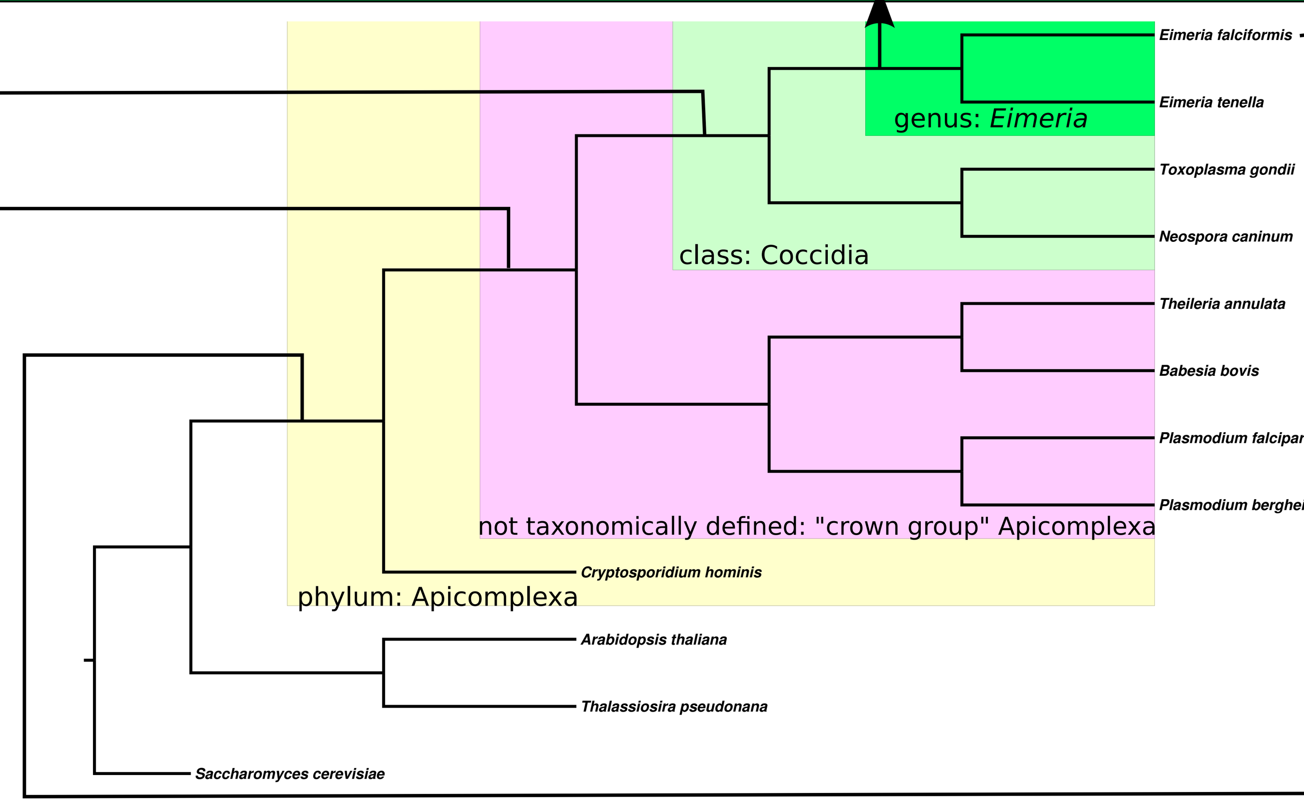
Id	description	Annotated	In group	Expected	p-value
GO:0001071	nucleic acid binding transcription factor activity	18	14	2.65	3.0e-09
GO:0003700	sequence-specific DNA binding transcription factor activity	18	14	2.65	3.0e-09
GO:0008270	zinc ion binding	162	40	23.81	3.4e-4
GO:0005515	protein binding	547	104	80.41	8.7e-3
GO:0046914	transition metal ion binding	181	40	26.61	0.003
GO:0016773	phosphotransferase activity, alcohol group as acceptor	132	31	19.40	0.003
GO:0004672	protein kinase activity	100	25	14.70	0.003
GO:0016301	kinase activity	135	31	19.84	0.005
GO:0005488	binding	1633	258	240.04	0.010
GO:0016772	transferase activity, transferring phosphorus-containing groups	211	43	31.02	0.011
GO:0006355	regulation of transcription, DNA-dependent	39	15	4.25	4.8e-06
GO:0043412	macromolecule modification	194	39	21.15	3.4e-05
GO:0010468	regulation of gene expression	45	15	4.91	3.6e-05
GO:0006464	cellular protein modification process	170	35	18.54	5.7e-05
IPR001471	AP2/ERF domain	17	14	1.919	3.0e-11
IPR021288	Sporozoite TA4 surface antigen	11	10	1.246	3.6e-09
IPR011009	Protein kinase-like domain	114	29	12.813	3.6e-05
IPR013083	Zinc finger, RING/FYVE/PHD-type	57	17	6.444	1.4e-04
IPR000571	Zinc finger, CCCH-type	20	9	2.270	1.7e-04
IPR000719	Protein kinase, catalytic domain	96	23	10.835	0.001
IPR002290	Serine/threonine- / dual-specificity protein kinase	86	21	9.715	0.001
IPR001611	Leucine-rich repeat	20	8	2.272	0.001
IPR002013	Synaptojanin, N-terminal	3	3	0.342	0.001
IPR016024	Armadillo-type fold	99	22	11.189	0.002
IPR003591	Leucine-rich repeat, typical subtype	6	4	0.683	0.002
IPR001841	Zinc finger, RING-type	32	10	3.633	0.002
IPR007087	Zinc finger, C2H2	14	6	1.593	0.003
IPR001965	Zinc finger, PHD-type	10	5	1.138	0.003
IPR019786	Zinc finger, PHD-type, conserved site	7	4	0.797	0.004
IPR011011	Zinc finger, FYVE/PHD-type	12	5	1.366	0.008
IPR011990	Tetratricopeptide-like helical	65	15	7.371	0.009
IPR002937	Amine oxidase	5	3	0.570	0.012
IPR004855	Transcription factor IIA, alpha/beta subunit	2	2	0.228	0.013
IPR013771	Bifunctional trypsin/alpha-amylase inhibitor helical domain	2	2	0.228	0.013
IPR019515	Vacuolar protein sorting-associated protein 54	2	2	0.228	0.013
IPR019562	Micronemal adhesive repeat, sialic-acid binding	2	2	0.228	0.013
IPR020635	Tyrosine-protein kinase, catalytic domain	2	2	0.228	0.013
IPR021869	Ribonuclease Zc3h12a-like	2	2	0.228	0.013
IPR019787	Zinc finger, PHD-finger	9	4	1.025	0.013
IPR020683	Ankyrin repeat-containing domain	26	7	2.959	0.023
IPR001357	BRCT domain	11	4	1.254	0.029
IPR011989	Armadillo-like helical	76	15	8.629	0.029
IPR001179	Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	3	2	0.342	0.036
IPR001778	Pollen allergen Poa pIX/Phl pVI	3	2	0.342	0.036
IPR003152	PIK-related kinase, FATC	3	2	0.342	0.036
IPR003653	Peptidase C48, SUMO/Sentrin/Ubl1	3	2	0.342	0.036
IPR005522	Inositol polyphosphate kinase	3	2	0.342	0.036
IPR017877	Myb-like domain	3	2	0.342	0.036
IPR000403	Phosphatidylinositol 3-/4-kinase, catalytic domain	7	3	0.798	0.037
IPR001752	Kinesin, motor domain	17	5	1.937	0.037
IPR002110	Ankyrin repeat	24	6	2.734	0.049
00513	Various types of N-glycan biosynthesis	7	2	0.218	0.021
00510	N-Glycan biosynthesis	9	2	0.281	0.034

Id	description	Annotated	In group	Expected	p-value
GO:0005509	calcium ion binding	66	21	7.30	3.3e-06
GO:0004112	cyclic-nucleotide phosphodiesterase	11	7	1.22	4.2e-05
GO:0008081	phosphoric diester hydrolase activity	16	8	1.77	0.00012
GO:0004252	serine-type endopeptidase activity	20	9	2.21	0.00012
GO:0008236	serine-type peptidase activity	26	10	2.87	0.00024
GO:0005515	protein binding	547	80	60.48	0.00185
GO:0042578	phosphoric ester hydrolase activity	44	12	4.87	0.00211
GO:0004609	phosphatidylserine decarboxylase	3	2	0.33	0.03388
GO:0044763	single-organism cellular process	387	60	40.12	0.00014
GO:0044699	single-organism process	417	62	43.23	0.00039
GO:0007165	signal transduction	62	15	6.43	0.00107
GO:0023052	signaling	62	15	6.43	0.00107
GO:0044700	single organism signaling	62	15	6.43	0.00107
GO:0065007	biological regulation	157	28	16.28	0.00178
GO:0007154	cell communication	65	15	6.74	0.00179
GO:0050794	regulation of cellular process	140	25	14.52	0.00317
GO:0051716	cellular response to stimulus	101	19	10.47	0.00568
GO:0050789	regulation of biological process	148	25	15.34	0.00685
IPR015500	Peptidase S8, subtilisin-related	9	7	0.824	1.7e-06
IPR000209	Peptidase S8/S53, subtilisin/kexin/sedolisin	10	7	0.915	5.1e-06
IPR023828	Peptidase S8, subtilisin, Ser-active site	8	6	0.733	1.4e-05
IPR002073	3'5'-cyclic nucleotide phosphodiesterase, catalytic domain	13	7	1.190	5.7e-05
IPR023088	3'5'-cyclic nucleotide phosphodiesterase	10	6	0.916	9.1e-05
IPR023827	Peptidase S8, subtilisin, Asp-active site	7	5	0.642	1.2e-04
IPR011992	EF-hand-like domain	64	16	5.830	1.7e-04
IPR006210	Epidermal growth factor-like	8	5	0.734	2.9e-04
IPR022398	Peptidase S8, subtilisin, His-active site	5	4	0.459	3.3e-04
IPR017986	WD40-repeat-containing domain	117	23	10.631	0.001
IPR023393	START-like domain	9	5	0.826	0.001
IPR015943	WD40/YVTN repeat-like-containing domain	121	23	10.999	0.001
IPR001680	WD40 repeat	100	20	9.102	0.001
IPR000152	EGF-type aspartate/asparagine hydroxylation site	6	4	0.551	0.001
IPR001881	EGF-like calcium-binding	6	4	0.551	0.001
IPR023174	3'5'-cyclic nucleotide phosphodiesterase, conserved site	10	5	0.917	0.001
IPR018249	EF-HAND 2	53	12	4.845	0.003
IPR003607	HD/PDEase domain	9	4	0.827	0.006
IPR001810	F-box domain, cyclin-like	5	3	0.460	0.007
IPR018097	EGF-like calcium-binding, conserved site	5	3	0.460	0.007
IPR002048	Calcium-binding EF-hand	32	8	2.932	0.007
IPR000172	Glucose-methanol-choline oxidoreductase, N-terminal	2	2	0.184	0.008
IPR004326	Mlo-related protein	2	2	0.184	0.008
IPR005221	Phosphatidylserine decarboxylase	2	2	0.184	0.008
IPR007751	Domain of unknown function DUF676, lipase-like	2	2	0.184	0.008
IPR007867	Glucose-methanol-choline oxidoreductase, C-terminal	2	2	0.184	0.008
IPR000884	Thrombospondin, type 1 repeat	15	5	1.377	0.009
IPR001214	SET domain	15	5	1.377	0.009
IPR009030	Growth factor, receptor	17	5	1.561	0.016
IPR000133	ER lumen protein retaining receptor	3	2	0.276	0.024
IPR000782	FAS1 domain	3	2	0.276	0.024
IPR000800	Notch domain	3	2	0.276	0.024
IPR000845	Nucleoside phosphorylase domain	3	2	0.276	0.024
IPR003817	Phosphatidylserine decarboxylase-related	3	2	0.276	0.024
IPR023395	Mitochondrial carrier domain	19	5	1.745	0.026
IPR018488	Cyclic nucleotide-binding, conserved site	8	3	0.736	0.031
IPR014710	RmlC-like jelly roll fold	14	4	1.286	0.034
IPR011990	Tetratricopeptide-like helical	71	12	6.503	0.036
IPR000595	Cyclic nucleotide-binding domain	9	3	0.828	0.043
IPR000742	Epidermal growth factor-like domain	9	3	0.828	0.043
IPR018490	Cyclic nucleotide-binding-like	9	3	0.828	0.043
IPR000436	Sushi/SCR/CCP	4	2	0.368	0.045
IPR002913	Lipid-binding START	4	2	0.368	0.045
IPR003298	Apical membrane antigen 1	4	2	0.368	0.045
IPR019775	WD40 repeat, conserved site	50	9	4.585	0.045
00563	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	8	2	0.226	0.023
00512	Mucin type O-glycan biosynthesis	1	1	0.029	0.031
00311	Penicillin and cephalosporin biosynthesis	1	1	0.029	0.031
00230	Purine metabolism	61	5	1.572	0.032



Id	description	Annotated	In group	Expected	p-value
GO:0050515	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	1	1	0	0.0013
GO:0006721	terpenoid metabolic process	4	1	0.01	0.0053
GO:0006720	isoprenoid metabolic process	7	1	0.01	0.0093
GO:0008610	lipid biosynthetic process	26	1	0.03	0.0345
IPR013200	HAD superfamily hydrolase-like, type 3	5	3	0.004	1.6e-08
IPR023214	HAD-like domain	39	3	0.036	1.4e-05
IPR004424	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	1	1	0.001	0.001
IPR010909	PLAC	1	1	0.001	0.001
IPR006379	HAD-superfamily hydrolase, subfamily IIB	5	1	0.005	0.006
IPR014721	Ribosomal protein S5 domain 2-type fold, subgroup	16	1	0.018	0.020
IPR020568	Ribosomal protein S5 domain 2-type fold	25	1	0.029	0.032

Id	description	Annotated	In group	Expected	p-value
GO:0005515	protein binding	547	53	36.72	0.0014
GO:0060589	nucleoside-triphosphatase regulator activity	22	6	1.48	0.0025
GO:0043169	cation binding	287	31	19.27	0.0036
GO:0008047	enzyme activator activity	17	5	1.14	0.0041
GO:0005044	scavenger receptor activity	2	2	0.13	0.0045
GO:0038024	cargo receptor activity	2	2	0.13	0.0045
GO:0048038	quinone binding	2	2	0.13	0.0045
GO:0046872	metal ion binding	279	30	18.73	0.0046
GO:0004872	receptor activity	6	3	0.40	0.0051
GO:0005083	small GTPase regulator activity	19	5	1.28	0.0069
GO:0007154	cell communication	65	16	3.83	3.3e-07
GO:0007165	signal transduction	62	15	3.65	1.1e-06
GO:0023052	signaling	62	15	3.65	1.1e-06
GO:0044700	single organism signaling	62	15	3.65	1.1e-06
GO:0044699	single-organism process	417	42	24.55	3.5e-05
GO:0050794	regulation of cellular process	140	20	8.24	8.7e-05
GO:0035556	intracellular signal transduction	42	10	2.47	9.3e-05
GO:0051716	cellular response to stimulus	101	16	5.95	0.00014
GO:0050789	regulation of biological process	148	20	8.71	0.00019
GO:0044763	single-organism cellular process	387	38	22.78	0.00021
IPR004043	LCCL	4	4	0.269	2.1e-05
IPR008973	C2 calcium/lipid-binding domain, CaLB	7	5	0.471	2.6e-05
IPR000008	C2 calcium-dependent membrane targeting	6	4	0.404	2.8e-04
IPR000772	Ricin B lectin domain	6	4	0.404	2.8e-04
IPR018029	C2 membrane targeting protein	6	4	0.404	2.8e-04
IPR021691	Protein of unknown function DUF3273	3	3	0.202	3.1e-04
IPR008979	Galactose-binding domain-like	7	4	0.471	0.001
IPR022086	Inner membrane complex protein	8	4	0.539	0.001
IPR001251	CRAL-TRIO domain	9	4	0.606	0.002
IPR011074	CRAL/TRIO, N-terminal domain	5	3	0.337	0.003
IPR002110	Ankyrin repeat	24	6	1.614	0.004
IPR001190	Speract/scavenger receptor	2	2	0.135	0.005
IPR002181	Fibrinogen, alpha/beta/gamma chain, C-terminal globular	2	2	0.135	0.005
IPR003104	Actin-binding FH2/DRF autoregulatory	2	2	0.135	0.005
IPR003131	Potassium channel tetramerisation-type BTB domain	2	2	0.135	0.005
IPR006685	Mechanosensitive ion channel MscS	2	2	0.135	0.005
IPR015801	Copper amine oxidase, N2/N3-terminal	2	2	0.135	0.005
IPR017448	Speract/scavenger receptor-related	2	2	0.135	0.005
IPR019385	Phosphorylated adapter RNA export protein, RNA-binding domain	2	2	0.135	0.005
IPR020683	Ankyrin repeat-containing domain	26	6	1.749	0.007
IPR011333	BTB/POZ fold	7	3	0.472	0.009
IPR000315	Zinc finger, B-box	3	2	0.203	0.013
IPR000421	Coagulation factor 5/8 C-terminal type domain	3	2	0.203	0.013
IPR000756	Diacylglycerol kinase, accessory domain	3	2	0.203	0.013
IPR001173	Glycosyl transferase, family 2	3	2	0.203	0.013
IPR001206	Diacylglycerol kinase, catalytic domain	3	2	0.203	0.013
IPR011658	PA14	3	2	0.203	0.013
IPR015425	Actin-binding FH2	3	2	0.203	0.013
IPR004087	K Homology domain	8	3	0.540	0.013
IPR013320	Concanavalin A-like lectin/glucanase, subgroup	8	3	0.540	0.013
IPR023393	START-like domain	8	3	0.540	0.013
IPR013083	Zinc finger, RING/FYVE/PHD-type	57	9	3.827	0.014
IPR023214	HAD-like domain	39	7	2.622	0.015
IPR008985	Concanavalin A-like lectin/glucanase	15	4	1.011	0.016
IPR001841	Zinc finger, RING-type	32	6	2.154	0.019
IPR004088	K Homology domain, type 1	9	3	0.607	0.019
IPR001401	Dynamin, GTPase domain	4	2	0.270	0.025
IPR002913	Lipid-binding START	4	2	0.270	0.025
IPR011016	Zinc finger, RING-CH-type	4	2	0.270	0.025
IPR013714	Golgi apparatus membrane protein TVP15	4	2	0.270	0.025
IPR011701	Major facilitator superfamily	18	4	1.214	0.030
IPR000195	Rab-GTPase-TBC domain	11	3	0.742	0.034
IPR013783	Immunoglobulin-like fold	11	3	0.742	0.034
IPR000169	Cysteine peptidase, cysteine active site	5	2	0.338	0.040
IPR000225	Armadillo	5	2	0.338	0.040
IPR000668	Peptidase C1A, papain C-terminal	5	2	0.338	0.040
IPR025660	Cysteine peptidase, histidine active site	5	2	0.338	0.040
00740	Riboflavin metabolism	2	1	0.035	0.038

Id	description	Annotated	In group	Expected	p-value
GO:0005216	ion channel activity	7	4	0.45	0.00051
GO:0015267	channel activity	7	4	0.45	0.00051
GO:0022803	passive transmembrane transporter activity	7	4	0.45	0.00051
GO:0022838	substrate-specific channel activity	7	4	0.45	0.00051
GO:0003735	structural constituent of ribosome	100	15	6.49	0.00155
GO:0022836	gated channel activity	5	3	0.32	0.00244
GO:0022839	ion gated channel activity	5	3	0.32	0.00244
GO:0015075	ion transmembrane transporter activity	56	10	3.64	0.00262
GO:0005198	structural molecule activity	121	16	7.86	0.00413
GO:0004129	cytochrome-c oxidase activity	2	2	0.13	0.00419
GO:0044267	cellular protein metabolic process	429	38	25.83	0.0032
GO:0006813	potassium ion transport	2	2	0.12	0.0036
GO:0006412	translation	169	19	10.17	0.0040
GO:0010467	gene expression	311	28	18.72	0.0117
GO:0019538	protein metabolic process	516	41	31.06	0.0167
GO:0009405	pathogenesis	5	2	0.30	0.0318
GO:0051704	multi-organism process	5	2	0.30	0.0318
GO:0044260	cellular macromolecule metabolic process	675	49	40.64	0.0432
GO:0006397	mRNA processing	14	3	0.84	0.0474
GO:0032259	methylation	14	3	0.84	0.0474
IPR006387	CPW-WPC domain	5	4	0.291	5.6e-05
IPR011641	Tyrosine-protein kinase ephrin type A/B receptor-like	3	3	0.175	2.0e-04
IPR012677	Nucleotide-binding, alpha-beta plait	65	12	3.747	3.3e-04
IPR005135	Endonuclease/exonuclease/phosphatase	8	4	0.466	0.001
IPR013584	RAP domain	9	4	0.524	0.001
IPR000504	RNA recognition motif domain	55	10	3.180	0.001
IPR000001	Kringle	2	2	0.117	0.003
IPR002483	Splicing factor PWI	2	2	0.117	0.003
IPR003929	Potassium channel, calcium-activated, BK, alpha subunit	2	2	0.117	0.003
IPR007621	TPM domain	2	2	0.117	0.003
IPR010441	Protein of unknown function DUF1042	2	2	0.117	0.003
IPR013099	Ion transport 2	2	2	0.117	0.003
IPR013806	Kringle-like fold	2	2	0.117	0.003
IPR021150	Ubiquinol-cytochrome c chaperone/UPF0174	2	2	0.117	0.003
IPR025677	OST-HTH associated domain	2	2	0.117	0.003
IPR001461	Peptidase A1	6	3	0.350	0.004
IPR009007	Peptidase aspartic, catalytic	6	3	0.350	0.004
IPR003409	MORN motif	12	4	0.699	0.004
IPR021109	Peptidase aspartic	8	3	0.467	0.009
IPR009069	MTCP1	3	2	0.175	0.010
IPR002877	Ribosomal RNA methyltransferase FtsJ domain	4	2	0.234	0.019
IPR003298	Apical membrane antigen 1	4	2	0.234	0.019
IPR008907	P25-alpha	4	2	0.234	0.019
IPR009543	Vacuolar protein sorting-associated protein	4	2	0.234	0.019
IPR012295	Beta2-adaptin/TBP, C-terminal domain	4	2	0.234	0.019
IPR023115	Translation initiation factor IF- 2, domain 3	4	2	0.234	0.019
IPR001849	Pleckstrin homology domain	5	2	0.292	0.030
IPR018355	SPla/RYanodine receptor subgroup	6	2	0.350	0.044
00240	Pyrimidine metabolism	52	3	0.413	0.018