Package ‘tRNAdbImport’

April 4, 2024

Title Importing from tRNAdb and mitoRNadb as GRanges objects
Version 1.20.1
Date 2020-01-13
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
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BugReports https://github.com/FelixErnst/tRNAdbImport/issues
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R topics documented:

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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 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.
refence  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 =
    "GCCGATTTAGCTCAGTTGGGAGAGCGCCAGACTGAAGATCTGGAGGTCCTGTGTTCGATCCACAGAATTCGCA")
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)

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 tRNAdb and mitotRNAdb as GRanges**

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**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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