

Resource Summary Report

Generated by T1D on Aug 9, 2026

HIPPIE

RRID:SCR_014651

Type: Tool

Proper Citation

HIPPIE (RRID:SCR_014651)

Resource Information

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

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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: 20260808T190015+0000

Ratings and Alerts

No rating or validation information has been found for HIPPIE.

No alerts have been found for HIPPIE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 142 mentions in open access literature.

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

Karthick V, et al. (2026) Quantum-augmented graph differential geometry enhances accuracy in protein-protein interaction prediction. Scientific reports, 16(1).

Mohtar MA, et al. (2026) Genetic regulatory axis between AGR2 and ESR1 promotes breast cancer progression. PloS one, 21(7), e0351873.

Rincic M, et al. (2026) Structural variations in evolutionary novel genomic regions: new insights into neurodevelopmental disorders by long-read DNA Sequencing. Molecular medicine (Cambridge, Mass.), 32(1), 17.

Mohtar MA, et al. (2026) RNA-Seq analysis reveals regulatory networks driven by EpCAM overexpression in esophageal adenocarcinoma cells. PeerJ, 14, e20877.

Ma K, et al. (2026) Multilabel prediction of virus target proteins via multimodal graph representation learning. PLoS computational biology, 22(5), e1014320.

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

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.

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.

Yavuz BR, et al. (2025) Discovering anticancer drug target combinations via network-informed signaling-based approach. Communications medicine, 5(1), 428.

Bankier S, et al. (2025) Circulating causal protein networks linked to future risk of myocardial infarction. Nature communications, 17(1), 448.

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.

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

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.

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.

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.

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.

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

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).