Package ‘tRNAdbImport’

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Title Importing from tRNAdb and mitotRNAdb as GRanges objects
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Description tRNAdbImport imports the entries of the tRNAdb and mtRNAdb (http://trna.bioinf.uni-leipzig.de) as GRanges object.
License GPL-3 + file LICENSE
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LazyData false
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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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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 or 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**: an 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 \(\backslash(\) or >\(\backslash(\) dot bracket annotation.
Description

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

Usage

```r
istRNAdbGRanges(x)
```

## S4 method for signature 'GRanges'

istRNAdbGRanges(x)

Arguments

- `x` the GRanges object to test

Value

a logical value
**Examples**

```r
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**

```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("tdb00000785")
  open_mtdbID("mtdb00000090")
}


**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/](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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