Resource Summary Report

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pymzML

RRID:SCR_002500
Type: Tool

Proper Citation

pymzML (RRID:SCR_002500)

Resource Information

URL: http://pymzml.github.io/

Proper Citation: pymzML (RRID:SCR_002500)

Description: Python module to parse mzML data in Python based on cElementTree. It is an extension to Python that offers (i) an easy access to mass spectrometry (MS) data that allows the rapid development of tools, (ii) a very fast parser for mzML data and (iii) a set of functions to compare or handle spectra.

Resource Type: software resource

Defining Citation: PMID:22302572

Keywords: standalone software, python, bio.tools

Funding:

Availability: GNU Lesser General Public License, Acknowledgement requested

Resource Name: pymzML

Resource ID: SCR_002500

Alternate IDs: biotools:pymzml, OMICS_03355

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

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250410T064914+0000

Ratings and Alerts

No rating or validation information has been found for pymzML.

No alerts have been found for pymzML.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Chatterjee P, et al. (2025) Quorum sensing mediates morphology and motility transitions in the model archaeon Haloferax volcanii. bioRxiv : the preprint server for biology.

McCausland JW, et al. (2025) Bacterial and host enzymes modulate the inflammatory response produced by the peptidoglycan of the Lyme disease agent. bioRxiv : the preprint server for biology.

Gul A, et al. (2024) Immunopeptidomics Mapping of Listeria monocytogenes T Cell Epitopes in Mice. Molecular & cellular proteomics : MCP, 23(9), 100829.

Urban J, et al. (2024) Predicting glycan structure from tandem mass spectrometry via deep learning. Nature methods, 21(7), 1206.

Schiller H, et al. (2024) Identification of structural and regulatory cell-shape determinants in Haloferax volcanii. Nature communications, 15(1), 1414.

Bonin M, et al. (2024) Engineering of a chitin deacetylase to generate tailor-made chitosan polymers. PLoS biology, 22(1), e3002459.

Böttcher B, et al. (2024) A highly conserved tRNA modification contributes to C. albicans filamentation and virulence. Microbiology spectrum, 12(5), e0425522.

Wallmann G, et al. (2023) Data-Driven Optimization of DIA Mass-Spectrometry by DO-MS. bioRxiv : the preprint server for biology.

Schulze S, et al. (2021) Comprehensive glycoproteomics shines new light on the complexity and extent of glycosylation in archaea. PLoS biology, 19(6), e3001277.

Wandy J, et al. (2019) In Silico Optimization of Mass Spectrometry Fragmentation Strategies in Metabolomics. Metabolites, 9(10).

Wandy J, et al. (2018) Ms2lda.org: web-based topic modelling for substructure discovery in mass spectrometry. Bioinformatics (Oxford, England), 34(2), 317.

Ozawa SI, et al. (2018) Configuration of Ten Light-Harvesting Chlorophyll a/b Complex I Subunits in Chlamydomonas reinhardtii Photosystem I. Plant physiology, 178(2), 583.

Sarin LP, et al. (2018) Nano LC-MS using capillary columns enables accurate quantification of modified ribonucleosides at low femtomol levels. RNA (New York, N.Y.), 24(10), 1403.

Ni Z, et al. (2017) LPPtiger software for lipidome-specific prediction and identification of oxidized phospholipids from LC-MS datasets. Scientific reports, 7(1), 15138.

Castelletto V, et al. (2017) Self-Assembly and Anti-Amyloid Cytotoxicity Activity of Amyloid beta Peptide Derivatives. Scientific reports, 7, 43637.

Rocca-Serra P, et al. (2016) Data standards can boost metabolomics research, and if there is a will, there is a way. Metabolomics : Official journal of the Metabolomic Society, 12, 14.