



GO term	Description	Enrich	FDR,adj	Enrichment (S.R. & z)	Gene
GO:0001567	regulation of keratinocyte migration	7.71E-4	1E0	5.33530 (10672.3,1.0)	141 Show gene
GO:0001549	positive regulation of keratinocyte migration	3.71E-4	1E0	5.33530 (10672.3,1.0)	141 Show gene
GO:0001543	negative regulation of interleukin-1 biosynthetic process	4.12E-4	1E0	6.350 (10671.6,0.53)	141 Show gene
GO:0001544	apoptotic process involved in keratinocyte	4.58E-4	1E0	59.05 (10672.2,1.782)	141 Show gene
GO:0001540	cellular response to exogenous DNA	3.19E-4	1E0	13.157 (10674.6,2.654)	141 Show gene
GO:0001576	negative regulation of gene silencing by RNA	6.56E-4	1E0	1.254 (10671.7,1.0)	141 Show gene
GO:0001566	regulation of gene silencing by siRNA	6.56E-4	1E0	1.254 (10671.7,1.0)	141 Show gene
GO:0001568	regulation of gene silencing by siRNA	6.56E-4	1E0	1.254 (10671.7,1.0)	141 Show gene
GO:0001569	regulation of gene silencing by siRNA	6.56E-4	1E0	1.254 (10671.7,1.0)	141 Show gene
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Species used: *Homo sapiens*

The system has recognized 11992 genes out of 12030 gene terms entered by the user.

2 duplicate genes were removed (keeping the highest ranking instance of each gene) leaving a total of 11930 genes

Only 10671 of these genes are associated with a GO term

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

The GOvella database was last updated on Apr 5, 2014.

P-value^a is the enrichment p-value computed according to the mHG or HG model. This p-value is not corrected for multiple testing of 10845 GO terms.

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

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

Enrichment (N, R, n, b) 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
- b - is the number of genes in the intersection

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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