Package ‘tRNAdbImport’

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Title Importing from tRNAdb and mitoRNAdb as GRanges objects

Version 1.20.1

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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, httptest, BiocStyle, rtracklayer

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VignetteBuilder knitr

RoxygenNote 7.2.3

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

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import.tRNAdb  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.mttRNAdb.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(),
)
import.tRNAdb

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

import.mtTRNAdb(
    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 mtTRNAdb 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

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

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("tdb0000000785")
  open_mtdbID("mtdb00000090")
}
```
tRNAdbImport

**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/](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**


**See Also**

[import.tRNAdb()] for examples
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