Resource Summary Report

Generated by dkNET on May 19, 2025

mzMatch

RRID:SCR_000543
Type: Tool

Proper Citation

mzMatch (RRID:SCR_000543)

Resource Information

URL: http://mzmatch.sourceforge.net/

Proper Citation: mzMatch (RRID:SCR_000543)

Description: A software to provide small tools for common processing tasks for LC/MS data. It is an extension to the metabolomics analysis pipeline mzMatch.R. The software is modular, open source, platform independent and written in Java.

Resource Type: software resource, software toolkit

Defining Citation: PMID:23162054

Keywords: metabolomics, analysis, java, tool, peak extraction, filtering, normalization, derivative detection, identification, bio.tools

Funding:

Availability: Open Source

Resource Name: mzMatch

Resource ID: SCR_000543

Alternate IDs: biotools:mzmatch, OMICS_02642

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

Record Creation Time: 20220129T080202+0000

Record Last Update: 20250513T060236+0000

Ratings and Alerts

No rating or validation information has been found for mzMatch.

No alerts have been found for mzMatch.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Ó Fearghail F, et al. (2021) A LCMS Metabolomic Workflow to Investigate Metabolic Patterns in Human Intestinal Cells Exposed to Hydrolyzed Crab Waste Materials. Frontiers in bioengineering and biotechnology, 9, 629083.

Howe CCF, et al. (2018) Untargeted Metabolomics Profiling of an 80.5 km Simulated Treadmill Ultramarathon. Metabolites, 8(1).

Del Carratore F, et al. (2017) RankProd 2.0: a refactored bioconductor package for detecting differentially expressed features in molecular profiling datasets. Bioinformatics (Oxford, England), 33(17), 2774.

Chokkathukalam A, et al. (2013) mzMatch-ISO: an R tool for the annotation and relative quantification of isotope-labelled mass spectrometry data. Bioinformatics (Oxford, England), 29(2), 281.

Jankevics A, et al. (2012) Separating the wheat from the chaff: a prioritisation pipeline for the analysis of metabolomics datasets. Metabolomics : Official journal of the Metabolomic Society, 8(Suppl 1), 29.