

## Genes GENES - KEGG Annotations

## Used notations:

- **List Hits** - the number of genes annotated by the considered KEGG category or annotation cluster within the analyzed list of target genes
- **List Total** - the number of genes within the analyzed list of target genes having at least one KEGG annotation
- **Population Hits** - the number of genes, available on the entire microarray, annotated by the considered KEGG category or annotation cluster
- **Population Total** - the number of genes available on the entire microarray and having at least one KEGG annotation
- **P-value** - the significance p-value of the gene enrichment of the considered KEGG category or annotation cluster, calculated with a unilateral Fisher exact test

## Terms

Rank	ID	Term	List Hits	List Total	Population Hits	Population Total	P-value	Genes ID's	Genes Names
1	04141	Protein processing in endoplasmic reticulum	36	304	167	5981	4.3e-14		hypoxia up-regulated 1
2	05016	Huntington's disease	33	304	183	5981	9.37e-11		ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d
3	00190	Oxidative phosphorylation	30	304	132	5981	1.53e-12		ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d
4	05010	Alzheimer's disease	29	304	167	5981	3.47e-09		ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d
5	05012	Parkinson's disease	26	304	130	5981	1.02e-09		ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d
6	03010	Ribosome	25	304	92	5981	1.7e-12		ribosomal protein S17-like
7	05322	Systemic lupus erythematosus	18	304	138	5981	1.92e-04		histone cluster 4, H4
8	04260	Cardiac muscle contraction	13	304	77	5981	1.13e-04		cytochrome c oxidase subunit VIa polypeptide 1
9	03040	Spliceosome	12	304	128	5981	2.88e-02		breast carcinoma amplified sequence 2
10	04978	Mineral absorption	11	304	51	5981	3.74e-05		solute carrier family 34 (sodium phosphate), member 2
11	04142	Lysosome	11	304	121	5981	4.29e-02		clathrin, heavy chain (Hc)
12	05110	Vibrio cholerae infection	10	304	54	5981	3.23e-04		KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
13	04612	Antigen processing and presentation	10	304	78	5981	5.77e-03		protein disulfide isomerase family A, member 3
14	05120	Epithelial cell signaling in Helicobacter pylori infection	8	304	68	5981	2.11e-02		nucleotide-binding oligomerization domain containing 1
15	04962	Vasopressin-regulated water reabsorption	7	304	44	5981	6.18e-03		adenylate cyclase 9
16	03060	Protein export	7	304	23	5981	9.9e-05		Sec61 alpha 1 subunit (S. cerevisiae)
17	04961	Endocrine and other factor-regulated calcium reabsorption	6	304	49	5981	3.65e-02		adenylate cyclase 9
18	00510	N-Glycan biosynthesis	6	304	49	5981	3.65e-02		defender against cell death 1

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