

# Package ‘tRNA’

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**Title** Analyzing tRNA sequences and structures

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**Description** The tRNA package allows tRNA sequences and structures to be accessed and used for subsetting. In addition, it provides visualization tools to compare feature parameters of multiple tRNA sets and correlate them to additional data. The tRNA package uses GRanges objects as inputs requiring only few additional column data sets.

**License** GPL-3 + file LICENSE

**Encoding** UTF-8

**LazyData** true

**biocViews** Software, Visualization

**Depends** R (>= 3.5), GenomicRanges, Structstrings

**Imports** stringr, S4Vectors, methods, BiocGenerics, IRanges, XVector, Biostrings, Modstrings, ggplot2, scales

**Suggests** knitr, rmarkdown, testthat, BiocStyle, tRNAscanImport

**Collate** 'tRNA.R' 'AllGenerics.R' 'tRNA-checks.R' 'tRNA-dotbracket.R' 'tRNA-features.R' 'tRNA-plot.R' 'tRNA-sequences.R' 'tRNA-structures.R' 'tRNA-subset.R' 'tRNA-utils.R' 'utils.R'

**VignetteBuilder** knitr

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gettRNABasePairing	<i>Accessing Dot Bracket annotation of tRNAs</i>
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## Description

gettRNABasePairing converts the dot bracket annotation into a DotBracketDataFrame. Base pairing is indicated by corresponding numbers in the forward and reverse columns. For more detail have a look at [getBasePairing](#).

gettRNALoopIDs converts the dot bracket annotation into a LoopIDList. For more details have a look at [getLoopIDList](#).

## Usage

```
gettRNABasePairing(x, with.nucleotides = FALSE)
```

```
gettRNALoopIDs(x)
```

```
## S4 method for signature 'GRanges'
gettRNABasePairing(x, with.nucleotides = FALSE)
```

```
## S4 method for signature 'GRanges'
gettRNALoopIDs(x)
```

## Arguments

**x** a GRanges object created by `import.tRNAscanAsGRanges` or `GRanges` with equivalent information. The `tRNA_str` and `tRNA_seq` columns will be used to construct a `StructuredXStringSet` and used for input into `getBasePairing`.

**with.nucleotides** a single logical value: should the nucleotides be saved alongside the base pairing information in the 'base' column?

**Value**

gettrNABasePairing: The result is a DotBracketDataFrame with following columns: pos, forward, reverse, character and base. If a position is unpaired, forward and reverse will be 0, otherwise it will match the base paired positions.

gettrNALoopIDs: return a list of list of loop ids.

**Examples**

```
data("gr", package = "tRNA")
gettrNABasePairing(gr[1])
gettrNALoopIDs(gr[1])
```

---

gettrNAFeaturePlots     *Graphical summary of tRNA features*

---

**Description**

gettrNAFeaturePlots generates a plot for every feature found with gettrNASummary. Based on the datatype, it will generate suitable point or bar plots. Names of the GRangesList will be used as sample identifiers and used for colouring.

The options tRNA\_colour\_palette, tRNA\_colour\_yes and tRNA\_colour\_no will be used for colours.

**Usage**

```
gettrNAFeaturePlots(x, plotScores = FALSE, scores = NA, scoreLabel = "Score")

## S4 method for signature 'GRangesList'
gettrNAFeaturePlots(x, plotScores = FALSE, scores = NA, scoreLabel = "Score")
```

**Arguments**

x	a named GRangesList object.
plotScores	logical value, whether to plot scores. If scores are not provided with an additional argument, it will try to use the column "score" of the GRanges objects.
scores	a list of scores, which have to have the same dimensions as the GRangesList or GRanges object.
scoreLabel	a string to use as a label for the x axis.

**Value**

a list of ggplot2 plots. These can be customized further.

**Examples**

```

data("gr", package = "tRNA")
data("gr_eco", package = "tRNA")
gr1 <- GRangesList(Sce = gr,
                  Eco = gr_eco)
plots <- gettRNAFeaturePlots(gr1)

# customized plots
plots$length$layers <- plots$length$layers[c(-1,-2)]
plots$length + ggplot2::geom_boxplot()

```

---

```
gettRNAstructureGRanges
```

*tRNA structures and sequences*

---

**Description**

gettRNAstructureGRanges returns a list of GRanges describing the boundaries of tRNA structures as extracted from the dot bracket annotation. The dot bracket annotation is parsed using gettRNABasePairing, which internally uses getBasePairing.

gettRNAstructureSeqs returns split or partial tRNA sequences based on the structure information. Variations in the length of structure features can be padded to retrieve sequences of equal length. If sequences are joined by setting joinCompletely = FALSE, the boundaries of the tRNA structure are stored in the result as metadata. They can be accessed as an IRanges object by using metadata(seq)[["tRNA\_structures"]].

**Usage**

```

gettRNAstructureGRanges(x, structure = "")

gettRNAstructureSeqs(
  x,
  structure = "",
  joinCompletely = FALSE,
  joinFeatures = FALSE,
  padSequences = TRUE
)

## S4 method for signature 'GRanges'
gettRNAstructureSeqs(
  x,
  structure = "",
  joinCompletely = FALSE,
  joinFeatures = FALSE,
  padSequences = TRUE
)

```

```
## S4 method for signature 'GRanges'
gettrNAstructureGRanges(x, structure = "")
```

### Arguments

- |                |  |
|----------------|--|
| x              | a GRanges object with tRNA information. It has to pass the <code>istrNAGRanges</code> function.  |
| structure      | optional parameter for returning just partial sequences. The following values are accepted: <code>anticodonStem</code> , <code>Dprime5</code> , <code>DStem</code> , <code>Dloop</code> , <code>Dprime3</code> , <code>acceptorStem</code> , <code>anticodonloop</code> , <code>variableLoop</code> , <code>TStem</code> , <code>Tloop</code> , <code>discriminator</code> . (default: <code>structure = ""</code> ) |
| joinCompletely | Should the sequence parts, which are to be returned, be joined into one sequence? (default: <code>joinCompletely = FALSE</code> ) Setting this to <code>TRUE</code> excludes <code>joinFeatures</code> be set to <code>TRUE</code> as well. In addition, <code>joinCompletely = TRUE</code> uses automatically all sequence structures.  |
| joinFeatures   | Should the sequence parts, which are to be returned and are from the same structure type, be joined into one sequence? (default: <code>joinCompletely = FALSE</code> ) Setting this to <code>TRUE</code> excludes <code>joinCompletely</code> be set to <code>TRUE</code> as well. <code>joinCompletely</code> takes precedence.   |
| padSequences   | parameter whether sequences of the same type should be returned with the same length. For stems missing positions will be filled up in the middle, for loops at the ends. (default: <code>padSequences = TRUE</code> ). If <code>joinCompletely == TRUE</code> this is set to <code>TRUE</code> automatically.   |

### Value

a list of GRanges or DNASTringSet objects. In case `joinCompletely` is set to `TRUE` a single DNASTringSet is returned.

### Examples

```
data("gr", package = "tRNA")
gettrNAstructureGRanges(gr, structure = "anticodonLoop")
gettrNAstructureSeqs(gr, structure = "anticodonLoop")
gettrNABasePairing(gr[1:10])
```

---

gettrNASummary

*Summary of tRNA features*

---

### Description

`gettrNASummary` prepares a DataFrame with the aggregated features of tRNAs from a GRanges object. Logical values are converted to numeric values.

**Usage**

```

gettRNAsummary(x)

## S4 method for signature 'GRangesList'
gettRNAsummary(x)

## S4 method for signature 'GRanges'
gettRNAsummary(x)

```

**Arguments**

x a GRanges or a GRangesList object. All elements have to pass the `istRNAGRanges` test.

**Value**

a DataFrame object

**Examples**

```

data("gr", package = "tRNA")
gettRNAsummary(gr)

```

---

hasTStem

*Subsetting tRNAs*

---

**Description**

The functions `has*` can be used to subset the GRanges object containing information about tRNAs. Please note that the settings `mismatches` and `bulged` take precedence before `unpaired` or `paired`. This means that by setting either `mismatches` or `bulged` to either `TRUE` or `FALSE`, `unpaired = TRUE` or `paired = TRUE` are automatically set to allow specific subsetting. If this removes elements from the results, please consider constructing a logical vectors with two calls as suggested in the examples.

**Usage**

```

hasTStem(x, length = NA, unpaired = NA, mismatches = NA, bulged = NA)

hasDStem(x, length = NA, unpaired = NA, mismatches = NA, bulged = NA)

hasAcceptorStem(x, length = NA, unpaired = NA, mismatches = NA, bulged = NA)

hasAnticodonStem(x, length = NA, unpaired = NA, mismatches = NA, bulged = NA)

hasTloop(x, length = NA)

```

```

hasDloop(x, length = NA)

hasAnticodonLoop(x, length = NA)

hasVariableLoop(x, length = NA, paired = NA, mismatches = NA, bulged = NA)

## S4 method for signature 'GRanges'
hasTStem(x, length = NA, unpaired = NA, mismatches = NA, bulged = NA)

## S4 method for signature 'GRanges'
hasDStem(x, length = NA, unpaired = NA, mismatches = NA, bulged = NA)

## S4 method for signature 'GRanges'
hasAcceptorStem(x, length = NA, unpaired = NA, mismatches = NA, bulged = NA)

## S4 method for signature 'GRanges'
hasAnticodonStem(x, length = NA, unpaired = NA, mismatches = NA, bulged = NA)

## S4 method for signature 'GRanges'
hasTloop(x, length = NA)

## S4 method for signature 'GRanges'
hasDloop(x, length = NA)

## S4 method for signature 'GRanges'
hasAnticodonLoop(x, length = NA)

## S4 method for signature 'GRanges'
hasVariableLoop(x, length = NA, paired = NA, mismatches = NA, bulged = NA)

```

### Arguments

x	a GRanges object from a tRNAscan import or with equivalent information
length	the length as integer
unpaired	logical: has unpaired nucleotides
mismatches	logical: has mismatched nucleotides
bulged	logical: has mismatched nucleotides of different length creating a bulge
paired	logical: has paired nucleotides (only used for loops)

### Value

a logical vector of the length or input GRanges object

### Examples

```

data("gr", package = "tRNA")
hasTStem(gr, length = 5, mismatches = TRUE)
gr[hasTStem(gr, length = 5, mismatches = TRUE)]
gr[hasDStem(gr, unpaired = FALSE) & hasDStem(gr, mismatches = FALSE)]

```

---

istRNAGRanges	<i>tRNA compatibility check</i>
---------------	---------------------------------

---

### Description

istRNAGRanges checks whether a GRanges object contains the information expected for a tRNA result. This is used internally to ensure the the required data is present in the input.

### Usage

```
istRNAGRanges(x)

## S4 method for signature 'GRanges'
istRNAGRanges(x)
```

### Arguments

x                    the GRanges object to test for compatibility.

### Value

a logical value

### Examples

```
data("gr", package = "tRNA")
istRNAGRanges(gr)
```

---

tRNA	<i>tRNA: analyzing tRNA sequences and structures</i>
------	--

---

### Description

The tRNA package allows feature information of tRNAs to be accessed and list of tRNA to be subset based on these features. The main purpose is to unify overlapping functions from the tRNAscanImport and tRNAdbImport packages. The functionality is currently under development and may change. The package expects a GRanges object with certain columns as input. The following columns are a requirement: tRNA\_length, tRNA\_type, tRNA\_anticodon, tRNA\_seq, tRNA\_str, tRNA\_CCA.end. Outputs of tRNAscanImport and tRNAdbImport meet these requirements.

Have a look at the vignette for an overview of the functionality. Additional functions are planned to be added in the future.

### Author(s)

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**See Also**

Useful links:

- Report bugs at <https://github.com/FelixErnst/tRNA/issues>

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tRNA-data

*tRNA example data*

---

**Description**

Example data for using the tRNA package

**Usage**

```
data(gr)
```

```
data(gr_human)
```

```
data(gr_human2)
```

```
data(gr_eco)
```

**Format**

object of class GRanges

An object of class GRanges of length 596.

An object of class GRanges of length 631.

An object of class GRanges of length 89.

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