

Resource Summary Report

Generated by SPARC SAWG on Jul 30, 2026

Protein interaction and molecular information database

RRID:SCR_002096

Type: Tool

Proper Citation

Protein interaction and molecular information database (RRID:SCR_002096)

Resource Information

URL: <https://omictools.com/protein-interactions-and-molecular-information-database-tool>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on August 26, 2016. PRIME is a developed version of Kinase Pathway Database which 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 1,510,000 and orthologous tables. Further, using other organisms interaction data, interaction prediction is also possible.

Synonyms: PRIME

Resource Type: data or information resource, database

Keywords: eukaryote, kinase pathway, protein, structure

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Protein interaction and molecular information database

Resource ID: SCR_002096

Alternate IDs: nif-0000-20899

Old URLs: <http://prime.ontology.ims.u-tokyo.ac.jp:8081/>

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260729T044020+0000

Ratings and Alerts

No rating or validation information has been found for Protein interaction and molecular information database.

No alerts have been found for Protein interaction and molecular information database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.