

Resource Summary Report

Generated by T1D on Aug 2, 2026

ProSight Lite

RRID:SCR_016908

Type: Tool

Proper Citation

ProSight Lite (RRID:SCR_016908)

Resource Information

URL: <http://prosightlite.northwestern.edu/>

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Description: Software application for matching a single candidate protein sequence and its modifications against a set of mass spectrometric observations. Used to analyze top-down mass spectrometry data.

Resource Type: data processing software, data analysis software, software application, software resource

Defining Citation: [DOI:10.1002/pmic.201400313](https://doi.org/10.1002/pmic.201400313)

Keywords: matching, single, protein, sequence, proteomics, top-down proteomics, mass, spectrometric, data, bio.tools

Funding: NIGMS R01 GM067193;
NIDA P30 DA018310

Availability: Free, Available for download, Freely available

Resource Name: ProSight Lite

Resource ID: SCR_016908

Alternate IDs: biotools:prosigh_lite

Alternate URLs: https://bio.tools/prosight_lite

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260801T190545+0000

Ratings and Alerts

No rating or validation information has been found for ProSight Lite.

No alerts have been found for ProSight Lite.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Skinner KA, et al. (2025) Next-Generation Protein Sequencing and individual ion mass spectrometry enable complementary analysis of interleukin-6. bioRxiv : the preprint server for biology.

Holzner C, et al. (2025) Protocol for producing brain-derived neurotrophic factor and neurotrophin-4 in their pro and active form in Escherichia coli. STAR protocols, 6(2), 103715.

Skinner KA, et al. (2025) Next-generation protein sequencing and individual ion mass spectrometry enable complementary analysis of interleukin-6. Analytical and bioanalytical chemistry, 417(28), 6291.

Moreno RY, et al. (2023) Distinctive interactomes of RNA polymerase II phosphorylation during different stages of transcription. iScience, 26(9), 107581.

Adams LM, et al. (2023) Mapping the KRAS proteoform landscape in colorectal cancer identifies truncated KRAS4B that decreases MAPK signaling. The Journal of biological chemistry, 299(1), 102768.

Schachner LF, et al. (2022) High-Throughput, Quantitative Analysis of Peptide-Exchanged MHCI Complexes by Native Mass Spectrometry. Analytical chemistry, 94(42), 14593.

Diao J, et al. (2021) Inhibition of Escherichia coli Lipoprotein Diacylglycerol Transferase Is Insensitive to Resistance Caused by Deletion of Braun's Lipoprotein. Journal of bacteriology, 203(13), e0014921.

Havlikova J, et al. (2021) Liquid Extraction Surface Analysis Mass Spectrometry of ESKAPE Pathogens. Journal of the American Society for Mass Spectrometry, 32(6), 1345.

Havlikova J, et al. (2020) Direct identification of bacterial and human proteins from infected wounds in living 3D skin models. Scientific reports, 10(1), 11900.

Whitelegge J, et al. (2020) Targeting a Subset of the Membrane Proteome for Top-Down Mass Spectrometry: Introducing the Proteolipidome. Proteomes, 8(1).

Mayfield JE, et al. (2019) Tyr1 phosphorylation promotes phosphorylation of Ser2 on the C-terminal domain of eukaryotic RNA polymerase II by P-TEFb. *eLife*, 8.

Kocurek KI, et al. (2017) Top-Down LESA Mass Spectrometry Protein Analysis of Gram-Positive and Gram-Negative Bacteria. *Journal of the American Society for Mass Spectrometry*, 28(10), 2066.

Savaryn JP, et al. (2016) Targeted analysis of recombinant NF kappa B (RelA/p65) by denaturing and native top down mass spectrometry. *Journal of proteomics*, 134, 76.

Lee AE, et al. (2016) Preparing to read the ubiquitin code: characterization of ubiquitin trimers by top-down mass spectrometry. *Journal of mass spectrometry : JMS*, 51(4), 315.