Resource Summary Report

Generated by NIF on Apr 17, 2025

Interaction Reference Index

RRID:SCR_002085
Type: Tool

Proper Citation

Interaction Reference Index (RRID:SCR_002085)

Resource Information

URL: http://irefindex.org

Proper Citation: Interaction Reference Index (RRID:SCR_002085)

Description: An index of protein interactions available in a number of primary interaction databases including BIND, BioGRID, CORUM, DIP, HPRD, IntAct, MINT, MPact, MPPI and OPHID. This index includes multiple interaction types including physical and genetic (mapped to their corresponding protein products) as determined by a multitude of methods. This index allows the user to search for a protein and retrieve a non-redundant list of interactors for that protein. iRefIndex uses the Sequence Global Unique Identifier (SEGUID) to group proteins and interactions into redundant groups. This method allows users to integrate their own data with the iRefIndex in a way that ensures proteins with the exact same sequence will be represented only once. iRefIndex project has three long term objectives: # to facilitate exchange of interaction data between interaction databases. # to consolidate interaction data from multiple sources. # to provide feedback to source interaction databases. iRefIndex is made available in a number of formats: MITAB tab-delimited text files, iRefWeb interface, iRefScape plugin for Cytoscape, PSICQUIC Web services, and an interface for the R programming language environment.

Abbreviations: iRefIndex

Resource Type: database, data or information resource

Defining Citation: PMID:18823568

Keywords: genetic, interaction, protein, protein interaction, protein-protein interaction

Funding:

Availability: Creative Commons Attribution License, 2.5 Generic

Resource Name: Interaction Reference Index

Resource ID: SCR_002085

Alternate IDs: nif-0000-20860

Old URLs: http://irefindex.uio.no

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250412T054648+0000

Ratings and Alerts

No rating or validation information has been found for Interaction Reference Index.

No alerts have been found for Interaction Reference Index.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Vasovi? LM, et al. (2023) Intrinsically disordered proteins and liquid-liquid phase separation in SARS-CoV-2 interactomes. Journal of cellular biochemistry.

Kondoh K, et al. (2022) Identification of Key Genes and Pathways Associated with Preeclampsia by a WGCNA and an Evolutionary Approach. Genes, 13(11).

Shu T, et al. (2020) Plasma Proteomics Identify Biomarkers and Pathogenesis of COVID-19. Immunity, 53(5), 1108.

Takahashi Y, et al. (2020) Systems Level Analysis and Identification of Pathways and Key Genes Associated with Delirium. Genes, 11(10).

Capriotti E, et al. (2019) Integrating molecular networks with genetic variant interpretation for precision medicine. Wiley interdisciplinary reviews. Systems biology and medicine, 11(3), e1443.

Genov N, et al. (2019) A Multi-Layered Study on Harmonic Oscillations in Mammalian Genomics and Proteomics. International journal of molecular sciences, 20(18).

Huang JK, et al. (2018) Systematic Evaluation of Molecular Networks for Discovery of Disease Genes. Cell systems, 6(4), 484.

Archer TC, et al. (2018) Proteomics, Post-translational Modifications, and Integrative Analyses Reveal Molecular Heterogeneity within Medulloblastoma Subgroups. Cancer cell, 34(3), 396.

Webber JT, et al. (2018) Integration of Tumor Genomic Data with Cell Lines Using Multi-dimensional Network Modules Improves Cancer Pharmacogenomics. Cell systems, 7(5), 526.

Lv BM, et al. (2018) Drug Repurposing for Japanese Encephalitis Virus Infection by Systems Biology Methods. Molecules (Basel, Switzerland), 23(12).

Kumar P, et al. (2017) A Human Tyrosine Phosphatase Interactome Mapped by Proteomic Profiling. Journal of proteome research, 16(8), 2789.

Lima Lde A, et al. (2016) An integrative approach to investigate the respective roles of single-nucleotide variants and copy-number variants in Attention-Deficit/Hyperactivity Disorder. Scientific reports, 6, 22851.

Wang L, et al. (2015) iCTNet2: integrating heterogeneous biological interactions to understand complex traits. F1000Research, 4, 485.

Mora A, et al. (2013) A survey of protein interaction data and multigenic inherited disorders. BMC bioinformatics, 14, 47.

Han K, et al. (2013) SHANK3 overexpression causes manic-like behaviour with unique pharmacogenetic properties. Nature, 503(7474), 72.

Rodionov A, et al. (2011) A new, fast algorithm for detecting protein coevolution using maximum compatible cliques. Algorithms for molecular biology : AMB, 6, 17.

Razick S, et al. (2011) iRefScape. A Cytoscape plug-in for visualization and data mining of protein interaction data from iRefIndex. BMC bioinformatics, 12, 388.

Mora A, et al. (2011) iRefR: an R package to manipulate the iRefIndex consolidated protein interaction database. BMC bioinformatics, 12, 455.

Turner B, et al. (2010) iRefWeb: interactive analysis of consolidated protein interaction data and their supporting evidence. Database : the journal of biological databases and curation, 2010, baq023.

Razick S, et al. (2008) iRefIndex: a consolidated protein interaction database with provenance. BMC bioinformatics, 9, 405.