Resource Summary Report

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Search Tool for Interactions of Chemicals

RRID:SCR_007947
Type: Tool

Proper Citation

Search Tool for Interactions of Chemicals (RRID:SCR_007947)

Resource Information

URL: http://stitch.embl.de

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Description: Database to explore known and predicted interactions of chemicals and proteins. It integrates information about interactions from metabolic pathways, crystal structures, binding experiments and drug-target relationships. Inferred information from phenotypic effects, text mining and chemical structure similarity is used to predict relations between chemicals. STITCH further allows exploring the network of chemical relations, also in the context of associated binding proteins. Each proposed interaction can be traced back to the original data sources. The database contains interaction information for over 68,000 different chemicals, including 2200 drugs, and connects them to 1.5 million genes across 373 genomes and their interactions contained in the STRING database.

Abbreviations: STITCH

Synonyms: STITCH: Chemical-Protein Interactions

Resource Type: data or information resource, database

Defining Citation: PMID:22075997, PMID:19897548, PMID:18084021

Keywords: drug-target relationship, chemical, chemical-protein interaction, chemical relationship, crystal structure, metabolic pathway interaction, protein, interaction, small molecule, drug, interaction network, FASEB list

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ProBioC

Resource Name: Search Tool for Interactions of Chemicals

Resource ID: SCR_007947

Alternate IDs: r3d100012165, OMICS_01589, nif-0000-03499

Alternate URLs: https://doi.org/10.17616/R3606X, https://doi.org/10.17616/R3606X

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260729T044157+0000

Ratings and Alerts

No rating or validation information has been found for Search Tool for Interactions of Chemicals.

No alerts have been found for Search Tool for Interactions of Chemicals.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 754 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Lahusen A, et al. (2025) An immune responsive tumor microenvironment imprints into PBMCs and predicts outcome in advanced pancreatic cancer: lessons from the PREDICT trial. Molecular cancer, 24(1), 202.

Saraphol B, et al. (2025) Analysis of the fecal microbiome and metabolome in dairy cows with different body condition scores. PloS one, 20(3), e0319461.

Ran B, et al. (2025) Analysis of Toxicity and Mechanisms of Bisphenol Analogs in Male Infertility: Insights from Network Toxicology and Molecular Docking Approaches. The world journal of men's health, 43(3), 721.

Ye H, et al. (2025) Improvement of the accuracy of breeding value prediction for egg production traits in Muscovy duck using low-coverage whole-genome sequence data. Poultry science, 104(2), 104812.

Xu Y, et al. (2025) Identification of tacrolimus-related genes in familial combined hyperlipidemia and development of a diagnostic model using bioinformatics analysis. Heliyon, 11(3), e41705.

Bumbaca B, et al. (2025) Network analyses of brain tumor multiomic data reveal pharmacological opportunities to alter cell state transitions. NPJ systems biology and applications, 11(1), 14.

Yin Y, et al. (2025) G0S2 modulates normal vitreous-induced proliferation in endothelial cells. Communications biology, 8(1), 560.

Ji L, et al. (2025) Role of Ca2+/calmodulin and PI3K/AKT signaling pathways and active ingredients of BaoTaiYin in treatment of recurrent miscarriage. Frontiers in molecular biosciences, 12, 1573294.

Aksorn N, et al. (2025) Particulate Matter 2.5 Induces FGFR1-mediated Integrin Switch to Promote Non-small Cell Lung Cancer Metastasis. Cancer genomics & proteomics, 22(4), 632.

Sagulkoo P, et al. (2025) Integrative bioinformatics frameworks for abdominal aortic aneurysm using GWAS meta-analysis, biological network construction, and structural modeling. Scientific reports, 15(1), 22331.

Jing R, et al. (2025) Investigating the mechanism of Gentiopicroside in rheumatoid arthritis through network pharmacology, molecular docking, and experimental validation. Scientific reports, 15(1), 19871.

Zyrianova T, et al. (2025) Pharmacological activation of BK channels protects against LPS-induced pneumonia. Scientific reports, 15(1), 30307.

Chang S, et al. (2025) The updated evidence of pirfenidone treated silicosis based on network pharmacology, molecular docking and experimental validation. Frontiers in medicine, 12, 1573241.

Zhang T, et al. (2025) Aspartame and ischemic stroke: unraveling the molecular link through network toxicology and molecular docking analysis. Scientific reports, 15(1), 23871.

Li R, et al. (2025) Phosphoproteomic insights into the regulation of root length in rice (Oryza sativa L. cv. KDML 105): uncovering key events and pathways involving phosphorylated proteins. PeerJ, 13, e19361.

Zhang L, et al. (2025) Erchen Decoction Offers Health Benefits in Regulating Obesity: Component Analysis, Network Pharmacology, and Experiment Verification. Food science & nutrition, 13(8), e70592.

Karimi I, et al. (2025) The anti-aging potential of antihypertensive peptides of Pariset, a dataset of algal peptides. Frontiers in aging, 6, 1618082.

Varl?? M, et al. (2025) Targeting heat shock protein 90 with usnic acid relieves immune suppression via aryl hydrocarbon receptor-mediated mechanisms in lung cancer. Molecular biomedicine, 6(1), 81.

Salemi A, et al. (2025) Niosome-loaded silibinin and methotrexate for synergistic breast cancer combination chemotherapy: in silico and in vitro study. Cancer cell international, 25(1), 336.

Abou-Taleb BA, et al. (2025) Comparison of Peganum harmala L. leaves extract nanoformulations against herpes simplex virus type 1 guided by network pharmacology analysis. Scientific reports, 15(1), 40395.