

Supplementary Table 1 – GO Term results: Gene ontology results obtained from PantherDB [32,33] for protein sequences containing conserved disordered-structured sites.

Supplementary table 1.

Sheet1

		Molecular Function		
#	GO Term	Count	% Proteins	% Terms
Homo sapiens				
1	binding (GO:0005488)	1127	34.40%	53.30%
2	catalytic activity (GO:0003824)	652	19.90%	30.80%
3	structural molecule activity (GO:0005198)	101	3.10%	4.80%
4	transporter activity (GO:0005215)	97	3.00%	4.60%
5	signal transducer activity (GO:0004871)	56	1.70%	2.60%
6	receptor activity (GO:0004872)	55	1.70%	2.60%
7	translation regulator activity (GO:0045182)	25	0.80%	1.20%
8	channel regulator activity (GO:0016247)	2	0.10%	0.10%
Arabidopsis thaliana				
1	binding (GO:0005488)	574	22.20%	43.00%
2	catalytic activity (GO:0003824)	527	20.40%	39.50%
3	structural molecule activity (GO:0005198)	114	4.40%	8.50%
4	transporter activity (GO:0005215)	44	1.70%	3.30%
5	translation regulator activity (GO:0045182)	38	1.50%	2.80%
6	receptor activity (GO:0004872)	15	0.60%	1.10%
7	signal transducer activity (GO:0004871)	12	0.50%	0.90%
8	antioxidant activity (GO:0016209)	11	0.40%	0.80%
Saccharomyces cerevisiae				
1	binding (GO:0005488)	274	31.50%	40.50%
2	catalytic activity (GO:0003824)	268	30.80%	39.60%
3	structural molecule activity (GO:0005198)	78	9.00%	11.50%
4	transporter activity (GO:0005215)	26	3.00%	3.80%
5	translation regulator activity (GO:0045182)	23	2.60%	3.40%
6	signal transducer activity (GO:0004871)	4	0.50%	0.60%
7	receptor activity (GO:0004872)	3	0.30%	0.40%
8	antioxidant activity (GO:0016209)	1	0.10%	0.10%
Plasmodium falciparum				
1	binding (GO:0005488)	157	29.50%	41.80%
2	catalytic activity (GO:0003824)	146	27.40%	38.80%
3	structural molecule activity (GO:0005198)	36	6.80%	9.60%
4	transporter activity (GO:0005215)	18	3.40%	4.80%
5	translation regulator activity (GO:0045182)	17	3.20%	4.50%
6	receptor activity (GO:0004872)	1	0.20%	0.30%
7	antioxidant activity (GO:0016209)	1	0.20%	0.30%

Supplementary table 1.

Biological Process			
#	GO Term	Count	% Proteins % Terms
Homo sapiens			
1	cellular process (GO:0009987)	1533	46.80% 30.10%
2	metabolic process (GO:0008152)	1218	37.20% 23.90%
3	cellular component organization or biogenesis (GO:0071840)	529	16.20% 10.40%
4	biological regulation (GO:0065007)	369	11.30% 7.20%
5	developmental process (GO:0032502)	362	11.10% 7.10%
6	localization (GO:0051179)	329	10.00% 6.50%
7	response to stimulus (GO:0050896)	314	9.60% 6.20%
8	multicellular organismal process (GO:0032501)	244	7.50% 4.80%
9	immune system process (GO:0002376)	64	2.00% 1.30%
10	biological adhesion (GO:0022610)	54	1.60% 1.10%
11	locomotion (GO:0040011)	42	1.30% 0.80%
12	reproduction (GO:0000003)	31	0.90% 0.60%
13	rhythmic process (GO:0048511)	5	0.20% 0.10%
14	growth (GO:0040007)	4	0.10% 0.10%
Arabidopsis thaliana			
1	metabolic process (GO:0008152)	903	34.90% 35.30%
2	cellular process (GO:0009987)	894	34.50% 34.90%
3	cellular component organization or biogenesis (GO:0071840)	294	11.40% 11.50%
4	localization (GO:0051179)	164	6.30% 6.40%
5	response to stimulus (GO:0050896)	134	5.20% 5.20%
6	biological regulation (GO:0065007)	104	4.00% 4.10%
7	developmental process (GO:0032502)	32	1.20% 1.30%
8	reproduction (GO:0000003)	20	0.80% 0.80%
9	multicellular organismal process (GO:0032501)	11	0.40% 0.40%
10	rhythmic process (GO:0048511)	2	0.10% 0.10%
Saccharomyces cerevisiae			
1	cellular process (GO:0009987)	478	54.90% 35.40%
2	metabolic process (GO:0008152)	434	49.80% 32.10%
3	cellular component organization or biogenesis (GO:0071840)	226	25.90% 16.70%
4	localization (GO:0051179)	95	10.90% 7.00%
5	response to stimulus (GO:0050896)	59	6.80% 4.40%
6	biological regulation (GO:0065007)	55	6.30% 4.10%
7	reproduction (GO:0000003)	4	0.50% 0.30%
8	developmental process (GO:0032502)	1	0.10% 0.10%
Plasmodium falciparum			
1	cellular process (GO:0009987)	275	51.60% 37.60%
2	metabolic process (GO:0008152)	251	47.10% 34.30%

Supplementary table 1.

Sheet1

3 cellular component organization or biogenesis (GO:0071840)	103	19.30%	14.10%
4 localization (GO:0051179)	54	10.10%	7.40%
5 response to stimulus (GO:0050896)	24	4.50%	3.30%
6 biological regulation (GO:0065007)	17	3.20%	2.30%
7 reproduction (GO:0000003)	4	0.80%	0.50%
8 locomotion (GO:0040011)	2	0.40%	0.30%
9 developmental process (GO:0032502)	1	0.20%	0.10%

Supplementary table 1.

Cellular Component				
#	GO Term	Count	% Proteins	% Terms
Homo sapiens				
1	cell part (GO:0044464)	1248	38.10%	38.90%
2	organelle (GO:0043226)	976	29.80%	30.40%
3	macromolecular complex (GO:0032991)	553	16.90%	17.20%
4	membrane (GO:0016020)	295	9.00%	9.20%
5	extracellular region (GO:0005576)	60	1.80%	1.90%
6	cell junction (GO:0030054)	31	0.90%	1.00%
7	synapse (GO:0045202)	29	0.90%	0.90%
8	extracellular matrix (GO:0031012)	16	0.50%	0.50%
Arabidopsis thaliana				
1	cell part (GO:0044464)	936	36.20%	42.00%
2	organelle (GO:0043226)	712	27.50%	32.00%
3	macromolecular complex (GO:0032991)	450	17.40%	20.20%
4	membrane (GO:0016020)	118	4.60%	5.30%
5	extracellular region (GO:0005576)	9	0.30%	0.40%
6	nucleoid (GO:0009295)	1	0.00%	0.00%
7	cell junction (GO:0030054)	1	0.00%	0.00%
Saccharomyces cerevisiae				
1	cell part (GO:0044464)	484	55.60%	40.20%
2	organelle (GO:0043226)	365	41.90%	30.30%
3	macromolecular complex (GO:0032991)	294	33.80%	24.40%
4	membrane (GO:0016020)	61	7.00%	5.10%
5	extracellular region (GO:0005576)	1	0.10%	0.10%
Plasmodium falciparum				
1	cell part (GO:0044464)	243	45.60%	39.60%
2	organelle (GO:0043226)	189	35.50%	30.80%
3	macromolecular complex (GO:0032991)	152	28.50%	24.80%
4	membrane (GO:0016020)	27	5.10%	4.40%
5	extracellular region (GO:0005576)	3	0.60%	0.50%

Supplementary table 1.

Protein Class				
#	GO Term	Count	% Proteins	% Terms
Homo sapiens				
1	nucleic acid binding (PC00171)	529	16.20%	24.30%
2	transcription factor (PC00218)	367	11.20%	16.90%
3	hydrolase (PC00121)	209	6.40%	9.60%
4	enzyme modulator (PC00095)	178	5.40%	8.20%
5	cytoskeletal protein (PC00085)	129	3.90%	5.90%
6	transferase (PC00220)	122	3.70%	5.60%
7	membrane traffic protein (PC00150)	87	2.70%	4.00%
8	signaling molecule (PC00207)	79	2.40%	3.60%
9	transporter (PC00227)	55	1.70%	2.50%
10	receptor (PC00197)	53	1.60%	2.40%
11	ligase (PC00142)	47	1.40%	2.20%
12	transfer/carrier protein (PC00219)	45	1.40%	2.10%
13	calcium-binding protein (PC00060)	40	1.20%	1.80%
14	chaperone (PC00072)	31	0.90%	1.40%
15	oxidoreductase (PC00176)	29	0.90%	1.30%
16	cell adhesion molecule (PC00069)	29	0.90%	1.30%
17	transmembrane receptor regulatory/adaptor protein (PC00217)	27	0.80%	1.20%
18	defense/immunity protein (PC00090)	26	0.80%	1.20%
19	cell junction protein (PC00070)	26	0.80%	1.20%
20	extracellular matrix protein (PC00102)	22	0.70%	1.00%
21	structural protein (PC00211)	16	0.50%	0.70%
22	isomerase (PC00135)	15	0.50%	0.70%
23	lyase (PC00144)	11	0.30%	0.50%
24	viral protein (PC00237)	1	0.00%	0.00%
25	surfactant (PC00212)	1	0.00%	0.00%
Arabidopsis thaliana				
1	nucleic acid binding (PC00171)	403	15.60%	32.10%
2	hydrolase (PC00121)	175	6.80%	13.90%
3	transferase (PC00220)	112	4.30%	8.90%
4	transcription factor (PC00218)	97	3.70%	7.70%
5	oxidoreductase (PC00176)	64	2.50%	5.10%
6	enzyme modulator (PC00095)	63	2.40%	5.00%
7	cytoskeletal protein (PC00085)	56	2.20%	4.50%
8	transporter (PC00227)	45	1.70%	3.60%
9	membrane traffic protein (PC00150)	41	1.60%	3.30%
10	lyase (PC00144)	39	1.50%	3.10%
11	ligase (PC00142)	36	1.40%	2.90%

Supplementary table 1.

12 isomerase (PC00135)	30	1.20%	2.40%
13 chaperone (PC00072)	22	0.90%	1.80%
14 transfer/carrier protein (PC00219)	19	0.70%	1.50%
15 calcium-binding protein (PC00060)	17	0.70%	1.40%
16 defense/immunity protein (PC00090)	7	0.30%	0.60%
17 signaling molecule (PC00207)	6	0.20%	0.50%
18 structural protein (PC00211)	6	0.20%	0.50%
19 receptor (PC00197)	6	0.20%	0.50%
20 extracellular matrix protein (PC00102)	3	0.10%	0.20%
21 transmembrane receptor regulatory/adaptor protein (PC00021)	3	0.10%	0.20%
22 cell adhesion molecule (PC00069)	3	0.10%	0.20%
23 storage protein (PC00210)	2	0.10%	0.20%
Saccharomyces cerevisiae			
1 nucleic acid binding (PC00171)	227	26.10%	37.50%
2 hydrolase (PC00121)	68	7.80%	11.20%
3 transferase (PC00220)	50	5.70%	8.30%
4 enzyme modulator (PC00095)	44	5.10%	7.30%
5 transcription factor (PC00218)	39	4.50%	6.40%
6 transporter (PC00227)	25	2.90%	4.10%
7 ligase (PC00142)	23	2.60%	3.80%
8 membrane traffic protein (PC00150)	22	2.50%	3.60%
9 cytoskeletal protein (PC00085)	20	2.30%	3.30%
10 oxidoreductase (PC00176)	20	2.30%	3.30%
11 lyase (PC00144)	14	1.60%	2.30%
12 transfer/carrier protein (PC00219)	13	1.50%	2.10%
13 chaperone (PC00072)	10	1.10%	1.70%
14 calcium-binding protein (PC00060)	7	0.80%	1.20%
15 isomerase (PC00135)	7	0.80%	1.20%
16 signaling molecule (PC00207)	5	0.60%	0.80%
17 cell junction protein (PC00070)	4	0.50%	0.70%
18 receptor (PC00197)	4	0.50%	0.70%
19 defense/immunity protein (PC00090)	1	0.10%	0.20%
20 structural protein (PC00211)	1	0.10%	0.20%
21 storage protein (PC00210)	1	0.10%	0.20%
Plasmodium falciparum			
1 nucleic acid binding (PC00171)	143	26.80%	37.40%
2 hydrolase (PC00121)	48	9.00%	12.60%
3 enzyme modulator (PC00095)	34	6.40%	8.90%
4 transferase (PC00220)	28	5.30%	7.30%
5 cytoskeletal protein (PC00085)	18	3.40%	4.70%

Supplementary table 1.

Sheet1

6 ligase (PC00142)	17	3.20%	4.50%
7 membrane traffic protein (PC00150)	15	2.80%	3.90%
8 transporter (PC00227)	14	2.60%	3.70%
9 transcription factor (PC00218)	13	2.40%	3.40%
10 calcium-binding protein (PC00060)	8	1.50%	2.10%
11 transfer/carrier protein (PC00219)	8	1.50%	2.10%
12 chaperone (PC00072)	8	1.50%	2.10%
13 isomerase (PC00135)	8	1.50%	2.10%
14 oxidoreductase (PC00176)	5	0.90%	1.30%
15 lyase (PC00144)	3	0.60%	0.80%
16 extracellular matrix protein (PC00102)	2	0.40%	0.50%
17 signaling molecule (PC00207)	2	0.40%	0.50%
18 cell junction protein (PC00070)	2	0.40%	0.50%
19 structural protein (PC00211)	2	0.40%	0.50%
20 receptor (PC00197)	2	0.40%	0.50%
21 transmembrane receptor regulatory/adaptor protein (PC00090)	1	0.20%	0.30%
22 defense/immunity protein (PC00090)	1	0.20%	0.30%

Supplementary table 1.

#	GO Term	Pathway	Count	% Proteins	% Term
Homo sapiens					
1	Wnt signaling pathway (P00057)		75	2.30%	6.90%
2	Gonadotropin-releasing hormone receptor pathway (P06664)		64	2.00%	5.90%
3	Integrin signalling pathway (P00034)		40	1.20%	3.70%
4	PDGF signaling pathway (P00047)		38	1.20%	3.50%
5	CCKR signaling map (P06959)		37	1.10%	3.40%
6	Inflammation mediated by chemokine and cytokine signaling pathway (P00031)		36	1.10%	3.30%
7	Angiogenesis (P00005)		35	1.10%	3.20%
8	Alzheimer disease-presenilin pathway (P00004)		30	0.90%	2.80%
9	Cadherin signaling pathway (P00012)		30	0.90%	2.80%
10	Huntington disease (P00029)		26	0.80%	2.40%
11	FGF signaling pathway (P00021)		25	0.80%	2.30%
12	EGF receptor signaling pathway (P00018)		25	0.80%	2.30%
13	Apoptosis signaling pathway (P00006)		23	0.70%	2.10%
14	Transcription regulation by bZIP transcription factor (P00055)		20	0.60%	1.90%
15	TGF-beta signaling pathway (P00052)		20	0.60%	1.90%
16	Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway (P00017)		18	0.50%	1.70%
17	T cell activation (P00053)		17	0.50%	1.60%
18	Cytoskeletal regulation by Rho GTPase (P00016)		17	0.50%	1.60%
19	p53 pathway (P00059)		16	0.50%	1.50%
20	Parkinson disease (P00049)		16	0.50%	1.50%
21	General transcription regulation (P00023)		15	0.50%	1.40%
22	Endothelin signaling pathway (P00019)		15	0.50%	1.40%
23	B cell activation (P00010)		15	0.50%	1.40%
24	VEGF signaling pathway (P00056)		14	0.40%	1.30%
25	Interleukin signaling pathway (P00036)		14	0.40%	1.30%
26	Alzheimer disease-amyloid secretase pathway (P00003)		13	0.40%	1.20%
27	p53 pathway feedback loops 2 (P04398)		13	0.40%	1.20%
28	Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway (P00018)		13	0.40%	1.20%
29	Toll receptor signaling pathway (P00054)		12	0.40%	1.10%
30	Nicotinic acetylcholine receptor signaling pathway (P00044)		12	0.40%	1.10%
31	Ras Pathway (P04393)		11	0.30%	1.00%
32	Muscarinic acetylcholine receptor 1 and 3 signaling pathway (P00042)		10	0.30%	0.90%
33	Insulin/IGF pathway-protein kinase B signaling cascade (P00033)		10	0.30%	0.90%
34	Axon guidance mediated by netrin (P00009)		9	0.30%	0.80%
35	Ubiquitin proteasome pathway (P00060)		9	0.30%	0.80%
36	Hypoxia response via HIF activation (P00030)		9	0.30%	0.80%
37	5HT2 type receptor mediated signaling pathway (P04374)		9	0.30%	0.80%

Supplementary table 1.

38 Oxidative stress response (P00046)	8	0.20%	0.70%
39 Notch signaling pathway (P00045)	8	0.20%	0.70%
40 Thyrotropin-releasing hormone receptor signaling pathway (P04394)	8	0.20%	0.70%
41 p38 MAPK pathway (P05918)	8	0.20%	0.70%
42 DNA replication (P00017)	8	0.20%	0.70%
43 Synaptic vesicle trafficking (P05734)	7	0.20%	0.60%
44 Ionotropic glutamate receptor pathway (P00037)	7	0.20%	0.60%
45 Interferon-gamma signaling pathway (P00035)	7	0.20%	0.60%
46 Oxytocin receptor mediated signaling pathway (P04391)	7	0.20%	0.60%
47 Histamine H1 receptor mediated signaling pathway (P04385)	7	0.20%	0.60%
48 PI3 kinase pathway (P00048)	6	0.20%	0.60%
49 Hedgehog signaling pathway (P00025)	6	0.20%	0.60%
50 Angiotensin II-stimulated signaling through G proteins and beta-arrestin (P05911)	6	0.20%	0.60%
51 Circadian clock system (P00015)	6	0.20%	0.60%
52 Cell cycle (P00013)	6	0.20%	0.60%
53 Axon guidance mediated by Slit/Robo (P00008)	5	0.20%	0.50%
54 Alpha adrenergic receptor signaling pathway (P00002)	5	0.20%	0.50%
55 mRNA splicing (P00058)	5	0.20%	0.50%
56 GABA-B receptor II signaling (P05731)	5	0.20%	0.50%
57 Insulin/IGF pathway-mitogen activated protein kinase kinase/MAP kinase cascade (P0003)	5	0.20%	0.50%
58 Nicotine pharmacodynamics pathway (P06587)	5	0.20%	0.50%
59 Blood coagulation (P00011)	5	0.20%	0.50%
60 Beta2 adrenergic receptor signaling pathway (P04378)	5	0.20%	0.50%
61 Beta1 adrenergic receptor signaling pathway (P04377)	5	0.20%	0.50%
62 TCA cycle (P00051)	4	0.10%	0.40%
63 De novo pyrimidine ribonucleotides biosynthesis (P02740)	4	0.10%	0.40%
64 Metabotropic glutamate receptor group II pathway (P00040)	4	0.10%	0.40%
65 Metabotropic glutamate receptor group III pathway (P00039)	4	0.10%	0.40%
66 Vasopressin synthesis (P04395)	4	0.10%	0.40%
67 P53 pathway feedback loops 1 (P04392)	4	0.10%	0.40%
68 Opioid proopiomelanocortin pathway (P05917)	4	0.10%	0.40%
69 Opioid proenkephalin pathway (P05915)	4	0.10%	0.40%
70 Dopamine receptor mediated signaling pathway (P05912)	4	0.10%	0.40%
71 Adrenaline and noradrenaline biosynthesis (P00001)	3	0.10%	0.30%
72 Heme biosynthesis (P02746)	3	0.10%	0.30%
73 Plasminogen activating cascade (P00050)	3	0.10%	0.30%
74 Muscarinic acetylcholine receptor 2 and 4 signaling pathway (P00043)	3	0.10%	0.30%
75 Metabotropic glutamate receptor group I pathway (P00041)	3	0.10%	0.30%
76 Endogenous cannabinoid signaling (P05730)	3	0.10%	0.30%
77 JAK/STAT signaling pathway (P00038)	3	0.10%	0.30%

Supplementary table 1.

78 p53 pathway by glucose deprivation (P04397)	3	0.10%	0.30%
79 General transcription by RNA polymerase I (P00022)	3	0.10%	0.30%
80 Pyruvate metabolism (P02772)	3	0.10%	0.30%
81 Corticotropin releasing factor receptor signaling pathway (P04380)	3	0.10%	0.30%
82 5HT4 type receptor mediated signaling pathway (P04376)	3	0.10%	0.30%
83 5HT3 type receptor mediated signaling pathway (P04375)	3	0.10%	0.30%
84 5HT1 type receptor mediated signaling pathway (P04373)	3	0.10%	0.30%
85 Axon guidance mediated by semaphorins (P00007)	2	0.10%	0.20%
86 Methylmalonyl pathway (P02755)	2	0.10%	0.20%
87 Isoleucine biosynthesis (P02748)	2	0.10%	0.20%
88 De novo purine biosynthesis (P02738)	2	0.10%	0.20%
89 ATP synthesis (P02721)	2	0.10%	0.20%
90 Vitamin D metabolism and pathway (P04396)	2	0.10%	0.20%
91 Glycolysis (P00024)	2	0.10%	0.20%
92 Succinate to proprionate conversion (P02777)	2	0.10%	0.20%
93 FAS signaling pathway (P00020)	2	0.10%	0.20%
94 5-Hydroxytryptamine degradation (P04372)	2	0.10%	0.20%
95 SCW signaling pathway (P06216)	1	0.00%	0.10%
96 GBB signaling pathway (P06214)	1	0.00%	0.10%
97 DPP signaling pathway (P06213)	1	0.00%	0.10%
98 DPP-SCW signaling pathway (P06212)	1	0.00%	0.10%
99 BMP/activin signaling pathway-drosophila (P06211)	1	0.00%	0.10%
100 Pyridoxal-5-phosphate biosynthesis (P02759)	1	0.00%	0.10%
101 Mannose metabolism (P02752)	1	0.00%	0.10%
102 Lipoate_biosynthesis (P02750)	1	0.00%	0.10%
103 Fructose galactose metabolism (P02744)	1	0.00%	0.10%
104 De novo pyrimidine deoxyribonucleotide biosynthesis (P02739)	1	0.00%	0.10%
105 Cysteine biosynthesis (P02737)	1	0.00%	0.10%
106 Arginine biosynthesis (P02728)	1	0.00%	0.10%
107 Vitamin B6 metabolism (P02787)	1	0.00%	0.10%
108 Valine biosynthesis (P02785)	1	0.00%	0.10%
109 Anandamide degradation (P05728)	1	0.00%	0.10%
110 Opioid prodynorphin pathway (P05916)	1	0.00%	0.10%
111 Salvage pyrimidine ribonucleotides (P02775)	1	0.00%	0.10%
112 Enkephalin release (P05913)	1	0.00%	0.10%
113 Pyridoxal phosphate salvage pathway (P02770)	1	0.00%	0.10%
114 Proline biosynthesis (P02768)	1	0.00%	0.10%
115 Beta3 adrenergic receptor signaling pathway (P04379)	1	0.00%	0.10%
116 Pentose phosphate pathway (P02762)	1	0.00%	0.10%

Arabidopsis thaliana

Supplementary table 1.

1 General transcription regulation (P00023)	17	0.70%	5.50%
2 Transcription regulation by bZIP transcription factor (P00055)	16	0.60%	5.20%
3 Ubiquitin proteasome pathway (P00060)	10	0.40%	3.30%
4 Huntington disease (P00029)	9	0.30%	2.90%
5 PDGF signaling pathway (P00047)	8	0.30%	2.60%
6 DNA replication (P00017)	8	0.30%	2.60%
7 Wnt signaling pathway (P00057)	7	0.30%	2.30%
8 Parkinson disease (P00049)	7	0.30%	2.30%
9 De novo purine biosynthesis (P02738)	7	0.30%	2.30%
10 Nicotinic acetylcholine receptor signaling pathway (P00044)	7	0.30%	2.30%
11 Ras Pathway (P04393)	7	0.30%	2.30%
12 EGF receptor signaling pathway (P00018)	7	0.30%	2.30%
13 Adrenaline and noradrenaline biosynthesis (P00001)	6	0.20%	2.00%
14 Histidine biosynthesis (P02747)	6	0.20%	2.00%
15 Heme biosynthesis (P02746)	6	0.20%	2.00%
16 Muscarinic acetylcholine receptor 2 and 4 signaling pathway (P00043)	6	0.20%	2.00%
17 Insulin/IGF pathway-mitogen activated protein kinase kinase/MAP kinase cascade (P0003)	6	0.20%	2.00%
18 Gonadotropin-releasing hormone receptor pathway (P06664)	5	0.20%	1.60%
19 Interleukin signaling pathway (P00036)	5	0.20%	1.60%
20 Inflammation mediated by chemokine and cytokine signaling pathway (P00031)	5	0.20%	1.60%
21 TCA cycle (P00051)	4	0.20%	1.30%
22 Oxidative stress response (P00046)	4	0.20%	1.30%
23 Ionotropic glutamate receptor pathway (P00037)	4	0.20%	1.30%
24 Tryptophan biosynthesis (P02783)	4	0.20%	1.30%
25 FGF signaling pathway (P00021)	4	0.20%	1.30%
26 FAS signaling pathway (P00020)	4	0.20%	1.30%
27 S-adenosylmethionine biosynthesis (P02773)	4	0.20%	1.30%
28 p53 pathway (P00059)	3	0.10%	1.00%
29 De novo pyrimidine ribonucleotides biosynthesis (P02740)	3	0.10%	1.00%
30 Muscarinic acetylcholine receptor 1 and 3 signaling pathway (P00042)	3	0.10%	1.00%
31 Metabotropic glutamate receptor group II pathway (P00040)	3	0.10%	1.00%
32 Arginine biosynthesis (P02728)	3	0.10%	1.00%
33 Metabotropic glutamate receptor group III pathway (P00039)	3	0.10%	1.00%
34 Integrin signalling pathway (P00034)	3	0.10%	1.00%
35 Thyrotropin-releasing hormone receptor signaling pathway (P04394)	3	0.10%	1.00%
36 Oxytocin receptor mediated signaling pathway (P04391)	3	0.10%	1.00%
37 p38 MAPK pathway (P05918)	3	0.10%	1.00%
38 Opioid proopiomelanocortin pathway (P05917)	3	0.10%	1.00%
39 Opioid prodynorphin pathway (P05916)	3	0.10%	1.00%
40 Opioid proenkephalin pathway (P05915)	3	0.10%	1.00%

Supplementary table 1.

41 Dopamine receptor mediated signaling pathway (P05912)	3	0.10%	1.00%
42 Pyruvate metabolism (P02772)	3	0.10%	1.00%
43 Corticotropin releasing factor receptor signaling pathway (P04380)	3	0.10%	1.00%
44 Beta3 adrenergic receptor signaling pathway (P04379)	3	0.10%	1.00%
45 Beta2 adrenergic receptor signaling pathway (P04378)	3	0.10%	1.00%
46 Beta1 adrenergic receptor signaling pathway (P04377)	3	0.10%	1.00%
47 5HT4 type receptor mediated signaling pathway (P04376)	3	0.10%	1.00%
48 5HT3 type receptor mediated signaling pathway (P04375)	3	0.10%	1.00%
49 5HT2 type receptor mediated signaling pathway (P04374)	3	0.10%	1.00%
50 5HT1 type receptor mediated signaling pathway (P04373)	3	0.10%	1.00%
51 Apoptosis signaling pathway (P00006)	2	0.10%	0.70%
52 O-antigen biosynthesis (P02757)	2	0.10%	0.70%
53 Methionine biosynthesis (P02753)	2	0.10%	0.70%
54 CCKR signaling map (P06959)	2	0.10%	0.70%
55 Lysine biosynthesis (P02751)	2	0.10%	0.70%
56 Fructose galactose metabolism (P02744)	2	0.10%	0.70%
57 TGF-beta signaling pathway (P00052)	2	0.10%	0.70%
58 PI3 kinase pathway (P00048)	2	0.10%	0.70%
59 Adenine and hypoxanthine salvage pathway (P02723)	2	0.10%	0.70%
60 Insulin/IGF pathway-protein kinase B signaling cascade (P00033)	2	0.10%	0.70%
61 p53 pathway feedback loops 2 (P04398)	2	0.10%	0.70%
62 Vitamin D metabolism and pathway (P04396)	2	0.10%	0.70%
63 General transcription by RNA polymerase I (P00022)	2	0.10%	0.70%
64 Pentose phosphate pathway (P02762)	2	0.10%	0.70%
65 Pyridoxal-5-phosphate biosynthesis (P02759)	1	0.00%	0.30%
66 N-acetylglucosamine metabolism (P02756)	1	0.00%	0.30%
67 Methylmalonyl pathway (P02755)	1	0.00%	0.30%
68 Isoleucine biosynthesis (P02748)	1	0.00%	0.30%
69 mRNA splicing (P00058)	1	0.00%	0.30%
70 Glutamine glutamate conversion (P02745)	1	0.00%	0.30%
71 Notch signaling pathway (P00045)	1	0.00%	0.30%
72 Chorismate biosynthesis (P02734)	1	0.00%	0.30%
73 Biotin biosynthesis (P02731)	1	0.00%	0.30%
74 Synaptic vesicle trafficking (P05734)	1	0.00%	0.30%
75 Ascorbate degradation (P02729)	1	0.00%	0.30%
76 Allantoin degradation (P02725)	1	0.00%	0.30%
77 Interferon-gamma signaling pathway (P00035)	1	0.00%	0.30%
78 Vitamin B6 metabolism (P02787)	1	0.00%	0.30%
79 Valine biosynthesis (P02785)	1	0.00%	0.30%
80 Hypoxia response via HIF activation (P00030)	1	0.00%	0.30%

Supplementary table 1.

81 Hedgehog signaling pathway (P00025)	1	0.00%	0.30%
82 Succinate to propionate conversion (P02777)	1	0.00%	0.30%
83 Serine glycine biosynthesis (P02776)	1	0.00%	0.30%
84 Salvage pyrimidine ribonucleotides (P02775)	1	0.00%	0.30%
85 Pyrimidine Metabolism (P02771)	1	0.00%	0.30%
86 Pyridoxal phosphate salvage pathway (P02770)	1	0.00%	0.30%
87 Circadian clock system (P00015)	1	0.00%	0.30%
88 Cell cycle (P00013)	1	0.00%	0.30%
89 Phenylethylamine degradation (P02766)	1	0.00%	0.30%
90 Peptidoglycan biosynthesis (P02763)	1	0.00%	0.30%
91 5-Hydroxytryptamine degradation (P04372)	1	0.00%	0.30%
Saccharomyces cerevisiae			
1 Transcription regulation by bZIP transcription factor (P00055)	16	1.80%	8.00%
2 General transcription regulation (P00023)	15	1.70%	7.50%
3 Parkinson disease (P00049)	14	1.60%	7.00%
4 Ubiquitin proteasome pathway (P00060)	13	1.50%	6.50%
5 Apoptosis signaling pathway (P00006)	10	1.10%	5.00%
6 Wnt signaling pathway (P00057)	10	1.10%	5.00%
7 Nicotinic acetylcholine receptor signaling pathway (P00044)	7	0.80%	3.50%
8 Glycolysis (P00024)	6	0.70%	3.00%
9 De novo purine biosynthesis (P02738)	5	0.60%	2.50%
10 TCA cycle (P00051)	4	0.50%	2.00%
11 EGF receptor signaling pathway (P00018)	4	0.50%	2.00%
12 DNA replication (P00017)	4	0.50%	2.00%
13 Isoleucine biosynthesis (P02748)	3	0.30%	1.50%
14 Heme biosynthesis (P02746)	3	0.30%	1.50%
15 PDGF signaling pathway (P00047)	3	0.30%	1.50%
16 Muscarinic acetylcholine receptor 2 and 4 signaling pathway (P00043)	3	0.30%	1.50%
17 Muscarinic acetylcholine receptor 1 and 3 signaling pathway (P00042)	3	0.30%	1.50%
18 Metabotropic glutamate receptor group II pathway (P00040)	3	0.30%	1.50%
19 ATP synthesis (P02721)	3	0.30%	1.50%
20 Valine biosynthesis (P02785)	3	0.30%	1.50%
21 Huntington disease (P00029)	3	0.30%	1.50%
22 FGF signaling pathway (P00021)	3	0.30%	1.50%
23 CCKR signaling map (P06959)	2	0.20%	1.00%
24 Leucine biosynthesis (P02749)	2	0.20%	1.00%
25 Toll receptor signaling pathway (P00054)	2	0.20%	1.00%
26 De novo pyrimidine ribonucleotides biosynthesis (P02740)	2	0.20%	1.00%
27 Arginine biosynthesis (P02728)	2	0.20%	1.00%
28 Tryptophan biosynthesis (P02783)	2	0.20%	1.00%

Supplementary table 1.

29 Endothelin signaling pathway (P00019)	2	0.20%	1.00%
30 Cell cycle (P00013)	2	0.20%	1.00%
31 B cell activation (P00010)	2	0.20%	1.00%
32 Pentose phosphate pathway (P02762)	2	0.20%	1.00%
33 SCW signaling pathway (P06216)	1	0.10%	0.50%
34 GBB signaling pathway (P06214)	1	0.10%	0.50%
35 DPP signaling pathway (P06213)	1	0.10%	0.50%
36 DPP-SCW signaling pathway (P06212)	1	0.10%	0.50%
37 BMP/activin signaling pathway-drosophila (P06211)	1	0.10%	0.50%
38 Gonadotropin-releasing hormone receptor pathway (P06664)	1	0.10%	0.50%
39 Pyridoxal-5-phosphate biosynthesis (P02759)	1	0.10%	0.50%
40 Angiogenesis (P00005)	1	0.10%	0.50%
41 Alzheimer disease-amyloid secretase pathway (P00003)	1	0.10%	0.50%
42 Mannose metabolism (P02752)	1	0.10%	0.50%
43 Lipoate_biosynthesis (P02750)	1	0.10%	0.50%
44 p53 pathway (P00059)	1	0.10%	0.50%
45 mRNA splicing (P00058)	1	0.10%	0.50%
46 Histidine biosynthesis (P02747)	1	0.10%	0.50%
47 VEGF signaling pathway (P00056)	1	0.10%	0.50%
48 Tetrahydrofolate biosynthesis (P02742)	1	0.10%	0.50%
49 TGF-beta signaling pathway (P00052)	1	0.10%	0.50%
50 Cysteine biosynthesis (P02737)	1	0.10%	0.50%
51 Notch signaling pathway (P00045)	1	0.10%	0.50%
52 Chorismate biosynthesis (P02734)	1	0.10%	0.50%
53 Synaptic vesicle trafficking (P05734)	1	0.10%	0.50%
54 Metabotropic glutamate receptor group III pathway (P00039)	1	0.10%	0.50%
55 Ionotropic glutamate receptor pathway (P00037)	1	0.10%	0.50%
56 Vitamin B6 metabolism (P02787)	1	0.10%	0.50%
57 Inflammation mediated by chemokine and cytokine signaling pathway (P00031)	1	0.10%	0.50%
58 Thyrotropin-releasing hormone receptor signaling pathway (P04394)	1	0.10%	0.50%
59 Oxytocin receptor mediated signaling pathway (P04391)	1	0.10%	0.50%
60 Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway (P00030)	1	0.10%	0.50%
61 Hedgehog signaling pathway (P00025)	1	0.10%	0.50%
62 Sulfate assimilation (P02778)	1	0.10%	0.50%
63 General transcription by RNA polymerase I (P00022)	1	0.10%	0.50%
64 Enkephalin release (P05913)	1	0.10%	0.50%
65 Dopamine receptor mediated signaling pathway (P05912)	1	0.10%	0.50%
66 FAS signaling pathway (P00020)	1	0.10%	0.50%
67 Histamine H2 receptor mediated signaling pathway (P04386)	1	0.10%	0.50%
68 Pyruvate metabolism (P02772)	1	0.10%	0.50%

Supplementary table 1.

69 Histamine H1 receptor mediated signaling pathway (P04385)	1	0.10%	0.50%
70 Pyridoxal phosphate salvage pathway (P02770)	1	0.10%	0.50%
71 Purine metabolism (P02769)	1	0.10%	0.50%
72 Beta2 adrenergic receptor signaling pathway (P04378)	1	0.10%	0.50%
73 Beta1 adrenergic receptor signaling pathway (P04377)	1	0.10%	0.50%
74 5HT2 type receptor mediated signaling pathway (P04374)	1	0.10%	0.50%
75 5HT1 type receptor mediated signaling pathway (P04373)	1	0.10%	0.50%
Plasmodium falciparum			
1 Ubiquitin proteasome pathway (P00060)	8	1.50%	#####
2 Huntington disease (P00029)	5	0.90%	6.30%
3 Transcription regulation by bZIP transcription factor (P00055)	4	0.80%	5.10%
4 General transcription regulation (P00023)	4	0.80%	5.10%
5 DNA replication (P00017)	4	0.80%	5.10%
6 Parkinson disease (P00049)	4	0.80%	5.10%
7 Wnt signaling pathway (P00057)	3	0.60%	3.80%
8 Nicotinic acetylcholine receptor signaling pathway (P00044)	3	0.60%	3.80%
9 p53 pathway (P00059)	2	0.40%	2.50%
10 mRNA splicing (P00058)	2	0.40%	2.50%
11 General transcription by RNA polymerase I (P00022)	2	0.40%	2.50%
12 Methylcitrate cycle (P02754)	2	0.40%	2.50%
13 Tryptophan biosynthesis (P02783)	2	0.40%	2.50%
14 CCKR signaling map (P06959)	2	0.40%	2.50%
15 De novo pyrimidine ribonucleotides biosynthesis (P02740)	2	0.40%	2.50%
16 Pyruvate metabolism (P02772)	2	0.40%	2.50%
17 Gonadotropin-releasing hormone receptor pathway (P06664)	2	0.40%	2.50%
18 De novo purine biosynthesis (P02738)	1	0.20%	1.30%
19 Purine metabolism (P02769)	1	0.20%	1.30%
20 Alzheimer disease-presenilin pathway (P00004)	1	0.20%	1.30%
21 Interleukin signaling pathway (P00036)	1	0.20%	1.30%
22 Alzheimer disease-amyloid secretase pathway (P00003)	1	0.20%	1.30%
23 Adrenaline and noradrenaline biosynthesis (P00001)	1	0.20%	1.30%
24 Insulin/IGF pathway-protein kinase B signaling cascade (P00033)	1	0.20%	1.30%
25 Inflammation mediated by chemokine and cytokine signaling pathway (P00031)	1	0.20%	1.30%
26 p53 pathway feedback loops 2 (P04398)	1	0.20%	1.30%
27 Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway (P00032)	1	0.20%	1.30%
28 Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway (P00030)	1	0.20%	1.30%
29 Vitamin D metabolism and pathway (P04396)	1	0.20%	1.30%
30 Ras Pathway (P04393)	1	0.20%	1.30%
31 FGF signaling pathway (P00021)	1	0.20%	1.30%
32 FAS signaling pathway (P00020)	1	0.20%	1.30%

Supplementary table 1.

33 ATP synthesis (P02721)	1	0.20%	1.30%
34 TCA cycle (P00051)	1	0.20%	1.30%
35 Endothelin signaling pathway (P00019)	1	0.20%	1.30%
36 EGF receptor signaling pathway (P00018)	1	0.20%	1.30%
37 PI3 kinase pathway (P00048)	1	0.20%	1.30%
38 PDGF signaling pathway (P00047)	1	0.20%	1.30%
39 Heme biosynthesis (P02746)	1	0.20%	1.30%
40 Cell cycle (P00013)	1	0.20%	1.30%
41 Cadherin signaling pathway (P00012)	1	0.20%	1.30%
42 Muscarinic acetylcholine receptor 2 and 4 signaling pathway (P00043)	1	0.20%	1.30%
43 Salvage pyrimidine ribonucleotides (P02775)	1	0.20%	1.30%