

Resource Summary Report

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HPRD - Human Protein Reference Database

RRID:SCR_007027

Type: Tool

Proper Citation

HPRD - Human Protein Reference Database (RRID:SCR_007027)

Resource Information

URL: <http://www.hprd.org>

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Description: Database that represents a centralized platform to visually depict and integrate information pertaining to domain architecture, post-translational modifications, interaction networks and disease association for each protein in the human proteome. All the information in HPRD has been manually extracted from the literature by expert biologists who read, interpret and analyze the published data.

Abbreviations: HPRD

Synonyms: Human Protein Reference Database

Resource Type: data or information resource, database

Defining Citation: [PMID:18988627](#), [PMID:16381900](#), [PMID:14525934](#)

Keywords: protein, disease, network, post-translational, proteome, protein binding, protein s, protein c, pathway, protein-protein interaction, protein expression, subcellular localization, phosphorylation motif, signaling pathway, protein sequence, blast, molecule, domain, motif, post-translational modification, protein isoform, FASEB list

Availability: Acknowledgement requested, Free, Non-commercial, Commercial requires license

Resource Name: HPRD - Human Protein Reference Database

Resource ID: SCR_007027

Alternate IDs: nif-0000-00137, r3d100010978

Alternate URLs: <https://doi.org/10.17616/R3MK9N>

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260804T043320+0000

Ratings and Alerts

No rating or validation information has been found for HPRD - Human Protein Reference Database.

No alerts have been found for HPRD - Human Protein Reference Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1266 mentions in open access literature.

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

Zeng M, et al. (2025) Drug-target interaction prediction based on graph convolutional autoencoder with dynamic weighting residual GCN. BMC bioinformatics, 26(1), 200.

Karunakaran KB, et al. (2025) Spatial and functional profiles distinguish target sets of Parkinson's disease and antipsychotic drugs with different clinical effects. Translational psychiatry, 15(1), 124.

Ray S, et al. (2025) A graph neural network-based approach for predicting SARS-CoV-2-human protein interactions from multiview data. PloS one, 20(9), e0332794.

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

Wright SN, et al. (2025) State of the interactomes: an evaluation of molecular networks for generating biological insights. Molecular systems biology, 21(1), 1.

Zhai Y, et al. (2025) Network pharmacology: a crucial approach in traditional Chinese medicine research. Chinese medicine, 20(1), 8.

Bhaumik D, et al. (2025) Implementation challenges of the new federal nursing home staffing rules will vary across states. Health affairs scholar, 3(2), qxaf009.

Tian D, et al. (2025) Causal association of cholesterol metabolism-related proteins with hepatocellular carcinoma and dysfunction-associated steatotic liver disease: a mendelian randomization study. Discover oncology, 16(1), 987.

Fei H, et al. (2025) Molecular mechanisms and genetic predisposition to osteoarthritis and osteosarcoma through Mendelian inheritance patterns. Discover oncology, 16(1), 2093.

Bögershausen N, et al. (2025) SEC24C deficiency causes trafficking and glycosylation abnormalities in an epileptic encephalopathy with cataracts and dyserythropoiesis. *JCI insight*, 10(9).

Ni T, et al. (2025) Integrated Transcriptome Analysis Reveals Novel Molecular Signatures for Schizophrenia Characterization. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(2), e2407628.

Yang G, et al. (2025) DTI-MHAPR: optimized drug-target interaction prediction via PCA-enhanced features and heterogeneous graph attention networks. *BMC bioinformatics*, 26(1), 11.

Bernhard C, et al. (2025) A coregulatory influence map of glioblastoma heterogeneity and plasticity. *NPJ precision oncology*, 9(1), 110.

Sun L, et al. (2025) ISLRWR: A network diffusion algorithm for drug-target interactions prediction. *PloS one*, 20(1), e0302281.

Corkran K, et al. (2025) An agent-based model to assess the impact of shared staff and occupancy rate on infectious disease burden in nursing homes. *BMC infectious diseases*, 25(1), 635.

Kubo H, et al. (2025) Sage extract and ascorbic acid derivative inhibit melanogenesis via downregulating keratinocyte-derived GM-CSF. *PloS one*, 20(6), e0325242.

Noh SG, et al. (2025) Co-regulation of Nr1d1 and Ppar γ in age-related changes of lipid metabolism and its modulation by calorie restriction. *Aging*, 17(7), 1810.

Lu D, et al. (2025) Identifying potential risk genes for clear cell renal cell carcinoma with deep reinforcement learning. *Nature communications*, 16(1), 3591.

Mugoma S, et al. (2025) The impact of COVID-19 and public health measures on homicide and suicide trends in Botswana using an interrupted time series analysis. *Injury epidemiology*, 12(1), 42.

Qian H, et al. (2025) Exploring the mechanism of *Inula japonica* Thunb. against non-small cell lung cancer using a computer-aided drug design approach. *Medicine*, 104(51), e46660.