

Table A – Reactome analysis of the AAE6 interactors selected with the Protein-Pathway method. The pathways with a significant FDR (<0.05) are bolded

Pathway name	Entities found	Entities p-value	Entities FDR	UniProt number	Entities protein name
(1) Loss of Function of FBXW7 in Cancer and NOTCH1 Signaling	3/6	3.31E-05	0.012	P62877 Q969H0-1 Q969H0-4	E3 ubiquitin-protein ligase <i>RBX1</i> F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 1 F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 4
(2) FBXW7 Mutants and NOTCH1 in Cancer	3/6	3.31E-05	0.012	P62877 Q969H0-1 Q969H0-4	E3 ubiquitin-protein ligase <i>RBX1</i> F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 1 F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 4
(3) NOTCH1 Intracellular Domain Regulates Transcription	5/48	1.30E-04	0.019	P49336 P62877 Q969H0-1 Q969H0-4 Q92830	Cyclin-dependent kinase 8 <i>CDK8</i> E3 ubiquitin-protein ligase <i>RBX1</i> F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 1 F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 4 Histone acetyltransferase <i>KAT2A</i>
(4) Regulation of TP53 Expression	2/2	1.94E-04	0.019	P04637 O75626	Cellular tumour antigen <i>P53</i> PR domain zinc finger protein 1 <i>PRDM1</i>
(5) Defective Base Excision Repair Associated with MUTYH	2/2	1.94E-04	0.019	Q9UIF7-3 Q9UIF7-6	Adenine DNA glycosylase <i>MUTYH</i> isoform 3 Adenine DNA glycosylase <i>MUTYH</i> isoform 6
(6) Pyrophosphate hydrolysis	2/2	1.94E-04	0.019	Q9H2U2 Q15181	Inorganic pyrophosphatase 2, mitochondrial <i>IPYR2</i> Inorganic pyrophosphatase <i>IPYR</i>
(7) Defective MUTYH substrate processing	2/2	1.94E-04	0.019	Q9UIF7-3 Q9UIF7-6	Adenine DNA glycosylase <i>MUTYH</i> isoform 3 Adenine DNA glycosylase <i>MUTYH</i> isoform 6
(8) TP53 Regulates Metabolic Genes	6/88	2.70E-04	0.019	P42345 Q9UGJ0 P04637 P14854 P10599 Q9HCJ0	Serine/threonine-protein kinase mTOR <i>MTOR</i> 5'-AMP-activated protein kinase subunit gamma-2 <i>AAKG2</i> Cellular tumour antigen <i>P53</i> Cytochrome c oxidase subunit 6B1 <i>CX6B1</i> Thioredoxin <i>THIO</i> Trinucleotide repeat-containing gene 6C protein <i>TNR6C</i>
(9) Constitutive Signaling by NOTCH1 HD+PEST Domain Mutants	5/59	3.34E-04	0.019	P49336 P62877 Q969H0-1 Q969H0-4 Q92830	Cyclin-dependent kinase 8 <i>CDK8</i> E3 ubiquitin-protein ligase <i>RBX1</i> F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 1 F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 4 Histone acetyltransferase <i>KAT2A</i>

Pathway name	Entities found	Entities p-value	Entities FDR	UniProt number	Entities protein name
(10) Signaling by NOTCH1 HD+PEST Domain Mutants in Cancer	5/59	3.34E-04	0.019	P49336 P62877 Q969H0-1 Q969H0-4 Q92830	Cyclin-dependent kinase 8 <i>CDK8</i> E3 ubiquitin-protein ligase <i>RBX1</i> F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 1 F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 4 Histone acetyltransferase <i>KAT2A</i>
(11) Signaling by NOTCH1 PEST Domain Mutants in Cancer	5/59	3.34E-04	0.019	P49336 P62877 Q969H0-1 Q969H0-4 Q92830	Cyclin-dependent kinase 8 <i>CDK8</i> E3 ubiquitin-protein ligase <i>RBX1</i> F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 1 F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 4 Histone acetyltransferase <i>KAT2A</i>
(12) Constitutive Signaling by NOTCH1 PEST Domain Mutants	5/59	3.34E-04	0.019	P49336 P62877 Q969H0-1 Q969H0-4 Q92830	Cyclin-dependent kinase 8 <i>CDK8</i> E3 ubiquitin-protein ligase <i>RBX1</i> F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 1 F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 4 Histone acetyltransferase <i>KAT2A</i>
(13) Signaling by NOTCH1 in Cancer	5/59	3.34E-04	0.019	P49336 P62877 Q969H0-1 Q969H0-4 Q92830	Cyclin-dependent kinase 8 <i>CDK8</i> E3 ubiquitin-protein ligase <i>RBX1</i> F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 1 F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 4 Histone acetyltransferase <i>KAT2A</i>
(14) Signaling by WNT	10/299	8.48E-04	0.044	P25054 Q13237 P09497 P62877 P56545 Q9P219 P35913 Q8N474 O14641 Q9HCJ0	Adenomatous polyposis coli protein <i>APC</i> cGMP-dependent protein kinase 2 <i>KGP2</i> Clathrin light chain B <i>CLCB</i> E3 ubiquitin-protein ligase <i>RBX1</i> PC-terminal-binding protein 2 <i>CTBP2</i> Protein Daple <i>DAPLE</i> Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit beta <i>PDE6B</i> Secreted frizzled-related protein 1 <i>SFRP1</i> Segment polarity protein dishevelled homolog <i>DVL2</i> Trinucleotide repeat-containing gene 6C protein <i>TNR6C</i>

Pathway name	Entities found	Entities p-value	Entities FDR	UniProt number	Entities protein name
(15) Signaling by NOTCH1	5/74	9.23E-04	0.045	P49336 P62877 Q969H0-1 Q969H0-4 Q92830	Cyclin-dependent kinase 8 <i>CDK8</i> E3 ubiquitin-protein ligase <i>RBX1</i> F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 1 F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 4 Histone acetyltransferase <i>KAT2A</i>
(16) Signaling by NOTCH	8/205	0.0011	0.049	P04637 P49336 P62877 Q969H0-1 Q969H0-4 Q92830 Q14186 Q9HCJ0	Cellular tumour antigen <i>P53</i> Cyclin-dependent kinase 8 <i>CDK8</i> E3 ubiquitin-protein ligase <i>RBX1</i> F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 1 F-box/WD repeat-containing protein 7 <i>FBXW7</i> isoform 4 Histone acetyltransferase <i>KAT2A</i> Transcription factor Dp-1 <i>TFDP1</i> Trinucleotide repeat-containing gene 6C protein <i>TNR6C</i>
(17) Negative regulation of TCF-dependent signaling by DVL-interacting proteins	2/5	0.0012	0.049	Q9P219 O14641	Protein Daple <i>DAPLE</i> Segment polarity protein dishevelled homolog <i>DVL2</i>
(18) Activation of NOXA and translocation to mitochondria	2/5	0.0012	0.049	P04637 Q14186	Cellular tumour antigen <i>P53</i> Transcription factor Dp-1 <i>TFDP1</i>
(19) Diseases of Base Excision Repair	2/7	0.0023	0.087	Q9UIF7-3 Q9UIF7-6	Adenine DNA glycosylase <i>MUTYH</i> isoform 3 Adenine DNA glycosylase <i>MUTYH</i> isoform 6
(20) Insulin processing	3/27	0.0026	0.091	P16870 Q12840 P33176	Carboxypeptidase E <i>CBPE</i> Kinesin heavy chain isoform 5A <i>KIF5A</i> Kinesin-1 heavy chain <i>KINH</i>
(21) Oxidative Stress Induced Senescence	5/94	0.0026	0.091	P04637 P01100 P10599 Q14186 Q9HCJ0	Cellular tumour antigen <i>P53</i> Proto-oncogene c-Fos <i>FOS</i> Thioredoxin <i>THIO</i> Transcription factor Dp-1 <i>TFDP1</i> Trinucleotide repeat-containing gene 6C protein <i>TNR6C</i>
(22) Pre-NOTCH Transcription and Translation	4/62	0.0036	0.113	P04637 Q92830 Q14186 Q9HCJ0	Cellular tumour antigen <i>P53</i> Histone acetyltransferase <i>KAT2A</i> Transcription factor Dp-1 <i>TFDP1</i> Trinucleotide repeat-containing gene 6C protein <i>TNR6C</i>

Pathway name	Entities found	Entities p-value	Entities FDR	UniProt number	Entities protein name
(23) Activation of PUMA and translocation to mitochondria	2/9	0.0038	0.113	P04637 Q14186	Cellular tumour antigen <i>P53</i> Transcription factor Dp-1 <i>TFDP1</i>
(24) Transcriptional Regulation by TP53	10/367	0.0038	0.113	Q9UGJ0 Q92851 P04637 P14854 O75626 P01100 P42345 P10599 Q14186 Q9HCJ0	5'-AMP-activated protein kinase subunit gamma-2 <i>AAKG2</i> Caspase-10 <i>CASP10</i> Cellular tumour antigen <i>p53</i> Cytochrome c oxidase subunit 6B1 <i>CX6B1</i> PR domain zinc finger protein 1 <i>PRDM1</i> Proto-oncogene c-Fos <i>FOS</i> Serine/threonine-protein kinase mTOR <i>MTOR</i> Thioredoxin <i>THIO</i> Transcription factor Dp-1 <i>TFDP1</i> Trinucleotide repeat-containing gene 6C protein <i>TNR6C</i>
(25) FOXO-mediated transcription	4/66	0.0045	0.124	Q8N139 Q969P5 P23511 P10599	ATP-binding cassette sub-family A member 6 <i>ABCA6</i> F-box only protein 32 <i>FBX32</i> Nuclear transcription factor Y subunit alpha <i>NFYA</i> Thioredoxin <i>THIO</i>

Table B – Reactome analysis of the EPE6 interactors selected with the Protein-Pathway method

Pathway name	Entities found	Entities p-value	Entities FDR	UniProt number	Entities protein name
(1) Signaling by Hippo	3/20	4.21E-04	0.144	O14641 Q9UDY2 Q9GZV5	Segment polarity protein disheveled homolog <i>DVL-2</i> Tight junction protein <i>ZO-2</i> WW domain-containing transcription regulator protein 1 <i>WWTR1</i>
(2) Post-chaperonin tubulin folding pathway	3/23	6.31E-04	0.144	Q13509 O75347 Q9BTW9	Tubulin beta-3 chain <i>TUBB3</i> Tubulin-specific chaperone A <i>TBCA</i> Tubulin-specific chaperone D <i>TBCD</i>
(3) Activated NTRK3 signals through PI3K	2/6	8.81E-04	0.144	P35568 P27986	Insulin receptor substrate 1 <i>IRS1</i> Phosphatidylinositol 3-kinase regulatory subunit alpha <i>PIK3R1</i>
(4) RNA Polymerase III Transcription Initiation from Type 3 Promoter	3/28	0.0011	0.144	Q16533 Q5SXM2 A6H8Y1	snRNA-activating protein complex subunit 1 <i>SNAPC1</i> snRNA-activating protein complex subunit 4 <i>SNAPC4</i> Transcription factor TFIIIB component B'' homolog <i>BDP1</i>
(5) HDR through Homologous Recombination (HRR)	4/66	0.0013	0.144	Q99708 Q07864 P49959 P12004	DNA endonuclease <i>RBBP8</i> DNA polymerase epsilon catalytic subunit <i>POLE</i> Double strand break repair protein <i>MRE11</i> Proliferating cell nuclear antigen <i>PCNA</i>
(6) Erythrocytes take up oxygen and release carbon dioxide	2/8	0.0016	0.144	P69905 P68871	Hemoglobin subunit alpha <i>HBA1</i> Hemoglobin subunit beta <i>HBB</i>
(7) PI3K/AKT activation	2/9	0.0020	0.144	P35568 P27986	Insulin receptor substrate 1 <i>IRS1</i> Phosphatidylinositol 3-kinase regulatory subunit alpha <i>PIK3R1</i>
(8) RNA Polymerase III Transcription Initiation	3/36	0.0023	0.144	Q16533 Q5SXM2 A6H8Y1	snRNA-activating protein complex subunit 1 <i>SNAPC1</i> snRNA-activating protein complex subunit 4 <i>SNAPC4</i> Transcription factor TFIIIB component B'' homolog <i>BDP1</i>
(9) HDR through MMEJ (alt-NHEJ)	2/10	0.0024	0.144	Q99708 P49959	DNA endonuclease <i>RBBP8</i> Double strand break repair protein <i>MRE11</i>
(10) Signaling by MET	4/80	0.0027	0.144	Q8N307 P27986 Q6VN20 Q96B97	Mucin-20 <i>MUC20</i> Phosphatidylinositol 3-kinase regulatory subunit alpha <i>PIK3R1</i> Ran-binding protein 10 <i>RANBP10</i> SH3 domain-containing kinase-binding protein 1 <i>SH3KBP1</i>

Pathway name	Entities found	Entities p-value	Entities FDR	UniProt number	Entities protein name
(11) Metabolism of proteins	25/2012	0.0028	0.144	O95786 P07550 P04637 Q8IWV2 Q13618 Q13217 Q9Y297 P02671 Q92696 Q6ZVT0 P05019 P15088 Q8N307 P23511 Q9UBK2 Q14435 P12004 Q9Y6M0 P10599 Q9P031 Q5JRA6 Q13509 Q9Y4R7 O75347 Q9BTW9	Antiviral innate immune response receptor RIG-I <i>DDX58</i> Beta-2 adrenergic receptor <i>ADRB2</i> Cellular tumour antigen <i>p53</i> Contactin-4 <i>CNTN4</i> Cullin-3 <i>CUL3</i> DnaJ homolog subfamily C member 3 <i>DNAJC3</i> F-box/WD repeat-containing protein 1A <i>BTRC</i> Fibrinogen alpha chain <i>FGA</i> Geranylgeranyl transferase type-2 subunit alpha <i>RABGGATA</i> Inactive polyglycyclase <i>TTLL10</i> Insulin-like growth factor I <i>IGF1</i> Mast cell carboxypeptidase A <i>CPA3</i> Mucin-20 <i>MUC20</i> Nuclear transcription factor Y subunit alpha <i>NFYA</i> Peroxisome proliferator-activated receptor gamma coactivator 1-alpha <i>PPARGC1A</i> Polypeptide N-acetylgalactosaminyltransferase 3 <i>GLNT3</i> Proliferating cell nuclear antigen <i>PCNA</i> Testisin <i>PRSS21</i> Thioredoxin <i>THIO</i> Thyroid transcription factor 1-associated protein 26 <i>CCDC59</i> Transport and Golgi organization protein 1 homolog <i>MIA3</i> Tubulin beta-3 chain <i>TUBB3</i> Tubulin monoglycyclase <i>TTLL3</i> Tubulin-specific chaperone A <i>TBCA</i> Tubulin-specific chaperone D <i>TBCD</i>
(12) RNA Polymerase III Abortive and Retractive Initiation	3/41	0.0033	0.144	Q16533 Q5SXM2 A6H8Y1	snRNA-activating protein complex subunit 1 <i>SNAPC1</i> snRNA-activating protein complex subunit 4 <i>SNAPC4</i> Transcription factor TFIIIB component B'' homolog <i>BDP1</i>
(13) RNA Polymerase III Transcription	3/41	0.0033	0.144	Q16533 Q5SXM2 A6H8Y1	snRNA-activating protein complex subunit 1 <i>SNAPC1</i> snRNA-activating protein complex subunit 4 <i>SNAPC4</i> Transcription factor TFIIIB component B'' homolog <i>BDP1</i>
(14) Erythropoietin activates Phosphoinositide-3-kinase (PI3K)	2/12	0.0034	0.144	P27986 P48736	Phosphatidylinositol 3-kinase regulatory subunit alpha <i>PIK3R1</i> Thyroid transcription factor 1-associated protein 26 <i>CCDC59</i>

Pathway name	Entities found	Entities p-value	Entities FDR	UniProt number	Entities protein name
(15) MET activates RAS signaling	2/12	0.0034	0.144	Q8N307 Q6VN20	Mucin-20 <i>MUC20</i> Ran-binding protein 10 <i>RANBP10</i>
(16) Erythrocytes take up carbon dioxide and release oxygen	2/12	0.0034	0.144	P69905 P68871	Hemoglobin subunit alpha <i>HBA1</i> Hemoglobin subunit beta <i>HBB</i>
(17) O ₂ /CO ₂ exchange in erythrocytes	2/12	0.0034	0.144	P69905 P68871	Hemoglobin subunit alpha <i>HBA1</i> Hemoglobin subunit beta <i>HBB</i>
(18) Carboxyterminal post-translational modifications of tubulin	3/43	0.0037	0.145	Q6ZVT0 Q13509 Q9Y4R7	Inactive polyglycyclase <i>TTL10</i> Tubulin beta-3 chain <i>TUBB3</i> Tubulin monoglycyclase <i>TTL3</i>
(19) DNA Double-Strand Break Repair	5/148	0.0043	0.146	P04637 Q99708 Q07864 P49959 P12004	Cellular tumour antigen <i>p53</i> DNA endonuclease <i>RBBP8</i> DNA polymerase epsilon catalytic subunit <i>POLE</i> Double strand break repair protein <i>MRE11</i> Proliferating cell nuclear antigen <i>PCNA</i>
(20) TP53 regulates transcription of several additional cell death genes whose specific roles in p53-dependent apoptosis remain uncertain	2/14	0.0046	0.146	P04637 Q92696	Cellular tumour antigen <i>p53</i> Geranylgeranyl transferase type-2 subunit alpha <i>RABGGATA</i>
(21) SEMA3A-Plexin repulsion signaling by inhibiting Integrin adhesion	2/14	0.0046	0.146	O75051 Q14563	Plexin-A2 <i>PLXNA2</i> Semaphorin-3A <i>SEMA3</i>
(22) Transcriptional Regulation by TP53	8/367	0.0047	0.146	P04637 P50750 P14854 Q99708 P49959 Q92696 P12004 P10599	Cellular tumour antigen <i>p53</i> Cyclin-dependent kinase 9 <i>CDK9</i> Cytochrome c oxidase subunit 6B1 <i>COX6B1</i> DNA endonuclease <i>RBBP8</i> Double strand break repair protein <i>MRE11</i> Geranylgeranyl transferase type-2 subunit alpha <i>RABGGATA</i> Proliferating cell nuclear antigen <i>PCNA</i> Thioredoxin <i>THIO</i>
(23) Toll-like Receptor Cascades	5/156	0.0053	0.146	Q9Y297 P02671 Q9NWZ3 Q13233 Q9BT09	F-box/WD repeat-containing protein 1A <i>BTRC</i> Fibrinogen alpha chain <i>FGA</i> Interleukin-1 receptor-associated kinase 4 <i>IRAK4</i> Mitogen-activated protein kinase kinase kinase 1 <i>MAP3K1</i> Protein canopy homolog 3 <i>CNPY3</i>

Pathway name	Entities found	Entities p-value	Entities FDR	UniProt number	Entities protein name
(24) Signaling by EGFR	3/51	0.0060	0.146	O43184 P27986 Q96B97	Disintegrin and metalloproteinase domain-containing protein 12 <i>ADAM12</i> Phosphatidylinositol 3-kinase regulatory subunit alpha <i>PIK3R1</i> SH3 domain-containing kinase-binding protein 1 <i>SH3KBP1</i>
(25) CRMPs in Sema3A signaling	2/16	0.0060	0.146	O75051 Q14563	Plexin-A2 <i>PLXNA2</i> Semaphorin-3A <i>SEMA3</i>

Table C – Reactome analysis of the AAE6 and EPE6 overlapping interactors selected with the Protein-Pathway method

Pathway name	Entities found	Entities p-value	Entities FDR	UniProt number	Entities protein name
(1) TP53 Regulates Metabolic Genes	3/88	0.0005	0.094	P04637 P14854 P10599	Cellular tumour antigen <i>P53</i> Cytochrome c oxidase subunit 6B1 <i>CX6B1</i> Thioredoxin <i>THIO</i>
(2) Late endosomal microautophagy	2/34	0.0016	0.094	Q9H444 P68871	Charged multivesicular body protein 4b <i>CHMP4B</i> Hemoglobin subunit beta <i>HBB</i>
(3) Carboxyterminal post-translational modifications of tubulin	2/43	0.0026	0.094	Q6ZVT0 Q9Y4R7	Inactive polyglycylase <i>TTL10</i> Tubulin monoglycylase <i>TTL3</i>
(4) Regulation of TP53 Expression	1/2	0.0035	0.094	P04637	Cellular tumour antigen <i>P53</i>
(5) FOXO-mediated transcription	2/66	0.0059	0.094	P23511 P10599	Nuclear transcription factor Y subunit alpha <i>NFYA</i> Thioredoxin <i>THIO</i>
(6) Transcriptional activation of cell cycle inhibitor p21	1/4	0.0070	0.094	P04637	Cellular tumour antigen <i>P53</i>
(7) Transcriptional activation of p53 responsive genes	1/4	0.0070	0.094	P04637	Cellular tumour antigen <i>P53</i>
(8) Negative regulation of TCF-dependent signaling by DVL-interacting proteins	1/5	0.0087	0.094	O14641	Segment polarity protein dishevelled homolog <i>DVL2</i>
(9) Reelin signalling pathway	1/5	0.0087	0.094	Q96B97	SH3 domain-containing kinase-binding protein 1 <i>SH3KBP1</i>
(10) Activation of NOXA and translocation to mitochondria	1/5	0.0087	0.094	P04637	Cellular tumour antigen <i>P53</i>
(11) Protein repair	1/6	0.0105	0.094	P10599	Thioredoxin <i>THIO</i>
(12) Oxidative Stress Induced Senescence	2/94	0.0117	0.094	P04637 P10599	Cellular tumour antigen <i>P53</i> Thioredoxin <i>THIO</i>
(13) RUNX3 regulates CDKN1A transcription	1/7	0.0122	0.094	P04637	Cellular tumour antigen <i>P53</i>
(14) Cell Cycle, Mitotic	4/536	0.0129	0.094	P04637 Q13352 Q9H444 Q96GY3	Cellular tumour antigen <i>P53</i> Centromere protein R <i>CENPR</i> Charged multivesicular body protein 4b <i>CHMP4B</i> Protein lin-37 homolog <i>LIN37</i>
(15) WNT mediated activation of DVL	1/8	0.0139	0.094	O14641	Segment polarity protein dishevelled homolog <i>DVL2</i>

Pathway name	Entities found	Entities p-value	Entities FDR	UniProt number	Entities protein name
(16) Erythrocytes take up oxygen and release carbon dioxide	1/8	0.0139	0.094	P68871	Hemoglobin subunit beta <i>HBB</i>
(17) Cargo recognition for clathrin-mediated endocytosis	2/105	0.0145	0.094	O14641 Q96B97	Segment polarity protein dishevelled homolog DVL2 SH3 domain-containing kinase-binding protein 1 SH3KBP1
(18) Activation of PUMA and translocation to mitochondria	1/9	0.0157	0.094	P04637	Cellular tumour antigen <i>P53</i>
(19) PI5P Regulates TP53 Acetylation	1/9	0.0157	0.094	P04637	Cellular tumour antigen <i>P53</i>
(20) Metabolism of proteins	8/2012	0.0158	0.094	P04637 P02671 Q6ZVT0 P23511 Q9Y6M0 P10599 Q9P031 Q9Y4R7	Cellular tumour antigen P53 Fibrinogen alpha chain FGA Inactive polyglycylase TTLL10 Nuclear transcription factor Y subunit alpha NFYA Testisin PRSS21 Thioredoxin THIO Thyroid transcription factor 1-associated protein 26 CCDC59 Tubulin monoglycylase TTLL3
(21) ATF6 (ATF6-alpha) activates chaperone genes	1/10	0.0174	0.094	P23511	Nuclear transcription factor Y subunit alpha <i>NFYA</i>
(22) Regulation of FOXO transcriptional activity by acetylation	1/10	0.0174	0.094	P10599	Thioredoxin <i>THIO</i>
(23) TP53 Regulates Transcription of Death Receptors and Ligands	1/12	0.0209	0.094	P04637	Cellular tumour antigen <i>P53</i>
(24) TP53 Regulates Transcription of Caspase Activators and Caspases	1/12	0.0209	0.094	P04637	Cellular tumour antigen <i>P53</i>
(25) WNT5:FZD7-mediated leishmania damping	1/12	0.0209	0.094	O14641	Segment polarity protein dishevelled homolog <i>DVL2</i>