Package ‘tRNAdbImport’

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Title   Importing from tRNAdb and mitoRNAdb as GRanges objects
Version 1.22.0
Date    2024-01-13
Description tRNAdbImport imports the entries of the tRNAdb and mtRNAdb
(http://trna.bioinf.uni-leipzig.de) as GRanges object.
License GPL-3 + file LICENSE
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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       'tRNAdbImport-import.R' 'tRNAdbImport-open.R' 'utils.R'
VignetteBuilder knitr
RoxygenNote 7.2.3

BugReports https://github.com/FelixErnst/tRNAdbImport/issues
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Author Felix G.M. Ernst [aut, cre](<https://orcid.org/0000-0001-5064-0928>)
Maintainer Felix G.M. Ernst <felix.gm.ernst@outlook.com>
import.tRNAdb

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Description

import.tRNAdb(id(...)

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 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 taxonem 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.
istRNAdbGRanges

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 = "GCGGATTTAGCTCAGTTGGGAGAGCGCCAGACTGAAGATCTGGAGGTCCTGTGTTCGATCCACAGAATTCGCA")
import.mtRNAdb(organism = "Bos taurus",
               aminoacids = c("Phe","Ala"))
import.mtRNAdb.id(mtdbID = "mtdbD00000900")
**open_tdbID**

**Examples**

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

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**open_tdbID**  
*Open a tRNA db entry in a browser*

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**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**

```r
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**

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

**tRNAdbImport**: Importing from tRNAdb and mitotRNAdb as GRanges

**Description**

The tRNAdb and mitotRNAdb (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)**

Felix G M Ernst [aut]

**References**


**See Also**

`import.tRNAdb()` for examples
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