Resource Summary Report

Generated by NIF on May 4, 2025

Krogan Lab Interactome Database

RRID:SCR_008121
Type: Tool

Proper Citation

Krogan Lab Interactome Database (RRID:SCR_008121)

Resource Information

URL: http://interactome-cmp.ucsf.edu/

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Description: This database currently holds E-MAP scores (individual interactions and correlation coefficients) for budding yeast genes involved in the early secretory pathway and chromosome function (including DNA damage and repair, transcriptional control, chromosome segregation and telomere regulation). E-MAPs (Epistatic Mini Array Profiles) are formed by creating and quantifying high-density genetic interaction maps. With this method, observed double mutant colony sizes are compared to those that would be expected from a distribution of typical double mutant colonies of each strain. Each interaction is assigned a score, which indicates the magnitude of the difference from the expected value and the certainty of the score. Negative (or aggravating) scores (+2.5) corresponds to epistatic or suppressor interactions.

Synonyms: Interactome

Resource Type: database, data or information resource

Keywords: function, gene, chromosome, dna, pathway, secretory, telomere regulation, transcriptional control, yeast

Funding:

Resource Name: Krogan Lab Interactome Database

Resource ID: SCR_008121

Alternate IDs: nif-0000-20868

Record Creation Time: 20220129T080245+0000

Record Last Update: 20250503T060001+0000

Ratings and Alerts

No rating or validation information has been found for Krogan Lab Interactome Database.

No alerts have been found for Krogan Lab Interactome Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Macossay-Castillo M, et al. (2019) The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. Journal of molecular biology, 431(8), 1650.

Tian B, et al. (2017) A two-step framework for inferring direct protein-protein interaction network from AP-MS data. BMC systems biology, 11(Suppl 4), 82.

Vazquez HM, et al. (2016) Chemogenetic E-MAP in Saccharomyces cerevisiae for Identification of Membrane Transporters Operating Lipid Flip Flop. PLoS genetics, 12(7), e1006160.

Ou-Yang L, et al. (2016) Protein complex detection based on partially shared multi-view clustering. BMC bioinformatics, 17(1), 371.

Zhang XF, et al. (2015) Identifying binary protein-protein interactions from affinity purification mass spectrometry data. BMC genomics, 16, 745.

Ölmezer G, et al. (2015) DNA repair defects ascribed to pby1 are caused by disruption of Holliday junction resolvase Mus81-Mms4. DNA repair, 33, 17.

Braberg H, et al. (2013) From structure to systems: high-resolution, quantitative genetic analysis of RNA polymerase II. Cell, 154(4), 775.

Lei YK, et al. (2012) Assessing and predicting protein interactions by combining manifold embedding with multiple information integration. BMC bioinformatics, 13 Suppl 7(Suppl 7), S3.

Fokkens L, et al. (2012) Gene duplications contribute to the overrepresentation of interactions between proteins of a similar age. BMC evolutionary biology, 12, 99.

Schelhorn SE, et al. (2011) Inferring physical protein contacts from large-scale purification data of protein complexes. Molecular & cellular proteomics : MCP, 10(6), M110.004929.

Zheng J, et al. (2010) Epistatic relationships reveal the functional organization of yeast transcription factors. Molecular systems biology, 6, 420.

Srihari S, et al. (2010) MCL-CAw: a refinement of MCL for detecting yeast complexes from weighted PPI networks by incorporating core-attachment structure. BMC bioinformatics, 11, 504.

Fiedler D, et al. (2009) Functional organization of the S. cerevisiae phosphorylation network. Cell, 136(5), 952.

Fokkens L, et al. (2009) Cohesive versus flexible evolution of functional modules in eukaryotes. PLoS computational biology, 5(1), e1000276.

Wilmes GM, et al. (2008) A genetic interaction map of RNA-processing factors reveals links between Sem1/Dss1-containing complexes and mRNA export and splicing. Molecular cell, 32(5), 735.