## **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: 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: 20250507T061341+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: <u>SciCrunch Registry</u>

### **Usage and Citation Metrics**

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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.

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

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.

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.

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

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.

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).

Wang M, et al. (2018) Assembling the Community-Scale Discoverable Human Proteome. Cell systems, 7(4), 412.