

KEGG Pathways

Diagrams of molecular interactions, reactions, and relations.

Inputs - Data: Data set. - Reference: Referential data set.

Outputs - Selected Data: Data subset. - Unselected Data: Remaining data.

KEGG Pathways widget displays diagrams of molecular interactions, reactions and relations from the [KEGG Pathways Database](#). It takes data on gene expression as an input, matches the genes to the biological processes and displays a list of corresponding pathways. To explore the pathway, the user can click on any process from the list or arrange them by P-value to get the most relevant processes at the top.

Pathway	P value	Genes	Reference
09160 Human Diseases			
09167 Endocrine and metabolic diseases			
AGE-RAGE signaling pathway in diabetic complications - ...	0.58664	8 of 5849	8 of 6427
09150 Organismal Systems			
09149 Aging			
Longevity regulating pathway - multiple species - Sacch...	0.14856	36 of 5849	36 of 6427
09140 Cellular Processes			
09143 Cell growth and death			
Meiosis - yeast - Saccharomyces cerevisiae (budding ye...	0.00012	130 of 5849	130 of 6427
Cell cycle - yeast - Saccharomyces cerevisiae (budding ...	0.00014	126 of 5849	126 of 6427

1. Information on the input genes.
2. If you have a separate reference set in the input, tick *From signal* to use these data as reference.
3. To have pathways listed and displayed by vertical descent, tick *Show pathways in full orthology*.
4. To fit the image to screen, tick *Resize to fit*. Untick the box if you wish to explore the pathways.
5. To clear all locally cached KEGG data, press *Clear cache*.
6. When *Auto commit is on*, the widget will automatically apply the changes. Alternatively press *Commit*.
7. A list of pathways either as processes or in full orthology. Click on the process to display the pathway. You can sort the data by P-value to get the most relevant results at the top.

Example

This simple example shows how to visualize interactions with **KEGG Pathways**. We have loaded the *Caffeine effect: time courses and dose response* (GDS2914) data with the **GEO Data Sets** widget. Then we have observed the pathways in **KEGG Pathways**. We have used reference from signal and selected *AGE-RAGE signaling pathway in diabetic complications*.

Workflow: GEO Data Sets → Expression Data → Data → KEGG Pathways

Filter Table:

ID	Title	Organism	Samples
GDS2914	Caffeine effect: time course a...	Saccharomyces cerevisiae	36
GDS360	Breast cancer and docetaxel ...	Homo sapiens	24
GDS10	Type 1 diabetes gene expres...	Mus musculus	28
GDS100	UV exposure time course (ec...	Escherichia coli	8
GDS1001	Na,K-ATPase alpha 1 isoform...	Mus musculus	4
GDS1002	Lung response to urban parti...	Rattus norvegicus	5

Description: Analysis of cells treated with a low dose of caffeine at 2 mM or a high one at 20 mM for 5, 15, or 90 minutes. Caffeine is a natural purine analogue that elicits pleiotropic effects leading to cell death. Results provide insight into the mechanism of action of

Sample Annotations:

- dose
 - high
 - low

KEGG Pathways Widget:

Info: 5849 unique gene names on input

Reference: From signal

Orthology: Show pathways in full orthology image, Resize to fit

Cache Control: Commit Automatically

Pathway Diagram: AGE-RAGE signaling pathway in diabetic complications

Pathway Table:

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