

# Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

## KEGGgraph

RRID:SCR\_023788

Type: Tool

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### Proper Citation

KEGGgraph (RRID:SCR\_023788)

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### Resource Information

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

**Proper Citation:** KEGGgraph (RRID:SCR\_023788)

**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:** 20260904T000531+0000

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### Ratings and Alerts

No rating or validation information has been found for KEGGgraph.

No alerts have been found for KEGGgraph.

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### 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 [kravitz2](#) .

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.