

Resource Summary Report

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MSnbase

RRID:SCR_019317

Type: Tool

Proper Citation

MSnbase (RRID:SCR_019317)

Resource Information

URL: <https://bioconductor.org/packages/MSnbase/>

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Description: Software R package provides infrastructure for manipulation, processing and visualisation of mass spectrometry and proteomics data, ranging from raw to quantitative and annotated data. Used for isobaric tagged mass spectrometry data visualization, processing and quantitation.

Resource Type: data processing software, software toolkit, data analytics software, data visualization software, software resource, software application

Defining Citation: [PMID:22113085](#), [PMID:32902283](#)

Keywords: Mass spectrometry data processing, mass spectrometry data visualization, raw mass spectrometry data

Funding: BBSRC Tools and Resources Development Fund ; European Union 7th Framework Program

Availability: Free, Available for download, Freely available

Resource Name: MSnbase

Resource ID: SCR_019317

Record Creation Time: 20220129T080344+0000

Record Last Update: 20260731T043036+0000

Ratings and Alerts

No rating or validation information has been found for MSnbase.

No alerts have been found for MSnbase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Pombo-García K, et al. (2024) Membrane prewetting by condensates promotes tight-junction belt formation. *Nature*, 632(8025), 647.

Chua EW, et al. (2024) A concise guide to essential R packages for analyses of DNA, RNA, and proteins. *Molecules and cells*, 47(11), 100120.

Liu S, et al. (2024) UCHL1 is a potential molecular indicator and therapeutic target for neuroendocrine carcinomas. *Cell reports. Medicine*, 5(2), 101381.

Zhao S, et al. (2023) RNF14-dependent atypical ubiquitylation promotes translation-coupled resolution of RNA-protein crosslinks. *Molecular cell*, 83(23), 4290.

Johnson ECB, et al. (2022) Large-scale deep multi-layer analysis of Alzheimer's disease brain reveals strong proteomic disease-related changes not observed at the RNA level. *Nature neuroscience*, 25(2), 213.

Kim KQ, et al. (2022) N1-methylpseudouridine found within COVID-19 mRNA vaccines produces faithful protein products. *Cell reports*, 40(9), 111300.

Aslan M, et al. (2021) Oncogene-mediated metabolic gene signature predicts breast cancer outcome. *NPJ breast cancer*, 7(1), 141.

Kershaw CJ, et al. (2021) Integrated multi-omics reveals common properties underlying stress granule and P-body formation. *RNA biology*, 18(sup2), 655.

Olivier-Jimenez D, et al. (2019) A database of high-resolution MS/MS spectra for lichen metabolites. *Scientific data*, 6(1), 294.

Alqurashi M, et al. (2018) Early Responses to Severe Drought Stress in the *Arabidopsis thaliana* Cell Suspension Culture Proteome. *Proteomes*, 6(4).