

# Resource Summary Report

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## HIPPIE

RRID:SCR\_014651

Type: Tool

### Proper Citation

HIPPIE (RRID:SCR\_014651)

### Resource Information

**URL:** <http://cbdm.uni-mainz.de/hippie/>

**Proper Citation:** HIPPIE (RRID:SCR\_014651)

**Description:** Web tool used to generate confidence scored and functionally annotated human protein-protein interaction networks. Users can run a protein query using a UniProt identifier (ID or accession), gene symbol or Entrez gene id, or a network query using set fields.

**Synonyms:** Human Integrated Protein Protein Interaction Reference, Human Integrated Protein-Protein Interaction rEference, Human Integrated Protein-Protein Interaction rEference (HIPPIE)

**Resource Type:** web application, software resource

**Defining Citation:** [DOI:10.1371/journal.pone.0031826](https://doi.org/10.1371/journal.pone.0031826)

**Keywords:** web tool, web application, protein protein interaction, reference tool, protein query, network query, human protein protein interaction network

**Funding:** Helmholtz Alliance in Systems Biology ;  
BMBF 01GS08170

**Availability:** Available on the web, Available for download, Acknowledgement requested

**Resource Name:** HIPPIE

**Resource ID:** SCR\_014651

**Record Creation Time:** 20220129T080321+0000

**Record Last Update:** 20260728T043441+0000

### Ratings and Alerts

No rating or validation information has been found for HIPPIE.

No alerts have been found for HIPPIE.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 135 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Chakraborty T, et al. (2025) DensePPI-2: a bio-inspired update for sequence-based PPI prediction leveraging mutation rates. Briefings in bioinformatics, 26(4).

Mechelli R, et al. (2025) A disease-specific convergence of host and Epstein-Barr virus genetics in multiple sclerosis. Proceedings of the National Academy of Sciences of the United States of America, 122(14), e2418783122.

Liu D, et al. (2025) PLM-interact: extending protein language models to predict protein-protein interactions. Nature communications, 16(1), 9012.

Donahue CJ, et al. (2025) A protein-proximity screen reveals Ebola virus co-opts the mRNA decapping complex through the scaffold protein EDC4. Nature communications, 16(1), 8485.

Malakhov MM, et al. (2025) Co-expression-wide association studies link genetically regulated interactions with complex traits. Nature communications, 16(1), 11061.

Vagiona AC, et al. (2025) Unraveling cooperative and competitive interactions within protein triplets in the human interactome. Scientific reports, 15(1), 32548.

Zheng Y, et al. (2025) A deep generative model for deciphering cellular dynamics and in silico drug discovery in complex diseases. Nature biomedical engineering, 9(12), 2155.

Chen J, et al. (2025) Surface Formation Pathway of Nitrogen- and Sulfur-Containing Organic Compounds on Ammonium Sulfate. The journal of physical chemistry. A, 129(12), 2922.

Tang H, et al. (2025) Metabolism-associated protein network constructing and host-directed anti-influenza drug repurposing. Briefings in bioinformatics, 26(3).

Jalali P, et al. (2025) Bioinformatics analysis reveals shared molecular pathways for relationship between ulcerative colitis and primary sclerosing cholangitis. Genomics & informatics, 23(1), 12.

Bermudez-Lekerika P, et al. (2025) In-silico proteomic analysis of the role of IL-4 and IL-10 in IVD degeneration: Protein-protein interaction networks for candidate prioritisation.

Computational and structural biotechnology journal, 27, 1600.

Vagiona AC, et al. (2025) Prediction of protein interactions with function in protein (de-)phosphorylation. PloS one, 20(3), e0319084.

Santiago J, et al. (2025) Advanced Paternal Age and Sperm Proteome Dynamics: A Possible Explanation for Age-Associated Male Fertility Decline. Cells, 14(11).

Lindacher J, et al. (2025) 3D Tumor microenvironment interaction reveals AP-1 complex regulation and contact-mediated reprogramming of bone marrow stromal cells in chronic lymphocytic leukemia. HemaSphere, 9(8), e70199.

Zhao B, et al. (2025) DENetwork unveils non-differentially expressed genes with functional relevance across conditions through information flow perturbation. Nucleic acids research, 53(22).

Silkwood K, et al. (2024) Leveraging gene correlations in single cell transcriptomic data. BMC bioinformatics, 25(1), 305.

Taylor S, et al. (2024) In Situ Ambient Pressure Photoelectron Spectroscopy Study of the Plasma-Surface Interaction on Metal Foils. Langmuir : the ACS journal of surfaces and colloids, 40(27), 13950.

Zhao Y, et al. (2024) Transcriptomics and weighted protein network analyses of the LRRK2 protein interactome reveal distinct molecular signatures for sporadic and LRRK2 Parkinson's Disease. NPJ Parkinson's disease, 10(1), 144.

Shao L, et al. (2024) Active natural compounds perturb the melanoma risk-gene network. G3 (Bethesda, Md.), 14(2).

Blumenthal DB, et al. (2024) Emergence of power law distributions in protein-protein interaction networks through study bias. eLife, 13.