

Resource Summary Report

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Human Reference Protein Interactome Project

RRID:SCR_015670

Type: Tool

Proper Citation

Human Reference Protein Interactome Project (RRID:SCR_015670)

Resource Information

URL: <http://interactome.baderlab.org/>

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Description: Project portal for the Human Reference Protein Interactome Project, which aims generate a first reference map of the human protein-protein interactome network by identifying binary protein-protein interactions (PPIs). It achieves this by systematically interrogating all pairwise combinations of predicted human protein-coding genes using proteome-scale technologies.

Abbreviations: HuRI

Synonyms: HuRI: The Human Reference Protein Interactome Mapping Project

Resource Type: web application, project portal, data or information resource, database, software resource, portal

Defining Citation: [PMID:25416956](#)

Keywords: protein interactome, protein-protein interaction, ppi, pairwise combination, proteome, human reference

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NIH RC4HG006066;
NICHD ARRA R01HD065288;
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NICHD ARRA R01MH105524;
NIMH R01MH091350;

NSF CCF-1219007;
NSERC RGPIN-2014-03892

Availability: Freely Available, Free, Available for download

Resource Name: Human Reference Protein Interactome Project

Resource ID: SCR_015670

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260729T044358+0000

Ratings and Alerts

No rating or validation information has been found for Human Reference Protein Interactome Project.

No alerts have been found for Human Reference Protein Interactome Project.

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 [SPARC SAWG](#) .

Scholtes C, et al. (2024) Identification of a chromatin-bound ERR α interactome network in mouse liver. Molecular metabolism, 83, 101925.

Sevilla LM, et al. (2024) Glucocorticoid receptor controls atopic dermatitis inflammation via functional interactions with P63 and autocrine signaling in epidermal keratinocytes. Cell death & disease, 15(7), 535.

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

Dufour CR, et al. (2022) The mTOR chromatin-bound interactome in prostate cancer. Cell reports, 38(12), 110534.

Piette BL, et al. (2021) Comprehensive interactome profiling of the human Hsp70 network highlights functional differentiation of J domains. Molecular cell, 81(12), 2549.

Kazazian K, et al. (2020) FAM46C/TENT5C functions as a tumor suppressor through inhibition of Plk4 activity. Communications biology, 3(1), 448.

Maiorino E, et al. (2020) Discovering the genes mediating the interactions between chronic respiratory diseases in the human interactome. Nature communications, 11(1),

MacNamara A, et al. (2020) Network and pathway expansion of genetic disease associations identifies successful drug targets. *Scientific reports*, 10(1), 20970.

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.

Ugidos N, et al. (2019) Interactome of the Autoimmune Risk Protein ANKRD55. *Frontiers in immunology*, 10, 2067.

Ghadie M, et al. (2019) Estimating dispensable content in the human interactome. *Nature communications*, 10(1), 3205.

Ramos PIP, et al. (2019) Leveraging User-Friendly Network Approaches to Extract Knowledge From High-Throughput Omics Datasets. *Frontiers in genetics*, 10, 1120.

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

Pan J, et al. (2018) Interrogation of Mammalian Protein Complex Structure, Function, and Membership Using Genome-Scale Fitness Screens. *Cell systems*, 6(5), 555.

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Himmelstein DS, et al. (2017) Systematic integration of biomedical knowledge prioritizes drugs for repurposing. *eLife*, 6.

Bueno R, et al. (2017) Changes in gene expression variability reveal a stable synthetic lethal interaction network in BRCA2-ovarian cancers. *Methods (San Diego, Calif.)*, 131, 74.

Satoh J, et al. (2013) A Comprehensive Profile of ChIP-Seq-Based STAT1 Target Genes Suggests the Complexity of STAT1-Mediated Gene Regulatory Mechanisms. *Gene regulation and systems biology*, 7, 41.

Bhattacharjee M, et al. (2013) A multilectin affinity approach for comparative glycoprotein profiling of rheumatoid arthritis and spondyloarthritis. *Clinical proteomics*, 10(1), 11.

Tabunoki H, et al. (2012) Molecular network profiling of U373MG human glioblastoma cells following induction of apoptosis by novel marine-derived anti-cancer 1,2,3,4-tetrahydroisoquinoline alkaloids. *Cancer cell international*, 12(1), 14.