

Package ‘biodbHmdb’

November 4, 2024

Title biodbHmdb, a library for connecting to the HMDB Database

Version 1.13.0

Description The biodbHmdb library is an extension of the biodb framework package that provides access to the HMDB Metabolites database. It allows to download the whole HMDB Metabolites database locally, access entries and search for entries by name or description. A future version of this package will also include a search by mass and mass spectra annotation.

URL <https://github.com/pkrog/biodbHmdb>

BugReports <https://github.com/pkrog/biodbHmdb/issues>

biocViews Software, Infrastructure, DataImport

Depends R (>= 4.1)

License AGPL-3

Encoding UTF-8

VignetteBuilder knitr

Suggests BiocStyle, roxygen2, devtools, testthat (>= 2.0.0), knitr, rmarkdown, covr, lgr

Imports R6, biodb (>= 1.3.2), Rcpp, zip

LinkingTo Rcpp, testthat

NeedsCompilation yes

RoxygenNote 7.2.3

Collate 'HmdbMetabolitesConn.R' 'HmdbMetabolitesEntry.R' fcts.R
RcppExports.R 'package.R' 'catch-routine-registration.R'

git_url <https://git.bioconductor.org/packages/biodbHmdb>

git_branch devel

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Repository Bioconductor 3.21

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