

Additional File 5: Table S4. Genes overrepresented in the ferret brain. Ontology analysis of genes that are at least twofold higher expressed in the visual cortex of the ferret compared to the hooded seal visual cortex. A. The GO terms for the domains "molecular function" and "biological process", and the "protein class" are given. B and C. PANTHER Overrepresentation Test of the domains "molecular function", "biological process", and "protein class" using the complete (B) and PANTHER GO-slim terms.

A	Category name	Accession	number of genes	Percent of gene hit against total	Function hits
Molecular function					
1	protein binding transcription factor	(GO:0000988)	9	0.80%	0.80%
2	nucleic acid binding transcription factor	(GO:0001071)	44	3.70%	4.10%
3	catalytic activity	(GO:0003824)	374	31.60%	34.80%
4	receptor	(GO:0004872)	41	3.50%	3.80%
5	structural molecule	(GO:0005198)	103	8.70%	9.60%
6	transporter	(GO:0005215)	68	5.70%	6.30%
7	binding	(GO:0005488)	351	29.70%	32.60%
8	antioxidant	(GO:0016209)	4	0.30%	0.40%
9	channel regulator	(GO:0016247)	1	0.10%	0.10%
10	enzyme regulator	(GO:0030234)	63	5.30%	5.90%
11	translation regulator	(GO:0045182)	18	1.50%	1.70%
Biological process					
1	cellular component organization or biogenesis	(GO:0071840)	107	9.00%	6.00%
2	cellular process	(GO:0009987)	384	32.50%	21.40%
3	localization	(GO:0051179)	188	15.90%	10.50%
4	apoptotic process	(GO:0006915)	23	1.90%	1.30%
5	reproduction	(GO:0000003)	16	1.40%	0.90%
6	biological regulation	(GO:0065007)	191	16.10%	10.60%
7	response to stimulus	(GO:0050896)	68	5.70%	3.80%
8	developmental process	(GO:0032502)	95	8.00%	5.30%
9	multicellular organismal process	(GO:0032501)	83	7.00%	4.60%
10	locomotion	(GO:0040011)	1	0.10%	0.10%
11	biological adhesion	(GO:0022610)	21	1.80%	1.20%
12	metabolic process	(GO:0008152)	575	48.60%	32.00%
13	growth	(GO:0040007)	2	0.20%	0.10%
14	immune system process	(GO:0002376)	44	3.70%	2.40%
Protein class					
1	extracellular matrix protein	(PC00102)	7	0.60%	0.70%
2	protease	(PC00190)	16	1.40%	1.50%
3	cytoskeletal protein	(PC00085)	41	3.50%	3.90%

4	transporter	(PC00227)	66	5.60%	6.30%
5	transmembrane receptor regulatory/adaptor protein	(PC00226)	5	0.40%	0.50%
6	transferase	(PC00220)	83	7.00%	7.90%
7	oxidoreductase	(PC00176)	62	5.20%	5.90%
8	lyase	(PC00144)	10	0.80%	1.00%
9	cell adhesion molecule	(PC00069)	11	0.90%	1.00%
10	ligase	(PC00142)	26	2.20%	2.50%
11	nucleic acid binding	(PC00171)	181	15.30%	17.30%
12	signaling molecule	(PC00207)	44	3.70%	4.20%
13	enzyme modulator	(PC00095)	86	7.30%	8.20%
14	calcium-binding protein	(PC00060)	37	3.10%	3.50%
15	defense/immunity protein	(PC00090)	8	0.70%	0.80%
16	hydrolase	(PC00121)	75	6.30%	7.10%
17	transfer/carrier protein	(PC00219)	33	2.80%	3.10%
18	membrane traffic protein	(PC00150)	58	4.90%	5.50%
19	phosphatase	(PC00181)	17	1.40%	1.60%
20	transcription factor	(PC00218)	47	4.00%	4.50%
21	chaperone	(PC00072)	27	2.30%	2.60%
22	cell junction protein	(PC00070)	4	0.30%	0.40%
23	surfactant	(PC00212)	2	0.20%	0.20%
24	structural protein	(PC00211)	2	0.20%	0.20%
25	kinase	(PC00137)	41	3.50%	3.90%
26	storage protein	(PC00210)	1	0.10%	0.10%
27	receptor	(PC00197)	45	3.80%	4.30%
28	isomerase	(PC00135)	14	1.20%	1.30%

B. Overrepresentation test complete

GO molecular function complete	Homo sapiens - REFLIS T (20814)	Client Text Box Input (1175)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (P-value)
structural constituent of ribosome (GO:0003735)	163	70	9.2	+	> 5	1.43E-34
proton-transporting ATPase activity, rotational mechanism (GO:0046961)	22	9	1.24	+	> 5	1.53E-02
ATPase activity, coupled to transmembrane movement of ions, rotational mechanism (GO:0044769)	25	10	1.41	+	> 5	5.74E-03
NADH dehydrogenase (quinone) activity (GO:0050136)	47	18	2.65	+	> 5	1.21E-06
NADH dehydrogenase (ubiquinone) activity (GO:0008137)	47	18	2.65	+	> 5	1.21E-06
NADH dehydrogenase activity (GO:0003954)	48	18	2.71	+	> 5	1.67E-06
hydrogen-exporting ATPase activity (GO:0036442)	27	10	1.52	+	> 5	1.12E-02
SNAP receptor activity	39	13	2.2	+	> 5	1.40E-03

(GO:0005484)						
oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor (GO:0016655)	61	18	3.44	+	> 5	6.33E-05
hydrogen ion transmembrane transporter activity (GO:0015078)	111	29	6.27	+	4.63	6.94E-08
cation-transporting ATPase activity (GO:0019829)	54	14	3.05	+	4.59	9.50E-03
ATPase activity, coupled to transmembrane movement of ions (GO:0042625)	55	14	3.1	+	4.51	1.17E-02
SNARE binding (GO:0000149)	119	28	6.72	+	4.17	1.52E-06
syntaxin binding (GO:0019905)	84	19	4.74	+	4.01	1.47E-03
ion channel binding (GO:0044325)	98	20	5.53	+	3.62	3.56E-03
oxidoreductase activity, acting on NAD(P)H (GO:0016651)	105	21	5.93	+	3.54	2.69E-03
translation factor activity, RNA binding (GO:0008135)	107	19	6.04	+	3.15	4.40E-02
structural molecule activity (GO:0005198)	639	90	36.07	+	2.49	2.26E-11
poly(A) RNA binding (GO:0044822)	1152	153	65.03	+	2.35	8.71E-19
RNA binding (GO:0003723)	1559	194	88.01	+	2.2	1.68E-21
monovalent inorganic cation transmembrane transporter activity (GO:0015077)	373	43	21.06	+	2.04	3.58E-02
protein domain specific binding (GO:0019904)	591	63	33.36	+	1.89	5.16E-03
oxidoreductase activity (GO:0016491)	742	79	41.89	+	1.89	2.75E-04
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides (GO:0016818)	815	80	46.01	+	1.74	5.14E-03
hydrolase activity, acting on acid anhydrides (GO:0016817)	817	80	46.12	+	1.73	5.62E-03
pyrophosphatase activity (GO:0016462)	812	79	45.84	+	1.72	8.19E-03
identical protein binding (GO:0042802)	1173	108	66.22	+	1.63	1.67E-03
enzyme binding (GO:0019899)	1604	143	90.55	+	1.58	1.48E-04
catalytic activity (GO:0003824)	5667	441	319.92	+	1.38	2.42E-11
nucleoside phosphate binding (GO:1901265)	2326	180	131.31	+	1.37	2.43E-02
nucleotide binding (GO:0000166)	2325	179	131.25	+	1.36	3.45E-02
small molecule binding (GO:0036094)	2593	198	146.38	+	1.35	1.83E-02
protein binding (GO:0005515)	10420	779	588.23	+	1.32	4.83E-26
heterocyclic compound binding (GO:1901363)	5826	401	328.89	+	1.22	6.09E-03

organic cyclic compound binding (GO:0097159)	5899	406	333.01	+	1.22	5.04E-03
binding (GO:0005488)	13955	950	787.79	+	1.21	8.77E-23
molecular_function (GO:0003674)	16648	1072	939.82	+	1.14	7.55E-23
DNA binding (GO:0003677)	2421	73	136.67	-	0.53	5.86E-07
molecular transducer activity (GO:0060089)	1848	48	104.32	-	0.46	3.09E-07
Unclassified (UNCLASSIFIED)	4166	106	235.18	-	0.45	0.00E+00
nucleic acid binding transcription factor activity (GO:0001071)	1166	29	65.82	-	0.44	3.67E-04
transcription factor activity, sequence-specific DNA binding (GO:0003700)	1166	29	65.82	-	0.44	3.67E-04
signal transducer activity (GO:0004871)	1644	40	92.81	-	0.43	3.60E-07
receptor activity (GO:0004872)	1567	35	88.46	-	0.4	5.47E-08
signaling receptor activity (GO:0038023)	1360	27	76.78	-	0.35	4.04E-08
transmembrane signaling receptor activity (GO:0004888)	1259	24	71.07	-	0.34	8.14E-08
G-protein coupled receptor activity (GO:0004930)	868	12	49	-	0.24	3.68E-07
response to stimulus (GO:0050896)	2170	68	122.5	0.56	-	2.95E-06
transcription, DNA-dependent (GO:0006351)	1941	60	109.57	0.55	-	1.12E-05
regulation of transcription from RNA polymerase II promoter (GO:0006357)	1319	40	74.46	0.54	-	1.13E-03
regulation of nucleobase-containing compound metabolic process (GO:0019219)	1700	50	95.97	0.52	-	1.48E-05
mesoderm development (GO:0007498)	671	17	37.88	0.45	-	2.16E-02
ectoderm development (GO:0007398)	663	15	37.43	0.4	-	4.83E-03
sensory perception (GO:0007600)	455	9	25.69	0.35	-	2.74E-02
cell-cell adhesion (GO:0016337)	391	7	22.07	0.32	-	3.75E-02
skeletal system development (GO:0001501)	232	1	13.1	< 0.2	-	6.00E-03
GO biological process complete	Homo sapiens - REFLIST (20814)	Client Text Box Input (1175)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (P-value)
mitochondrial ATP synthesis coupled proton transport (GO:0042776)	19	9	1.07	+	> 5	1.50E-02
translational termination (GO:0006415)	171	73	9.65	+	> 5	1.73E-35
SRP-dependent cotranslational protein	109	46	6.15	+	> 5	3.51E-21

targeting to membrane (GO:0006614)						
cytoplasmic translation (GO:0002181)	31	13	1.75	+	> 5	3.40E-04
viral transcription (GO:0019083)	111	46	6.27	+	> 5	7.29E-21
cotranslational protein targeting to membrane (GO:0006613)	112	46	6.32	+	> 5	1.04E-20
ribosomal large subunit biogenesis (GO:0042273)	39	16	2.2	+	> 5	1.33E-05
translational elongation (GO:0006414)	200	82	11.29	+	> 5	5.69E-39
protein targeting to ER (GO:0045047)	113	46	6.38	+	> 5	1.49E-20
establishment of protein localization to endoplasmic reticulum (GO:0072599)	117	47	6.6	+	> 5	8.07E-21
mitochondrial ATP synthesis coupled electron transport (GO:0042775)	68	27	3.84	+	> 5	8.45E-11
ATP synthesis coupled electron transport (GO:0042773)	68	27	3.84	+	> 5	8.45E-11
mitochondrial electron transport, NADH to ubiquinone (GO:0006120)	46	18	2.6	+	> 5	2.74E-06
cellular protein complex disassembly (GO:0043624)	200	78	11.29	+	> 5	1.89E-35
viral gene expression (GO:0019080)	121	46	6.83	+	> 5	2.26E-19
glutamate secretion (GO:0014047)	29	11	1.64	+	> 5	9.59E-03
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)	119	45	6.72	+	> 5	8.31E-19
oxidative phosphorylation (GO:0006119)	77	29	4.35	+	> 5	3.32E-11
multi-organism metabolic process (GO:0044033)	127	47	7.17	+	> 5	2.24E-19
respiratory electron transport chain (GO:0022904)	135	49	7.62	+	> 5	5.91E-20
electron transport chain (GO:0022900)	137	49	7.73	+	> 5	1.09E-19
protein complex disassembly (GO:0043241)	220	78	12.42	+	> 5	1.12E-32
translational initiation (GO:0006413)	232	82	13.1	+	> 5	2.06E-34
protein localization to endoplasmic reticulum (GO:0070972)	136	48	7.68	+	> 5	5.34E-19
mitochondrial translational elongation (GO:0070125)	84	29	4.74	+	> 5	2.86E-10
mitochondrial translational initiation (GO:0070124)	84	29	4.74	+	> 5	2.86E-10
macromolecular complex disassembly (GO:0032984)	229	79	12.93	+	> 5	2.45E-32
mitochondrial translational termination (GO:0070126)	86	29	4.85	+	> 5	5.08E-10

mitochondrial translation (GO:0032543)	107	35	6.04	+	> 5	3.29E-12
cellular respiration (GO:0045333)	185	59	10.44	+	> 5	9.33E-22
nuclear-transcribed mRNA catabolic process (GO:0000956)	181	56	10.22	+	> 5	6.64E-20
spliceosomal snRNP assembly (GO:0000387)	39	12	2.2	+	> 5	2.69E-02
mRNA catabolic process (GO:0006402)	193	57	10.9	+	> 5	2.34E-19
mitochondrial transmembrane transport (GO:1990542)	51	15	2.88	+	> 5	2.97E-03
ribosome assembly (GO:0042255)	51	15	2.88	+	> 5	2.97E-03
RNA catabolic process (GO:0006401)	222	61	12.53	+	4.87	2.41E-19
protein targeting to membrane (GO:0006612)	186	51	10.5	+	4.86	1.03E-15
translation (GO:0006412)	397	108	22.41	+	4.82	3.83E-36
ATP metabolic process (GO:0046034)	178	48	10.05	+	4.78	2.33E-14
purine ribonucleoside triphosphate metabolic process (GO:0009205)	193	52	10.9	+	4.77	9.44E-16
purine nucleoside triphosphate metabolic process (GO:0009144)	201	53	11.35	+	4.67	1.05E-15
aerobic respiration (GO:0009060)	57	15	3.22	+	4.66	1.15E-02
ribonucleoside triphosphate metabolic process (GO:0009199)	199	52	11.23	+	4.63	3.37E-15
peptide biosynthetic process (GO:0043043)	420	109	23.71	+	4.6	1.03E-34
hydrogen ion transmembrane transport (GO:1902600)	116	30	6.55	+	4.58	1.29E-07
purine ribonucleoside monophosphate metabolic process (GO:0009167)	202	49	11.4	+	4.3	6.30E-13
purine nucleoside monophosphate metabolic process (GO:0009126)	203	49	11.46	+	4.28	7.60E-13
nucleoside triphosphate metabolic process (GO:0009141)	220	53	12.42	+	4.27	4.58E-14
dicarboxylic acid transport (GO:0006835)	63	15	3.56	+	4.22	3.80E-02
amide biosynthetic process (GO:0043604)	480	114	27.1	+	4.21	5.41E-33
ribonucleoside monophosphate metabolic process (GO:0009161)	215	51	12.14	+	4.2	3.58E-13
viral life cycle (GO:0019058)	241	57	13.61	+	4.19	5.75E-15
establishment of protein localization to membrane (GO:0090150)	273	64	15.41	+	4.15	6.19E-17
peptide metabolic process (GO:0006518)	517	117	29.19	+	4.01	4.75E-32
nucleoside monophosphate	226	51	12.76	+	4	2.54E-12

metabolic process (GO:0009123)						
energy derivation by oxidation of organic compounds (GO:0015980)	342	76	19.31	+	3.94	2.90E-19
neurotransmitter secretion (GO:0007269)	122	27	6.89	+	3.92	3.45E-05
regulation of synaptic plasticity (GO:0048167)	133	29	7.51	+	3.86	1.30E-05
establishment of protein localization to organelle (GO:0072594)	348	74	19.65	+	3.77	1.30E-17
neurotransmitter transport (GO:0006836)	160	34	9.03	+	3.76	1.02E-06
mitochondrial transport (GO:0006839)	153	32	8.64	+	3.7	5.18E-06
ribonucleoprotein complex assembly (GO:0022618)	182	38	10.27	+	3.7	1.40E-07
ribonucleoprotein complex subunit organization (GO:0071826)	192	40	10.84	+	3.69	4.44E-08
proton transport (GO:0015992)	153	31	8.64	+	3.59	1.98E-05
generation of precursor metabolites and energy (GO:0006091)	411	83	23.2	+	3.58	1.04E-18
ribosome biogenesis (GO:0042254)	218	44	12.31	+	3.58	1.10E-08
protein localization to membrane (GO:0072657)	388	78	21.9	+	3.56	2.69E-17
nucleobase-containing compound catabolic process (GO:0034655)	344	69	19.42	+	3.55	6.16E-15
hydrogen transport (GO:0006818)	155	31	8.75	+	3.54	2.66E-05
synaptic vesicle localization (GO:0097479)	110	22	6.21	+	3.54	4.79E-03
synaptic vesicle transport (GO:0048489)	108	21	6.1	+	3.44	1.32E-02
establishment of synaptic vesicle localization (GO:0097480)	108	21	6.1	+	3.44	1.32E-02
ribonucleoprotein complex biogenesis (GO:0022613)	346	67	19.53	+	3.43	1.12E-13
ribonucleotide metabolic process (GO:0009259)	324	62	18.29	+	3.39	3.14E-12
purine ribonucleoside metabolic process (GO:0046128)	277	53	15.64	+	3.39	4.43E-10
purine ribonucleotide metabolic process (GO:0009150)	309	59	17.44	+	3.38	1.80E-11
rRNA processing (GO:0006364)	147	28	8.3	+	3.37	4.06E-04
mitochondrion organization (GO:0007005)	410	78	23.15	+	3.37	6.21E-16
ribose phosphate metabolic process (GO:0019693)	337	64	19.02	+	3.36	1.48E-12
purine nucleoside metabolic process (GO:0042278)	280	53	15.81	+	3.35	6.69E-10

cellular amide metabolic process (GO:0043603)	666	125	37.6	+	3.32	7.06E-27
regulation of neurotransmitter levels (GO:0001505)	155	29	8.75	+	3.31	3.43E-04
heterocycle catabolic process (GO:0046700)	386	72	21.79	+	3.3	4.71E-14
protein targeting (GO:0006605)	423	78	23.88	+	3.27	3.56E-15
mRNA metabolic process (GO:0016071)	564	104	31.84	+	3.27	3.25E-21
aromatic compound catabolic process (GO:0019439)	396	73	22.36	+	3.27	5.09E-14
purine nucleotide metabolic process (GO:0006163)	331	61	18.69	+	3.26	2.83E-11
rRNA metabolic process (GO:0016072)	152	28	8.58	+	3.26	7.95E-04
cellular nitrogen compound catabolic process (GO:0044270)	386	71	21.79	+	3.26	1.63E-13
organic cyclic compound catabolic process (GO:1901361)	427	78	24.11	+	3.24	6.01E-15
cellular component disassembly (GO:0022411)	493	89	27.83	+	3.2	3.93E-17
ribonucleoside metabolic process (GO:0009119)	301	54	16.99	+	3.18	3.05E-09
regulation of synapse structure or activity (GO:0050803)	218	37	12.31	+	3.01	6.28E-05
nucleoside metabolic process (GO:0009116)	326	55	18.4	+	2.99	1.93E-08
mRNA splicing, via spliceosome (GO:0000398)	226	38	12.76	+	2.98	5.06E-05
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (GO:0000377)	226	38	12.76	+	2.98	5.06E-05
establishment of vesicle localization (GO:0051650)	186	31	10.5	+	2.95	1.46E-03
RNA splicing, via transesterification reactions (GO:0000375)	229	38	12.93	+	2.94	7.11E-05
nucleotide metabolic process (GO:0009117)	484	80	27.32	+	2.93	5.51E-13
vesicle localization (GO:0051648)	194	32	10.95	+	2.92	1.17E-03
purine-containing compound metabolic process (GO:0072521)	378	62	21.34	+	2.91	2.52E-09
single-organism cellular localization (GO:1902580)	845	138	47.7	+	2.89	3.54E-24
nucleoside phosphate metabolic process (GO:0006753)	490	80	27.66	+	2.89	1.08E-12
protein localization to organelle (GO:0033365)	528	86	29.81	+	2.89	8.52E-14
glycosyl compound metabolic process (GO:1901657)	344	56	19.42	+	2.88	4.73E-08
Golgi vesicle transport (GO:0048193)	246	39	13.89	+	2.81	1.51E-04

organonitrogen compound biosynthetic process (GO:1901566)	1007	159	56.85	+	2.8	6.93E-27
positive regulation of protein ubiquitination (GO:0031398)	165	26	9.31	+	2.79	3.69E-02
signal release (GO:0023061)	189	29	10.67	+	2.72	1.79E-02
single-organism membrane organization (GO:0044802)	715	109	40.36	+	2.7	3.45E-16
vesicle organization (GO:0016050)	214	32	12.08	+	2.65	9.38E-03
membrane organization (GO:0061024)	877	131	49.51	+	2.65	2.30E-19
cellular macromolecule catabolic process (GO:0044265)	764	114	43.13	+	2.64	2.21E-16
intracellular protein transport (GO:0006886)	727	108	41.04	+	2.63	3.21E-15
nucleobase-containing small molecule metabolic process (GO:0055086)	547	81	30.88	+	2.62	1.27E-10
modulation of synaptic transmission (GO:0050804)	266	39	15.02	+	2.6	1.10E-03
protein polyubiquitination (GO:0000209)	198	29	11.18	+	2.59	4.28E-02
cytoplasmic transport (GO:0016482)	713	104	40.25	+	2.58	5.18E-14
viral process (GO:0016032)	674	98	38.05	+	2.58	6.03E-13
multi-organism cellular process (GO:0044764)	678	98	38.27	+	2.56	8.73E-13
interspecies interaction between organisms (GO:0044419)	749	108	42.28	+	2.55	2.53E-14
symbiosis, encompassing mutualism through parasitism (GO:0044403)	749	108	42.28	+	2.55	2.53E-14
single-organism intracellular transport (GO:1902582)	1168	165	65.94	+	2.5	8.35E-23
RNA splicing (GO:0008380)	338	46	19.08	+	2.41	7.21E-04
regulation of cellular amide metabolic process (GO:0034248)	311	42	17.56	+	2.39	3.14E-03
regulation of translation (GO:0006417)	289	39	16.31	+	2.39	8.20E-03
exocytosis (GO:0006887)	297	40	16.77	+	2.39	6.29E-03
neurotrophin signaling pathway (GO:0038179)	397	53	22.41	+	2.36	1.43E-04
neurotrophin TRK receptor signaling pathway (GO:0048011)	394	52	22.24	+	2.34	2.78E-04
intracellular transport (GO:0046907)	1353	178	76.38	+	2.33	1.72E-21
macromolecule catabolic process (GO:0009057)	899	118	50.75	+	2.33	5.94E-13
organonitrogen compound metabolic process (GO:1901564)	1727	226	97.49	+	2.32	2.44E-28
protein transport (GO:0015031)	1224	160	69.1	+	2.32	1.26E-18
establishment of protein localization (GO:0045184)	1307	170	73.78	+	2.3	8.09E-20

cellular macromolecular complex assembly (GO:0034622)	608	79	34.32	+	2.3	1.59E-07
organophosphate metabolic process (GO:0019637)	834	108	47.08	+	2.29	3.22E-11
establishment of organelle localization (GO:0051656)	294	38	16.6	+	2.29	2.99E-02
mRNA processing (GO:0006397)	396	51	22.36	+	2.28	7.86E-04
cellular protein localization (GO:0034613)	1138	145	64.24	+	2.26	1.47E-15
cellular macromolecule localization (GO:0070727)	1146	145	64.69	+	2.24	2.68E-15
organelle localization (GO:0051640)	368	46	20.77	+	2.21	7.30E-03
ncRNA metabolic process (GO:0034660)	409	51	23.09	+	2.21	2.04E-03
establishment of localization in cell (GO:0051649)	1812	219	102.29	+	2.14	1.04E-22
oxidation-reduction process (GO:0055114)	1034	123	58.37	+	2.11	1.40E-10
protein localization (GO:0008104)	1689	200	95.35	+	2.1	2.83E-19
synaptic transmission (GO:0007268)	560	66	31.61	+	2.09	2.91E-04
secretion by cell (GO:0032940)	484	57	27.32	+	2.09	2.53E-03
protein complex subunit organization (GO:0071822)	1406	164	79.37	+	2.07	1.89E-14
cellular localization (GO:0051641)	2174	252	122.73	+	2.05	2.43E-24
positive regulation of cellular catabolic process (GO:0031331)	416	48	23.48	+	2.04	3.62E-02
RNA processing (GO:0006396)	705	81	39.8	+	2.04	2.45E-05
organophosphate biosynthetic process (GO:0090407)	447	51	25.23	+	2.02	2.51E-02
macromolecule localization (GO:0033036)	2013	227	113.64	+	2	8.04E-20
organic substance transport (GO:0071702)	1899	211	107.2	+	1.97	2.50E-17
secretion (GO:0046903)	589	65	33.25	+	1.95	3.60E-03
macromolecular complex subunit organization (GO:0043933)	2074	228	117.08	+	1.95	1.52E-18
cellular catabolic process (GO:0044248)	1448	156	81.74	+	1.91	1.13E-10
organic substance catabolic process (GO:1901575)	1509	161	85.19	+	1.89	8.96E-11
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	783	81	44.2	+	1.83	1.90E-03
phosphorylation (GO:0016310)	1269	130	71.64	+	1.81	6.20E-07
single-organism biosynthetic process (GO:0044711)	1333	136	75.25	+	1.81	2.82E-07
macromolecular complex assembly (GO:0065003)	1177	118	66.44	+	1.78	1.71E-05

single-organism transport (GO:0044765)	3104	310	175.23	+	1.77	1.55E-20
catabolic process (GO:0009056)	1764	176	99.58	+	1.77	1.48E-09
phosphate-containing compound metabolic process (GO:0006796)	2020	201	114.03	+	1.76	2.47E-11
single-organism localization (GO:1902578)	3296	326	186.07	+	1.75	2.83E-21
phosphorus metabolic process (GO:0006793)	2067	204	116.69	+	1.75	3.27E-11
cellular protein metabolic process (GO:0044267)	3575	351	201.82	+	1.74	5.87E-23
vesicle-mediated transport (GO:0016192)	1150	112	64.92	+	1.73	2.04E-04
carbohydrate derivative metabolic process (GO:1901135)	1029	99	58.09	+	1.7	2.38E-03
neuron development (GO:0048666)	982	94	55.44	+	1.7	5.94E-03
neuron projection development (GO:0031175)	838	80	47.31	+	1.69	4.44E-02
transport (GO:0006810)	3742	357	211.24	+	1.69	3.11E-21
establishment of localization (GO:0051234)	3851	367	217.4	+	1.69	5.47E-22
small molecule metabolic process (GO:0044281)	2233	212	126.06	+	1.68	3.96E-10
ion transport (GO:0006811)	1263	114	71.3	+	1.6	6.55E-03
protein metabolic process (GO:0019538)	4241	380	239.41	+	1.59	3.93E-18
localization (GO:0051179)	4683	415	264.37	+	1.57	1.03E-19
cellular component organization or biogenesis (GO:0071840)	5188	455	292.87	+	1.55	1.09E-21
organelle organization (GO:0006996)	2912	255	164.39	+	1.55	4.28E-09
cellular component biogenesis (GO:0044085)	1978	173	111.66	+	1.55	5.82E-05
cellular component organization (GO:0016043)	5066	439	285.99	+	1.54	1.88E-19
single-organism organelle organization (GO:1902589)	1970	165	111.21	+	1.48	2.16E-03
single-organism metabolic process (GO:0044710)	4494	375	253.7	+	1.48	1.19E-12
cellular nitrogen compound metabolic process (GO:0034641)	5112	419	288.58	+	1.45	1.13E-13
gene expression (GO:0010467)	3825	307	215.93	+	1.42	2.75E-07
nitrogen compound metabolic process (GO:0006807)	5475	436	309.08	+	1.41	2.47E-12
regulation of cellular component organization (GO:0051128)	2160	172	121.94	+	1.41	2.52E-02
regulation of cellular protein metabolic process (GO:0032268)	2364	188	133.45	+	1.41	8.72E-03
nervous system development (GO:0007399)	2271	179	128.2	+	1.4	2.83E-02
cellular metabolic process	8573	669	483.97	+	1.38	1.01E-23

(GO:0044237)						
regulation of protein metabolic process (GO:0051246)	2530	195	142.82	+	1.37	3.91E-02
cellular nitrogen compound biosynthetic process (GO:0044271)	3407	261	192.33	+	1.36	9.48E-04
nucleobase-containing compound metabolic process (GO:0006139)	4372	331	246.81	+	1.34	2.80E-05
primary metabolic process (GO:0044238)	8697	657	490.97	+	1.34	1.12E-18
cellular macromolecule metabolic process (GO:0044260)	6753	507	381.22	+	1.33	9.07E-11
heterocycle metabolic process (GO:0046483)	4573	343	258.16	+	1.33	3.50E-05
cellular aromatic compound metabolic process (GO:0006725)	4575	342	258.27	+	1.32	5.42E-05
metabolic process (GO:0008152)	9928	742	560.46	+	1.32	1.06E-22
regulation of biological quality (GO:0065008)	3134	233	176.92	+	1.32	4.81E-02
organic substance metabolic process (GO:0071704)	9008	669	508.52	+	1.32	3.01E-17
cellular biosynthetic process (GO:0044249)	4493	331	253.64	+	1.3	4.96E-04
organic cyclic compound metabolic process (GO:1901360)	4818	354	271.99	+	1.3	1.72E-04
organic substance biosynthetic process (GO:1901576)	4587	335	258.95	+	1.29	9.53E-04
biosynthetic process (GO:0009058)	4673	340	263.8	+	1.29	1.06E-03
macromolecule metabolic process (GO:0043170)	7438	533	419.89	+	1.27	5.81E-08
single-organism cellular process (GO:0044763)	11415	777	644.4	+	1.21	1.82E-11
cellular process (GO:0009987)	14147	947	798.63	+	1.19	1.65E-18
single-organism process (GO:0044699)	12755	839	720.05	+	1.17	1.77E-09
biological_process (GO:0008150)	16542	1062	933.84	+	1.14	3.99E-20
tissue development (GO:0009888)	1601	52	90.38	-	0.58	3.21E-02
G-protein coupled receptor signaling pathway (GO:0007186)	1197	35	67.57	-	0.52	4.62E-02
Unclassified (UNCLASSIFIED)	4272	115	241.16	-	0.48	0.00E+00
sensory perception (GO:0007600)	945	24	53.35	-	0.45	2.88E-02
anatomical structure formation involved in morphogenesis (GO:0048646)	974	23	54.98	-	0.42	4.47E-03
detection of chemical stimulus (GO:0009593)	496	4	28	-	< 0.2	1.24E-04

detection of stimulus involved in sensory perception (GO:0050906)	514	3	29.02	-	< 0.2	6.56E-06
PANTHER Protein Class	Homo sapiens - REFLIST (20814)	Client Text Box Input (1175)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (P-value)
SNARE protein (PC00034)	42	14	2.37	+	> 5	4.33E-05
ribosomal protein (PC00202)	225	73	12.7	+	> 5	1.33E-29
membrane traffic protein (PC00150)	366	58	20.66	+	2.81	1.47E-09
RNA binding protein (PC00031)	859	133	48.49	+	2.74	1.15E-22
membrane trafficking regulatory protein (PC00151)	119	18	6.72	+	2.68	4.31E-02
chaperone (PC00072)	196	27	11.06	+	2.44	6.57E-03
oxidoreductase (PC00176)	609	62	34.38	+	1.8	2.07E-03
nucleic acid binding (PC00171)	2297	181	129.67	+	1.4	6.55E-04
Unclassified (UNCLASSIFIED)	9675	487	546.18	-	0.89	0.00E+00
transcription factor (PC00218)	1565	47	88.35	-	0.53	9.34E-05
receptor (PC00197)	1596	45	90.1	-	0.5	8.81E-06
cell adhesion molecule (PC00069)	507	11	28.62	-	0.38	2.74E-02
G-protein coupled receptor (PC00021)	468	9	26.42	-	0.34	1.52E-02
defense/immunity protein (PC00090)	551	8	31.11	-	0.26	1.44E-04
cytokine receptor (PC00084)	293	3	16.54	-	< 0.2	1.12E-02
cytokine (PC00083)	196	1	11.06	-	< 0.2	3.67E-02
KRAB box transcription factor (PC00029)	341	1	19.25	-	< 0.2	1.55E-05

C. Overrepresentation test GO-slim

PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20814)	Client Text Box Input (1175)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (P-value)
structural constituent of ribosome (GO:0003735)	180	57	10.16	+	> 5	1.90E-22
hydrogen ion transmembrane transporter activity (GO:0015078)	41	10	2.31	+	4.32	2.50E-02
translation initiation factor activity (GO:0003743)	97	16	5.48	+	2.92	3.08E-02
oxidoreductase activity (GO:0016491)	626	65	35.34	+	1.84	5.71E-04
RNA binding (GO:0003723)	454	46	25.63	+	1.79	2.57E-02
structural molecule activity (GO:0005198)	1034	103	58.37	+	1.76	5.73E-06
catalytic activity (GO:0003824)	5209	373	294.06	+	1.27	2.19E-05

Unclassified (UNCLASSIFIED)	10020	528	565.65	-	0.93	0.00E+00
sequence-specific DNA binding transcription factor activity (GO:0003700)	1462	44	82.53	-	0.53	2.05E-04
DNA binding (GO:0003677)	1878	53	106.02	-	0.5	4.18E-07
nucleic acid binding transcription factor activity (GO:0001071)	1646	44	92.92	-	0.47	6.85E-07
receptor activity (GO:0004872)	1636	41	92.36	-	0.44	7.91E-08
serine-type peptidase activity (GO:0008236)	322	4	18.18	-	0.22	1.13E-02
cytokine activity (GO:0005125)	230	1	12.98	-	< 0.2	5.10E-03
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20814)	Client Text Box Input (1175)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (P- value)
oxidative phosphorylation (GO:0006119)	56	15	3.16	+	4.74	2.65E-04
translation (GO:0006412)	435	90	24.56	+	3.66	8.77E-23
protein localization (GO:0008104)	116	19	6.55	+	2.9	1.15E-02
respiratory electron transport chain (GO:0022904)	217	33	12.25	+	2.69	1.28E-04
generation of precursor metabolites and energy (GO:0006091)	274	41	15.47	+	2.65	8.80E-06
synaptic transmission (GO:0007268)	331	36	18.69	+	1.93	4.70E-02
organelle organization (GO:0006996)	571	56	32.23	+	1.74	1.59E-02
vesicle-mediated transport (GO:0016192)	895	83	50.52	+	1.64	2.39E-03
protein metabolic process (GO:0019538)	2692	240	151.97	+	1.58	1.21E-10
protein transport (GO:0015031)	1082	91	61.08	+	1.49	3.03E-02
cellular component organization or biogenesis (GO:0071840)	1316	107	74.29	+	1.44	2.83E-02
transport (GO:0006810)	2473	184	139.61	+	1.32	1.54E-02
metabolic process (GO:0008152)	8247	572	465.56	+	1.23	4.33E-08
primary metabolic process (GO:0044238)	6825	463	385.29	+	1.2	2.48E-04
Unclassified (UNCLASSIFIED)	8629	409	487.13	-	0.84	0.00E+00
developmental process (GO:0032502)	2456	95	138.65	-	0.69	4.69E-03
immune system process (GO:0002376)	1391	44	78.53	-	0.56	1.99E-03
transcription from RNA polymerase II promoter (GO:0006366)	1723	54	97.27	-	0.56	1.12E-04

response to stimulus (GO:0050896)	2170	68	122.5	-	0.56	2.95E-06
transcription, DNA- dependent (GO:0006351)	1941	60	109.57	-	0.55	1.12E-05
regulation of transcription from RNA polymerase II promoter (GO:0006357)	1319	40	74.46	-	0.54	1.13E-03
regulation of nucleobase- containing compound metabolic process (GO:0019219)	1700	50	95.97	-	0.52	1.48E-05
mesoderm development (GO:0007498)	671	17	37.88	-	0.45	2.16E-02
ectoderm development (GO:0007398)	663	15	37.43	-	0.4	4.83E-03
sensory perception (GO:0007600)	455	9	25.69	-	0.35	2.74E-02
cell-cell adhesion (GO:0016337)	391	7	22.07	-	0.32	3.75E-02
skeletal system development (GO:0001501)	232	1	13.1	-	< 0.2	6.00E-03