

Resource Summary Report

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Interaction Reference Index Web Interface

RRID:SCR_008118

Type: Tool

Proper Citation

Interaction Reference Index Web Interface (RRID:SCR_008118)

Resource Information

URL: <http://wodaklab.org/iRefWeb/>

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Description: iRefWeb is an interface to a relational database containing the latest build of the interaction Reference Index (iRefIndex) which integrates protein interaction data from nine different interaction databases: BioGRID, BIND, CORUM, DIP, HPRD, INTACT, MINT, MPPI, MPACT and OPHID. Integration is achieved through a rigorously documented procedure for mapping protein IDs across databases, enabling systematic backtracking of the links used to establish the identity of the interaction partners. The iRefWeb interface groups interaction records from the different databases into a single non-redundant view. In particular iRefWeb facilitates comparing interaction records as seen by the various source databases relative to the PubMeds they were annotated from. iRefWeb is one of several views of the iRefIndex resource. Data are also available in a tab-delimited plain-text format (PSI-MITAB) as well as planned releases of a PSI-XML formatted version and a Cytoscape plugin. Further details about the iRefIndex project as well as data downloads are available from [here](#). The method used to build iRefIndex is described in a recent publication.

Synonyms: iRefWeb

Resource Type: data or information resource, database

Keywords: bind, biogrid, corum, dip, hprd, intact, interaction, mint, mpact, mppi, ophid, protein

Resource Name: Interaction Reference Index Web Interface

Resource ID: SCR_008118

Alternate IDs: nif-0000-20861, r3d100012725

Alternate URLs: <https://doi.org/10.17616/R31B8K>, <https://doi.org/10.17616/R31B8K>

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260729T044200+0000

Ratings and Alerts

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

No alerts have been found for Interaction Reference Index Web Interface.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Marino GB, et al. (2025) GeneSetCart: assembling, augmenting, combining, visualizing, and analyzing gene sets. GigaScience, 14.

Peng R, et al. (2023) Mapping the protein-protein interactome in the tumor immune microenvironment. Antibody therapeutics, 6(4), 311.

Ieremie I, et al. (2022) TransformerGO: predicting protein-protein interactions by modelling the attention between sets of gene ontology terms. Bioinformatics (Oxford, England), 38(8), 2269.

Unsal-Beyge S, et al. (2022) Functional stratification of cancer drugs through integrated network similarity. NPJ systems biology and applications, 8(1), 11.

Chen S, et al. (2022) A full-proteome, interaction-specific characterization of mutational hotspots across human cancers. Genome research, 32(1), 135.

Azadian S, et al. (2021) Reconstruction of Intercellular Signaling Network by Cytokine-Receptor Interactions. Iranian journal of biotechnology, 19(1), e2560.

Arici MK, et al. (2021) Performance Assessment of the Network Reconstruction Approaches on Various Interactomes. Frontiers in molecular biosciences, 8, 666705.

Milewska A, et al. (2020) MASS SPECTROMETRY IN VIROLOGICAL SCIENCES. Mass spectrometry reviews, 39(5-6), 499.

Ku AA, et al. (2020) Integration of multiple biological contexts reveals principles of synthetic lethality that affect reproducibility. Nature communications, 11(1), 2375.

Wilson JL, et al. (2018) PathFX provides mechanistic insights into drug efficacy and safety for regulatory review and therapeutic development. PLoS computational biology, 14(12), e1006614.

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.

Salavaty A, et al. (2017) Bioinformatic Analysis of Circadian Expression of Oncogenes and Tumor Suppressor Genes. Bioinformatics and biology insights, 11, 1177932217746991.

Rouleau M, et al. (2017) Endogenous Protein Interactome of Human UDP-Glucuronosyltransferases Exposed by Untargeted Proteomics. Frontiers in pharmacology, 8, 23.

Alonso-Lopez D, et al. (2016) APID interactomes: providing proteome-based interactomes with controlled quality for multiple species and derived networks. Nucleic acids research, 44(W1), W529.

Delahaye-Duriez A, et al. (2016) Rare and common epilepsies converge on a shared gene regulatory network providing opportunities for novel antiepileptic drug discovery. Genome biology, 17(1), 245.

Wilson JL, et al. (2016) Pathway-based network modeling finds hidden genes in shRNA screen for regulators of acute lymphoblastic leukemia. Integrative biology : quantitative biosciences from nano to macro, 8(7), 761.

Sabetian S, et al. (2015) Identification of putative drug targets for human sperm-egg interaction defect using protein network approach. BMC systems biology, 9, 37.

Pu S, et al. (2015) Extracting high confidence protein interactions from affinity purification data: at the crossroads. Journal of proteomics, 118, 63.

Budak G, et al. (2015) Reconstruction of the temporal signaling network in Salmonella-infected human cells. Frontiers in microbiology, 6, 730.

Wang Z, et al. (2015) Dynamics of the discovery process of protein-protein interactions from low content studies. BMC systems biology, 9, 26.