

Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

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 or information resource, service resource, storage service resource, data repository

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, r3d100010889, biotools:peptideatlas

Alternate URLs: <https://bio.tools/peptideatlas>, <https://doi.org/10.17616/R3BK61>

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260810T040436+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 511 mentions in open access literature.

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

Al-Momani SS, et al. (2026) A Landscape Analysis of Human SUMOylation. Molecular & cellular proteomics : MCP, 25(5), 101571.

Hickson SM, et al. (2026) Genomic, proteolytic, and phenotypic characterization of Pseudomonas aeruginosa isolates causing infective endocarditis. Microbiology spectrum, 14(6), e0374225.

Deng S, et al. (2026) SPAID: a comprehensive database for disease-specific autoantigens in autoimmune disorders. Advanced biotechnology, 4(2).

Schilling V, et al. (2026) The State of Peptide Detectability in Computational Proteomics and Guidelines for AI Applications. Computational and structural biotechnology journal, 35(1), 0037.

Kusebauch U, et al. (2026) A Labrador PeptideAtlas and DIA spectral assay library - resources for proteomics research in dogs. Scientific data, 13(1).

Nde J, et al. (2026) Integrative Structural Modeling of Intrinsically Disordered Regions in a Human HDAC2 Chromatin Remodeling Complex. *bioRxiv : the preprint server for biology*.

Misra S, et al. (2026) Cross-Platform Proteomics and Machine Learning Algorithms Nominate Plasma Biomarkers of Stroke Diagnosis. *Journal of the American Heart Association*, 15(6), e048249.

Pathirana R, et al. (2026) *Helicobacter pylori* induces the production of interleukin-37 to promote broad immunosuppression and enhance colonization. *Gut microbes*, 18(1), 2618860.

Deutsch EW, et al. (2026) Expanding the human proteome with microproteins and peptideins. *Nature*, 654(8119), 813.

Wacholder A, et al. (2026) Community benchmarking and evaluation of human unannotated microprotein detection by mass spectrometry based proteomics. *Nature communications*, 17(1), 1241.

Jachmann C, et al. (2026) The *Escherichia coli* PeptideAtlas Build: Characterizing the Observed *Escherichia coli* Pan-Proteome and Its Post-Translational Modifications. *Journal of proteome research*, 25(2), 1027.

Larrea-Sebal A, et al. (2026) Blood proteomics: insights from public data. *Genome biology*, 27(1).

Fast L, et al. (2026) Regulation of NAT1 activity in modern humans by a novel phosphorylation site. *Science advances*, 12(23), eady1666.

Yao Y, et al. (2026) Development of a High-Throughput LC-MS/MS Method for Simultaneous Quantification of Four Therapeutic Monoclonal Antibodies in Human Serum: Application in Clinical Therapeutic Drug Monitoring. *Biomedical chromatography : BMC*, 40(3), e70350.

Delgado-Sequera A, et al. (2026) Targeted Quantitative Analysis of Specific Proteins in Cytosolic, Mitochondrial, and Nuclear Fractions Using PRM. *Journal of proteome research*, 25(4), 2183.

Warren JM, et al. (2026) The Effects of Rapid Mitochondrial Gene Loss on Organellar Proteomes. *Genome biology and evolution*, 18(6).

Liang Q, et al. (2026) Diagnostic importance of serum markers in lung cancer. *Molecular medicine reports*, 33(5).

J??rvinen E, et al. (2026) Automated Mag-Net Enrichment Unlocks Deep and Cost-Effective LC-MS Plasma Proteomics. *Journal of proteome research*, 25(2), 618.

Vivek AT, et al. (2026) Integrative multi-omics analysis widens annotation and functional insights into long non-coding RNAs of *Arabidopsis thaliana*. *Biology direct*, 21(1), 14.

Skubitz APN, et al. (2026) Repurposing the liquid-based Pap test for the detection of ovarian cancer protein biomarkers. *Clinical proteomics*, 23(1).