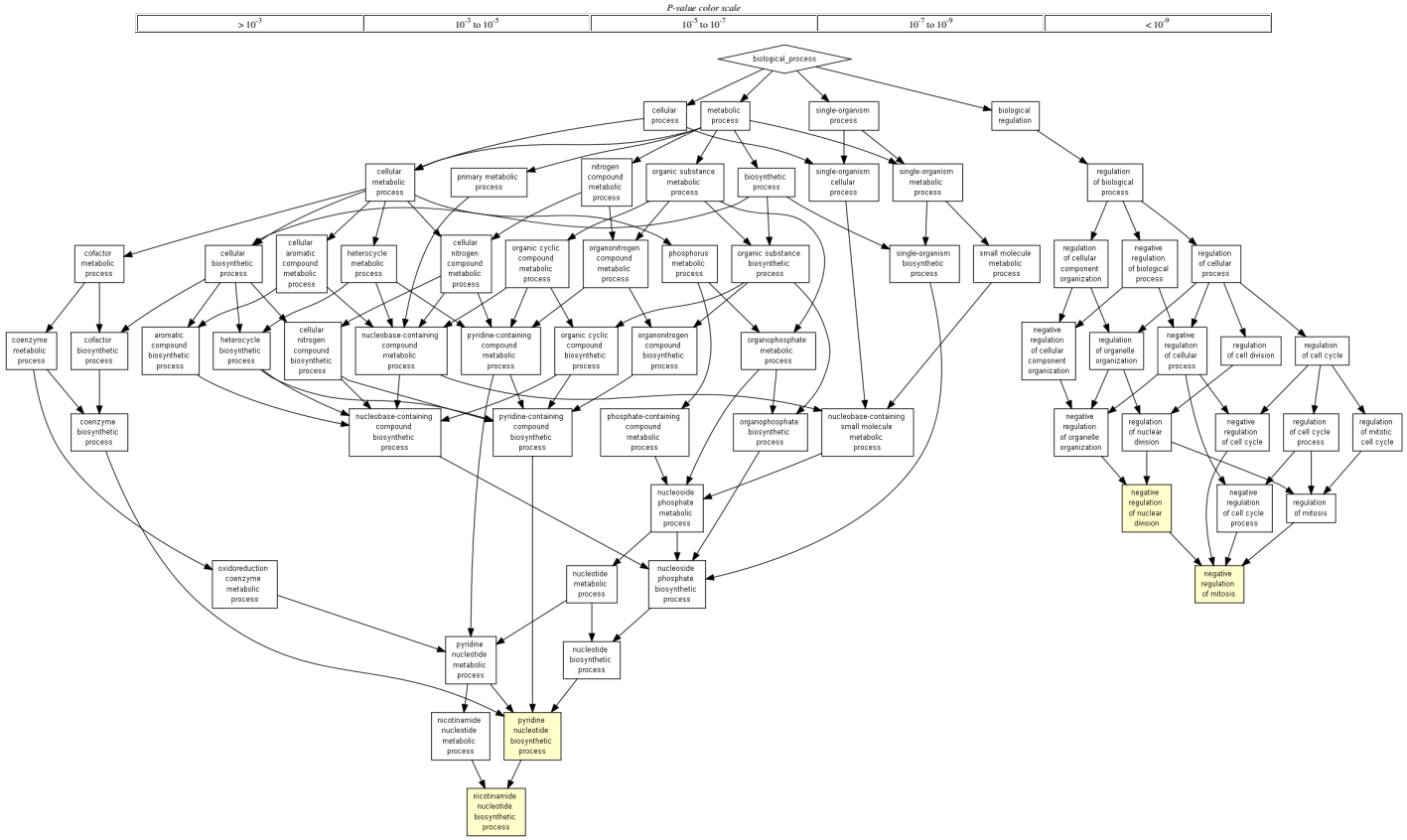

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0045839	negative regulation of mitosis	6.94E-4	1E0	5.05 (1595,11,201,7)	[+] Show genes
GO:0051784	negative regulation of nuclear division	6.94E-4	1E0	5.05 (1595,11,201,7)	[+] Show genes
GO:0019363	pyridine nucleotide biosynthetic process	9.64E-4	1E0	31.90 (1595,2,50,2)	[+] Show genes
GO:0019359	nicotinamide nucleotide biosynthetic process	9.64E-4	1E0	31.90 (1595,2,50,2)	[+] Show genes

Species used: Homo sapiens

The system has recognized 1648 genes out of 1649 gene terms entered by the user.
1648 genes were recognized by gene symbol and 0 genes by other gene IDs .
Only 1595 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 5937 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-value * 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

Back to the GOrilla main page