

# Package ‘tRNAdbImport’

November 15, 2025

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

**Version** 1.29.0

**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

**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>

**git\_branch** devel

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Contents

|                 |          |
|-----------------|----------|
| import.tRNAdb   | 2        |
| istRNAdbGRanges | 4        |
| open_tdbID      | 5        |
| tRNAdbImport    | 6        |
| <b>Index</b>    | <b>7</b> |

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|               |                                                                 |
|---------------|-----------------------------------------------------------------|
| import.tRNAdb | <i>Importing information from the tRNA db as GRanges object</i> |
|---------------|-----------------------------------------------------------------|

---

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 =
"GCGGATTAGCTCAGTTGGGAGAGCGCCAGACTGAAGATCTGGAGGTCCTGTGTTTCGATCCACAGAATTCGCA")
import.mttrRNAdb(organism = "Bos taurus",
                 aminoacids = c("Phe","Ala"))
import.mttrRNAdb.id(mtdbID = "mtdbD00000900")
```

---

|                 |                                   |
|-----------------|-----------------------------------|
| istRNAdbGRanges | <i>tRNAdb compatibility check</i> |
|-----------------|-----------------------------------|

---

**Description**

istRNAdbGRanges checks whether a GRanges object contains the information expected for a tR-  
NAdb 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)
```

---

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("tdbD00000785")
  open_mtdbID("mtdbD00000907")
}
```

---

tRNAdbImport

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

---

### 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

# Index

## \* **datasets**

`import.tRNAdb`, [2](#)

`import.mttrRNAdb (import.tRNAdb)`, [2](#)

`import.tRNAdb`, [2](#)

`istRNAdbGRanges`, [4](#)

`istRNAdbGRanges, GRanges-method`  
`(istRNAdbGRanges)`, [4](#)

`open_mtdbID (open_tdbID)`, [5](#)

`open_tdbID`, [5](#)

`TRNA_DB_URL (import.tRNAdb)`, [2](#)

`TRNA_DB_URL_MT (import.tRNAdb)`, [2](#)

`tRNAdb2GFF (import.tRNAdb)`, [2](#)

`tRNAdbImport`, [6](#)