Package 'biodbHmdb'

April 23, 2025

Title biodbHmdb, a library for connecting to the HMDB Database

Version 1.14.0

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 RELEASE_3_21

git_last_commit a7f0a0f

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-04-23

Author Pierrick Roger [aut, cre] (ORCID:
<https://orcid.org/0000-0001-8177-4873>)

Maintainer Pierrick Roger <pierrick.roger@cea.fr>

Contents