

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

Reactome Knowledgebase

RRID:SCR_023504

Type: Tool

Proper Citation

Reactome Knowledgebase (RRID:SCR_023504)

Resource Information

URL: <https://reactome.org/>

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Description: Open source relational database of signaling and metabolic molecules and their relations organized into biological pathways and processes. Core unit of Reactome data model is the reaction. Entities (nucleic acids, proteins, complexes, vaccines, anti-cancer therapeutics and small molecules) participating in reactions form network of biological interactions and are grouped into pathways including classical intermediary metabolism, signaling, transcriptional regulation, apoptosis and disease. External domain expert provides expertise, curator formalizes it into database structure, and external domain expert reviews representation. System of evidence tracking ensures that all assertions are backed up by primary literature. Website is designed to give the user graphical map of known biological processes and pathways that is also an interface. Database and website enable to find, organize, and utilize biological information to support data visualization, integration and analysis.

Synonyms: Reactome

Resource Type: data access protocol, software resource, web service, data or information resource, database

Keywords: signaling and metabolic molecules relations, biological pathways and processes, intermediary metabolism, signaling, transcriptional regulation, apoptosis, disease

Funding: NHGRI U24 HG012198

Availability: Free, Freely available

Resource Name: Reactome Knowledgebase

Resource ID: SCR_023504

Record Creation Time: 20230426T050216+0000

Record Last Update: 20260731T043137+0000

Ratings and Alerts

No rating or validation information has been found for Reactome Knowledgebase.

No alerts have been found for Reactome Knowledgebase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 445 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Arcego DM, et al. (2026) Sex-specific interaction effects of Syntaxin 1A coexpression network and childhood trauma on adult depressive symptoms. *EBioMedicine*, 123, 106062.

Luan F, et al. (2025) Comprehensive pan-cancer analysis reveals NTN1 as an immune infiltrate risk factor and its potential prognostic value in SKCM. *Scientific reports*, 15(1), 3223.

da Silva JCT, et al. (2025) Label-free proteomic analysis of Duchenne and Becker muscular dystrophy showed decreased sarcomere proteins and increased ubiquitination-related proteins. *Scientific reports*, 15(1), 3293.

Chen C, et al. (2025) Identification of Three Distinct Subgroups in Antiphospholipid Syndrome: Implication for Sex Differences and Prognostic Outcomes from a Multicenter Study. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(15), e2415291.

Lago-Baameiro N, et al. (2025) Intra and inter-organ communication through extracellular vesicles in obesity: functional role of obesosomes and steatosomes. *Journal of translational medicine*, 23(1), 207.

Liu FF, et al. (2025) Gene Expression Signatures of Smoking and Acute Myocardial Infarction: A Blood Transcriptome Analysis. *Mediators of inflammation*, 2025, 2431090.

Auddino S, et al. (2025) Comprehensive sequencing profile and functional analysis of lsmiRs in human pancreatic islets and beta cells. *Diabetologia*, 68(6), 1261.

Han R, et al. (2025) Upregulation of PD-L1 contributes to improving the apoptosis of granulosa cells via the PI3K/AKT pathway in PCOS. *Journal of assisted reproduction and genetics*, 42(2), 611.

Sharma D, et al. (2025) Light-dark shift promotes colon carcinogenesis through accelerated colon aging. *iScience*, 28(1), 111560.

Wang C, et al. (2025) Integrated multi-omics analysis identifies lipid metabolism biomarkers in ONFH and reveals therapeutic potential of retinoic acid. *Scientific reports*, 15(1), 30716.

Satitsri S, et al. (2025) The natural statin β , β -dehydromonacolin K exerts anti-secretory effect in human intestinal epithelial cells via a nonsense-mediated mRNA decay-dependent mechanism. *Pharmaceutical biology*, 63(1), 645.

Bauer M, et al. (2025) Association of the composition of the bone marrow tumor microenvironment in BCR::ABL1-negative myeloproliferative neoplasms with IFN- γ signaling and driver mutations. *Leukemia*, 39(10), 2391.

Wang P, et al. (2025) Integrative Proteomic and Phosphoproteomic Profiling Reveals Molecular Mechanisms of Hypoxic Adaptation in Brandt's Voles (*Lasiopodomys brandtii*) Brain Tissue. *Cells*, 14(7).

Giovannetti F, et al. (2025) Conjunctival MicroRNA Expression Signature in Primary Sjögren's Syndrome Dry Eye: A NanoString-Based Bioinformatic Analysis. *Investigative ophthalmology & visual science*, 66(4), 80.

Wang Q, et al. (2025) Knowledge graph and its application in the study of neurological and mental disorders. *Frontiers in psychiatry*, 16, 1452557.

Li J, et al. (2025) Repeated Evolution of Transcript Dosage Compensation of Independently Formed Nematode Neo-X Chromosomes. *Genome biology and evolution*, 17(4).

Wang K, et al. (2025) Vesicle-mediated transport-related gene SEC23A promotes cell proliferation by regulating cell cycle leading to gastric cancer progression. *Acta biochimica et biophysica Sinica*, 57(9), 1433.

Ye C, et al. (2025) Comprehensive analysis of single-cell and bulk RNA sequencing data reveals an EGFR signature for predicting immunotherapy response and prognosis in pan-cancer. *Frontiers in immunology*, 16, 1604394.

Zheng Y, et al. (2025) A deep generative model for deciphering cellular dynamics and in silico drug discovery in complex diseases. *Nature biomedical engineering*, 9(12), 2155.

Hermansen JU, et al. (2025) Proteasome inhibition overcomes resistance to targeted therapies in B-cell malignancy models and in an index patient. *Cell death & disease*, 16(1), 555.