

Resource Summary Report

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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: data repository, data or information resource, database, 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, r3d100010889, biotools:peptideatlas

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

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260804T043314+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 479 mentions in open access literature.

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

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

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

Maquedano M, et al. (2025) The state of the human coding gene catalogues. Database : the journal of biological databases and curation, 2025.

Sinn LR, et al. (2025) Slice-PASEF: Maximising Ion Utilisation in LC-MS Proteomics. bioRxiv : the preprint server for biology.

Qiu B, et al. (2025) Computational analysis reveals non-consensus N-glycosylation sequons in antibody Fab region. mAbs, 17(1), 2574406.

Ran Z, et al. (2025) Deciphering the MHC immunopeptidome of human cancers with Ligand.MHC atlas. *Briefings in bioinformatics*, 26(4).

Bae D, et al. (2025) AI-guided discovery and optimization of antimicrobial peptides through species-aware language model. *Briefings in bioinformatics*, 26(4).

Ho CW, et al. (2025) LncRNA-Encoded Micropeptides: Expression Validation, Translational Mechanisms, and Roles in Cellular Metabolism. *International journal of molecular sciences*, 26(12).

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).

Tzvetkov J, et al. (2025) Searching for Sulfotyrosines (sY) in a HA(pY)STACK. *Journal of proteome research*, 24(3), 1250.

Xiao C, et al. (2025) Oncogenic roles of young human de novo genes and their potential as neoantigens in cancer immunotherapy. *Cell genomics*, 5(9), 100928.

Wen B, et al. (2025) DeepMVP: deep learning models trained on high-quality data accurately predict PTM sites and variant-induced alterations. *Nature methods*, 22(9), 1857.

Scifo E, et al. (2025) Proteomic aging signatures across mouse organs and life stages. *The EMBO journal*, 44(16), 4631.

Sissala N, et al. (2025) Comparative evaluation of Olink Explore 3072 and mass spectrometry with peptide fractionation for plasma proteomics. *Communications chemistry*, 8(1), 327.

Gomez-Artiguez L, et al. (2025) *Candida albicans*: A Comprehensive View of the Proteome. *Journal of proteome research*, 24(4), 1636.

Welp LM, et al. (2025) Chemical crosslinking extends and complements UV crosslinking in analysis of RNA/DNA nucleic acid-protein interaction sites by mass spectrometry. *Nucleic acids research*, 53(15).

Rodriguez JM, et al. (2025) An audit of the PeptideAtlas database uncovers evidence for repurposed pseudogenes and co-opted retroviral ORFs. *BMC genomics*, 26(1), 1087.

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.