

Resource Summary Report

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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

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: 20260725T190725+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

Usage and Citation Metrics

We found 174 mentions in open access literature.

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

Matzanke T, et al. (2025) Cysteine-Directed Isobaric Labeling Combined with GeLC-FAIMS-MS for Quantitative Top-Down Proteomics. *Journal of proteome research*, 24(3), 1470.

Willems P, et al. (2025) Maximizing Immunopeptidomics-Based Bacterial Epitope Discovery by Multiple Search Engines and Rescoring. *Journal of proteome research*, 24(4), 2141.

Blüchl C, et al. (2025) Fc Proteoforms of ACPA IgG Discriminate Autoimmune Responses in Plasma and Synovial Fluid of Rheumatoid Arthritis Patients and Associate with Disease Activity. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(15), e2408769.

Deng Z, et al. (2025) Identification of protein-degraders in an anaerobic digester by protein stable isotope probing and metagenomics. *Applied microbiology and biotechnology*, 109(1), 87.

Suwatthanarak T, et al. (2025) Profiling plasma protease activity with charge-changing peptides enables detection and classification of gastrointestinal cancers. *Scientific reports*, 15(1), 32184.

Hu H, et al. (2025) Structure and mechanism of the Zorya anti-phage defence system. *Nature*, 639(8056), 1093.

Kajimura Y, et al. (2025) An in vivo "turning model" reveals new RanBP9 interactions in lung macrophages. *Cell death discovery*, 11(1), 171.

Ingham A, et al. (2025) CRAMP1-dependent histone H1 biogenesis is essential for topoisomerase II inhibitor tolerance. *Molecular cell*, 85(13), 2487.

Da Dalt L, et al. (2025) Increased mitochondrial fusion via systemic OPA1 overexpression promotes dyslipidemia and atherosclerosis in LDLR deficient mice. *Molecular metabolism*, 102, 102256.

Sissala N, et al. (2025) Comparative evaluation of Olink Explore 3072 and mass spectrometry with peptide fractionation for plasma proteomics. *Communications chemistry*, 8(1), 327.

Ming Y, et al. (2025) Nucleolar MED19 regulates 2'-O-methylation of rRNA in supporting cancer cell growth. *Nucleic acids research*, 53(22).

Pan Y, et al. (2025) Functional-proteomics-based investigation of the cellular response to farnesyltransferase inhibition in lung cancer. *iScience*, 28(2), 111864.

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.

Fendler NL, et al. (2025) Identification and characterization of a human MORC2 DNA binding region that is required for gene silencing. *Nucleic acids research*, 53(4).

Roulstone V, et al. (2025) Palbociclib and dsRNA sensor co-operate to enhance anti-cancer effects through ER stress and modulation of immune evasion. *Nature communications*, 16(1), 4855.

Olivella R, et al. (2025) QSample: An Automated System for Rapid Monitoring of Quality Indicators in Proteomics Samples. *Journal of proteome research*, 24(9), 4816.

Daduang R, et al. (2025) LC-MS determination of *Nicotiana benthamiana* host plant proteins in the drug products of recombinant plant-produced pembrolizumab. *Scientific reports*, 15(1), 25635.

Kittitruji K, et al. (2025) Proteomic Analysis of Plant-Derived hIGF-1-Fc Reveals Proteome Abundance Changes Associated with Wound Healing and Cell Proliferation. *Proteomes*, 13(4).

Sadia M, et al. (2025) A stochastic approach for parameter optimization of feature detection algorithms for non-target screening in mass spectrometry. *Analytical and bioanalytical chemistry*, 417(27), 6033.

Sajic T, et al. (2025) Depletion-dependent activity-based protein profiling using SWATH/DIA-MS detects serine hydrolase lipid remodeling in lung adenocarcinoma progression. *Nature communications*, 16(1), 4889.