Resource Summary Report

Generated by NIF on Apr 29, 2025

Human Proteinpedia

RRID:SCR_002948
Type: Tool

Proper Citation

Human Proteinpedia (RRID:SCR_002948)

Resource Information

URL: http://www.humanproteinpedia.org/

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Description: A community portal for sharing and integration of human protein data that allows research laboratories to contribute and maintain protein annotations. The Human Protein Reference Database (HPRD) integrates data that is deposited along with the existing literature curated information in the context of an individual protein. Data pertaining to post-translational modifications, protein-protein interactions, tissue expression, expression in cell lines, subcellular localization and enzyme substrate relationships can be submitted.

Abbreviations: Human Proteinpedia

Resource Type: database, service resource, data or information resource, storage service resource, data repository

Defining Citation: PMID:18259167

Keywords: enzyme, protein expression, post-translational modification, protein-protein interaction, subcellular localization, enzyme substrate, tissue expression, protein, protein binding, peptide, mass spectrometry, mass spectrometry spectra, immunohistochemistry, western blotting, microarray, co-immunoprecipitation, fluorescence, annotation, cell line expression, disease tissue expression, FASEB list

Funding:

Availability: The community can contribute to this resource, Public

Resource Name: Human Proteinpedia

Resource ID: SCR_002948

Alternate IDs: nif-0000-02999

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250429T054814+0000

Ratings and Alerts

No rating or validation information has been found for Human Proteinpedia.

No alerts have been found for Human Proteinpedia.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 32 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Peerapen P, et al. (2023) Protein network analysis and functional enrichment via computational biotechnology unravel molecular and pathogenic mechanisms of kidney stone disease. Biomedical journal, 46(2), 100577.

Lite C, et al. (2021) SARS-CoV-2/human interactome reveals ACE2 locus crosstalk with the immune regulatory network in the host. Pathogens and disease, 79(2).

Ahmed SSSJ, et al. (2020) Regulatory Cross Talk Between SARS-CoV-2 Receptor Binding and Replication Machinery in the Human Host. Frontiers in physiology, 11, 802.

Arfaoui A, et al. (2019) A genome-wide RNAi screen reveals essential therapeutic targets of breast cancer stem cells. EMBO molecular medicine, 11(10), e9930.

Rioualen C, et al. (2017) HTS-Net: An integrated regulome-interactome approach for establishing network regulation models in high-throughput screenings. PloS one, 12(9), e0185400.

Chiang AW, et al. (2017) Identification of Entry Factors Involved in Hepatitis C Virus Infection Based on Host-Mimicking Short Linear Motifs. PLoS computational biology, 13(1), e1005368.

Mukherjee S, et al. (2016) Proteomics in India: the clinical aspect. Clinical proteomics, 13, 21.

Fernandes M, et al. (2016) CanisOme--The protein signatures of Canis lupus familiaris diseases. Journal of proteomics, 136, 193.

Pawar H, et al. (2015) Downregulation of S100 Calcium Binding Protein A9 in Esophageal Squamous Cell Carcinoma. TheScientificWorldJournal, 2015, 325721.

Subbannayya T, et al. (2015) Macrophage migration inhibitory factor - a therapeutic target in gallbladder cancer. BMC cancer, 15, 843.

Rauniyar N, et al. (2015) Parallel Reaction Monitoring: A Targeted Experiment Performed Using High Resolution and High Mass Accuracy Mass Spectrometry. International journal of molecular sciences, 16(12), 28566.

Wohlgemuth I, et al. (2015) Studying macromolecular complex stoichiometries by peptide-based mass spectrometry. Proteomics, 15(5-6), 862.

Chen T, et al. (2015) Web resources for mass spectrometry-based proteomics. Genomics, proteomics & bioinformatics, 13(1), 36.

Perez-Riverol Y, et al. (2015) Making proteomics data accessible and reusable: current state of proteomics databases and repositories. Proteomics, 15(5-6), 930.

Subbannayya Y, et al. (2015) Identification of differentially expressed serum proteins in gastric adenocarcinoma. Journal of proteomics, 127(Pt A), 80.

Giulietti M, et al. (2014) How much do we know about the coupling of G-proteins to serotonin receptors? Molecular brain, 7, 49.

Frantzi M, et al. (2014) Clinical proteomic biomarkers: relevant issues on study design & technical considerations in biomarker development. Clinical and translational medicine, 3(1), 7.

Murthy KR, et al. (2014) Proteomic analysis of human vitreous humor. Clinical proteomics, 11(1), 29.

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

Fan S, et al. (2013) Layered signaling regulatory networks analysis of gene expression involved in malignant tumorigenesis of non-resolving ulcerative colitis via integration of cross-study microarray profiles. PloS one, 8(6), e67142.