

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

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: database, data or information resource

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: 20260808T190401+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 1311 mentions in open access literature.

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

Angelis NV, et al. (2026) Ole-4, a novel synthetic derivative of Oleuropein, enhances antitumor immunity and modulates kinase activity-dependent signaling. Journal of translational medicine, 24(1).

Rychlik KA, et al. (2026) Prenatal arsenic exposure and gene expression in fetal liver, heart, lung, and placenta. Toxicology, 522, 154420.

Myers IK, et al. (2026) Vagus Nerve Stimulation Paired With Tones Alters the Auditory Cortex Proteome in a Rat Model of Rett Syndrome. Developmental neurobiology, 86(3), e70032.

Kotlyar M, et al. (2026) IID 2025: Physical protein interaction data with detection types, co-purified protein sets, molecular docking, and immune cell networks. Nucleic acids research, 54(D1), D593.

Gersting SW, et al. (2026) Peroxisomal interactome mapping enables network-based modelling of function and disease. Life science alliance, 9(9).

Kumar APKA, et al. (2026) Phosphoproteome landscape of ARID1A and its implications in DNA damage response and breast cancer pathogenesis. Discover oncology, 17(1), 312.

Choudhary A, et al. (2026) Extracellular vesicles from stem cells rescue cellular phenotypes and behavioral deficits in SHANK3-associated ASD neuronal and mouse models. Cell death & disease, 17(1).

Palollathil A, et al. (2026) Integrative phosphoproteomic analysis reveals co-regulatory phosphorylation networks of rhotekin in cancer progression. Discover oncology, 17(1).

Sujina A, et al. (2026) Differential phosphorylation of PHIP phosphopeptides with implications in insulin signaling. BMC molecular and cell biology, 27(1).

Poojari TR, et al. (2026) Meta-cancer phosphoproteomic analysis unveils association of Tau phosphosites with DNA damage response. Frontiers in systems biology, 6, 1819794.

Palollathil A, et al. (2026) Integrative phosphoproteomic analysis identifies functional roles of TRPM7 phosphosites in oncogenesis. Frontiers in bioinformatics, 6, 1757645.

Gopalakrishnan V, et al. (2026) Exploring the Phosphoregulatory Network of Human Sucrose Non-Fermenting 1-Related Kinase. Biology, 15(9).

Zhong J, et al. (2026) Splitpea: a Python package for protein-protein interaction network rewiring analysis due to alternative splicing. Bioinformatics (Oxford, England), 42(4).

Ullanat V, et al. (2026) Learning the language of protein-protein interactions. Nature communications, 17(1), 1199.

Zhao Y, et al. (2026) Integrative Analysis of Triphala's Therapeutic Mechanisms in Periodontitis: Network Pharmacology-guided Investigation with Experimental Validation in Cellular and Animal Models. Oral health & preventive dentistry, 24, 375.

Noh SG, et al. (2026) Calorie Restriction Modulates Gene Expression of IL19 and IL24 during Renal Aging. Annals of geriatric medicine and research, 30(1), 28.

Palollathil A, et al. (2026) Proteome-Wide Analysis of Functional Phosphosites in the FGFR Family of Proteins: Insights from Large-Scale Phosphoproteomic Analysis. Proteomes, 14(1).

Khanum A, et al. (2026) Computational Phosphosite-Specific Network Analysis of YES1 Y426 Reveals Cancer-Associated Phosphorylation Patterns. Proteomes, 14(2).

Vijayan J, et al. (2026) Co-Phosphoregulatory Network Underlying Functional Coherence of TLK1 and TLK2 Kinase Paralogs. International journal of molecular sciences, 27(12).

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