Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

FunCoup

RRID:SCR_018711
Type: Tool

Proper Citation

FunCoup (RRID:SCR_018711)

Resource Information

URL: http://funcoup.sbc.su.se/search/

Proper Citation: FunCoup (RRID:SCR_018711)

Description: Database of genome wide functional coupling networks. Provides tools to explore predicted networks and to retrieve detailed information about data underlying each prediction. Web service for functional coupling search.

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

Defining Citation: PMID:24185702

Keywords: Genome, genome functional coupling network, coupling network, functional coupling, functional couplings search, gene identifier, genome data

Funding: Swedish Research Council ;
Stockholm University

Availability: Free, Freely available

Resource Name: FunCoup

Resource ID: SCR_018711

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260808T190114+0000

Ratings and Alerts

No rating or validation information has been found for FunCoup.

No alerts have been found for FunCoup.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Jin X, et al. (2020) The prohibitin-binding compound fluorizoline affects multiple components of the translational machinery and inhibits protein synthesis. The Journal of biological chemistry, 295(29), 9855.

Ogris C, et al. (2017) A novel method for crosstalk analysis of biological networks: improving accuracy of pathway annotation. Nucleic acids research, 45(2), e8.

Wan Y, et al. (2016) Transcriptome analysis reveals a ribosome constituents disorder involved in the RPL5 downregulated zebrafish model of Diamond-Blackfan anemia. BMC medical genomics, 9, 13.