



New! Fisher's Exact with FDR multiple test correction now available for Gene List Analysis. [View release notes](#) here.

Analysis Summary: Please report in publication [?](#)

Analysis Type: PANTHER Overrepresentation Test (Released 20171205)	
Annotation Version and Release Date: PANTHER version 13.0 Released 2017-11-12	
Analyzed List:	Client Text Box Input (Homo sapiens) Change
Reference List:	Homo sapiens (all genes in database) Change
Annotation Data Set:	PANTHER GO-Slim Biological Process ▼
Test Type: <input checked="" type="radio"/> Fisher's Exact with FDR multiple test correction <input type="radio"/> Binomial	

Results [?](#)

	Reference list	Client Text Box Input
Mapped IDs:	21042 out of 21042	24 out of 24
Unmapped IDs:	0	0
Multiple mapping information:	0	0

[Export results](#) View: [-- Please select a chart to display --](#) ▼

Displaying all results; [click here to display only results with False Discovery Rate < 0.05](#)

	Homo sapiens (REF)	Client Text Box Input (.Hierarchy.) NEW! ?				
	▲ #	#	expected	Fold Enrichment	+/-	raw P value
PANTHER GO-Slim Biological Process	1	0	.00	< 0.01	-	1.00E00 3
multi-multicellular organism process	1479	0	1.69	< 0.01	-	4.10E-01 3
↳ multicellular organismal process	1	0	.00	< 0.01	-	1.00E00 3
vitamin catabolic process	30	0	.03	< 0.01	-	1.00E00 1
↳ vitamin metabolic process	5416	18	6.18	2.91	+	6.33E-07 1
↳ metabolic process	1	0	.00	< 0.01	-	1.00E00 3
pinocytosis	372	0	.42	< 0.01	-	1.00E00 1
↳ endocytosis	800	0	.91	< 0.01	-	1.00E00 2
↳ vesicle-mediated transport	1668	0	1.90	< 0.01	-	2.55E-01 2
↳ transport	1970	0	2.25	< 0.01	-	1.62E-01 1
↳ localization	1	0	.00	< 0.01	-	1.00E00 3
endoderm development	1569	0	1.79	< 0.01	-	2.55E-01 2
↳ developmental process	1	0	.00	< 0.01	-	1.00E00 3
nitrogen utilization	2435	13	2.78	4.68	+	4.92E-07 1
↳ nitrogen compound metabolic process	2	0	.00	< 0.01	-	1.00E00 5
nitric oxide biosynthetic process	2	0	.00	< 0.01	-	1.00E00 4
mammary gland development	357	0	.41	< 0.01	-	1.00E00 3
↳ system development	2	0	.00	< 0.01	-	1.00E00 4
bile acid metabolic process	100	0	.11	< 0.01	-	1.00E00 1
↳ steroid metabolic process	572	0	.65	< 0.01	-	1.00E00 1
↳ lipid metabolic process	4346	18	4.96	3.63	+	1.75E-08 7
↳ primary metabolic process	2	0	.00	< 0.01	-	1.00E00 4
disaccharide metabolic process	344	0	.39	< 0.01	-	1.00E00 1
↳ carbohydrate metabolic process	3	0	.00	< 0.01	-	1.00E00 4
termination of RNA polymerase II transcription	192	0	.22	< 0.01	-	1.00E00 1
↳ transcription from RNA polymerase II promoter	485	0	.55	< 0.01	-	1.00E00 1
↳ transcription, DNA-dependent	1023	6	1.17	5.14	+	8.44E-04 2
↳ RNA metabolic process	2050	18	2.34	7.70	+	5.05E-14 4
↳ nucleobase-containing compound metabolic process	3	0	.00	< 0.01	-	1.00E00 4
ferredoxin metabolic process						

protein metabolic process	1714	2	1.95	1.02	+	1.00E00	2
prosthetic group metabolic process	3	0	.00	< 0.01	-	1.00E00	3
nitric oxide mediated signal transduction	3	0	.00	< 0.01	-	1.00E00	3
intracellular signal transduction	1000	0	1.14	< 0.01	-	6.28E-01	4
signal transduction	2162	0	2.47	< 0.01	-	1.67E-01	1
cell communication	2509	0	2.86	< 0.01	-	1.05E-01	1
cellular process	7905	17	9.02	1.89	+	1.17E-03	2
sex determination	4	0	.00	< 0.01	-	1.00E00	6
7-methylguanosine mRNA capping	5	0	.01	< 0.01	-	1.00E00	5
mRNA processing	221	2	.25	7.93	+	2.64E-02	3
regulation of vasoconstriction	5	0	.01	< 0.01	-	1.00E00	5
regulation of biological process	3358	4	3.83	1.04	+	7.86E-01	5
biological regulation	3653	4	4.17	.96	-	1.00E00	2
secondary metabolic process	5	0	.01	< 0.01	-	1.00E00	5
unsaturated fatty acid biosynthetic process	5	0	.01	< 0.01	-	1.00E00	5
fatty acid biosynthetic process	56	0	.06	< 0.01	-	1.00E00	1
fatty acid metabolic process	178	0	.20	< 0.01	-	1.00E00	2
regulation of binding	6	0	.01	< 0.01	-	1.00E00	6
regulation of molecular function	412	0	.47	< 0.01	-	1.00E00	1
blood coagulation	6	0	.01	< 0.01	-	1.00E00	6
response to external stimulus	294	0	.34	< 0.01	-	1.00E00	1
response to stimulus	2677	9	3.05	2.95	+	1.90E-03	3
peroxisomal transport	6	0	.01	< 0.01	-	1.00E00	5
regulation of cellular amino acid metabolic process	6	0	.01	< 0.01	-	1.00E00	5
cellular amino acid metabolic process	227	0	.26	< 0.01	-	1.00E00	2
protein ADP-ribosylation	6	0	.01	< 0.01	-	1.00E00	5
protein glycosylation	103	0	.12	< 0.01	-	1.00E00	1
cellular protein modification process	799	0	.91	< 0.01	-	1.00E00	1
sensory perception of pain	8	0	.01	< 0.01	-	1.00E00	3
sensory perception	409	0	.47	< 0.01	-	1.00E00	1
neurological system process	816	0	.93	< 0.01	-	1.00E00	1
system process	910	0	1.04	< 0.01	-	6.24E-01	4
single-multicellular organism process	1463	0	1.67	< 0.01	-	4.08E-01	3
pentose-phosphate shunt	8	0	.01	< 0.01	-	1.00E00	3
monosaccharide metabolic process	102	0	.12	< 0.01	-	1.00E00	1
cell killing	8	0	.01	< 0.01	-	1.00E00	3
viral process	8	0	.01	< 0.01	-	1.00E00	3
polyphosphate catabolic process	8	0	.01	< 0.01	-	1.00E00	3
phosphate-containing compound metabolic process	858	4	.98	4.09	+	1.54E-02	2
mRNA transcription	10	0	.01	< 0.01	-	1.00E00	2
hemopoiesis	11	0	.01	< 0.01	-	1.00E00	4
antigen processing and presentation	11	0	.01	< 0.01	-	1.00E00	4
immune system process	268	0	.31	< 0.01	-	1.00E00	1
asymmetric protein localization	12	0	.01	< 0.01	-	1.00E00	2
protein localization	484	0	.55	< 0.01	-	1.00E00	1
vitamin transport	12	0	.01	< 0.01	-	1.00E00	2
DNA catabolic process	12	0	.01	< 0.01	-	1.00E00	1
DNA metabolic process	381	18	.43	41.42	+	8.15E-27	9
circadian rhythm	13	0	.01	< 0.01	-	1.00E00	2
rhythmic process	13	0	.01	< 0.01	-	1.00E00	2
skeletal system development	13	0	.01	< 0.01	-	1.00E00	2
pteridine-containing compound metabolic process	14	0	.02	< 0.01	-	1.00E00	1
response to toxic substance	14	0	.02	< 0.01	-	1.00E00	1
dorsal/ventral axis specification	14	0	.02	< 0.01	-	1.00E00	1
pattern specification process	104	0	.12	< 0.01	-	1.00E00	1
vitamin biosynthetic process	16	0	.02	< 0.01	-	1.00E00	2

angiogenesis	16	0	.02	< 0.01	-	1.00E00	2
female gamete generation	16	0	.02	< 0.01	-	1.00E00	2
↳ gamete generation	161	0	.18	< 0.01	-	1.00E00	1
↳ reproduction	266	0	.30	< 0.01	-	1.00E00	1
anterior/posterior axis specification	16	0	.02	< 0.01	-	1.00E00	2
JAK-STAT cascade	17	0	.02	< 0.01	-	1.00E00	1
lysosomal transport	17	0	.02	< 0.01	-	1.00E00	1
blood circulation	17	0	.02	< 0.01	-	1.00E00	1
heart development	18	0	.02	< 0.01	-	1.00E00	1
phosphate ion transport	19	0	.02	< 0.01	-	1.00E00	2
mitochondrial translation	19	0	.02	< 0.01	-	1.00E00	2
↳ translation	141	0	.16	< 0.01	-	1.00E00	1
↳ mitochondrion organization	110	0	.13	< 0.01	-	1.00E00	3
↳ organelle organization	1152	0	1.31	< 0.01	-	6.40E-01	4
↳ cellular component organization	1543	0	1.76	< 0.01	-	2.55E-01	2
↳ cellular component organization or biogenesis	1685	0	1.92	< 0.01	-	2.56E-01	2
muscle organ development	19	0	.02	< 0.01	-	1.00E00	2
digestive tract mesoderm development	19	0	.02	< 0.01	-	1.00E00	2
↳ mesoderm development	278	0	.32	< 0.01	-	1.00E00	2
fatty acid beta-oxidation	20	0	.02	< 0.01	-	1.00E00	1
tricarboxylic acid cycle	21	0	.02	< 0.01	-	1.00E00	3
gluconeogenesis	23	0	.03	< 0.01	-	1.00E00	1
regulation of carbohydrate metabolic process	23	1	.03	38.12	+	2.70E-02	3
mRNA polyadenylation	24	0	.03	< 0.01	-	1.00E00	1
↳ mRNA 3'-end processing	35	0	.04	< 0.01	-	1.00E00	1
cellular glucose homeostasis	24	0	.03	< 0.01	-	1.00E00	1
↳ homeostatic process	262	0	.30	< 0.01	-	1.00E00	1
porphyrin-containing compound metabolic process	26	0	.03	< 0.01	-	1.00E00	1
cytokine production	27	0	.03	< 0.01	-	1.00E00	2
carbohydrate transport	27	0	.03	< 0.01	-	1.00E00	2
transcription elongation from RNA polymerase II promoter	29	0	.03	< 0.01	-	1.00E00	1
glycolysis	29	0	.03	< 0.01	-	1.00E00	1
↳ generation of precursor metabolites and energy	151	0	.17	< 0.01	-	1.00E00	1
cholesterol metabolic process	29	0	.03	< 0.01	-	1.00E00	1
pyrimidine nucleobase metabolic process	30	0	.03	< 0.01	-	1.00E00	1
sensory perception of sound	31	0	.04	< 0.01	-	1.00E00	1
regulation of sequence-specific DNA binding transcription factor activity	32	0	.04	< 0.01	-	1.00E00	1
JNK cascade	32	0	.04	< 0.01	-	1.00E00	1
↳ MAPK cascade	329	0	.38	< 0.01	-	1.00E00	2
chromatin remodeling	34	0	.04	< 0.01	-	1.00E00	1
glycogen metabolic process	35	0	.04	< 0.01	-	1.00E00	1
↳ polysaccharide metabolic process	92	0	.10	< 0.01	-	1.00E00	1
acyl-CoA metabolic process	37	0	.04	< 0.01	-	1.00E00	3
↳ coenzyme metabolic process	71	0	.08	< 0.01	-	1.00E00	1
protein methylation	39	0	.04	< 0.01	-	1.00E00	1
chromatin assembly	40	0	.05	< 0.01	-	1.00E00	1
induction of apoptosis	40	0	.05	< 0.01	-	1.00E00	1
↳ apoptotic process	440	0	.50	< 0.01	-	1.00E00	2
↳ cell death	460	0	.52	< 0.01	-	1.00E00	1
↳ death	460	0	.52	< 0.01	-	1.00E00	1
sensory perception of taste	40	0	.05	< 0.01	-	1.00E00	1
↳ sensory perception of chemical stimulus	280	0	.32	< 0.01	-	1.00E00	1
regulation of translation	41	0	.05	< 0.01	-	1.00E00	1
mitochondrial transport	41	0	.05	< 0.01	-	1.00E00	1
I-kappaB kinase/NF-kappaB cascade	43	0	.05	< 0.01	-	1.00E00	2
tRNA aminoacylation for protein translation	44	0	.05	< 0.01	-	1.00E00	1
cell growth	44	0	.05	< 0.01	-	1.00E00	1

growth	50	0	.06	< 0.01	-	1.00E00	1
transcription initiation from RNA polymerase II promoter	48	0	.05	< 0.01	-	1.00E00	2
fertilization	48	0	.05	< 0.01	-	1.00E00	2
DNA recombination	49	0	.06	< 0.01	-	1.00E00	1
neuron-neuron synaptic transmission	49	0	.06	< 0.01	-	1.00E00	1
synaptic transmission	328	0	.37	< 0.01	-	1.00E00	1
cell-cell signaling	513	0	.59	< 0.01	-	1.00E00	1
oxidative phosphorylation	50	0	.06	< 0.01	-	1.00E00	1
cellular amino acid catabolic process	53	0	.06	< 0.01	-	1.00E00	1
cell-matrix adhesion	53	0	.06	< 0.01	-	1.00E00	1
cell adhesion	336	0	.38	< 0.01	-	1.00E00	4
biological adhesion	336	0	.38	< 0.01	-	1.00E00	4
neuromuscular synaptic transmission	54	0	.06	< 0.01	-	1.00E00	1
calcium-mediated signaling	54	0	.06	< 0.01	-	1.00E00	1
regulation of gene expression, epigenetic	56	0	.06	< 0.01	-	1.00E00	1
purine nucleobase metabolic process	57	0	.07	< 0.01	-	1.00E00	1
meiosis	57	0	.07	< 0.01	-	1.00E00	1
cell cycle	814	5	.93	5.39	+	2.01E-03	3
response to interferon-gamma	58	0	.07	< 0.01	-	1.00E00	1
immune response	355	0	.40	< 0.01	-	1.00E00	2
protein lipidation	58	0	.07	< 0.01	-	1.00E00	1
cell proliferation	60	0	.07	< 0.01	-	1.00E00	1
cellular amino acid biosynthetic process	63	0	.07	< 0.01	-	1.00E00	1
protein acetylation	63	0	.07	< 0.01	-	1.00E00	1
transmembrane receptor protein serine/threonine kinase signaling pathway	64	0	.07	< 0.01	-	1.00E00	1
cell surface receptor signaling pathway	1110	0	1.27	< 0.01	-	6.36E-01	4
synaptic vesicle exocytosis	65	0	.07	< 0.01	-	1.00E00	1
exocytosis	245	0	.28	< 0.01	-	1.00E00	1
neurotransmitter secretion	37	0	.04	< 0.01	-	1.00E00	3
visual perception	69	0	.08	< 0.01	-	1.00E00	1
lipid transport	69	0	.08	< 0.01	-	1.00E00	1
RNA catabolic process	70	2	.08	25.05	+	3.03E-03	5
cytokine-mediated signaling pathway	74	0	.08	< 0.01	-	1.00E00	1
response to abiotic stimulus	75	0	.09	< 0.01	-	1.00E00	1
behavior	76	0	.09	< 0.01	-	1.00E00	1
cyclic nucleotide metabolic process	76	0	.09	< 0.01	-	1.00E00	1
sulfur compound metabolic process	78	0	.09	< 0.01	-	1.00E00	1
amino acid transport	79	0	.09	< 0.01	-	1.00E00	2
segment specification	80	0	.09	< 0.01	-	1.00E00	1
protein phosphorylation	80	0	.09	< 0.01	-	1.00E00	1
RNA localization	82	0	.09	< 0.01	-	1.00E00	2
cellular calcium ion homeostasis	85	0	.10	< 0.01	-	1.00E00	1
complement activation	86	0	.10	< 0.01	-	1.00E00	1
B cell mediated immunity	87	0	.10	< 0.01	-	1.00E00	2
spermatogenesis	88	0	.10	< 0.01	-	1.00E00	1
cation transport	89	0	.10	< 0.01	-	1.00E00	1
ion transport	361	0	.41	< 0.01	-	1.00E00	1
protein folding	89	0	.10	< 0.01	-	1.00E00	1
cell recognition	92	0	.10	< 0.01	-	1.00E00	1
chromosome segregation	95	0	.11	< 0.01	-	1.00E00	2
embryo development	95	0	.11	< 0.01	-	1.00E00	2
negative regulation of apoptotic process	98	0	.11	< 0.01	-	1.00E00	1
receptor-mediated endocytosis	103	0	.12	< 0.01	-	1.00E00	1
defense response to bacterium	104	0	.12	< 0.01	-	1.00E00	1
cellular defense response	106	0	.12	< 0.01	-	1.00E00	1
nucleobase-containing compound transport	107	0	.12	< 0.01	-	1.00E00	1
rRNA metabolic process	111	0	.13	< 0.01	-	1.00E00	3

muscle contraction	112	0	.13	< 0.01	-	1.00E00	1
tRNA metabolic process	112	2	.13	15.66	+	7.41E-03	1
respiratory electron transport chain	117	0	.13	< 0.01	-	1.00E00	3
nuclear transport	119	0	.14	< 0.01	-	1.00E00	4
cell-cell adhesion	121	0	.14	< 0.01	-	1.00E00	1
cytokinesis	131	0	.15	< 0.01	-	1.00E00	1
RNA splicing, via transesterification reactions	139	0	.16	< 0.01	-	1.00E00	1
↳ RNA splicing	150	0	.17	< 0.01	-	1.00E00	1
response to biotic stimulus	147	0	.17	< 0.01	-	1.00E00	1
transmembrane receptor protein tyrosine kinase signaling pathway	151	0	.17	< 0.01	-	1.00E00	1
DNA replication	156	17	.18	95.54	+	5.17E-31	1
protein targeting	160	0	.18	< 0.01	-	1.00E00	1
↳ intracellular protein transport	688	0	.78	< 0.01	-	1.00E00	2
↳ protein transport	720	0	.82	< 0.01	-	1.00E00	1
mRNA splicing, via spliceosome	161	2	.18	10.89	+	1.47E-02	2
DNA repair	162	9	.18	48.71	+	1.46E-13	8
regulation of cell cycle	164	0	.19	< 0.01	-	1.00E00	1
phospholipid metabolic process	177	0	.20	< 0.01	-	1.00E00	2
phagocytosis	178	0	.20	< 0.01	-	1.00E00	2
ectoderm development	206	0	.23	< 0.01	-	1.00E00	2
response to endogenous stimulus	219	0	.25	< 0.01	-	1.00E00	4
anion transport	220	0	.25	< 0.01	-	1.00E00	4
mitosis	221	0	.25	< 0.01	-	1.00E00	4
protein complex assembly	237	0	.27	< 0.01	-	1.00E00	1
↳ protein complex biogenesis	1	0	.00	< 0.01	-	1.00E00	3
↳ cellular component biogenesis	504	0	.57	< 0.01	-	1.00E00	1
nervous system development	238	0	.27	< 0.01	-	1.00E00	1
sensory perception of smell	240	0	.27	< 0.01	-	1.00E00	2
locomotion	253	0	.29	< 0.01	-	1.00E00	2
chromatin organization	255	0	.29	< 0.01	-	1.00E00	1
regulation of catalytic activity	338	0	.39	< 0.01	-	1.00E00	2
cellular component morphogenesis	339	0	.39	< 0.01	-	1.00E00	2
↳ anatomical structure morphogenesis	470	0	.54	< 0.01	-	1.00E00	1
cytoskeleton organization	379	0	.43	< 0.01	-	1.00E00	1
cellular component movement	407	0	.46	< 0.01	-	1.00E00	1
proteolysis	420	0	.48	< 0.01	-	1.00E00	1
cell differentiation	459	0	.52	< 0.01	-	1.00E00	1
G-protein coupled receptor signaling pathway	470	0	.54	< 0.01	-	1.00E00	1
regulation of phosphate metabolic process	479	0	.55	< 0.01	-	1.00E00	1
regulation of transcription from RNA polymerase II promoter	548	3	.63	4.80	+	2.39E-02	3
↳ regulation of nucleobase-containing compound metabolic process	1151	3	1.31	2.29	+	1.42E-01	1
response to stress	684	9	.78	11.54	+	3.60E-08	1
catabolic process	1127	4	1.29	3.11	+	3.72E-02	4
biosynthetic process	1659	13	1.89	6.87	+	5.15E-09	2
Unclassified	10635	6	12.13	.49	-	1.37E-02	2