

Package: RforMassSpectrometry (via r-universe)

September 3, 2024

Title R for MassSpectrometry meta-package

Version 0.1.5

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

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

RoxygenNote 7.1.2

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

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

RemoteRef HEAD

RemoteSha 5f8650383f7a066a0568b4fa0e07168e40bab903

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.

Index

RforMassSpectrometry, [2](#)