

Supplementary Files

Nevirapine induced mitochondrial dysfunction in HepG2 cells

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Supplemental File S1: Full list of annotation clusters identified by DAVID

Supplemental File S2: Full list of cellular components identified by PANTHER

Functional Annotation Clustering

[Help and Manual](#)

Current Gene List: [List_2](#)
















































Current Background: [Homo sapiens](#)

33 DAVID IDs

Options Classification Stringency Medium

15 Cluster(s)

 [Download File](#)

	Annotation Cluster 1	Enrichment Score: 3.22	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial part	RT		12	1.3E-8	1.5E-6
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial matrix	RT		9	1.5E-8	8.3E-7
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial lumen	RT		9	1.5E-8	8.3E-7
<input type="checkbox"/>	GOTERM_CC_FAT	nucleoid	RT		5	4.8E-7	1.8E-5
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial nucleoid	RT		5	4.8E-7	1.8E-5
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrion	RT		13	7.0E-7	2.0E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT		9	7.5E-7	2.4E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	transit peptide	RT		9	8.3E-7	6.2E-5
<input type="checkbox"/>	SP_PIR_KEYWORDS	mitochondrion	RT		10	5.8E-6	2.2E-4
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial membrane	RT		8	1.3E-5	3.0E-4
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial envelope	RT		8	1.9E-5	3.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT	organelle envelope	RT		9	2.9E-5	4.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT	envelope	RT		9	2.9E-5	4.2E-4
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial inner membrane	RT		7	3.5E-5	4.4E-4
<input type="checkbox"/>	GOTERM_CC_FAT	organelle inner membrane	RT		7	5.2E-5	5.9E-4
<input type="checkbox"/>	GOTERM_CC_FAT	intracellular organelle lumen	RT		12	5.6E-4	5.8E-3
<input type="checkbox"/>	GOTERM_CC_FAT	organelle lumen	RT		12	6.8E-4	6.5E-3
<input type="checkbox"/>	GOTERM_CC_FAT	membrane-enclosed lumen	RT		12	8.1E-4	7.1E-3
<input type="checkbox"/>	GOTERM_CC_FAT	organelle membrane	RT		8	6.4E-3	4.8E-2
<input type="checkbox"/>	KEGG_PATHWAY	Parkinson's disease	RT		4	8.2E-3	7.1E-2
<input type="checkbox"/>	KEGG_PATHWAY	Alzheimer's disease	RT		4	1.6E-2	9.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	oxidative phosphorylation	RT		3	1.6E-2	4.2E-1
<input type="checkbox"/>	KEGG_PATHWAY	Huntington's disease	RT		4	2.1E-2	1.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial membrane part	RT		3	2.8E-2	1.7E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	mitochondrion inner membrane	RT		3	4.1E-2	3.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	Oxidative phosphorylation	RT		3	6.9E-2	2.7E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	ion transport	RT		4	7.0E-2	4.4E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	transport	RT		6	1.4E-1	6.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ion transport	RT		4	2.0E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	phosphorylation	RT		4	2.1E-1	9.0E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	hydrolase	RT		5	2.6E-1	8.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	phosphorus metabolic process	RT		4	3.1E-1	9.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	phosphate metabolic process	RT		4	3.1E-1	9.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	transmembrane transport	RT		3	3.2E-1	9.5E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	membrane	RT		10	7.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	plasma membrane	RT		6	9.4E-1	1.0E0
	Annotation Cluster 2	Enrichment Score: 2.47	G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	gluconeogenesis	RT		4	4.0E-6	2.0E-4
<input type="checkbox"/>	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT		4	9.4E-4	3.3E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	glycolysis	RT		3	2.4E-3	4.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	glucose metabolic process	RT		4	3.4E-3	4.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	glycolysis	RT		3	3.9E-3	3.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	glucose catabolic process	RT		3	5.9E-3	4.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	hexose metabolic process	RT		4	6.4E-3	4.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	hexose catabolic process	RT		3	8.3E-3	4.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	monosaccharide catabolic process	RT		3	8.8E-3	4.2E-1

	Annotation Cluster	Enrichment Score	Gene	Bar	Count	P_Value	Benjamini
<input type="checkbox"/>	Annotation Cluster 1	3.22					
<input type="checkbox"/>	GOTERM_BP_FAT	monosaccharide metabolic process	RT		4	9.5E-3	4.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	alcohol catabolic process	RT		3	1.1E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular carbohydrate catabolic process	RT		3	1.2E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	carbohydrate catabolic process	RT		3	2.0E-2	4.1E-1
<input type="checkbox"/>	Annotation Cluster 3	2.43					
<input type="checkbox"/>	GOTERM_MF_FAT	NAD or NADH binding	RT		4	1.5E-4	2.8E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	oxidoreductase	RT		7	2.9E-4	8.5E-3
<input type="checkbox"/>	GOTERM_BP_FAT	oxidation reduction	RT		7	1.4E-3	2.9E-1
<input type="checkbox"/>	GOTERM_MF_FAT	cofactor binding	RT		5	2.2E-3	9.4E-2
<input type="checkbox"/>	GOTERM_MF_FAT	coenzyme binding	RT		4	7.5E-3	1.8E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	nadp	RT		3	2.8E-2	2.4E-1
<input type="checkbox"/>	INTERPRO	NAD(P)-binding domain	RT		3	3.3E-2	8.3E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	nad	RT		3	3.9E-2	3.1E-1
<input type="checkbox"/>	Annotation Cluster 4	2.2					
<input type="checkbox"/>	KEGG_PATHWAY	Propanoate metabolism	RT		3	4.9E-3	8.5E-2
<input type="checkbox"/>	KEGG_PATHWAY	Butanoate metabolism	RT		3	5.5E-3	6.5E-2
<input type="checkbox"/>	KEGG_PATHWAY	Valine, leucine and isoleucine degradation	RT		3	9.2E-3	6.4E-2
<input type="checkbox"/>	Annotation Cluster 5	1.67					
<input type="checkbox"/>	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT		12	1.2E-2	8.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	non-membrane-bounded organelle	RT		12	1.2E-2	8.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cytoskeleton	RT		7	6.4E-2	3.0E-1
<input type="checkbox"/>	Annotation Cluster 6	1.57					
<input type="checkbox"/>	GOTERM_BP_FAT	ATP biosynthetic process	RT		3	1.4E-2	4.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT		3	1.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT		3	1.7E-2	4.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT		3	1.7E-2	4.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT		3	1.7E-2	4.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ATP metabolic process	RT		3	1.8E-2	4.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT		3	2.3E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT		3	2.3E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT		3	2.3E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT		3	2.4E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT		3	2.5E-2	4.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	nitrogen compound biosynthetic process	RT		4	2.6E-2	4.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT		3	2.8E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT		3	3.1E-2	4.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ribonucleotide metabolic process	RT		3	3.4E-2	4.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	purine nucleotide biosynthetic process	RT		3	3.5E-2	4.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	purine nucleotide metabolic process	RT		3	5.3E-2	5.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	nucleotide biosynthetic process	RT		3	5.3E-2	5.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	RT		3	5.6E-2	5.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	nucleobase, nucleoside and nucleotide biosynthetic process	RT		3	5.6E-2	5.7E-1
<input type="checkbox"/>	Annotation Cluster 7	1.38					
<input type="checkbox"/>	GOTERM_CC_FAT	pigment granule	RT		4	8.5E-4	6.9E-3
<input type="checkbox"/>	GOTERM_CC_FAT	melanosome	RT		4	8.5E-4	6.9E-3
<input type="checkbox"/>	GOTERM_CC_FAT	membrane-bounded vesicle	RT		5	3.0E-2	1.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	vesicle	RT		5	5.0E-2	2.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT		4	1.1E-1	4.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic vesicle	RT		4	1.5E-1	5.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum	RT		3	6.1E-1	9.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular region	RT		4	8.2E-1	1.0E0
<input type="checkbox"/>	Annotation Cluster 8	1.17					
<input type="checkbox"/>	SP_PIR_KEYWORDS	P-loop	RT		4	9.3E-4	2.3E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	nucleotide-binding	RT		9	5.3E-3	7.7E-2
<input type="checkbox"/>	GOTERM_MF_FAT	nucleotide binding	RT		12	6.6E-3	1.8E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	gtp-binding	RT		4	1.7E-2	1.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	purine ribonucleotide binding	RT		9	4.3E-2	6.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	ribonucleotide binding	RT		9	4.3E-2	6.4E-1

Annotation Cluster 1		Enrichment Score: 3.22	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	GTP binding	RT		4	4.9E-2	6.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	guanyl ribonucleotide binding	RT		4	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	guanyl nucleotide binding	RT		4	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	purine nucleotide binding	RT		9	5.4E-2	6.1E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	atp-binding	RT		6	6.6E-2	4.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT		3	8.7E-2	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	purine nucleoside binding	RT		7	1.4E-1	8.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	nucleoside binding	RT		7	1.4E-1	8.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cell surface	RT		3	1.7E-1	5.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	phosphorylation	RT		4	2.1E-1	9.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	ATP binding	RT		6	2.3E-1	9.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT		6	2.4E-1	9.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	adenyl nucleotide binding	RT		6	2.7E-1	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	phosphorus metabolic process	RT		4	3.1E-1	9.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	phosphate metabolic process	RT		4	3.1E-1	9.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT		3	4.8E-1	1.0E0
Annotation Cluster 9		Enrichment Score: 0.93	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	response to organic substance	RT		6	1.3E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to organic cyclic substance	RT		3	2.4E-2	4.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	soluble fraction	RT		4	2.8E-2	1.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to hormone stimulus	RT		3	1.7E-1	8.8E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cell fraction	RT		5	1.9E-1	6.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to endogenous stimulus	RT		3	1.9E-1	9.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cytosol	RT		5	3.1E-1	8.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	membrane fraction	RT		3	5.2E-1	9.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	insoluble fraction	RT		3	5.4E-1	9.6E-1
Annotation Cluster 10		Enrichment Score: 0.88	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	protein homooligomerization	RT		3	1.5E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein oligomerization	RT		3	4.7E-2	5.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	lipid binding	RT		4	7.8E-2	7.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein complex assembly	RT		3	2.7E-1	9.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein complex biogenesis	RT		3	2.7E-1	9.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecular complex assembly	RT		3	3.9E-1	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecular complex subunit organization	RT		3	4.2E-1	9.8E-1
Annotation Cluster 11		Enrichment Score: 0.73	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of apoptosis	RT		3	1.6E-1	8.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of programmed cell death	RT		3	1.6E-1	8.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cell death	RT		3	1.6E-1	8.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of apoptosis	RT		4	2.1E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of programmed cell death	RT		4	2.2E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell death	RT		4	2.2E-1	9.0E-1
Annotation Cluster 12		Enrichment Score: 0.66	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	intracellular protein transport	RT		3	1.7E-1	8.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein transport	RT		4	1.9E-1	9.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	establishment of protein localization	RT		4	2.0E-1	9.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular protein localization	RT		3	2.0E-1	8.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecule localization	RT		3	2.0E-1	8.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein localization	RT		4	2.6E-1	9.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	intracellular transport	RT		3	3.8E-1	9.8E-1
Annotation Cluster 13		Enrichment Score: 0.6	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	synaptic transmission	RT		3	1.2E-1	8.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	transmission of nerve impulse	RT		3	1.5E-1	8.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	behavior	RT		3	2.4E-1	9.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cell-cell signaling	RT		3	3.4E-1	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	neurological system process	RT		3	7.1E-1	1.0E0
Annotation Cluster 14		Enrichment Score: 0.17	G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	calcium ion binding	RT		4	3.4E-1	9.9E-1
<input type="checkbox"/>	GOTERM_MF_FAT	ion binding	RT		10	6.4E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	metal-binding	RT		5	7.5E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	metal ion binding	RT		9	7.5E-1	1.0E0

Annotation Cluster 1		Enrichment Score: 3.22		G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	cation binding	RT			9	7.6E-1	1.0E0
<input type="checkbox"/>	GOTERM_MF_FAT	transition metal ion binding	RT			4	9.6E-1	1.0E0
Annotation Cluster 15		Enrichment Score: 0.03		G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell membrane	RT			4	7.2E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	plasma membrane	RT			6	9.4E-1	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	RT			4	9.9E-1	1.0E0
<input type="checkbox"/>	SP_PIR_KEYWORDS	transmembrane	RT			4	9.9E-1	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	integral to membrane	RT			4	1.0E0	1.0E0
<input type="checkbox"/>	GOTERM_CC_FAT	intrinsic to membrane	RT			4	1.0E0	1.0E0

42 terms were not clustered.



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

Analysis Type: PANTHER Overrepresentation Test (release 20160715)	
Annotation Version and Release Date: GO Ontology database Released 2016-11-30	
Analyzed List:	upload_1 (Homo sapiens) Change
Reference List:	Homo sapiens (all genes in database) Change
Annotation Data Set:	GO cellular component complete v
<input checked="" type="checkbox"/> Use the Bonferroni correction for multiple testing ?	

Results [?](#)

	Reference list	upload_1
Mapped IDs:	20972 out of 20972	33 out of 36
Unmapped IDs:	0	0
Multiple mapping information:	0	3

Bonferroni count: 1304

[Export results](#)

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

	Homo sapiens (REF)	upload_1 (v Hierarchy NEW! ?)				
	#	#	expected	Fold Enrichment	+/-	P value
GO cellular component complete						
mitochondrial nucleoid	45	5	.08	64.73	+	2.12E-05
↳ organelle	13117	35	22.52	1.55	+	1.35E-03
↳ mitochondrion	1725	14	2.96	4.73	+	5.58E-04
↳ cytoplasmic part	8168	30	14.02	2.14	+	7.74E-05
↳ cytoplasm	10829	32	18.59	1.72	+	3.13E-03
↳ membrane-bounded organelle	12169	34	20.89	1.63	+	1.44E-03
↳ nucleoid	47	5	.08	61.97	+	2.62E-05
↳ mitochondrial part	1002	11	1.72	6.40	+	7.61E-04
↳ mitochondrial matrix	428	9	.73	12.25	+	4.58E-05
myelin sheath	179	9	.31	29.29	+	2.40E-08
mitochondrial inner membrane	505	8	.87	9.23	+	2.44E-03
↳ mitochondrial membrane	700	8	1.20	6.66	+	2.63E-02
↳ mitochondrial envelope	741	8	1.27	6.29	+	3.94E-02
↳ organelle envelope	1155	11	1.98	5.55	+	3.05E-03
↳ envelope	1161	11	1.99	5.52	+	3.21E-03
↳ organelle inner membrane	563	8	.97	8.28	+	5.43E-03

extracellular matrix	522	8	.90	8.93	+ 3.11E-03
↳ extracellular region part	3841	28	6.59	4.25	+ 1.90E-11
↳ extracellular region	4564	29	7.83	3.70	+ 1.30E-10
adherens junction	684	8	1.17	6.81	+ 2.23E-02
↳ anchoring junction	702	8	1.21	6.64	+ 2.68E-02
extracellular exosome	2750	26	4.72	5.51	+ 9.88E-13
↳ extracellular vesicle	2764	26	4.74	5.48	+ 1.12E-12
↳ vesicle	4051	27	6.95	3.88	+ 1.01E-09
↳ extracellular organelle	2765	26	4.75	5.48	+ 1.13E-12