

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 2, 2026

## mzMatch

RRID:SCR\_000543

Type: Tool

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### Proper Citation

mzMatch (RRID:SCR\_000543)

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### 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:** 20260801T191031+0000

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### 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 [PRECISE-TBI](#) .

?? 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.