

Resource Summary Report

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ProteomeTools

RRID:SCR_018535

Type: Tool

Proper Citation

ProteomeTools (RRID:SCR_018535)

Resource Information

URL: <http://www.proteometools.org/index.php?id=home>

Proper Citation: ProteomeTools (RRID:SCR_018535)

Description: Project for building molecular and digital tools from human proteome to facilitate biomedical research, drug discovery, personalized medicine and life science research.

Resource Type: data or information resource, portal, project portal

Defining Citation: [PMID:28135259](#)

Keywords: Molecular tool, human proteome, proteome, human, peptide, data

Funding: Alexander von Humboldt Foundation ;
American Recovery and Reinvestment Act ;
European Research Council ;
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NCRR S10 RR027584;
NHGRI RC2 HG005805;
NIGMS P50 GM076547;
NIGMS R01 GM087221;
Swiss National Science Foundation

Availability: Free, Freely available

Resource Name: ProteomeTools

Resource ID: SCR_018535

Alternate URLs: <http://www.proteometools.org>

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260821T194130+0000

Ratings and Alerts

No rating or validation information has been found for ProteomeTools.

No alerts have been found for ProteomeTools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Klaproth-Andrade D, et al. (2026) Modanovo: A Unified Model for Post-translational Modification-Aware De Novo Sequencing Using Experimental Spectra From In Vivo and Synthetic Peptides. *Molecular & cellular proteomics : MCP*, 25(2), 101501.

Nameni A, et al. (2026) iDeepLC: Chemical Structure Information Yields Improved Retention Time Prediction of Peptides with Unseen Modifications. *Analytical chemistry*, 98(24), 17707.

Palmer AS, et al. (2025) Integrated fibre-specific methylome and proteome profiling of human skeletal muscle across males and females with fibre-type deconvolution. *Skeletal muscle*, 15(1), 28.

Abdul-Khalek N, et al. (2025) To Fly, or Not to Fly, That Is the Question: A Deep Learning Model for Peptide Detectability Prediction in Mass Spectrometry. *Journal of proteome research*, 24(6), 2709.

Carlson HL, et al. (2025) Human lung microvascular endothelial cell protein modification by 2-chlorohexadecanoic acid: RhoA mediates 2-chlorohexadecanoic acid-elicited endothelial activation. *Redox biology*, 82, 103596.

Madej D, et al. (2025) PyViscount: Validating False Discovery Rate Estimation Methods via Random Search Space Partition. *Journal of proteome research*, 24(3), 1118.

Quiñones-Vega M, et al. (2025) Proteomics and Metabolomics Profiles of Unvaccinated Nonagenarian Patients with Severe SARS-CoV-2 Infection. *Journal of proteome research*, 24(11), 5453.

Carlson HL, et al. (2025) 2-chlorofatty acid modification of neutrophil proteins: identification, localization and role in NETosis. *Cell communication and signaling : CCS*, 23(1), 461.

Hamaneh MB, et al. (2025) FastSpel: A Method for Fast Spectral Library Generation. *Journal of proteome research*, 24(10), 4952.

Adams C, et al. (2024) Fragment ion intensity prediction improves the identification rate of non-tryptic peptides in timsTOF. *Nature communications*, 15(1), 3956.

Liu K, et al. (2024) SpecEncoder: deep metric learning for accurate peptide identification in proteomics. *Bioinformatics (Oxford, England)*, 40(Suppl 1), i257.

Wiebach V, et al. (2023) "What I wish I had known before starting my PhD". *Analytical science advances*, 4(1-2), 6.

Will A, et al. (2023) Peptide collision cross sections of 22 post-translational modifications. *Analytical and bioanalytical chemistry*, 415(27), 6633.

Wildschut MHE, et al. (2023) Proteogenetic drug response profiling elucidates targetable vulnerabilities of myelofibrosis. *Nature communications*, 14(1), 6414.

Wamsley NT, et al. (2023) Targeted Proteomic Quantitation of NRF2 Signaling and Predictive Biomarkers in HNSCC. *Molecular & cellular proteomics : MCP*, 22(11), 100647.

Bittremieux W, et al. (2022) A learned embedding for efficient joint analysis of millions of mass spectra. *Nature methods*, 19(6), 675.

Rehfeldt TG, et al. (2022) Variability analysis of LC-MS experimental factors and their impact on machine learning. *GigaScience*, 12.

Zhou WJ, et al. (2022) pValid 2: A deep learning based validation method for peptide identification in shotgun proteomics with increased discriminating power. *Journal of proteomics*, 251, 104414.

Meier F, et al. (2021) Deep learning the collisional cross sections of the peptide universe from a million experimental values. *Nature communications*, 12(1), 1185.

van Bentum M, et al. (2021) An Introduction to Advanced Targeted Acquisition Methods. *Molecular & cellular proteomics : MCP*, 20, 100165.