



GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0044772	mitotic cell cycle phase transition	5.86E-4	1E0	1.77 (4545,127,891,44)	[+1 Show genes]
GO:0007017	microtubule-based process	6.09E-4	1E0	3.48 (4545,151,121,14)	[+1 Show genes]
GO:0006626	protein targeting to mitochondrion	7.01E-4	1E0	4.47 (4545,26,352,9)	[+1 Show genes]
GO:0072655	establishment of protein localization to mitochondrion	7.01E-4	1E0	4.47 (4545,26,352,9)	[+1 Show genes]
GO:0000132	establishment of mitotic spindle orientation	7.54E-4	1E0	26.22 (4545,8,65,3)	[+1 Show genes]
GO:0051438	regulation of ubiquitin-protein ligase activity	7.97E-4	1E0	2.32 (4545,44,891,20)	[+1 Show genes]
GO:0044770	cell cycle phase transition	8.5E-4	1E0	1.74 (4545,129,891,44)	[+1 Show genes]

Species used: Homo sapiens

The system has recognized 4864 genes out of 4873 gene terms entered by the user.
4864 genes were recognized by gene symbol and 0 genes by other gene IDs .
Only 4545 of these genes are associated with a GO term.

The GOrilla database is periodically updated using the [GO database](#) and other sources.
The GOrilla database was last updated on Apr 5, 2014

This results page will be available on this site for one month from now (until May 8, 2014). You can bookmark this page and come back to it later.

'P-value' is the enrichment p-value computed according to the mHG or HG model. This p-value is not corrected for multiple testing of 8250 GO terms.

'FDR q-value' is the correction of the above p-value for multiple testing using the Benjamini and Hochberg (1995) method.
Namely, for the i^{th} term (ranked according to p-value) the FDR q-value is $(p\text{-value} * \text{number of GO terms}) / i$.

Enrichment (N, B, n, b) is defined as follows:

N - is the total number of genes
B - is the total number of genes associated with a specific GO term
n - is the number of genes in the top of the user's input list or in the target set when appropriate
b - is the number of genes in the intersection
 $Enrichment = (b/n) / (B/N)$

Genes: For each GO term you can see the list of associated genes that appear in the optimal top of the list.
Each gene name is specified by gene symbol followed by a short description of the gene

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