Resource Summary Report

Generated by dkNET on Apr 22, 2025

Reactome

RRID:SCR_003485
Type: Tool

Proper Citation

Reactome (RRID:SCR_003485)

Resource Information

URL: http://www.reactome.org

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Description: Collection of pathways and pathway annotations. The core unit of the Reactome data model is the reaction. Entities (nucleic acids, proteins, complexes and small molecules) participating in reactions form a network of biological interactions and are grouped into pathways (signaling, innate and acquired immune function, transcriptional regulation, translation, apoptosis and classical intermediary metabolism) . Provides website to navigate pathway knowledge and a suite of data analysis tools to support the pathway-based analysis of complex experimental and computational data sets.

Synonyms: Reactome Functional Interaction Network

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

Defining Citation: PMID:21082427, PMID:21067998

Keywords: pathway, interaction, reaction, nucleic acid, protein, complex, small molecule, signaling pathway, immune function, transcriptional regulation, translation, apoptosis, metabolism, ortholog, visualization, protein-protein interaction, web service, book, biomart, gold standard, bio.tools, FASEB list

Funding: Ontario Research Fund ;
European Molecular Biology Laboratory ;
NHGRI P41 HG003751;
European Union FP6 ENFIN LSHG-CT-2005-518254;
NIGMS GM080223;

NIGMS R01 GM100039

Availability: Open source, Public, Freely available

Resource Name: Reactome

Resource ID: SCR_003485

Alternate IDs: nif-0000-03390, biotools:reactome

Alternate URLs: https://bio.tools/reactome

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250422T055123+0000

Ratings and Alerts

No rating or validation information has been found for Reactome.

No alerts have been found for Reactome.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3580 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Sridhar S, et al. (2025) Targeting TREM2 signaling shows limited impact on cerebrovascular calcification. Life science alliance, 8(1).

Liu YK, et al. (2025) Application of integrated omics in aseptic loosening of prostheses after hip replacement. Molecular medicine reports, 31(3).

Sui Z, et al. (2025) Mesenchymal stromal cells promote the formation of lung cancer organoids via Kindlin-2. Stem cell research & therapy, 16(1), 7.

Palomino Lago E, et al. (2025) Identification of a global gene expression signature associated with the genetic risk of catastrophic fracture in iPSC-derived osteoblasts from Thoroughbred horses. Animal genetics, 56(1), e13504.

Mahmud MS, et al. (2025) Computational network analysis of two popular skin cancers provides insights into the molecular mechanisms and reveals common therapeutic targets.

Heliyon, 11(1), e41688.

Jiang J, et al. (2025) Identification and validation of glucose metabolism-related gene signature in endometrial cancer. BMC cancer, 25(1), 30.

Liu L, et al. (2025) Revealing the role of cancer-associated fibroblast senescence in prognosis and immune landscape in pancreatic cancer. iScience, 28(1), 111612.

Zhang X, et al. (2025) Fluo-Cast-Bright: a deep learning pipeline for the non-invasive prediction of chromatin structure and developmental potential in live oocytes. Communications biology, 8(1), 141.

Doron-Mandel E, et al. (2025) SEC-MX: an approach to systematically study the interplay between protein assembly states and phosphorylation. Nature communications, 16(1), 1176.

Peterson JM, et al. (2025) A window into intracellular events in myositis through subcellular proteomics. Inflammation research : official journal of the European Histamine Research Society ... [et al.], 74(1), 31.

Alfayyadh MM, et al. (2025) PathVar: A Customisable NGS Variant Calling Algorithm Implicates Novel Candidate Genes and Pathways in Hemiplegic Migraine. Clinical genetics, 107(2), 157.

Rosner S, et al. (2025) Divergent Clinical and Immunologic Outcomes Based on STK11 Co-mutation Status in Resectable KRAS-Mutant Lung Cancers Following Neoadjuvant Immune Checkpoint Blockade. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(2), 339.

Bae S, et al. (2025) Lonafarnib Protects Against Muscle Atrophy Induced by Dexamethasone. Journal of cachexia, sarcopenia and muscle, 16(1), e13665.

Ge J, et al. (2025) TGF-? signaling orchestrates cancer-associated fibroblasts in the tumor microenvironment of human hepatocellular carcinoma: unveiling insights and clinical significance. BMC cancer, 25(1), 113.

Aghila Rani KG, et al. (2025) Medwakh smoking induces alterations in salivary proteins and cytokine expression: a clinical exploratory proteomics investigation. Clinical proteomics, 22(1), 2.

Altab G, et al. (2025) Unravelling the transcriptomic symphony of muscle ageing: key pathways and hub genes altered by ageing and caloric restriction in rat muscle revealed by RNA sequencing. BMC genomics, 26(1), 29.

Tat VY, et al. (2025) Characterizing temporal and global host innate immune responses against SARS-CoV-1 and -2 infection in pathologically relevant human lung epithelial cells. PloS one, 20(1), e0317921.

Koponen L, et al. (2025) A deep intronic PHEX variant associated with X-linked hypophosphatemia in a Finnish family. JBMR plus, 9(2), ziae169.

Guo H, et al. (2025) Depot-specific acetylation profiles of adipose tissues-therapeutic targets for metabolically unhealthy obesity. Diabetology & metabolic syndrome, 17(1), 36.

Gralewska P, et al. (2025) Olaparib Combined with DDR Inhibitors Effectively Prevents EMT and Affects miRNA Regulation in TP53-Mutated Epithelial Ovarian Cancer Cell Lines. International journal of molecular sciences, 26(2).