

Package ‘tRNAdbImport’

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Title Importing from tRNAdb and mitotRNAdb as GRanges objects

Version 1.2.2

Date 2019-06-11

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 true

biocViews Software, Visualization, DataImport

Depends R (>= 3.5), GenomicRanges, Modstrings, Structstrings, tRNA

Imports Biostrings, BiocGenerics, stringr, xml2, S4Vectors, assertive, methods, httr, IRanges, utils

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

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

VignetteBuilder knitr

RoxygenNote 6.1.1

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

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

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|-----------------|-----------------------------------|
| 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 | <i>Open a tRNA db entry in a browser</i> |
|------------|--|

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

```
open_tdbID("tdbD00000785")  
open_mtdbID("mtdbD00000907")
```

| | |
|--------------|---|
| tRNAdbImport | <i>tRNAdbImport: Importing from to tRNAdb and mitotRNAdb as GRanges</i> |
|--------------|---|

Description

The tRNAdb and mttRNAdb (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)

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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

 TRNA_DB_URL

Importing information from the tRNA db as GRanges object

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 http 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 $\backslash(\backslash)$ 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 <code>isTRNAdbGRanges</code> check |

Format

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 =
  "GCGGATTTAGCTCAGTTGGGAGAGCGCCAGACTGAAGATCTGGAGTCCTGTGTTTCGATCCACAGAATTCGCA")
import.mtRNAdb(organism = "Bos taurus",
               aminoacids = c("Phe", "Ala"))
import.mtRNAdb.id(mtdbID = "mtdbD00000900")
```

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