

Resource Summary Report

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KEGGgraph

RRID:SCR_023788

Type: Tool

Proper Citation

KEGGgraph (RRID:SCR_023788)

Resource Information

URL: <https://bioconductor.org/packages/KEGGgraph/>

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Description: Software R package interface between KEGG pathway and graph object as well as collection of tools to analyze, dissect and visualize these graphs.

Synonyms: Kyoto Encyclopedia of Genes and Genomes graph

Resource Type: software resource, software toolkit

Defining Citation: [PMID:19307239](#)

Keywords: Kyoto Encyclopedia of Genes and Genomes, KEGG, KEGG pathways, graph models, graph object, graphs visualization,

Availability: Free, Available for download, Freely available

Resource Name: KEGGgraph

Resource ID: SCR_023788

Record Creation Time: 20230714T050221+0000

Record Last Update: 20260821T194244+0000

Ratings and Alerts

No rating or validation information has been found for KEGGgraph.

No alerts have been found for KEGGgraph.

Data and Source Information

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Dragunas G, et al. (2026) A beneficial environment promotes immune resilience through epigenetic regulation. *Science advances*, 12(9), eady7317.

Wang J, et al. (2025) Integrated metabolomic and transcriptomic analysis of anthocyanin metabolism in wheat pericarp. *BMC genomic data*, 26(1), 3.

Thompson S, et al. (2025) Menadione reduces the expression of virulence- and colonization-associated genes in *Helicobacter pylori*. *Microbiology (Reading, England)*, 171(3).

Liang YJ, et al. (2025) SMART 2.0 Statistical Metabolomics Analysis: An R Tool 2.0. *Analytical chemistry*, 97(46), 25453.

Zhang Z, et al. (2024) Priority index for critical Covid-19 identifies clinically actionable targets and drugs. *Communications biology*, 7(1), 189.

Newsham I, et al. (2024) Early detection and diagnosis of cancer with interpretable machine learning to uncover cancer-specific DNA methylation patterns. *Biology methods & protocols*, 9(1), bpae028.

Simons CCJM, et al. (2022) Polymorphisms in the mTOR-PI3K-Akt pathway, energy balance-related exposures and colorectal cancer risk in the Netherlands Cohort Study. *BioData mining*, 15(1), 2.

Saw NMMT, et al. (2021) Influence of Extraction Solvent on Nontargeted Metabolomics Analysis of Enrichment Reactor Cultures Performing Enhanced Biological Phosphorus Removal (EBPR). *Metabolites*, 11(5).

Piran M, et al. (2020) Can We Assume the Gene Expression Profile as a Proxy for Signaling Network Activity? *Biomolecules*, 10(6).

Kim TR, et al. (2019) Topological integration of RPPA proteomic data with multi-omics data for survival prediction in breast cancer via pathway activity inference. *BMC medical genomics*, 12(Suppl 5), 94.

Kim SY, et al. (2019) Robust pathway-based multi-omics data integration using directed random walks for survival prediction in multiple cancer studies. *Biology direct*, 14(1), 8.

Bastounis EE, et al. (2019) Subendothelial stiffness alters endothelial cell traction force generation while exerting a minimal effect on the transcriptome. *Scientific reports*, 9(1), 18209.

Yu H, et al. (2016) Prediction of drugs having opposite effects on disease genes in a directed network. BMC systems biology, 10 Suppl 1(Suppl 1), 2.

Vizoso M, et al. (2015) Aberrant DNA methylation in non-small cell lung cancer-associated fibroblasts. Carcinogenesis, 36(12), 1453.

Song KH, et al. (2014) Sho-saiko-to, a traditional herbal medicine, regulates gene expression and biological function by way of microRNAs in primary mouse hepatocytes. BMC complementary and alternative medicine, 14, 14.