

Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

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: German Federal Ministry of Education and Research ;
Alexander von Humboldt Foundation ;
American Recovery and Reinvestment Act ;
NHGRI RC2 HG005805;
NIGMS R01 GM087221;
NCRR S10 RR027584;
NIGMS P50 GM076547;
European Research Council ;
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: 20260731T043036+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 21 mentions in open access literature.

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

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.

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.

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.

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

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.

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

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.

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.

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

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

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

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.

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.

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

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.

Guan S, et al. (2019) Prediction of LC-MS/MS Properties of Peptides from Sequence by Deep Learning. *Molecular & cellular proteomics : MCP*, 18(10), 2099.

Sánchez LFH, et al. (2019) PathwayMatcher: proteoform-centric network construction enables fine-granularity multiomics pathway mapping. *GigaScience*, 8(8).