

Resource Summary Report

Generated by SPARC SAWG on Aug 10, 2026

Kinase Pathway Database

RRID:SCR_008199

Type: Tool

Proper Citation

Kinase Pathway Database (RRID:SCR_008199)

Resource Information

URL: <http://kinasedb.ontology.ims.u-tokyo.ac.jp>

Proper Citation: Kinase Pathway Database (RRID:SCR_008199)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 23, 2016. KinasePathwayDatabase is an integrated database concerning completed sequenced major eukaryotes, which contains the classification of protein kinases and their functional conservation and orthologous tables among species, protein-protein interaction data, domain information, structural information, and automatic pathway graph image interface. The protein-protein interactions are extracted by natural language processing (NLP) from abstracts using basic word pattern and protein name dictionary GENA: developed by our group. In this system, pathways are easily compared among species using protein interactions data more than 47,000 and orthologous tables.

Synonyms: Kinase Pathway Database

Resource Type: database, data or information resource

Keywords: eukaryote, functional, automatic, classification, conservation, domain, interaction, intermolecular interactions and signaling pathways databases, kinase, orthologous, pathway, protein, sequence, specie, structural, image

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Kinase Pathway Database

Resource ID: SCR_008199

Alternate IDs: nif-0000-21235

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260808T190421+0000

Ratings and Alerts

No rating or validation information has been found for Kinase Pathway Database.

No alerts have been found for Kinase Pathway Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Wang H, et al. (2019) HKPocket: human kinase pocket database for drug design. BMC bioinformatics, 20(1), 617.

Krallinger M, et al. (2005) Text-mining and information-retrieval services for molecular biology. Genome biology, 6(7), 224.