

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: 20260905T132718+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 184 mentions in open access literature.

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

Cai X, et al. (2026) A targeted proteomics assay for the preoperative diagnosis of thyroid nodules. *Cell reports. Medicine*, 7(3), 102664.

Brahadeeswaran S, et al. (2026) Proteomic mapping of *Rosa damascena* nanovesicles reveals plastid mitochondrial metabolic convergence and antimicrobial peptides. *Plant signaling & behavior*, 21(1), 2641285.

Kutchuashvili A, et al. (2026) Anticodon loop remodeling and D-stem shape drive the specific recognition of ANN-decoding tRNAs for t6A modification. *Nucleic acids research*, 54(11).

Kleiber N, et al. (2026) 2'-O-methylation-dependent installation of N2-methylguanosine in the U6 internal stem loop facilitates efficient spliceosome assembly. *Nature communications*, 17(1).

Intorasoot S, et al. (2026) Elucidation of the Antimycobacterial Activity of D-Form Human Lactoferricin 1-11 (D-Form hLF 1-11) Against *Mycobacterium smegmatis* Through Proteomics and Imaging Analysis. *Antibiotics (Basel, Switzerland)*, 15(6).

Zhu C, et al. (2026) Identification of non-canonical peptides with moPepGen. *Nature biotechnology*, 44(4), 568.

Thomé CC, et al. (2026) Distinct steps of nuclear maturation of human pre-60S complexes require the activity of GTPases including GNL3L. *Nucleic acids research*, 54(5).

Król J, et al. (2026) WNetAlign: fast and accurate spectra alignment using truncated Wasserstein distance and network simplex. *Briefings in bioinformatics*, 27(3).

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.

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 Immuno-peptidomics-Based Bacterial Epitope Discovery by Multiple Search Engines and Rescoring. *Journal of proteome research*, 24(4), 2141.

Blöchl 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.

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.

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).

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

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

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.