GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0005622	intracellular	2.89E-10	3.68E-7	2.78 (14414,373,639,46)	[+] Show genes
GO:0019908	nuclear cyclin-dependent protein kinase holoenzyme complex	8.67E-5	5.53E-2	22.56 (14414,3,639,3)	[+] 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 1274 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