

Package ‘tRNAdbImport’

November 30, 2024

Title Importing from tRNAdb and mitotRNAdb as GRanges objects

Version 1.25.0

Date 2024-01-13

Description tRNAdbImport imports the entries of the tRNAdb and mtRNAdb (<http://trna.bioinf.uni-leipzig.de>) as GRanges object.

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Encoding UTF-8

LazyData false

biocViews Software, Visualization, DataImport

Depends R (>= 3.6), GenomicRanges, Modstrings, Structstrings, tRNA

Imports Biostrings, stringr, httr2, xml2, S4Vectors, methods, IRanges, utils

Suggests BiocGenerics, knitr, rmarkdown, testthat, httpptest, BiocStyle, rtracklayer

Collate 'tRNAdbImport.R' 'AllGenerics.R' 'tRNAdbImport-checks.R' 'tRNAdbImport-import.R' 'tRNAdbImport-open.R' 'utils.R'

VignetteBuilder knitr

RoxygenNote 7.2.3

BugReports <https://github.com/FelixErnst/tRNAdbImport/issues>

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

git_branch devel

git_last_commit 6e54ea5

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2024-11-29

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| | |
|---------------|---|
| import.tRNAdb | <i>Importing information from the tRNA db as GRanges object</i> |
|---------------|---|

Description

title

Usage

TRNA_DB_URL

TRNA_DB_URL_MT

```
import.tRNAdb.id(
  tdbID,
  database = c("DNA", "RNA"),
  origin = c("allothers", "plastid", "mitochondrial"),
  dbURL = TRNA_DB_URL,
  verbose = FALSE
)
```

```
import.mtRNAdb.id(mtdbID, dbURL = TRNA_DB_URL_MT, verbose = FALSE)
```

```
import.tRNAdb.blast(
  blastSeq,
  database = c("DNA", "RNA"),
  origin = c("allothers", "plastid", "mitochondrial"),
  dbURL = TRNA_DB_URL,
  verbose = FALSE
)
```

```
import.tRNAdb(
  organism = "",
  strain = "",
  taxonomyID = "",
  aminoacids = "",
  anticodons = "",
  sequences = list(),
  structures = list(),
```

```

reference = "",
comment = "",
pubmed = "",
genes = "",
database = c("DNA", "RNA"),
origin = c("allothers", "plastid", "mitochondrial"),
dbURL = TRNA_DB_URL,
verbose = FALSE
)

import.mtRNAdb(
  organism = "",
  strain = "",
  taxonomyID = "",
  aminoacids = "",
  anticodons = "",
  sequences = list(),
  structures = list(),
  reference = "",
  comment = "",
  pubmed = "",
  genes = "",
  dbURL = TRNA_DB_URL_MT,
  verbose = FALSE
)

tRNAdb2GFF(input)

```

Arguments

| | |
|------------|---|
| tdbID | a tRNAdb ID |
| database | "RNA" or "DNA" |
| origin | one ore more of "plastid", "mitochondrial" or "allothers" |
| dbURL | the URL of the tRNA db |
| verbose | whether to report verbose information from the httr2 calls |
| mtdbID | a mtRNAdb ID |
| blastSeq | a sequence to use for a blast search |
| organism | a organism name as a character string |
| strain | a strain information as a character string |
| taxonomyID | organism and strain information as a taxonom ID |
| aminoacids | a character vector of amino acids as a three letter code |
| anticodons | a character vector of anticodon sequences |
| sequences | a named (1-15) list of sequences, which are used for the search |
| structures | a named (1-15) list of structures, which are used for the search. Please use the \(\) or >> dot bracket annotation. |

| | |
|-----------|---|
| reference | a reference as a character string |
| comment | a comment as a character string |
| pubmed | a pubmed ID |
| genes | a gene name as a character string |
| input | a GRanges object which passes the istRNAdbGRanges check |

Format

An object of class character of length 1.

An object of class character of length 1.

Value

a GRanges object containing the information from the tRNA db

Examples

```
import.tRNAdb(organism = "Saccharomyces cerevisiae",
              aminoacids = c("Phe","Ala"))
import.tRNAdb.id(tdbID = "tdbD00000785")
import.tRNAdb.blast(blastSeq =
"GCGGATTTAGCTCAGTTGGGAGAGCGCCAGACTGAAGATCTGGAGGTCCTGTGTTTCGATCCACAGAATTCGCA")
import.mtRNAdb(organism = "Bos taurus",
               aminoacids = c("Phe","Ala"))
import.mtRNAdb.id(mtdbID = "mtdbD00000900")
```

| | |
|-----------------|-----------------------------------|
| istRNAdbGRanges | <i>tRNAdb compatibility check</i> |
|-----------------|-----------------------------------|

Description

istRNAdbGRanges checks whether a GRanges object contains the information expected for a tRNAdb result.

Usage

```
istRNAdbGRanges(x)

## S4 method for signature 'GRanges'
istRNAdbGRanges(x)
```

Arguments

x the GRanges object to test

Value

a logical value

Examples

```
gr <- import.tRNAdb(organism = "Saccharomyces cerevisiae",
                    aminoacids = c("Phe","Ala"),
                    anticodons = c("GAA"))
istRNAdbGRanges(gr)
```

open_tdbID

Open a tRNA db entry in a browser

Description

open.tdbID is a wrapper for browseURL and opens a tab for a tRNAdb entry in a browser. Please note, that the tRNAdb server does not show the entry right away without a session ID. open twice upon first use.

Usage

```
open_tdbID(tdbID, dbURL = TRNA_DB_URL)
```

```
open_mtdbID(mtdbID, dbURL = TRNA_DB_URL_MT)
```

Arguments

| | |
|--------|------------------------|
| tdbID | a tRNA db |
| dbURL | the URL for the tRNAdb |
| mtdbID | a mtRNA db |

Value

opens a window in a default browser for tRNAdb entry selected

Examples

```
if(interactive()){
  open_tdbID("tdbD00000785")
  open_mtdbID("mtdbD00000907")
}
```

tRNAdbImport

tRNAdbImport: Importing from to tRNAdb and mitotRNAdb as GRanges

Description

The tRNAdb and mtRNAdb (Jühling et al. 2009) is a compilation of tRNA sequences and tRNA genes. It is a follow up version of the database of Sprinzl et al. 2005.

Using ‘tRNAdbImport’ the tRNAdb can be accessed as outlined on the website <http://trna.bioinf.uni-leipzig.de/> and the results are returned as a ‘GRanges’ object.

Manual

Please refer to the tRNAdbImport vignette for an example how to work and use the package: [tRNAdbImport](#)

Author(s)

Felix G M Ernst [aut]

References

Jühling F, Mörl M, Hartmann RK, Sprinzl M, Stadler PF, Pütz J. 2009. "tRNAdb 2009: compilation of tRNA sequences and tRNA genes." Nucleic Acids Research, Volume 37 (suppl_1): D159–162. doi:10.1093/nar/gkn772.

See Also

[`import.tRNAdb()`] for examples

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