

Resource Summary Report

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Mass spectrometry imaging workbench

RRID:SCR_017410

Type: Tool

Proper Citation

Mass spectrometry imaging workbench (RRID:SCR_017410)

Resource Information

URL: <https://usegalaxy.eu>

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Description: Software tool for analysis of mass spectrometry imaging data implemented in Galaxy framework. Provides options to analyze mass spectrometry imaging data in imzML file format, including quality control, visualization, preprocessing, statistical analysis, image co-registration and feature identification. Galaxy docker container for mass spectrometry imaging.

Resource Type: data processing software, software application, data analysis software, software resource

Defining Citation: [DOI:10.1101/628719](https://doi.org/10.1101/628719)

Keywords: Analysis, mass, spectrometry, imaging, data, Galaxy, framework, imzML, file, quality, control, visualization, statistics, docker, container

Availability: Free, Available for download, Freely available

Resource Name: Mass spectrometry imaging workbench

Resource ID: SCR_017410

Alternate URLs: <https://github.com/foellmelanie/docker-galaxy-msi>,
<https://galaxyproject.org/use/msi/>

License: MIT license

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260731T043020+0000

Ratings and Alerts

No rating or validation information has been found for Mass spectrometry imaging workbench.

No alerts have been found for Mass spectrometry imaging workbench.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 98 mentions in open access literature.

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

Erny E, et al. (2025) Downregulation of TCF19 and ATAD2 causes endothelial cell cycle arrest at the transition from cardiac hypertrophy to heart failure. Basic research in cardiology, 120(6), 1209.

Hurtado A, et al. (2025) A One Health approach for the genomic characterization of antibiotic-resistant Campylobacter isolates using Nanopore whole-genome sequencing. Frontiers in microbiology, 16, 1540210.

Stadager J, et al. (2025) CRISPR GENome and epigenome engineering improves loss-of-function genetic-screening approaches. Cell reports methods, 5(6), 101078.

Atac D, et al. (2024) Identification and Characterization of ATOH7-Regulated Target Genes and Pathways in Human Neuroretinal Development. Cells, 13(13).

Showers WM, et al. (2024) SCUBA implements a storage format-agnostic API for single-cell data access in R. F1000Research, 13, 1256.

Garcia-Fernandez A, et al. (2023) Antibiotic resistance, plasmids, and virulence-associated markers in human strains of Campylobacter jejuni and Campylobacter coli isolated in Italy. Frontiers in microbiology, 14, 1293666.

Siatra P, et al. (2023) Return of the Tbx5; lineage-tracing reveals ventricular cardiomyocyte-like precursors in the injured adult mammalian heart. NPJ Regenerative medicine, 8(1), 13.

Larivière D, et al. (2023) Scalable, accessible, and reproducible reference genome assembly and evaluation in Galaxy. bioRxiv : the preprint server for biology.

Koch DT, et al. (2023) Tigecycline causes loss of cell viability mediated by mitochondrial OXPHOS and RAC1 in hepatocellular carcinoma cells. Journal of translational medicine, 21(1), 876.

Brislinger-Engelhardt MM, et al. (2023) Temporal Notch signaling regulates mucociliary cell fates through Hes-mediated competitive de-repression. bioRxiv : the preprint server for biology.

Gladkikh AS, et al. (2023) Near complete genome sequences from Southern Vietnam revealed local features of genetic diversity and intergenerational changes in SARS- CoV-2 variants in 2020-2021. BMC infectious diseases, 23(1), 806.

Viljoen N, et al. (2023) A rabies-related lyssavirus from a *Nycticeinops schlieffeni* bat with neurological signs, South Africa. Microbiology resource announcements, 12(11), e0062123.

Ali O, et al. (2022) Transcriptomic changes induced by applications of a commercial extract of *Ascophyllum nodosum* on tomato plants. Scientific reports, 12(1), 8042.

Lee DW, et al. (2022) Genomic epidemiology of SARS- CoV-2 Omicron variants in the Republic of Korea. Scientific reports, 12(1), 22414.

Gjaltema RAF, et al. (2022) Distal and proximal cis-regulatory elements sense X chromosome dosage and developmental state at the Xist locus. Molecular cell, 82(1), 190.

Sun SW, et al. (2021) The complete mitochondrial genome of the wild silkworm *Antheraea yamamai* from Heilongjiang, China (Lepidoptera: Saturniidae). Mitochondrial DNA. Part B, Resources, 6(8), 2209.

Yol E, et al. (2021) A High-Density SNP Genetic Map Construction Using ddRAD-Seq and Mapping of Capsule Shattering Trait in Sesame. Frontiers in plant science, 12, 679659.

Bartas M, et al. (2021) The Changes in the p53 Protein across the Animal Kingdom Point to Its Involvement in Longevity. International journal of molecular sciences, 22(16).

Maier W, et al. (2021) Freely accessible ready to use global infrastructure for SARS-CoV-2 monitoring. bioRxiv : the preprint server for biology.

Hetz SA, et al. (2021) Burkholderiaceae Are Key Acetate Assimilators During Complete Denitrification in Acidic Cryoturbated Peat Circles of the Arctic Tundra. Frontiers in microbiology, 12, 628269.