Resource Summary Report

Generated by NIF on May 16, 2025

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

Funding:

Availability: Apache License

Resource Name: jmzReader

Resource ID: SCR_012050

Alternate IDs: OMICS_03341

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250420T014604+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 NIF.

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.