Expansion in the genus *Eimeria*

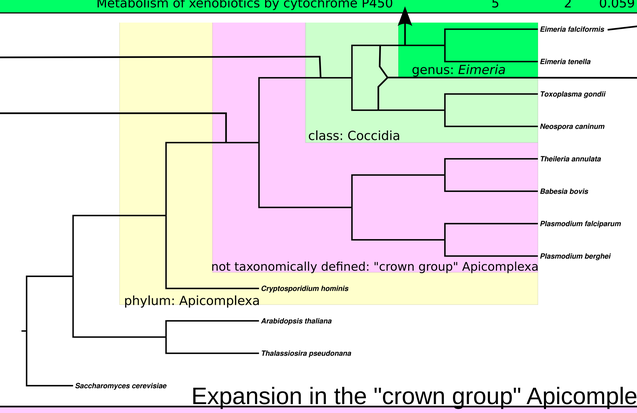
Id	description	Annotated	In group	Expected	p-value
GO:0003774	motor activity	31	22	2.57	3.9e-18
GO:0017111	nucleoside-triphosphatase activity	215	47	17.85	1.8e-11
GO:0016462	pyrophosphatase activity	218	47	18.09	3.0e-11
GO:0016818	hydrolase activity, acting on phosphorus-containing anhydrides	219	47	18.18	3.6e-11
GO:0016817	hydrolase activity, acting on acid anhydrides	222	47	18.43	6.1e-11
GO:0016787	hydrolase activity	413	68	34.28	1.3e-10
GO:0003777	microtubule motor activity	22	13	1.83	1.4e-09
GO:0008237	metallopeptidase activity	23	9	1.91	4.4e-05
GO:0008061	chitin binding	4	4	0.33	4.6e-05
GO:0097367	carbohydrate derivative binding	4	4	0.33	4.6e-05
GO:0007017	microtubule-based process	34	18	2.54	8.6e-13
GO:0006928	cellular component movement	27	16	2.02	1.8e-12
GO:0007018	microtubule-based movement	27	16	2.02	1.8e-12
GO:0006022	aminoglycan metabolic process	4	4	0.30	2.9e-05
GO:0006030	chitin metabolic process	4	4	0.30	2.9e-05
GO:0006040	amino sugar metabolic process	5	4	0.37	0.00014
GO:1901071	glucosamine-containing compound metabolic process	5	4	0.37	0.00014
GO:0006461	protein complex assembly	10	4	0.75	0.00435
GO:0070271	protein complex biogenesis	10	4	0.75	0.00435
GO:0007596	blood coagulation	2	2	0.15	0.00554
IPR004273	Dynein heavy chain	10	10	0.843	2.0e-11
IPR013602	Dynein heavy chain, domain-2	10	10	0.843	2.0e-11
IPR024743	Dynein heavy chain, coiled coil stalk	10	10	0.843	2.0e-11
IPR001609	Myosin head, motor domain	9	9	0.760	2.3e-10
IPR024317	Dynein heavy chain, P-loop containing D4 domain	9	9	0.760	2.3e-10
IPR011704	ATPase, dynein-related, AAA domain	8	7	0.678	2.4e-07
IPR003593	AAA+ ATPase domain	64	18	5.364	4.0e-06
IPR012779	Peptidase M1, alanyl aminopeptidase	5	5	0.425	4.5e-06
IPR013594	Dynein heavy chain, domain-1	5	5	0.425	4.5e-06
IPR014782	Peptidase M1, membrane alanine aminopeptidase, N-terminal	5	5	0.425	4.5e-06
IPR024601	Peptidase M1, alanyl aminopeptidase, C-terminal	5	5	0.425	4.5e-06
IPR009030	Growth factor, receptor	11	7	0.932	7.9e-06
IPR002557	Chitin binding domain	4	4	0.340	5.3e-05
IPR007120	DNA-directed RNA polymerase, subunit 2, domain 6	3	3	0.256	0.001
IPR007121	RNA polymerase, beta subunit, conserved site	3	3	0.256	0.001
IPR007641	RNA polymerase Rpb2, domain 7	3	3	0.256	0.001
IPR007644	RNA polymerase, beta subunit, protrusion	3	3	0.256	0.001
IPR007645	RNA polymerase Rpb2, domain 3	3	3	0.256	0.001
IPR011641	Tyrosine-protein kinase ephrin type A/B receptor-like	3	3	0.256	0.001
IPR013578	Peptidase M16C associated	3	3	0.256	0.001
IPR017871	ABC transporter, conserved site	14	6	1.189	0.001
IPR014756	Immunoglobulin E-set	11	5	0.935	0.001
IPR000048	IQ motif, EF-hand binding site	4	3	0.341	0.002
IPR018316	Tubulin/FtsZ, 2-layer sandwich domain	4	3	0.341	0.002
IPR013781	Glycoside hydrolase, catalytic domain	8	4	0.681	0.003
IPR003439	ABC transporter-like	18	6	1.530	0.003
IPR001140	ABC transporter, transmembrane domain	9	4	0.766	0.005
IPR011527	ABC transporter, transmembrane domain, type 1	9	4	0.766	0.005
IPR017940	ABC transporter, integral membrane type 1	9	4	0.766	0.005
IPR008280	Tubulin/FtsZ, C-terminal	5	3	0.426	0.005
IPR013093	ATPase, AAA-2	5	3	0.426	0.005
IPR019489	Clp ATPase, C-terminal	5	3	0.426	0.005
IPR023123	Tubulin, C-terminal	5	3	0.426	0.005
IPR000001	Kringle	2	2	0.171	0.007
IPR000177	Apple domain	2	2	0.171	0.007
IPR000741	Fructose-bisphosphate aldolase, class-I	2	2	0.171	0.007
IPR001190	Speract/scavenger receptor	2	2	0.171	0.007
IPR002328	Alcohol dehydrogenase, zinc-type, conserved site	2	2	0.171	0.007
IPR002453	Beta tubulin	2	2	0.171	0.007
IPR002498	Phosphatidylinositol-4-phosphate 5-kinase, core	2	2	0.171	0.007
IPR004882	LUC7-related	2	2	0.171	0.007
IPR006650	Adenosine/AMP deaminase active site	2	2	0.171	0.007
IPR007642	RNA polymerase Rpb2, domain 2	2	2	0.171	0.007
IPR013806	Kringle-like fold	2	2	0.171	0.007
IPR013838	Beta tubulin, autoregulation binding site	2	2	0.171	0.007
IPR016034	Phosphatidylinositol-4-phosphate 5-kinase, core, subgroup	2	2	0.171	0.007
IPR017448	Speract/scavenger receptor-related	2	2	0.171	0.007
IPR023795	Protease inhibitor I4, serpin, conserved site	2	2	0.171	0.007
IPR023796	Serpin domain	2	2	0.171	0.007
00590	Arachidonic acid metabolism	3	2	0.035	0.001
00480	Glutathione metabolism	13	2	0.155	0.014
00564	Glycerophospholipid metabolism	22	2	0.267	0.038
00980	Metabolism of xenobiotics by cytochrome P450	5	2	0.059	0.002

Expansion in *Eimeria falciformis*

Id	description	Annotated	In group	Expected	p-value
GO:0008237	metallopeptidase activity	23	8	0.36	5.5e-10
GO:0031177	phosphopantetheine binding	3	3	0.05	3.5e-06
GO:0072341	modified amino acid binding	3	3	0.05	3.5e-06
GO:0070011	peptidase activity, acting on L-amino acid peptides	75	8	1.19	1.1e-05
GO:0016597	amino acid binding	4	3	0.06	1.4e-05
GO:0008233	peptidase activity	80	8	1.26	1.8e-05
GO:0033218	amide binding	5	3	0.08	3.5e-05
GO:0008270	zinc ion binding	118	9	1.87	4.5e-05
GO:0019842	vitamin binding	7	3	0.11	0.00012
GO:0031406	carboxylic acid binding	7	3	0.11	0.00012
GO:0016567	protein ubiquitination	5	2	0.08	0.0023
GO:0032446	protein modification by small protein conjugation	6	2	0.09	0.0033
GO:0070647	protein modification by small protein conjugation or removal	6	2	0.09	0.0033
GO:0006508	proteolysis	81	5	1.27	0.0064
GO:0008654	phospholipid biosynthetic process	9	2	0.14	0.00078
GO:0006644	phospholipid metabolic process	14	2	0.22	0.0188
GO:0006511	ubiquitin-dependent protein catabolic process	20	2	0.31	0.0372
GO:0019941	modification-dependent protein catabolic process	20	2	0.31	0.0372
GO:0043632	modification-dependent macromolecule catabolic process	20	2	0.31	0.0372
GO:0008610	lipid biosynthetic process	23	2	0.36	0.0482
IPR021288	Sporozoite TA4 surface antigen	9	7	0.177	4.8e-11
IPR012779	Peptidase M1, alanyl aminopeptidase	5	5	0.100	3.5e-09
IPR014782	Peptidase M1, membrane alanine aminopeptidase, N-terminal	5	5	0.100	3.5e-09
IPR024601	Peptidase M1, alanyl aminopeptidase, C-terminal	5	5	0.100	3.5e-09
IPR009081	Acyl carrier protein-like	4	4	0.080	1.7e-07
IPR014031	Beta-ketoacyl synthase, C-terminal	5	4	0.100	8.5e-07
IPR006162	Phosphopantetheine attachment site	3	3	0.061	8.6e-06
IPR013578	Peptidase M16C associated	3	3	0.061	8.6e-06
IPR020806	Polyketide synthase, phosphopantetheine-binding domain	3	3	0.061	8.6e-06
IPR016038	Thiolase-like, subgroup	8	4	0.161	1.1e-05
IPR016039	Thiolase-like	8	4	0.161	1.1e-05
IPR001227	Acyl transferase domain	4	3	0.081	3.4e-05
IPR014030	Beta-ketoacyl synthase, N-terminal	4	3	0.081	3.4e-05
IPR014043	Acyl transferase	4	3	0.081	3.4e-05
IPR016036	Malonyl-CoA ACP transacylase, ACP-binding	4	3	0.081	3.4e-05
IPR020801	Polyketide synthase, acyl transferase domain	4	3	0.081	3.4e-05
IPR020841	Polyketide synthase, beta-ketoacyl synthase domain	4	3	0.081	3.4e-05
IPR020842	Polyketide synthase/Fatty acid synthase, KR	5	3	0.101	8.3e-05
IPR005221	Phosphatidylserine decarboxylase	2	2	0.041	4.2e-04
IPR013968	Polyketide synthase, KR	2	2	0.041	4.2e-04
IPR019474	Ubiquitin conjugation factor E4, core	2	2	0.041	4.2e-04
IPR020471	Aldo/keto reductase subgroup	2	2	0.041	4.2e-04
IPR020807	Polyketide synthase, dehydratase domain	2	2	0.041	4.2e-04
IPR016035	Acyl transferase/acyl hydrolase/lysophospholipase	8	3	0.162	0.0014
IPR016040	NAD(P)-binding domain	52	6	1.037	0.001
IPR002198	Short-chain dehydrogenase/reductase SDR	9	3	0.182	0.001
IPR007863	Peptidase M16, C-terminal	10	3	0.203	0.001
IPR011249	Metalloenzyme, LuxS/M16 peptidase-like, metal-binding	10	3	0.203	0.001
IPR003817	Phosphatidylserine decarboxylase-related	3	2	0.061	0.001
IPR006634	TRAM/LAG1/CLN8 homology domain	3	2	0.061	0.001
IPR013120	Male sterility, NAD-binding	3	2	0.061	0.001
IPR018201	Beta-ketoacyl synthase, active site	3	2	0.061	0.001
IPR005045	Protein of unknown function DUF284, transmembrane eukaryotic	4	2	0.082	0.002
IPR023174	3'5'-cyclic nucleotide phosphodiesterase, conserved site	5	2	0.102	0.004
IPR023210	NADP-dependent oxidoreductase domain	5	2	0.102	0.004
IPR001357	BRCT domain	6	2	0.122	0.006
IPR002073	3'5'-cyclic nucleotide phosphodiesterase, catalytic domain	6	2	0.122	0.006
IPR004274	NLI interacting factor	6	2	0.122	0.006
IPR023088	3'5'-cyclic nucleotide phosphodiesterase	6	2	0.122	0.006
IPR011237	Peptidase M16, core	8	2	0.163	0.011
IPR002347	Glucose/ribitol dehydrogenase	9	2	0.184	0.014
IPR000863	Sulfotransferase domain	1	1	0.021	0.021
IPR018170	Aldo/keto reductase, conserved site	1	1	0.021	0.021
00590	Arachidonic acid metabolism	3	2	0.035	0.001
00480	Glutathione metabolism	13	2	0.155	0.014
00564	Glycerophospholipid metabolism	22	2	0.267	0.038
00980	Metabolism of xenobiotics by cytochrome P450	5	2	0.059	0.002

Expansion in the class Coccidia

Id	description	Annotated	In group	Expected	p-value
GO:0003774	motor activity	31	20	2.31	2.9e-16
GO:0003777	microtubule motor activity	22	13	1.64	3.4e-10
GO:0016787	hydrolase activity	413	61	30.78	1.4e-09
GO:0016817	hydrolase activity, acting on acid anhydrides	222	41	16.55	3.5e-09
GO:0017111	nucleoside-triphosphatase activity	215	40	16.02	4.7e-09
GO:0016462	pyrophosphatase activity	218	40	16.25	7.3e-09
GO:0016818	hydrolase activity, acting on phosphorus-containing anhydrides	219	40	16.32	8.4e-09
GO:0008237	metallopeptidase activity	23	10	1.71	1.9e-06
GO:0008061	chitin binding	4	4	0.30	3.0e-05
GO:0097367	carbohydrate derivative binding	4	4	0.30	3.0e-05
GO:0007017	microtubule-based process	34	18	2.54	8.6e-13
GO:0006928	cellular component movement	27	16	2.02	1.8e-12
GO:0007018	microtubule-based movement	27	16	2.02	1.8e-12
GO:0006022	aminoglycan metabolic process	4	4	0.30	2.9e-05
GO:0006030	chitin metabolic process	4	4	0.30	2.9e-05
GO:0006040	amino sugar metabolic process	5	4	0.37	0.00014
GO:1901071	glucosamine-containing compound metabolic process	5	4	0.37	0.00014
GO:0006461	protein complex assembly	10	4	0.75	0.00435
GO:0070271	protein complex biogenesis	10	4	0.75	0.00435
GO:0007596	blood coagulation	2	2	0.15	0.00554
IPR004273	Dynein heavy chain	10	10	0.814	1.4e-11
IPR013602	Dynein heavy chain, domain-2	10	10	0.814	1.4e-11
IPR024743	Dynein heavy chain, coiled coil stalk	10	10	0.814	1.4e-11
IPR024317	Dynein heavy chain, P-loop containing D4 domain	9	9	0.734	1.7e-10
IPR011704	ATPase, dynein-related, AAA domain	8	7	0.655	1.9e-07
IPR001609	Myosin head, motor domain	9	7	0.737	7.9e-07
IPR012779	Peptidase M1, alanyl aminopeptidase	5	5	0.411	3.8e-06
IPR013594	Dynein heavy chain, domain-1	5	5	0.411	3.8e-06
IPR014782	Peptidase M1, membrane alanine aminopeptidase, N-terminal	5	5	0.411	3.8e-06
IPR024601	Peptidase M1, alanyl aminopeptidase, C-terminal	5	5	0.411	3.8e-06
IPR002557	Chitin binding domain	4	4	0.329	4.6e-05
IPR009081	Acyl carrier protein-like	4	4	0.329	4.6e-05
IPR003593	AAA+ ATPase domain	64	15	5.207	1.7e-04
IPR014031	Beta-ketoacyl synthase, C-terminal	5	4	0.411	2.1e-04
IPR006162	Phosphopantetheine attachment site	3	3	0.247	5.6e-04
IPR013120	Male sterility, NAD-binding	3	3	0.247	5.6e-04
IPR013578	Peptidase M16C associated	3	3	0.247	5.6e-04
IPR020806	Polyketide synthase, phosphopantetheine-binding domain	3	3	0.247	5.6e-04
IPR007863	Peptidase M16, C-terminal	10	5	0.822	6.7e-04
IPR011249	Metalloenzyme, LuxS/M16 peptidase-like, metal-binding	10	5	0.822	6.7e-04
IPR001227	Acyl transferase domain	4	3	0.330	0.002
IPR004043	LCCL	4	3	0.330	0.002
IPR014030	Beta-ketoacyl synthase, N-terminal	4	3	0.330	0.002
IPR014043	Acyl transferase	4	3	0.330	0.002
IPR016036	Malonyl-CoA ACP transacylase, ACP-binding	4	3	0.330	0.002
IPR018316	Tubulin/FtsZ, 2-layer sandwich domain	4	3	0.330	0.002
IPR020801	Polyketide synthase, acyl transferase domain	4	3	0.330	0.002
IPR020841	Polyketide synthase, beta-ketoacyl synthase domain	4	3	0.330	0.002
IPR003439	ABC transporter-like	18	6	1.478	0.003
IPR011237	Peptidase M16, core	8	4	0.658	0.003
IPR016035	Acyl transferase/acyl hydrolase/lysophospholipase	8	4	0.658	0.003
IPR016038	Thiolase-like, subgroup	8	4	0.658	0.003
IPR016039	Thiolase-like	8	4	0.658	0.003
IPR017871	ABC transporter, conserved site	14	5	1.151	0.004
IPR001140	ABC transporter, transmembrane domain	9	4	0.741	0.004
IPR011527	ABC transporter, transmembrane domain, type 1	9	4	0.741	0.004
IPR017940	ABC transporter, integral membrane type 1	9	4	0.741	0.004
IPR008280	Tubulin/FtsZ, C-terminal	5	3	0.412	0.004
IPR017975	Tubulin, conserved site	5	3	0.412	0.004
IPR020842	Polyketide synthase/Fatty acid synthase, KR	5	3	0.412	0.004
IPR023123	Tubulin, C-terminal	5	3	0.412	0.004
IPR001757	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	10	4	0.823	0.006
IPR023299	ATPase, P-type, cytoplasmic domain N	10	4	0.823	0.006
IPR001190	Speract/scavenger receptor	2	2	0.165	0.006
IPR002453	Beta tubulin	2	2	0.165	0.006
IPR006685	Mechanosensitive ion channel MscS	2	2	0.165	0.006
IPR007621	TPM domain	2	2	0.165	0.006
IPR013838	Beta tubulin, autoregulation binding site	2	2	0.165	0.006
IPR013968	Polyketide synthase, KR	2	2	0.165	0.006
IPR017448	Speract/scavenger receptor-related	2	2	0.165	0.006
IPR020807	Polyketide synthase, dehydratase domain	2	2	0.165	0.006
IPR018317	Tubulin	6	3	0.494	0.009
IPR003008	Tubulin/FtsZ, GTPase domain	6	3	0.494	0.009
IPR008984	SMAD/FHA domain	6	3	0.494	0.009
IPR009030	Growth factor, receptor	11	4	0.905	0.009
IPR018303	ATPase, P-type phosphorylation site	11	4	0.905	0.009
00625	Chloroalkane and chloroalkene degradation	3	2	0.247	0.020
00982	Drug metabolism - cytochrome P450	3	2	0.247	0.020
00565	Ether lipid metabolism	6	3	0.488	0.010
00010	Glycolysis / Gluconeogenesis	29	6	2.309	0.030
00680	Methane metabolism	16	4	1.297	0.040
00626	Naphthalene degradation	2	2	0.165	0.007
00830	Retinol metabolism	2	2	0.165	0.007



Expansion in the "crown group" Apicomplexa

Id	description	Annotated	In group	Expected	p-value
GO:0003735	structural constituent of ribosome	95	43	21.62	5.0e-07
GO:0005198	structural molecule activity	111	46	25.26	4.2e-06
GO:0003774	motor activity	31	17	7.05	9.3e-05
GO:0003899	DNA-directed RNA polymerase activity	23	13	5.23	0.00043
GO:0034062	RNA polymerase activity	23	13	5.23	0.00043
GO:0008061	chitin binding	4	4	0.91	0.00265
GO:0019207	kinase regulator activity	4	4	0.91	0.00265
GO:0019887	protein kinase regulator activity	4	4	0.91	0.00265
GO:0097367	carbohydrate derivative binding	4	4	0.91	0.00265
GO:0016779	nucleotidyltransferase activity	42	18	9.56	0.00267
GO:0006412	translation	158	61	38.59	1.5e-05
GO:0009059	macromolecule biosynthetic process	242	85	59.11	1.8e-05
GO:0034645	cellular macromolecule biosynthetic process	242	85	59.11	1.8e-05
GO:0010467	gene expression	265	88	64.72	0.00016
GO:0009058	biosynthetic process	348	110	85.00	0.00018
GO:1901576	organic substance biosynthetic process	334	106	81.58	0.00021
GO:0044267	cellular protein metabolic process	355	111	86.71	0.00029
GO:0044249	cellular biosynthetic process	334	105	81.58	0.00037
GO:0009987	cellular process	937	249	228.86	0.00070
GO:0019538	protein metabolic process	422	126	103.07	0.00091
IPR004273	Dynein heavy chain	10	10	2.234	3.1e-07
IPR013602	Dynein heavy chain, domain-2	10	10	2.234	3.1e-07
IPR024743	Dynein heavy chain, coiled coil stalk	10	10	2.234	3.1e-07
IPR024317	Dynein heavy chain, P-loop containing D4 domain	9	9	2.011	1.4e-06
IPR011704	ATPase, dynein-related, AAA domain	8	7	1.790	1.8e-04
IPR011332	Ribosomal protein, zinc-binding domain	5	5	1.120	0.001
IPR012779	Peptidase M1, alanyl aminopeptidase	5	5	1.120	0.001
IPR013594	Dynein heavy chain, domain-1	5	5	1.120	0.001
IPR014782	Peptidase M1, membrane alanine aminopeptidase, N-terminal	5	5	1.120	0.001
IPR024601	Peptidase M1, alanyl aminopeptidase, C-terminal	5	5	1.120	0.001
IPR001609	Myosin head, motor domain	9	7	2.014	0.001
IPR016024	Armadillo-type fold	72	5	16.278	0.001
IPR010920	Like-Sm (LSM) domain	14	9	3.131	0.001
IPR011989	Armadillo-like helical	58	4	13.095	0.002
IPR000555	JAB1/Mov34/MPN/PAD-1	4	4	0.896	0.003
IPR002557	Chitin binding domain	4	4	0.896	0.003
IPR001163	Ribonucleoprotein LSM domain	11	7	2.462	0.004
IPR023313	Ubiquitin-conjugating enzyme, active site	11	7	2.462	0.004
IPR000608	Ubiquitin-conjugating enzyme, E2	12	7	2.686	0.008
00190	Oxidative phosphorylation	33	12	6.864	0.048
00440	Phosphonate and phosphinate metabolism	4	4	0.844	0.002
00230	Purine metabolism	61	20	12.475	0.033
00240	Pyrimidine metabolism	52	21	10.400	0.001

Independent expansion in *Eimeria* and Sarcocystidae

Id	description	Annotated	In group	Expected	p-value
GO:0008237	metallopeptidase activity	23	5	0.23	1.8e-06
GO:0004332	fructose-bisphosphate aldolase activity	2	2	0.02	9.8e-05
GO:0016832	aldehyde-lyase activity	2	2	0.02	9.8e-05
GO:0016787	hydrolase activity	413	12	4.20	0.00010
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	31	4	0.32	0.00020
GO:0043492	ATPase activity, coupled to movement of substances	31	4	0.32	0.00020
GO:0016820	hydrolase activity, catalyzing transmembrane movement of substances	33	4	0.34	0.00025
GO:0015399	primary active transmembrane transporter activity	35	4	0.36	0.00032
GO:0015405	P-P-bond-hydrolysis-driven transmembrane transporter activity	35	4	0.36	0.00032
GO:0022857	transmembrane transporter activity	70	5	0.71	0.00048
GO:0051179	localization	184	7	2.12	0.0022
GO:0055085	transmembrane transport	66	4	0.76	0.0053
GO:0006096	glycolysis	12	2	0.14	0.0076
GO:0006007	glucose catabolic process	16	2	0.18	0.0135
GO:0016052	carbohydrate catabolic process	16	2	0.18	0.0135
GO:0019320	hexose catabolic process	16	2	0.18	0.0135
GO:0044724	single-organism carbohydrate catabolic process	16	2	0.18	0.0135
GO:0046365	monosaccharide catabolic process	16	2	0.18	0.0135
GO:0044699	single-organism process	332	8	3.82	0.0173
GO:0006006	glucose metabolic process	21	2	0.24	0.0228
IPR012779	Peptidase M1, alanyl aminopeptidase	5	5	0.043	6.0e-11
IPR014782	Peptidase M1, membrane alanine aminopeptidase, N-terminal	5	5	0.043	6.0e-11
IPR024601	Peptidase M1, alanyl aminopeptidase, C-terminal	5	5	0.043	6.0e-11
IPR001140	ABC transporter, transmembrane domain	9	4	0.079	8.3e-07
IPR011527	ABC transporter, transmembrane domain, type 1	9	4	0.079	8.3e-07
IPR017940	ABC transporter, integral membrane type 1	9	4	0.079	8.3e-07
IPR017871	ABC transporter, conserved site	14	4	0.123	6.4e-06
IPR003439	ABC transporter-like	18	4	0.158	1.9e-05
IPR000741	Fructose-bisphosphate aldolase, class-I	2	2	0.018	8.5e-05
IPR009543	Vacuolar protein sorting-associated protein	4	2	0.036	0.001
IPR023174	3'5'-cyclic nucleotide phosphodiesterase, conserved site	5	2	0.045	0.001
IPR002073	3'5'-cyclic nucleotide phosphodiesterase, catalytic domain	6	2	0.054	0.001
IPR023088	3'5'-cyclic nucleotide phosphodiesterase	6	2	0.054	0.001
IPR003593	AAA+ ATPase domain	64	4	0.565	0.003
IPR002259	Equilibrative nucleoside transporter	1	1	0.009	0.009
IPR008636	HOOK	1	1	0.009	0.009
IPR013534	Starch synthase, catalytic domain	1	1	0.009	0.009
IPR013785	Aldolase-type TIM barrel	17	2	0.154	0.011
IPR000177	Apple domain	2	1	0.018	0.019
IPR003014	PAN-1 domain	3	1	0.028	0.028
IPR003609	Apple-like	3	1	0.028	0.028
IPR021691	Protein of unknown function DUF3273	3	1	0.028	0.028
00710	Carbon fixation in photosynthetic organisms	14	2	0.272	0.035
00051	Fructose and mannose metabolism	11	2	0.213	0.022
00480	Glutathione metabolism	13	2	0.253	0.031
00680	Methane metabolism	16	2	0.312	0.045
00030	Pentose phosphate pathway	15	2	0.292	0.040