9ERS2, Q91WD5, Q91YT0	0.054882527766937
UP_KEYWORDS	Respiratory chain	9	0.8130081300813	0.003666049571888	Q9DC69, Q91VD9, Q9ERS2, Q9CZ13, Q91WD5, Q99LC3, Q9DB77, Q9CQ75, Q91YT0, P51432, P57716, Q91ZX7, Q8VBW6, Q9ERS2, Q03265, P70677, Q91WD5, Q9CQ75, Q9DC69, Q91VD9, Q9JHR7, P63328, P0DP26, Q9CZ13, P56383, P56480, Q99LC3, Q9DB77, Q91VR2, O89110, P49615, Q91YT0	0.012513449205378
KEGG_PATHWAY	mmu05010:Alzheimer's disease	23	2.0776874435411	0.004790994216994	Q9DC69, Q91VD9, Q9JHR7, P63328, P0DP26, Q9CZ13, P56383, P56480, Q99LC3, Q9DB77, Q91VR2, O89110, P49615, Q91YT0	0.041460526877835
GOTERM_CC_DIRECTIGO:0005747~mitochondrial respiratory chain complex		8	0.7226738934056	0.005286818264336	Q9DC69, Q91VD9, Q99LX0, Q9ERS2, Q91WD5, Q99LC3, Q9CQ75, Q91YT0	0.038677249407513
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	19	1.7163504968383	0.006718490920628	Q8BVE3, Q9ERS2, Q03265, P50516, Q91WD5, Q9Z1G3, Q9CQ75, Q9DC69, Q91VD9, P50518, Q9CZ13, P56383, P62814, P56480, Q99LC3, Q9DB77, Q91VR2, Q91YT0, Q9D819	0.050388681904711
UP_KEYWORDS	Iron-sulfur	8	0.7226738934056	0.0120622395728	Q91VD9, Q80Y14, Q9CQM9, Q8WTY4, Q91WD5, P33610, Q00519, Q91YT0	0.035906201519031
GOTERM_CC_DIRECTIGO:0070469~respiratory chain		8	0.7226738934056	0.016405448557325	Q9DC69, Q91VD9, Q9CZ13, Q91WD5, Q99LC3, Q9DB77, Q9CQ75, Q91YT0	0.095014889561174

Annotation Cluster 57		Enrichment Score: 1.5924540765210637						
Category	Term	Count	%	PValue	Genes			FDR
KEGG_PATHWAY	mmu00040:Penicillin biosynthesis	9	0.8130081300813	0.001419365558631	Q8VEE0, P45376, Q9JII6, Q99KP3, P45377, Q6ZQM8, Q91X52, Q91ZJ5, P21300			0.015207488128184
Annotation Cluster 58		Enrichment Score: 1.5901471719408036						
Category	Term	Count	%	PValue	Genes			FDR
INTERPRO	IPR000608:Ubiquitin-conjugating enzyme, E2	10	0.903342366757	9.51590216515237E-05	P62254, Q9CZY3, O88738, Q7TSS2, Q9Z255, P61087, P63280, Q9D2M8, P61082, Q8CFI2			0.005757120809917
INTERPRO	IPR016135:Ubiquitin-conjugating enzyme/RWD	10	0.903342366757	0.00086976061392	P62254, Q9CZY3, O88738, Q7TSS2, Q9Z255, P61087, P63280, Q9D2M8, P61082, Q8CFI2			0.03348578363592
GOTERM_MF_DIRECT	GO:0061631~ubiquitin conjugating enzyme activ	8	0.7226738934056	0.000901035192714	P62254, Q9CZY3, O88738, Q7TSS2, Q9Z255, P61087, Q9D2M8, Q8CFI2			0.01980360327815
Annotation Cluster 59		Enrichment Score: 1.5655942110235401						
Category	Term	Count	%	PValue	Genes			FDR
UP_KEYWORDS	GTP-binding	25	2.2583559168925	0.005331362786702	Q9Z0N1, Q922F4, Q9R1T4, Q69ZS7, Q5U3K5, Q9WTP7, P59325, Q05D44, P61027, P62835, P42208, P46664, P47758, Q80UG5, O35626, P53994, P36916, Q9QXB9, P32233, O08810, Q3UM18, P84096, Q8R050, P61750, P58252			0.017060360917446
Annotation Cluster 60		Enrichment Score: 1.498917995608888						
Category	Term	Count	%	PValue	Genes			FDR
UP_KEYWORDS	DNA recombination	9	0.8130081300813	0.0076957041669	Q8VEE4, P97386, P28352, P60122, Q99K48, Q9WMT5, Q9WUP7, P37913, Q9CQ71			0.024322225515139
UP_KEYWORDS	DNA repair	19	1.7163504968383	0.039224068780859	P62908, P97386, P28352, Q9Z255, Q3U1J4, Q99K48, O35593, Q9WMT5, Q9WUP7, P11103, P39749, P37913, Q9CQ71, P54726, Q8VEE4, Q8VUJ6, Q9JLV6, P60122, P17918			0.096551553922115
Annotation Cluster 61		Enrichment Score: 1.493796451874483						
Category	Term	Count	%	PValue	Genes			FDR
UP_KEYWORDS	Transferase	104	9.39476061427281	1.27798352765814E-05	Q91YR5, Q9CWQ0, Q8K1R7, Q62407, Q9WTP7, Q9DBL7, P11440, P68181, Q61036, Q8CAY6, Q9JK38, P12382, O88738, Q9JLV6, Q9Z120, Q6P9R2, P09411, P49138, P10649, Q9DBC7, Q91YQ5, P22907, Q64674, P18654, Q8K183, O54734, O09131, Q91WU5, P23492, Q9Z255, Q80X41, Q80WS3, Q93092, P33610, Q91ZJ5, P62254, Q8CIG8, Q8JZK9, Q91V92, Q9JJ78, P04184, P47856, P47857, Q8CFI2, Q7TSS2, Q8BWU5, O35654, Q64261, P08030, Q04447, Q5DW34, Q9D1G2, Q8BH69, Q8CIN4, P05201, Q61510, B2RQC6, P19096, Q8CGY8, Q07832, P30285, Q9CS42, Q8BY71, Q3THS6, Q1HFFZ0, Q9JKX6, P05132, P49615, Q3TX08, Q8CFV9, Q9WV85, Q3TRM8, P13439, Q9JLI6, Q9Z2A0, Q9DBG6, Q09200, P70218, Q68FH4, Q9D270, Q99K85, Q91YL3, O70551, O70310, P11103, Q9R0N0, Q99KQ4, Q3TW96, P31750, Q9CQ65, Q9CWJ9, Q9QZL0, Q04899, Q03963, P61087, O54988, Q6ZQM8, Q8VE10, Q9ESL4, A2BDX3, Q64737, P26450, P97930, Q9WUA3			7.60846007163918E-05
GOTERM_MF_DIRECT	GO:0016740~transferase activity	101	9.12375790424571	0.001291103371942	Q91YR5, Q9CWQ0, Q8K1R7, Q62407, Q9WTP7, Q9DBL7, P11440, P68181, Q61036, Q8CAY6, Q9JK38, P12382, Q9JLV6, Q9Z120, Q6P9R2, P49138, P10649, Q91YQ5, P22907, Q64674, P18654, Q8K183, O54734, O09131, Q91WU5, P23492, Q9CXY6, Q9Z255, Q80X41, Q80WS3, Q93092, P33610, Q91ZJ5, P62254, Q8CIG8, Q8JZK9, Q91V92, Q9JJ78, P04184, P47856, P47857, Q8CFI2, Q7TSS2, Q8BWU5, O35654, Q64261, P08030, Q04447, Q5DW34, Q9D1G2, Q8BH69, Q8CIN4, P05201, Q61510, B2RQC6, P19096, Q8CGY8, Q07832, P30285, Q9CS42, Q8BY71, Q3THS6, Q1HFFZ0, Q9JKX6, P05132, P49615, Q3TX08, Q8CFV9, Q9WV85, Q3TRM8, P13439, Q9JLI6, Q9Z2A0, Q9DBG6, Q09200, P70218, Q68FH4, Q9D270, Q99K85, Q91YL3, O70551, O70310, P11103, Q9R0N0, Q99KQ4, Q3TW96, P31750, Q9CQ65, Q9CWJ9, Q9QZL0, Q04899, Q03963, P61087, O54988, Q6ZQM8, Q8VE10, Q9ESL4, A2BDX3, Q64737, P97930, Q9WUA3			0.026151172219924
UP_KEYWORDS	Kinase	47	4.2457091237579	0.001401022613587	Q8K1R7, Q91YL3, O70551, Q62407, Q80X41, Q9WTP7, Q07832, Q9R0N0, P30285, Q9DBL7, P31750, Q9CS42, P11440, P68181, Q61036, P12382, Q9QZL0, Q9JLV6, Q03963, Q04899, Q9JJ78, Q6P9R2, O54988, P09411, P04184, P49138, P05132, P47857, P49615, Q9WV85, Q8CFV9, Q9DBC7, Q9ESL4, Q3TRM8, P26450, P97930, Q9Z2A0, P18654, P70218, Q68FH4, Q64261, Q04447, Q8K183, Q9D1G2, Q8BH69, Q9WUA3, Q8CIN4			0.005274438074679

UP_KEYWORDS	Serine/threonine-protein kinase	25	2.2583559168925	0.045941783224364	Q8K1R7, O70551, Q62407, Q80X41, Q07832, P30285, P31750, P11440, P68181, Q61036, Q9QZL0, Q03963, Q04899, Q9JJ78, Q6P9R2, O54988, P49138, P05132, P49615, Q9ESL4, Q9Z2A0, P18654, P70218, Q64261, Q8CIN4	0.10889904171701
<b>Annotation Cluster 62</b> Enrichment Score: 1.4932023379649095						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR007123:Gelsolin domain	5	0.4516711833785	0.002731916619757	Q9JJ28, P13020, P24452, Q01405, Q9D662	0.075866668096212
<b>Annotation Cluster 63</b> Enrichment Score: 1.4433117066215926						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Flavoprotein	14	1.2646793134598	0.002649187134765	Q8CFV9, Q9JMH6, Q8R2E9, Q9JHI5, Q64521, Q8R180, Q9DCN2, Q9DC69, Q9Z0X1, Q8C0L6, Q9JLT4, Q99LC3, Q00519, Q91YT0	0.009688455807139
UP_KEYWORDS	FAD	12	1.0840108401084	0.009153893761723	Q9DCN2, Q9DC69, Q8C0L6, Q9Z0X1, Q9JLT4, Q9JMH6, Q8R2E9, Q9JHI5, Q64521, Q99LC3, Q8R180, Q00519	0.027897580988109
<b>Annotation Cluster 64</b> Enrichment Score: 1.4369465057455773						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu00250:Alanine, aspartate and glutamate met	8	0.7226738934056	0.011813314709729	B2RQC6, Q91YI0, P16460, P46664, P47856, P54822, P05201, Q9JHW2	0.080545327566336
<b>Annotation Cluster 65</b> Enrichment Score: 1.383002609354318						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR001440:Tetratricopeptide TPR-1	6	0.5420054200542	0.002981015689982	Q60864, Q9CYG7, O70145, Q8CGY8, Q9D706, Q64378	0.080156199663952
UP_KEYWORDS	TPR repeat	13	1.1743450767841	0.015454207379133	Q60864, O70145, Q99MD9, Q8CGY8, Q9CR16, Q99L47, Q64378, Q9CYG7, O88447, Q80UM3, Q5SW19, Q9D706, Q9QYI3	0.044273073300363
<b>Annotation Cluster 66</b> Enrichment Score: 1.37053037212395						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECTIGO:0000776-kinetochore		13	1.1743450767841	0.009084783990891	Q9R1T4, Q07832, Q6P5F9, Q08788, Q9DBR7, P63168, A2AGT5, Q9Z0Y1, Q99P69, Q9CWU9, P42208, Q9WVA3, Q8R1Q8	0.058059079298105
UP_KEYWORDS	Centromere	12	1.0840108401084	0.021976620650512	A2AGT5, Q9Z0Y1, Q99P69, Q9R1T4, Q07832, P42208, Q9CWU9, P62715, Q9WVA3, Q8BK67, Q8R1Q8, Q76MZ3	0.059221209331905
UP_KEYWORDS	Kinetochore	9	0.8130081300813	0.041055078269062	A2AGT5, Q9Z0Y1, Q99P69, Q9R1T4, Q07832, P42208, Q9CWU9, Q9WVA3, Q8R1Q8	0.098618365666622
<b>Annotation Cluster 67</b> Enrichment Score: 1.3394336802536475						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Iron-sulfur	8	0.7226738934056	0.0120622395728	Q91VD9, Q80Y14, Q9CQM9, Q8WTY4, Q91WD5, P33610, Q00519, Q91YT0	0.035906201519031
<b>Annotation Cluster 68</b> Enrichment Score: 1.1812525374926601						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	SH3 domain	16	1.4453477868112	0.024611048802757	P27870, O70145, P26450, Q80TY0, A2AAY5, Q62418, Q9Z0R6, P97369, O08539, Q61792, P70248, P97814, Q62422, Q8CBW3, Q9JLQ0, Q9Z0U1	0.06495287106707
<b>Annotation Cluster 69</b> Enrichment Score: 1.1747530875240222						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Signal recognition particle	3	0.2710027100271	0.030686276724526	Q9D7A6, P49962, Q8BMA6	0.077779077638404
<b>Annotation Cluster 70</b> Enrichment Score: 1.1563978735527476						
Category	Term	Count	%	PValue	Genes	FDR
SMART	SM00360:RRM	20	1.806684733514	0.00439818298197	Q9CX86, Q91WT8, Q9CPN8, Q9JLI8, P97379, P29341, Q99K48, Q9Z1D1, P97855, P32067, Q9D883, Q62189, Q3UEB3, Q8BGD9, Q8VIJ6, O08583, Q6NVF9, Q8R4X3, Q8C166, Q9CQI7	0.092023520853528

<b>Annotation Cluster 71</b> Enrichment Score: 1.1027721989192003						
Category	Term	Count	%	PValue	Genes	FDR
INTERPRO	IPR010987:Glutathione S-transferase, C-termina	8	0.7226738934056	0.003979306568255	P10649, Q68FL6, Q9Z1Q9, Q8CGC7, Q9D8N0, O09131, Q9ER72, Q9QYB1	0.103959725254541
<b>Annotation Cluster 72</b> Enrichment Score: 1.081642017702263						
Category	Term	Count	%	PValue	Genes	FDR
SMART	SM00185:ARM	8	0.7226738934056	0.001863466739234	O35643, Q8BNU0, O35344, P30999, E9PVA8, P70188, P52293, P70168	0.047065879817901
<b>Annotation Cluster 73</b> Enrichment Score: 1.0628183391633939						
Category	Term	Count	%	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0031105--septin complex	3	0.2710027100271	0.01916356698515	Q9R1T4, P42208, Q80UG5	0.103446050910132
<b>Annotation Cluster 74</b> Enrichment Score: 1.0317128870571977						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Helicase	17	1.5356820234869	8.47286965413036E-05	Q61655, Q91VR5, P97310, Q6NZQ2, P97311, Q9WTM5, P97855, Q61881, Q62167, P54823, Q6NVF4, Q91VC3, P49718, Q9EPU0, P49717, P60122, P25206	0.000433810926291
GOTERM_MF_DIRECT	GO:0004386--helicase activity	16	1.4453477868112	0.002155823400252	Q61655, Q91VR5, P97310, Q6NZQ2, P97311, Q9WTM5, P97855, Q61881, Q62167, P54823, Q6NVF4, P49718, Q9EPU0, P49717, P60122, P25206	0.039767242365354
<b>Annotation Cluster 75</b> Enrichment Score: 1.030979709984985						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	mRNA transport	9	0.8130081300813	0.024564702983462	Q61655, O08583, Q9CPN8, Q3U0V1, P63242, P97379, Q6P5F9, Q9CWU9, Q91VC3	0.06495287106707
<b>Annotation Cluster 76</b> Enrichment Score: 1.0109753771736083						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu03430:Mismatch repair	6	0.5420054200542	0.014944953607737	Q8VEE4, O35654, P17918, P37913, Q9CQ71, Q9WUK4	0.096074701764022
<b>Annotation Cluster 77</b> Enrichment Score: 0.9776539255190654						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Porphyrin biosynthesis	3	0.2710027100271	0.039819611969733	P10518, P70697, P22907	0.097084006326207
<b>Annotation Cluster 78</b> Enrichment Score: 0.9339610750739368						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu00061:Fatty acid biosynthesis	5	0.4516711833785	0.012717496126741	P19096, Q9CZW4, E9Q4Z2, Q9QUJ7, P41216	0.084159900838725
<b>Annotation Cluster 79</b> Enrichment Score: 0.8819368888420165						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Pyridoxal phosphate	7	0.6323396567299	0.035673662612028	Q99K85, P19096, Q9JL16, Q9Z2Y8, Q99K01, Q8VCN5, P05201	0.088664637171644
<b>Annotation Cluster 80</b> Enrichment Score: 0.8373544318199488						
Category	Term	Count	%	PValue	Genes	FDR
KEGG_PATHWAY	mmu05161:Hepatitis B	19	1.7163504968383	0.011033435037741	Q9CQV8, Q60931, Q3U1J4, P26450, P68254, Q60591, P30285, P70677, P31750, Q62167, P52633, P42225, P63101, Q04207, Q07813, Q64261, P17918, P42227, O89110	0.077578840109118
<b>Annotation Cluster 81</b> Enrichment Score: 0.4714760870474071						
Category	Term	Count	%	PValue	Genes	FDR
UP_KEYWORDS	Protein phosphatase	11	0.9936766034327	0.041219395024721	Q9D358, Q9D967, P29351, P63328, Q9DAK9, Q61074, Q8CHP8, P62715, Q8BUM3, P62137, Q9D7X3	0.098618365666622