Resource Summary Report

Generated by NIF on Apr 26, 2025

mzML

RRID:SCR_003763
Type: Tool

Proper Citation

mzML (RRID:SCR_003763)

Resource Information

URL: http://www.psidev.info/index.php?q=node/257

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Description: Markup language for encoding raw spectrometer output. From 2005-2008 there has existed two separate XML formats for encoding raw spectrometer output: mzData developed by the PSI and mzXML developed at the Seattle Proteome Center at the Institute for Systems Biology. It was recognized that the existence of two separate formats for essentially the same thing generated confusion and required extra programming effort. Therefore the PSI, with full participation by ISB, has developed a new format by taking the best aspects of each of the precursor formats to form a single one. It is intended to replace the previous two formats. This new format was originally given a working name of dataXML. The final name is mzML.

Abbreviations: mzML

Synonyms: mzML Specification

Resource Type: markup language, interchange format, data or information resource, standard specification, narrative resource

Keywords: mass spectrometry, specification

Funding:

Resource Name: mzML

Resource ID: SCR_003763

Alternate IDs: nlx_158004

Record Creation Time: 20220129T080220+0000

Record Last Update: 20250426T055644+0000

Ratings and Alerts

No rating or validation information has been found for mzML.

No alerts have been found for mzML.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

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.

Hao L, et al. (2024) MzmL, a novel marine derived N-acyl homoserine lactonase from Mesoflavibacter zeaxanthinifaciens that attenuates Pectobacterium carotovorum subsp. carotovorum virulence. Frontiers in microbiology, 15, 1353711.

Niksirat H, et al. (2024) The quantification of zebrafish ocular-associated proteins provides hints for sex-biased visual impairments and perception. Heliyon, 10(12), e33057.

Fang Z, et al. (2024) GP-Plotter: Flexible Spectral Visualization for Proteomics Data with Emphasis on Glycoproteomics Analysis. Genomics, proteomics & bioinformatics, 22(5).

Zhang Q, et al. (2023) Mzion enables deep and precise identification of peptides in data-dependent acquisition proteomics. Scientific reports, 13(1), 7056.

Wang R, et al. (2023) 3D-MSNet: a point cloud-based deep learning model for untargeted feature detection and quantification in profile LC-HRMS data. Bioinformatics (Oxford, England), 39(5).

Bafiti V, et al. (2023) Bioenergetic Profiling in Glioblastoma Multiforme Patients with Different Clinical Outcomes. Metabolites, 13(3).

Overhoff M, et al. (2022) Autophagy regulates neuronal excitability by controlling

cAMP/protein kinase A signaling at the synapse. The EMBO journal, 41(22), e110963.

Karlsen J, et al. (2021) Slow Protein Turnover Explains Limited Protein-Level Response to Diurnal Transcriptional Oscillations in Cyanobacteria. Frontiers in microbiology, 12, 657379.

Codesido S, et al. (2021) New insights into the conversion of electropherograms to the effective electrophoretic mobility scale. Electrophoresis, 42(19), 1875.

Peris-Díaz MD, et al. (2021) Mass Spectrometry-Based Structural Analysis of Cysteine-Rich Metal-Binding Sites in Proteins with MetaOdysseus R Software. Journal of proteome research, 20(1), 776.

Breuer S, et al. (2021) Brain-Restricted Inhibition of IL-6 Trans-Signaling Mildly Affects Metabolic Consequences of Maternal Obesity in Male Offspring. Nutrients, 13(11).

Jahn M, et al. (2021) Protein allocation and utilization in the versatile chemolithoautotroph Cupriavidus necator. eLife, 10.

Matzinger M, et al. (2021) Cleavable Cross-Linkers and Mass Spectrometry for the Ultimate Task of Profiling Protein-Protein Interaction Networks in Vivo. Journal of proteome research, 20(1), 78.

Tully B, et al. (2020) Toffee - a highly efficient, lossless file format for DIA-MS. Scientific reports, 10(1), 8939.

Cao X, et al. (2020) Dataset of the phospholipidome and transcriptome of Campylobacter jejuni under different growth conditions. Data in brief, 33, 106349.

Wu Z, et al. (2020) PB-Net: Automatic peak integration by sequential deep learning for multiple reaction monitoring. Journal of proteomics, 223, 103820.

Polasky DA, et al. (2020) Fast and comprehensive N- and O-glycoproteomics analysis with MSFragger-Glyco. Nature methods, 17(11), 1125.

Lankinen Å, et al. (2018) Plant immunity in natural populations and agricultural fields: Low presence of pathogenesis-related proteins in Solanum leaves. PloS one, 13(11), e0207253.

Vialas V, et al. (2016) A comprehensive Candida albicans PeptideAtlas build enables deep proteome coverage. Journal of proteomics, 131, 122.