P-value color scale

$> 10^{-3}$	10^{-3} to 10^{-5}	10^{-5} to 10^{-7}	10^{-7} to 10^{-9}	$< 10^{-9}$

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0003677	DNA binding	1.07E-8	2.33E-5	1.65 (3290,558,424,119)	[+] Show genes
GO:0003676	nucleic acid binding	3.39E-5	3.68E-2	1.24 (3290,939,770,272)	[+] Show genes
GO:0043565	sequence-specific DNA binding	5.28E-5	3.82E-2	2.34 (3290,157,287,32)	[+] Show genes
GO:0005267	potassium channel activity	4.29E-4	2.33E-1	18.00 (3290,17,43,4)	[+] Show genes
GO:0070087	chromo shadow domain binding	4.5E-4	1.95E-1	16.05 (3290,3,205,3)	[+] Show genes
GO:0003682	chromatin binding	5.21E-4	1.88E-1	6.14 (3290,102,42,8)	[+] Show genes
GO:0022832	voltage-gated channel activity	6.93E-4	2.15E-1	16.11 (3290,19,43,4)	[+] Show genes

GO:0005244	voltage-gated ion channel activity	6.93E-4	1.88E-1	16.11 (3290,19,43,4)	[+] Show genes
GO:0035198	miRNA binding	7.8E-4	1.88E-1	71.52 (3290,4,23,2)	[+] Show genes
GO:0015079	potassium ion transmembrane transporter activity	9.16E-4	1.99E-1	15.30 (3290,20,43,4)	[+] Show genes

Species used: Homo sapiens

The system has recognized 3412 genes out of 3416 gene terms entered by the user.
3412 genes were recognized by gene symbol and 0 genes by other gene IDs .
1 duplicate genes were removed (keeping the highest ranking instance of each gene) leaving a total of 3411 genes.
Only 3290 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 2168 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

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