Resource Summary Report

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KEGG PATHWAY Database

RRID:SCR_018145
Type: Tool

Proper Citation

KEGG PATHWAY Database (RRID:SCR_018145)

Resource Information

URL: https://www.genome.jp/kegg/pathway.html

Proper Citation: KEGG PATHWAY Database (RRID:SCR_018145)

Description: Reference database for pathway mapping in KEGG Mapper. Collection of manually drawn pathway maps representing knowledge on molecular interaction, reaction and relation networks for metabolism, genetic information processing, environmental information processing, cellular processes, organisms systems, human diseases, drug development.

Synonyms: KEGG PATHWAY

Resource Type: data or information resource, database, service resource

Keywords: Pathway mapping, reference database, KEGG Mapper, molecular interaction, reaction and relation network, metabolism, genetic information processing, cellular process, organism system, human disease, drug development, data

Availability: Free, Freely available

Resource Name: KEGG PATHWAY Database

Resource ID: SCR_018145

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260905T133215+0000

Ratings and Alerts

No rating or validation information has been found for KEGG PATHWAY Database.

No alerts have been found for KEGG PATHWAY Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1224 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Du J, et al. (2026) Oxaliplatin triggers adipose and muscle wasting through cancer-independent metabolic and CNS pathways in mouse models. Communications biology.

M Naeini M, et al. (2026) Convergent genomic and molecular features predict risk of metachronous metastasis in clear cell renal cell carcinoma. Communications medicine, 6(1).

Kojima M, et al. (2026) Precision Oncology for Pediatric Solid Tumors Using In-Hospital Pediatric/AYA Malignancy-Specific Panel Sequencing. Cancer science, 117(3), 797.

Yu Q, et al. (2026) Gut microbiota-associated nutritional-immune status predicts prognosis in postoperative NSCLC patients. Gut microbes, 18(1), 2652460.

Elizondo G, et al. (2026) Acute arrhythmias in a long-chain 3-hydroxyacyl-CoA dehydrogenase deficiency mouse model. American journal of physiology. Heart and circulatory physiology, 330(2), H484.

Li N, et al. (2026) Pre-diagnostic metabolites in peripheral blood of Langerhans cell histiocytosis children with posterior pituitary involvement. Metabolomics : Official journal of the Metabolomic Society, 22(4).

Jiang M, et al. (2026) SIRT6-Mediated Regulation of TFAM: A Central Mechanism Connecting Nuclear and Mitochondrial Transcriptional Processes and Mitophagy. International journal of biological sciences, 22(1), 178.

Ye P, et al. (2026) Realgar-Induced CNS Toxicity: Exploring OTC-Mediated Ornithine Regulation of ZBTB7A Inhibits Astrocyte Glycolysis Based on the Liver-Brain Axis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(2), e02591.

Nagano T, et al. (2026) Multi-proteomics reveals integrated metabolic and regulatory networks for xylan catabolism in Streptomyces sp. SirexAA-E. Microbiology spectrum, 14(1), e0225125.

Shahid MA, et al. (2026) Profillin-1 and Transgelin-2: Actin Binding Proteins Expression in Early and Advanced Stages of Triple-Negative Breast Cancer Receiving Neoadjuvant Chemotherapy. Cancer reports (Hoboken, N.J.), 9(4), e70529.

Naidoo V, et al. (2026) An Evaluation of the Interaction of Brefeldin A with Mitogen-Activated Protein Kinase 1 (MAPK1) and Protein Kinase C Alpha (PrKC?): Insights from Molecular Modelling Studies. International journal of molecular sciences, 27(7).

Ahmad W, et al. (2026) Dysregulated host miRNAs with antiviral potential against SARS-CoV-2 identified from COVID-19 patients. Journal of translational medicine, 24(1).

Ozawa M, et al. (2026) PTBP1 supports mouse spermatogenesis by facilitating cytoskeletal organization through the mTORC2-PKC? pathway in Sertoli cells. Communications biology, 9(1).

Wang L, et al. (2026) Site-specific HPV18 integration facilitates cervical carcinogenesis through metabolic reprogramming-induced dysfunction of the SpHK1/S1P/S1PR1 pathway. Cell death & disease, 17(1), 24.

Tian JX, et al. (2026) Integrated hepatic transcriptome and metabolome reveal the mechanisms of Jiangtang Tiaozhi formula on improving glycolipid metabolic disorder. World journal of diabetes, 17(2), 111453.

Kolifarhood G, et al. (2026) Causal evidence linking chronic pain genetics to late-onset asthma via the nervous system. British journal of anaesthesia, 136(3), 933.

von der Decken I, et al. (2026) The potential of deep learning on the discovery of new genes implicated in differences of sex development. Computational and structural biotechnology journal, 31, 221.

Alexovi? M, et al. (2026) Peripheral blood CD14 + monocytes in luminal breast carcinoma subtypes: in preliminary research and overview of candidate biomarker proteins. Scientific reports, 16(1).

Zhang Z, et al. (2026) Discover the maze-like network for glabridin biosynthesis. Nature communications, 17(1).

Li S, et al. (2026) Comparative metagenomic and metatranscriptomic analyses reveal the role of the gayal rumen and hindgut microbiome in high-efficiency lignocellulose degradation. Journal of animal science and biotechnology, 17(1), 18.