Resource Summary Report

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Unified Human Interactome

RRID:SCR_005805
Type: Tool

Proper Citation

Unified Human Interactome (RRID:SCR_005805)

Resource Information

URL: http://www.unihi.org

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Description: A database of human molecular interaction networks that integrates human protein-protein and transcriptional regulatory interactions from 15 distinct resources and aims to give direct and easy access to the integrated data set and to enable users to perform network-based investigations. The database includes tools (i) to search for molecular interaction partners of query genes or proteins in the integrated dataset, (ii) to inspect the origin, evidence and functional annotation of retrieved proteins and interactions, (iii) to visualize and adjust the resulting interaction network, (iv) to filter interactions based on method of derivation, evidence and type of experiment as well as based on gene expression data or gene lists and (v) to analyze the functional composition of interaction networks.

Abbreviations: UniHI

Resource Type: data or information resource, database

Defining Citation: PMID:24214987, PMID:22218860, PMID:18984619, PMID:17158159

Keywords: molecular interaction network, interactome, protein, protein interaction network, protein interaction, pathway, function, visualization, protein-protein interaction, transcriptional regulatory interaction, network

Availability: Public, Non-commercial

Resource Name: Unified Human Interactome

Resource ID: SCR_005805

Alternate IDs: OMICS_01911, nif-0000-03609

Alternate URLs: http://www.mdc-berlin.de/unihi

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260729T044121+0000

Ratings and Alerts

No rating or validation information has been found for Unified Human Interactome.

No alerts have been found for Unified Human Interactome.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Shen Y, et al. (2023) Identification of eIF6 as a prognostic factor that drives tumor progression and predicts arsenic trioxide efficacy in lung adenocarcinoma. Molecular biology reports, 50(2), 1167.

Sun L, et al. (2021) eIF6 promotes the malignant progression of human hepatocellular carcinoma via the mTOR signaling pathway. Journal of translational medicine, 19(1), 216.

Shen L, et al. (2021) SIRT3 mediates mitofusin 2 ubiquitination and degradation to suppress ischemia reperfusion-induced acute kidney injury. Experimental cell research, 408(2), 112861.

Liu R, et al. (2020) Defect of SLC38A3 promotes epithelial-mesenchymal transition and predicts poor prognosis in esophageal squamous cell carcinoma. Chinese journal of cancer research = Chung-kuo yen cheng yen chiu, 32(5), 547.

Haenig C, et al. (2020) Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains. Cell reports, 32(7), 108050.

Schmidt A, et al. (2018) Time-resolved transcriptome and proteome landscape of human regulatory T cell (Treg) differentiation reveals novel regulators of FOXP3. BMC biology, 16(1), 47.

Miryala SK, et al. (2018) Discerning molecular interactions: A comprehensive review on biomolecular interaction databases and network analysis tools. Gene, 642, 84.

Xing P, et al. (2017) A fast approach to detect gene-gene synergy. Scientific reports, 7(1), 16437.

Chen H, et al. (2015) Pathway mapping and development of disease-specific biomarkers: protein-based network biomarkers. Journal of cellular and molecular medicine, 19(2), 297.

Stroedicke M, et al. (2015) Systematic interaction network filtering identifies CRMP1 as a novel suppressor of huntingtin misfolding and neurotoxicity. Genome research, 25(5), 701.

Kalathur RK, et al. (2015) The unfolded protein response and its potential role in Huntington's disease elucidated by a systems biology approach. F1000Research, 4, 103.

Mesak F, et al. (2015) Transcriptomics of diapause in an isogenic self-fertilizing vertebrate. BMC genomics, 16, 989.

Zaveri HP, et al. (2014) Identification of critical regions and candidate genes for cardiovascular malformations and cardiomyopathy associated with deletions of chromosome 1p36. PloS one, 9(1), e85600.

Pinto JP, et al. (2014) Targeting molecular networks for drug research. Frontiers in genetics, 5, 160.

Koch S, et al. (2013) Cathepsin D deficiency induces cytoskeletal changes and affects cell migration pathways in the brain. Neurobiology of disease, 50, 107.

Kollmann K, et al. (2013) Cell biology and function of neuronal ceroid lipofuscinosis-related proteins. Biochimica et biophysica acta, 1832(11), 1866.

Zhang J, et al. (2011) The BioAssay network and its implications to future therapeutic discovery. BMC bioinformatics, 12 Suppl 5(Suppl 5), S1.

Marras E, et al. (2010) Inferring modules from human protein interactome classes. BMC systems biology, 4, 102.

Jesmin J, et al. (2010) Gene regulatory network reveals oxidative stress as the underlying molecular mechanism of type 2 diabetes and hypertension. BMC medical genomics, 3, 45.