GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0006637	acyl-CoA metabolic process	1.36E-6	1.1E-2	6.63 (14414,34,639,10)	[+] Show genes
GO:0035383	thioester metabolic process	1.36E-6	5.49E-3	6.63 (14414,34,639,10)	[+] Show genes
GO:0006790	sulfur compound metabolic process	3.51E-6	9.42E-3	3.35 (14414,128,639,19)	[+] Show genes
GO:0034032	purine nucleoside bisphosphate metabolic process	1.11E-5	2.23E-2	5.37 (14414,42,639,10)	[+] Show genes
GO:0033865	nucleoside bisphosphate metabolic process	1.11E-5	1.79E-2	5.37 (14414,42,639,10)	[+] Show genes
GO:0033875	ribonucleoside bisphosphate metabolic process	1.11E-5	1.49E-2	5.37 (14414,42,639,10)	[+] Show genes
GO:0055088	lipid homeostasis	5.82E-5	6.69E-2	6.58 (14414,24,639,7)	[+] Show genes
GO:0033554	cellular response to stress	6.07E-5	6.11E-2	1.98 (14414,422,639,37)	[+] Show genes
GO:0006259	DNA metabolic process	1.87E-4	1.68E-1	2.09 (14414,302,639,28)	[+] Show genes
GO:0030309	poly-N-acetyllactosamine metabolic process	2.42E-4	1.94E-1	8.06 (14414,14,639,5)	[+] Show genes
GO:0030311	poly-N-acetyllactosamine biosynthetic process	2.42E-4	1.77E-1	8.06 (14414,14,639,5)	[+] Show genes
GO:0008203	cholesterol metabolic process	2.71E-4	1.82E-1	5.26 (14414,30,639,7)	[+] Show genes
GO:0006631	fatty acid metabolic process	2.91E-4	1.8E-1	2.92 (14414,108,639,14)	[+] Show genes
GO:0002143	tRNA wobble position uridine thiolation	3.35E-4	1.93E-1	16.92 (14414,4,639,3)	[+] Show genes
GO:0034227	tRNA thio-modification	3.35E-4	1.8E-1	16.92 (14414,4,639,3)	[+] Show genes
GO:0033292	T-tubule organization	3.35E-4	1.69E-1	16.92 (14414,4,639,3)	[+] Show genes
GO:0055092	sterol homeostasis	3.49E-4	1.65E-1	7.52 (14414,15,639,5)	[+] Show genes
GO:0042632	cholesterol homeostasis	3.49E-4	1.56E-1	7.52 (14414,15,639,5)	[+] Show genes
GO:1902652	secondary alcohol metabolic process	4.16E-4	1.76E-1	4.93 (14414,32,639,7)	[+] Show genes
GO:0044255	cellular lipid metabolic process	6.08E-4	2.44E-1	1.85 (14414,390,639,32)	[+] Show genes
GO:0034243	regulation of transcription elongation from RNA polymerase II promoter	6.68E-4	2.56E-1	6.63 (14414,17,639,5)	[+] Show genes
GO:0006974	cellular response to DNA damage stimulus	7.78E-4	2.84E-1	2.04 (14414,266,639,24)	[+] Show genes
GO:0010898	positive regulation of triglyceride catabolic process	8.11E-4	2.84E-1	13.53 (14414,5,639,3)	[+] Show genes
GO:0010896	regulation of triglyceride catabolic process	8.11E-4	2.72E-1	13.53 (14414,5,639,3)	[+] Show genes
GO:0030300	regulation of intestinal cholesterol absorption	8.11E-4	2.61E-1	13.53 (14414,5,639,3)	[+] Show genes
GO:1904729	regulation of intestinal lipid absorption	8.11E-4	2.51E-1	13.53 (14414,5,639,3)	[+] Show genes
GO:1904478	regulation of intestinal absorption	8.11E-4	2.42E-1	13.53 (14414,5,639,3)	[+] Show genes
GO:0045723	positive regulation of fatty acid biosynthetic process	8.11E-4	2.33E-1	13.53 (14414,5,639,3)	[+] Show genes
GO:0061365	positive regulation of triglyceride lipase activity	8.11E-4	2.25E-1	13.53 (14414,5,639,3)	[+] Show genes
GO:0042304	regulation of fatty acid biosynthetic process	8.11E-4	2.17E-1	13.53 (14414,5,639,3)	[+] Show genes
GO:0051004	regulation of lipoprotein lipase activity	8.11E-4	2.1E-1	13.53 (14414,5,639,3)	[+] Show genes
GO:0051006	positive regulation of lipoprotein lipase activity	8.11E-4	2.04E-1	13.53 (14414,5,639,3)	[+] Show genes
GO:0051716	cellular response to stimulus	9.56E-4	2.33E-1	1.61 (14414,644,639,46)	[+] Show genes
GO:0006695	cholesterol biosynthetic process	9.84E-4	2.33E-1	8.20 (14414,11,639,4)	[+] Show genes

Note that only 38.15% of the terms you entered were used in the analysis

Species used: Danio rerio (Zebrafish)

The system has recognized 17175 genes out of 37782 gene terms entered by the user.
0 genes were recognized by gene symbol and 17175 genes by other gene IDs .
756 duplicate genes were removed (keeping the highest ranking instance of each gene) leaving a total of 16419 genes.
Only 14414 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 Jul 7, 2018

This results page will be available on this site for one month from now (until Aug 10, 2018). 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 8046 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 ith 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