

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

[jmzReader](#)

RRID:SCR_012050

Type: Tool

Proper Citation

jmzReader (RRID:SCR_012050)

Resource Information

URL: <https://code.google.com/p/jmzreader/>

Proper Citation: jmzReader (RRID:SCR_012050)

Description: A collection of Java application programming interfaces (APIs) to parse the most commonly used peak list and XML-based mass spectrometry (MS) data formats: DTA, MS2, MGF, PKL, mzXML, mzData, and mzML.

Resource Type: software resource

Defining Citation: [PMID:22539430](#)

Keywords: standalone software, mac os x, unix/linux, windows, java

Availability: Apache License

Resource Name: jmzReader

Resource ID: SCR_012050

Alternate IDs: OMICS_03341

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260905T132719+0000

Ratings and Alerts

No rating or validation information has been found for jmzReader.

No alerts have been found for jmzReader.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Stricker T, et al. (2021) Adduct annotation in liquid chromatography/high-resolution mass spectrometry to enhance compound identification. Analytical and bioanalytical chemistry, 413(2), 503.

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.