

Package: RforMassSpectrometry (via r-universe)

October 14, 2026

Title R for MassSpectrometry meta-package

Version 0.2.2

Description The RforMassSpectrometry meta-package loads and manages the core packages of the R for Mass Spectrometry initiative, that provide efficient, thoroughly documented, tested and flexible R software for the analysis and interpretation of high throughput mass spectrometry assays.

Depends R (>= 3.5.0)

Imports MsExperiment, Spectra, QFeatures, MsCoreUtils, MetaboCoreUtils, PSMATCH, PTMods

Suggests BiocStyle, knitr, rmarkdown

URL <https://www.RforMassSpectrometry.org/>

BugReports <https://github.com/RforMassSpectrometry/RforMassSpectrometry/issues>

VignetteBuilder knitr

License Artistic-2.0

Encoding UTF-8

LazyData true

Config/roxygen2/version 8.0.0

Config/pak/sysreqs cmake libglib-dev make libicu-dev libuv1-dev libxml2-dev libssl-dev zlib1g-dev

Repository <https://rformassspectrometry.r-universe.dev>

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RemoteUrl <https://github.com/rformassspectrometry/RforMassSpectrometry>

RemoteRef HEAD

RemoteSha 2ae1dc1deec348e70a99b7ab3091491a7ca9a5cc

Contents

RforMassSpectrometry	2
Index	3

RforMassSpectrometry *The R for MassSpectrometry meta-package*

Description

RforMassSpectrometry is a meta-package, to manage and document the RforMassSpectrometry project. The goal of the project to provide efficient, thoroughly documented, tested and flexible R software for the analysis and interpretation of high throughput mass spectrometry assays, including proteomics and metabolomics experiments. The project formalises the longtime collaborative development efforts of its members under the RforMassSpectrometry organisation to facilitate dissemination and accessibility of their work.

Details

See <https://www.rformassspectrometry.org/> for details.

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See Also

Useful links:

- <https://www.RforMassSpectrometry.org/>
- Report bugs at <https://github.com/RforMassSpectrometry/RforMassSpectrometry/issues>

Index

RforMassSpectrometry, [2](#)
RforMassSpectrometry-package
 (RforMassSpectrometry), [2](#)