

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

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

Availability: Free, Available for download, Freely available,

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: 20260912T200223+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 [kravitz2](#) .

?? 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.