Resource Summary Report

Generated by dkNET on May 18, 2025

OpenMS

RRID:SCR_012042
Type: Tool

Proper Citation

OpenMS (RRID:SCR_012042)

Resource Information

URL: http://sourceforge.net/projects/open-ms/

Proper Citation: OpenMS (RRID:SCR_012042)

Description: An algorithm to align LC-MS samples and to match corresponding ion species across samples.

Resource Type: software resource

Defining Citation: PMID:17646306, DOI:10.1186/1471-2105-9-163

Keywords: standalone software, mac os x, unix/linux, windows, c++, python, bio.tools

Funding:

Availability: GNU Lesser General Public License

Resource Name: OpenMS

Resource ID: SCR_012042

Alternate IDs: biotools:openms

Alternate URLs: https://bio.tools/openms, https://sources.debian.org/src/openms/

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250420T014604+0000

Ratings and Alerts

No rating or validation information has been found for OpenMS.

No alerts have been found for OpenMS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 152 mentions in open access literature.

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

Canal-Garcia A, et al. (2025) Proteomic signatures of Alzheimer's disease and Lewy body dementias: A comparative analysis. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(1), e14375.

Kuhnen G, et al. (2024) Python workflow for the selection and identification of marker peptides-proof-of-principle study with heated milk. Analytical and bioanalytical chemistry, 416(14), 3349.

Struyf N, et al. (2024) Delineating functional and molecular impact of ex vivo sample handling in precision medicine. NPJ precision oncology, 8(1), 38.

Bianco V, et al. (2024) Regional Differences in the Small Intestinal Proteome of Control Mice and of Mice Lacking Lysosomal Acid Lipase. Journal of proteome research, 23(4), 1506.

Zhu C, et al. (2024) moPepGen: Rapid and Comprehensive Identification of Non-canonical Peptides. bioRxiv : the preprint server for biology.

Rempfer C, et al. (2024) Differential prolyl hydroxylation by six Physcomitrella prolyl-4 hydroxylases. Computational and structural biotechnology journal, 23, 2580.

Wang K, et al. (2024) Longitudinal molecular profiling elucidates immunometabolism dynamics in breast cancer. Nature communications, 15(1), 3837.

König S, et al. (2024) Observations from the Proteomics Bench. Proteomes, 12(1).

Xiong Y, et al. (2024) Proteomic stable isotope probing with an upgraded Sipros algorithm for improved identification and quantification of isotopically labeled proteins. Microbiome, 12(1), 148.

Sweatt AJ, et al. (2024) Proteome-wide copy-number estimation from transcriptomics. Molecular systems biology, 20(11), 1230.

Fendler NL, et al. (2024) Identification and characterization of a human MORC2 DNA binding

region that is required for gene silencing. bioRxiv : the preprint server for biology.

Zweigle J, et al. (2024) PF?Screen - an open-source tool for automated PFAS feature prioritization in non-target HRMS data. Analytical and bioanalytical chemistry, 416(2), 349.

Emanuelsson EB, et al. (2024) Remodeling of the human skeletal muscle proteome found after long-term endurance training but not after strength training. iScience, 27(1), 108638.

Yan S, et al. (2024) Inflammation causes insulin resistance in mice via interferon regulatory factor 3 (IRF3)-mediated reduction in FAHFA levels. Nature communications, 15(1), 4605.

Saha S, et al. (2024) TCF4 trinucleotide repeat expansions and UV irradiation increase susceptibility to ferroptosis in Fuchs endothelial corneal dystrophy. Redox biology, 77, 103348.

Wicke D, et al. (2024) The previously uncharacterized RnpM (YlxR) protein modulates the activity of ribonuclease P in Bacillus subtilis in vitro. Nucleic acids research, 52(3), 1404.

Kanwal N, et al. (2024) GPATCH4 regulates rRNA and snRNA 2'-O-methylation in both DHX15-dependent and DHX15-independent manners. Nucleic acids research, 52(4), 1953.

Dai C, et al. (2024) quantms: a cloud-based pipeline for quantitative proteomics enables the reanalysis of public proteomics data. Nature methods, 21(9), 1603.

Sharma N, et al. (2024) Defining the Soluble and Extracellular Vesicle Protein Compartments of Plasma Using In-Depth Mass Spectrometry-Based Proteomics. Journal of proteome research, 23(9), 4114.

Searfoss RM, et al. (2024) Top-down Proteomics for the Characterization and Quantification of Calreticulin Arginylation. bioRxiv : the preprint server for biology.