

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://FDILab.org) on Apr 17, 2025

PeptideAtlas

RRID:SCR_006783

Type: Tool

Proper Citation

PeptideAtlas (RRID:SCR_006783)

Resource Information

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

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Description: Multi-organism, publicly accessible compendium of peptides identified in a large set of tandem mass spectrometry proteomics experiments. Mass spectrometer output files are collected for human, mouse, yeast, and several other organisms, and searched using the latest search engines and protein sequences. All results of sequence and spectral library searching are subsequently processed through the Trans Proteomic Pipeline to derive a probability of correct identification for all results in a uniform manner to insure a high quality database, along with false discovery rates at the whole atlas level. The raw data, search results, and full builds can be downloaded for other uses. All results of sequence searching are processed through PeptideProphet to derive a probability of correct identification for all results in a uniform manner ensuring a high quality database. All peptides are mapped to Ensembl and can be viewed as custom tracks on the Ensembl genome browser. The long term goal of the project is full annotation of eukaryotic genomes through a thorough validation of expressed proteins. The PeptideAtlas provides a method and a framework to accommodate proteome information coming from high-throughput proteomics technologies. The online database administers experimental data in the public domain. You are encouraged to contribute to the database.

Abbreviations: PeptideAtlas

Synonyms: Peptide Atlas, PeptideAtlas

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

Defining Citation: [PMID:20013378](#), [PMID:23215161](#), [PMID:16381952](#), [PMID:15642101](#)

Keywords: proteomics, peptide, mass spectrometry, annotation, eukaryotic, genome, peptide sequence, high-throughput mass spectrometry, ensembl, peptideprophet, protein sequence, blood plasma, protein, eukaryotic cell, dna, bio.tools, FASEB list

Funding: NCI ;
NHGRI ;
NIGMS

Availability: Public, The community can contribute to this resource, Acknowledgement requested

Resource Name: PeptideAtlas

Resource ID: SCR_006783

Alternate IDs: nif-0000-03266, biotools:peptideatlas

Alternate URLs: <https://bio.tools/peptideatlas>

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250417T065254+0000

Ratings and Alerts

No rating or validation information has been found for PeptideAtlas.

No alerts have been found for PeptideAtlas.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 464 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Gomez-Artiguez L, et al. (2025) Candida albicans: a comprehensive view of the proteome. bioRxiv : the preprint server for biology.

Li D, et al. (2025) MicroEpitope: an atlas of immune epitopes derived from cancer microbiomes. *Nucleic acids research*, 53(D1), D1435.

Matsumoto M, et al. (2025) Missense mutations of the ephrin receptor EPHA1 associated with Alzheimer's disease disrupt receptor signaling functions. *The Journal of biological chemistry*, 301(2), 108099.

Döring S, et al. (2025) Challenges and Insights in Absolute Quantification of Recombinant Therapeutic Antibodies by Mass Spectrometry: An Introductory Review. *Antibodies (Basel, Switzerland)*, 14(1).

Zhou N, et al. (2025) Proteomic patterns associated with ketamine response in major depressive disorders. *Cell biology and toxicology*, 41(1), 26.

Ramsbottom KA, et al. (2024) Meta-Analysis of Rice Phosphoproteomics Data to Understand Variation in Cell Signaling Across the Rice Pan-Genome. *Journal of proteome research*, 23(7), 2518.

Evans KV, et al. (2024) Expression of the Arabidopsis redox-related LEA protein, SAG21 is regulated by ERF, NAC and WRKY transcription factors. *Scientific reports*, 14(1), 7756.

Massey S, et al. (2024) Novel CDKL5 targets identified in human iPSC-derived neurons. *Cellular and molecular life sciences : CMLS*, 81(1), 347.

Reis ALG, et al. (2024) Proteomic analysis of cerebrospinal fluid of amyotrophic lateral sclerosis patients in the presence of autologous bone marrow derived mesenchymal stem cells. *Stem cell research & therapy*, 15(1), 301.

Shi K, et al. (2024) PractiCPP: a deep learning approach tailored for extremely imbalanced datasets in cell-penetrating peptide prediction. *Bioinformatics (Oxford, England)*, 40(2).

Korchak JA, et al. (2024) IS-PRM-Based Peptide Targeting Informed by Long-Read Sequencing for Alternative Proteome Detection. *Journal of the American Society for Mass Spectrometry*, 35(11), 2614.

Svecla M, et al. (2024) ASGR1 deficiency diverts lipids toward adipose tissue but results in liver damage during obesity. *Cardiovascular diabetology*, 23(1), 42.

Xu X, et al. (2024) ACP-DRL: an anticancer peptides recognition method based on deep representation learning. *Frontiers in genetics*, 15, 1376486.

Sharma N, et al. (2024) Defining the Soluble and Extracellular Vesicle Protein Compartments of Plasma Using In-Depth Mass Spectrometry-Based Proteomics. *Journal of proteome research*, 23(9), 4114.

Kobak KA, et al. (2024) Effect of biological sex and short-term high-fat diet on cellular proliferation, ribosomal biogenesis, and targeted protein abundance in murine articular cartilage. *Osteoarthritis and cartilage open*, 6(3), 100495.

Hallal SM, et al. (2024) Size matters: Biomolecular compositions of small and large extracellular vesicles in the urine of glioblastoma patients. *Journal of extracellular biology*, 3(11), e70021.

Maquedano M, et al. (2024) More than 2,500 coding genes in the human reference gene set still have unsettled status. *bioRxiv : the preprint server for biology*.

Reddy PJ, et al. (2024) *Borrelia* PeptideAtlas: A proteome resource of common *Borrelia burgdorferi* isolates for Lyme research. *Scientific data*, 11(1), 1313.

Lv D, et al. (2024) CancerProteome: a resource to functionally decipher the proteome landscape in cancer. *Nucleic acids research*, 52(D1), D1155.

Lee JG, et al. (2024) PIBF1 regulates trophoblast syncytialization and promotes cardiovascular development. *Nature communications*, 15(1), 1487.