



GO term	Description	P-value	DR q-value	Enrichment (N, R, n)	Genes
<a href="#">GO:0000121</a>	positive regulation of cationic input into nucleus	6.44E-4	4.02E-1	125/34 (2869/213,406/53)	<a href="#">Go to this gene</a>
<a href="#">GO:0000124</a>	negative regulation of cellular macromolecular biosynthetic process	1.41E-4	5.38E-1	134/34 (2869/213,406/53)	<a href="#">Go to this gene</a>
<a href="#">GO:0000125</a>	negative regulation of macromolecular biosynthetic process	2.58E-4	6.03E-1	171/34 (2869/213,406/53)	<a href="#">Go to this gene</a>
<a href="#">GO:0000126</a>	regulation of gene silencing by siRNA	3.25E-4	6.10E-1	84/81 (2869/3,12/25)	<a href="#">Go to this gene</a>
<a href="#">GO:0000129</a>	regulation of gene silencing by RNA	1.25E-4	4.93E-1	84/81 (2869/3,12/25)	<a href="#">Go to this gene</a>
<a href="#">GO:0000130</a>	regulation of posttranscriptional gene silencing	3.25E-4	4.13E-1	84/81 (2869/3,12/25)	<a href="#">Go to this gene</a>
<a href="#">GO:0000131</a>	posttranscriptional gene silencing	3.25E-4	3.87E-1	159/2869 (435,534/132)	<a href="#">Go to this gene</a>
<a href="#">GO:0000132</a>	regulation of macromolecular metabolic process	1.87E-4	3.68E-1	150/2869 (499,373/124)	<a href="#">Go to this gene</a>
<a href="#">GO:0000133</a>	negative regulation of transcription, DNA-templated	4.13E-4	3.68E-1	179/2869 (534,406/47)	<a href="#">Go to this gene</a>
<a href="#">GO:0000134</a>	negative regulation of cellular biosynthetic process	5.3E-4	4.03E-1	146/2869 (226,406/54)	<a href="#">Go to this gene</a>
<a href="#">GO:0000135</a>	negative regulation of biosynthetic process	5.84E-4	4.44E-1	145/2869 (229,406/54)	<a href="#">Go to this gene</a>
<a href="#">GO:0000136</a>	regulation of primary metabolic process	6.06E-4	3.84E-1	132/2869 (538,373/127)	<a href="#">Go to this gene</a>
<a href="#">GO:0000137</a>	negative regulation of nucleoside-containing compound metabolic process	6.25E-4	3.66E-1	148/2869 (213,406/53)	<a href="#">Go to this gene</a>
<a href="#">GO:0000138</a>	negative regulation of RNA biosynthetic process	6.34E-4	3.63E-1	176/2869 (537,406/47)	<a href="#">Go to this gene</a>
<a href="#">GO:0000139</a>	positive regulation of metabolism, biosynthesis	7.55E-4	3.75E-1	109/2869 (34,53/5)	<a href="#">Go to this gene</a>
<a href="#">GO:0000140</a>	regulation of metabolic process	7.61E-4	3.77E-1	126/2869 (1023,373/173)	<a href="#">Go to this gene</a>
<a href="#">GO:0000141</a>	RNA biosynthetic process	8.21E-4	3.69E-1	131/2869 (406,534/106)	<a href="#">Go to this gene</a>
<a href="#">GO:0000142</a>	cellular response to stress	8.25E-4	3.40E-1	132/2869 (49,534/106)	<a href="#">Go to this gene</a>
<a href="#">GO:0000143</a>	pyruvate production	8.26E-4	3.53E-1	64/1 (2869/6,363/5)	<a href="#">Go to this gene</a>
<a href="#">GO:0000144</a>	cellular response to osmotic stress	8.75E-4	3.33E-1	170/2869 (2,21/5)	<a href="#">Go to this gene</a>
<a href="#">GO:0000145</a>	regulation of cellular macromolecular biosynthetic process	8.97E-4	3.28E-1	138/2869 (664,528/107)	<a href="#">Go to this gene</a>
<a href="#">GO:0000146</a>	post-translational modification of protein	9.27E-4	3.21E-1	133/2869 (518,534/132)	<a href="#">Go to this gene</a>
<a href="#">GO:0000147</a>	regulation of cellular metabolic process	9.46E-4	3.14E-1	137/2869 (52,373/106)	<a href="#">Go to this gene</a>

Species used: Homo sapiens

The system has recognized 2869 genes out of 2867 gene terms entered by the user.

2867 genes were recognized by gene symbol and 0 genes by other gene IDs.

1 duplicate gene was removed (keeping the highest ranking instance of each gene) leaving a total of 2862 genes.

Only 2860 of those genes are associated with a GO term.

The GOdb database is periodically updated using the [GO database](#) and other sources.

The GOdb database was last updated on April 5, 2014.

This results page will be available on this site for one month from now (until May 6, 2014). You can bookmark this page and come back to it later.

**P-value** is the enrichment p-value computed according to the [FDR](#) or [FDR](#) method. This p-value is not corrected for multiple testing of 7617 GO terms.

**FDR q-value** is the correction of the above p-value for multiple testing using the Benjamini and Hochberg (1995) method.

Simply, 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, R, n)** is defined as follows:

- N - is the total number of genes
  - R - 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
  - i - is the number of genes in the intersection
- Enrichment =  $(R/n) / (R/N)$

**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 GOdb main page](#)