Resource Summary Report

Generated by NIF on Apr 8, 2025

ProSight Lite

RRID:SCR_016908
Type: Tool

Proper Citation

ProSight Lite (RRID:SCR_016908)

Resource Information

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

Proper Citation: ProSight Lite (RRID:SCR_016908)

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

Defining Citation: DOI: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: 20250407T220344+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 11 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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

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 Diacylglyceryl 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.

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.

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.