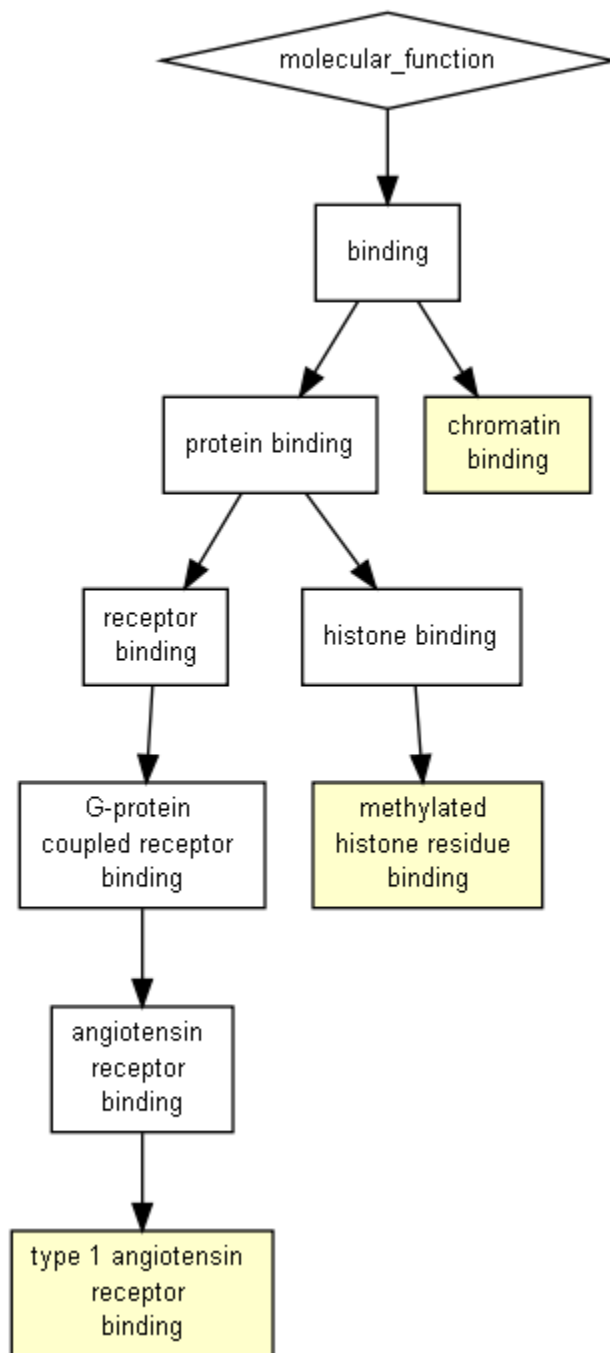


P-value color scale

| | | | | |
|-------------|------------------------|------------------------|------------------------|-------------|
| $> 10^{-3}$ | 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:0031702 | type 1 angiotensin receptor binding | 4.71E-4 | 1E0 | 15.98 (9174,3,574,3) | [+] Show genes |

| | | | | | |
|----------------------------|-----------------------------------|---------|---------|------------------------|---|
| GO:0003682 | chromatin binding | 5.34E-4 | 8.63E-1 | 1.83 (9174,210,981,41) | [+] Show genes |
| GO:0035064 | methyated histone residue binding | 7.79E-4 | 8.39E-1 | 30.18 (9174,24,38,3) | [+] Show genes |

Species used: Homo sapiens

The system has recognized 10385 genes out of 10422 gene terms entered by the user.

10385 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 10384 genes.

Only 9174 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 3229 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 $(\text{p-value} * \text{number of GO terms}) / i$.

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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