

Kyoto Encyclopedia of Genes and Genomes

Based on the KEGG database, KEGG enrichment analysis performs functional annotation and pathway enrichment analysis of genes in the gene collection.

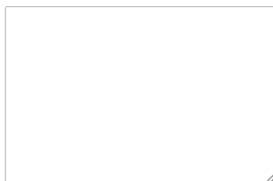
Usage:

1. Paste the gene list in the search box or upload the gene list file.
2. Adjust the parameters of the figure, including height, width, color, fontsize, fontcolor and fontweight. Click "submit" to submit.

Kyoto Encyclopedia of Genes and Genomes:

KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies. You can also go to the kegg website (<https://www.kegg.jp/>) to get more information.

Enter The Gene ID:







← Paste the gene list

Eg.MSU7

Data File : 未选择任何文件

← Upload the gene list file

Height(heatmap): <input type="text" value="50"/>	Fontsize: <input type="text" value="14"/>
Width(heatmap): <input type="text" value="100"/>	Fontcolor: <input type="text" value="#6b6b6b"/>
Color: <input type="radio"/>  <input checked="" type="radio"/>  <input type="radio"/>  <input type="radio"/> 	Fontweight: <input type="radio"/> bold <input checked="" type="radio"/> normal

← Adjust the parameters of the figure

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Click to submit

Results :

1. The list showing the top 10 results of KEGG enrichment analysis. Click the link at the top right to get all the results downloaded.
2. The barplot and dotplot of KEGG enrichment analysis results. Move mouse to drag the slider on the left to control the range of data displayed in the figure. Click the arrow at the top right to download the figure.

KEGG enrichment result

Top 10 results are listed in the table, if you want to get all information, please download the result file.

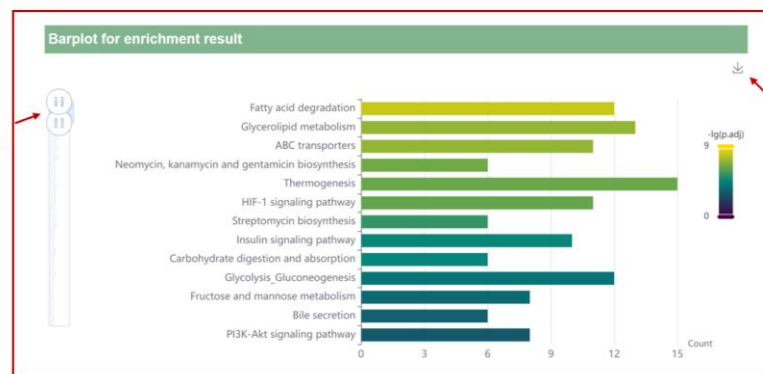
[Click here to download all the information.](#)

← **Click to download
all the results**

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
ko00071	Fatty acid degradation	12/99	52/5998	2.48076909548972e-11	3.94442286182866e-09	2.42854237768994e-09	12
ko02010	ABC transporters	11/99	53/5998	6.05320113194611e-10	3.27655745229733e-08	2.01734421094771e-08	11
ko00561	Glycerolipid metabolism	13/99	83/5998	6.18218387225911e-10	3.27655745229733e-08	2.01734421094771e-08	13
ko00524	Neomycin, kanamycin and gentamicin biosynthesis	6/99	10/5998	3.45749736087527e-09	1.37435520094792e-07	8.46176985687895e-08	6
ko04714	Thermogenesis	15/99	139/5998	5.72435861757401e-09	1.82034604038854e-07	1.12076916091449e-07	15
ko04066	HIF-1 signaling pathway	11/99	67/5998	8.43579794795849e-09	2.235486456209e-07	1.37636703361428e-07	11
ko00521	Streptomycin biosynthesis	6/99	15/5998	7.70706186018483e-08	1.75060405109913e-06	1.07782970375517e-06	6
ko04910	Insulin signaling pathway	10/99	78/5998	4.71086839251762e-07	9.36285093012876e-06	5.76461526979129e-06	10
ko04973	Carbohydrate digestion and absorption	6/99	20/5998	5.58253632414573e-07	9.86248083932413e-06	6.07223249293045e-06	6
ko00010	Glycolysis_Gluconeogenesis	12/99	141/5998	2.85878478211067e-06	4.54546780355596e-05	2.79859983932939e-05	12

Barplot

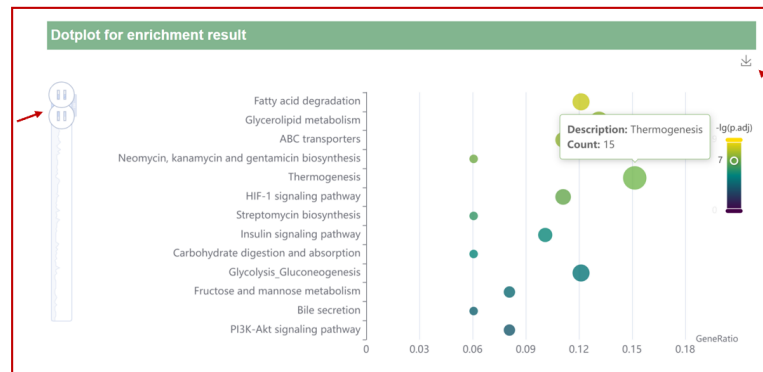
Drag to change
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displayed in the
figure.



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the figure

Dotplot

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the figure