

# Package ‘tRNAdbImport’

December 6, 2024

**Title** Importing from tRNAdb and mitotRNAdb as GRanges objects

**Version** 1.24.0

**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, httpptest, BiocStyle, rtracklayer

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

**VignetteBuilder** knitr

**RoxygenNote** 7.2.3

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

**git\_url** <https://git.bioconductor.org/packages/tRNAdbImport>

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import.tRNAdb	<i>Importing information from the tRNA db as GRanges object</i>
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**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 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.
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 =
"GCGGATTTAGCTCAGTTGGGAGAGCGCCAGACTGAAGATCTGGAGGTCTGTGTTTCGATCCACAGAATTCGCA")
import.mtRNAdb(organism = "Bos taurus",
               aminoacids = c("Phe", "Ala"))
import.mtRNAdb.id(mtdbID = "mtdbD00000900")
```

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istRNAdbGRanges	<i>tRNAdb compatibility check</i>
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**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)
```

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open_tdbID	<i>Open a tRNA db entry in a browser</i>
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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**

```
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")
}
```

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tRNAdbImport

*tRNAdbImport: Importing from to 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)**

Felix G M Ernst [aut]

**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

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