

# Package ‘EpiTxDb’

January 30, 2026

**Type** Package

**Title** Storing and accessing epitranscriptomic information using the AnnotationDbi interface

**Version** 1.22.0

**Date** 2025-09-23

**Description** EpiTxDb facilitates the storage of epitranscriptomic information. More specifically, it can keep track of modification identity, position, the enzyme for introducing it on the RNA, a specifier which determines the position on the RNA to be modified and the literature references each modification is associated with.

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**LazyData** false

**biocViews** Software, Epitranscriptomics

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**Imports** methods, utils, httr, xml2, curl, rex, GenomicFeatures, txdbmaker, GenomicRanges, Seqinfo, BiocGenerics, BiocFileCache, S4Vectors, IRanges, RSQLite, DBI, Biostrings, tRNAdbImport

**Suggests** BiocStyle, knitr, rmarkdown, testthat, httpptest, AnnotationHub, ensemblDb, ggplot2, EpiTxDb.Hs.hg38, BSgenome.Hsapiens.UCSC.hg38, BSgenome.Scerevisiae.UCSC.sacCer3, TxDb.Hsapiens.UCSC.hg38.knownGene

**Collate** 'AllGenerics.R' 'EpiTxDb-SELECT-helpers.R' 'EpiTxDb-schema.R' 'EpiTxDb.R' 'EpiTxDb-class.R' 'makeEpiTxDb.R' 'makeEpiTxDbFromGRanges.R' 'shiftGenomicToTranscript.R' 'makeEpiTxDbFromRMBase.R' 'makeEpiTxDbFromtRNAdb.R' 'modifications.R' 'modificationsBy.R' 'ranges-helpers.R' 'select-methods.R'

**RoxygenNote** 7.3.3

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

**URL** <https://github.com/FelixErnst/EpiTxDb>

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Contents

|                                    |           |
|------------------------------------|-----------|
| EpiTxDb-package . . . . .          | 2         |
| EpiTxDb-class . . . . .            | 3         |
| EpiTxDb-data . . . . .             | 4         |
| EpiTxDb-package#’ . . . . .        | 4         |
| makeEpiTxDb . . . . .              | 5         |
| makeEpiTxDbFromGRanges . . . . .   | 7         |
| makeEpiTxDbFromRMBase . . . . .    | 8         |
| makeEpiTxDbFromtRNAdb . . . . .    | 9         |
| modifications . . . . .            | 11        |
| positionSequence . . . . .         | 12        |
| rescale . . . . .                  | 13        |
| select . . . . .                   | 14        |
| shiftTranscriptToGenomic . . . . . | 15        |
| <b>Index</b>                       | <b>17</b> |

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|                 |                                                                                                       |
|-----------------|-------------------------------------------------------------------------------------------------------|
| EpiTxDb-package | <i>EpiTxDb: Storing and accessing epitranscriptomic information using the AnnotationDbi interface</i> |
|-----------------|-------------------------------------------------------------------------------------------------------|

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Description

EpiTxDb facilitates the storage of epitranscriptomic information. More specifically, it can keep track of modification identity, position, the enzyme for introducing it on the RNA, a specifier which determines the position on the RNA to be modified and the literature references each modification is associated with.

Author(s)

**Maintainer:** Felix G.M. Ernst <[felix.gm.ernst@outlook.com](mailto:felix.gm.ernst@outlook.com)> (**ORCID**)

See Also

- Useful links:
- <https://github.com/FelixErnst/EpiTxDb>
  - Report bugs at <https://github.com/FelixErnst/EpiTxDb/issues>

EpiTxDb-class

*EpiTxDb objects***Description**

The EpiTxDb class is a [AnnotationDb](#) type container for storing Epitranscriptomic information.

The information are typically stored on a per transcript and not as genomic coordinates, but the EpiTxDb class is agnostic to this. In case of genomic coordinates transcriptsBy will return modifications per chromosome.

**Usage**

```
## S4 method for signature 'EpiTxDb'
organism(object)
```

```
## S4 method for signature 'EpiTxDb'
seqinfo(x)
```

```
## S4 method for signature 'EpiTxDb'
seqlevels(x)
```

```
## S4 method for signature 'EpiTxDb'
as.list(x)
```

**Arguments**

x, object            a EpiTxDb object

**Value**

For

- organism() and seqlevels(): a character vector
- seqinfo(): a [Seqinfo](#) object
- as.list() a list

**See Also**

- [makeEpiTxDbFromGRanges](#) for creating a EpiTxDb object from a [GRanges](#) object and it's metadata columns
- [makeEpiTxDbFromRMBase](#) for creating a EpiTxDb object from RMBase online resources
- [makeEpiTxDbFromtRNadb](#) for creating a EpiTxDb object from tRNadb online resources
- [makeEpiTxDb](#) for creating a EpiTxDb object from data.frames
- [modifications](#), [modificationsBy](#) for getting epitranscriptomic modification locations
- [select](#) for using the default interface of [AnnotationDb](#) objects.
- [shiftGenomicToTranscript](#) and [shiftTranscriptToGenomic](#) for transferring genomic to transcript coordinates and back again.

Examples

```
etdb_file <- system.file("extdata", "EpiTxDb.Hs.hg38.snoRNAdb.sqlite",
                          package="EpiTxDb")
etdb <- loadDb(etdb_file)
etdb

# general methods
seqinfo(etdb) #
seqlevels(etdb) # easy access to all transcript names
```

---

|              |                              |
|--------------|------------------------------|
| EpiTxDb-data | <i>EpiTxDb internal data</i> |
|--------------|------------------------------|

---

Description

EpiTxDb internal data

Usage

```
data(rmbase_data)
```

Format

data.frame

---

|                   |                                                                                                        |
|-------------------|--------------------------------------------------------------------------------------------------------|
| EpiTxDb-package#' | <i>EpiTxDb - Storing and accessing epitranscriptomic information using the AnnotationDbi interface</i> |
|-------------------|--------------------------------------------------------------------------------------------------------|

---

Description

title

Author(s)

Felix G M Ernst [aut]

References

Jia-Jia Xuan, Wen-Ju Sun, Ke-Ren Zhou, Shun Liu, Peng-Hui Lin, Ling-Ling Zheng, Liang-Hu Qu, Jian-Hua Yang (2017): "RMBase v2.0: Deciphering the Map of RNA Modifications from Epitranscriptome Sequencing Data." Nucleic Acids Research, Volume 46, Issue D1, 4 January 2018, Pages D327–D334. doi: 10.1093/nar/gkx934

Jühling, Frank; Mörl, Mario; Hartmann, Roland K.; Sprinzl, Mathias; Stadler, Peter F.; Pütz, Jörn (2009): "TRNAdb 2009: Compilation of tRNA Sequences and tRNA Genes." Nucleic Acids Research 37 (suppl\_1): D159–D162. doi: 10.1093/nar/gkn772

Sprinzl, Mathias; Vassilenko, Konstantin S. (2005): "Compilation of tRNA Sequences and Sequences of tRNA Genes." Nucleic Acids Research 33 (suppl\_1): D139–D140. doi: 10.1093/nar/gki012

makeEpiTxDb

*Creating a EpiTxDb from user supplied annotations as data.frames*

## Description

makeEpiTxDb is a low-level constructor for creating a [EpiTxDb](#) object from user supplied annotations.

This functions typically will not be used by regular users.

## Usage

```
makeEpiTxDb(
  modifications,
  reactions = NULL,
  specifiers = NULL,
  references = NULL,
  metadata = NULL,
  reassign.ids = FALSE
)
```

## Arguments

**modifications** A data.frame containing the following columns:

- **mod\_id**: a unique integer value per modification.
- **mod\_type**: the modification type as a character or factor value. Must be a value from `shortName(ModRNAString())`.
- **mod\_name**: a character or factor name for the specific modification
- **mod\_start**: the start position for the modification as integer value. Usually `mod_start = mod_end`
- **mod\_end**: the end position for the modification as integer value. Usually `mod_start = mod_end`
- **mod\_strand**: the strand information for the modification as a character or factor.
- **sn\_id**: a integer value per unique sequence
- **sn\_name**: a character or factor as sequence name, e.g a chromosome or a transcript identifier like `chr1`.

The first six are mandatory, whereas one of the last two has to be set. `sn_id` will be generated from `sn_name`, if `sn_id` is not set.

**reactions** An optional data.frame containing the following columns:

- **mod\_id**: a integer value per modification and the link to the modification data.frame.
- **rx\_genename**: a character or factor referencing a genename for the enzyme incorporating the modification.
- **rx\_rank**: a integer for sorting enzyme reactions, if multiple enzymes are involved in the modification's incorporation/maintenance.
- **rx\_ensembl**: a character or factor with an ensembl identifier for the genename of the enzyme.

|                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|---------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                           | <ul style="list-style-type: none"> <li>• <code>rx_ensembltrans</code>: a character or factor with an ensembl identifier for the transcript being translated into the enzyme.</li> <li>• <code>rx_entrezid</code>: a character or factor with an entrezid for the genename of the enzyme.</li> </ul> <p>(default: <code>reactions = NULL</code>)</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <code>specifiers</code>   | <p>An optional <code>data.frame</code> containing the following columns:</p> <ul style="list-style-type: none"> <li>• <code>mod_id</code>: a integer value per modification and the link to the modification <code>data.frame</code>.</li> <li>• <code>spec_type</code>: a character or factor referencing a type of specifier, e.g. <code>snoRNA</code>. Not checked for validity.</li> <li>• <code>spec_genename</code>: a character or factor referencing a genename for the specifier directing an enzyme to the specific location for the modification to be incorporated.</li> <li>• <code>spec_ensembl</code>: a character or factor with an ensembl identifier for the genename of the specifier.</li> <li>• <code>spec_ensembltrans</code>: a character or factor with an ensembl identifier for the transcript being translated into the specifier.</li> <li>• <code>spec_entrezid</code>: a character or factor with an entrezid for the genename of the specifier.</li> </ul> <p>(default: <code>specifiers = NULL</code>)</p> |
| <code>references</code>   | <p>An optional <code>data.frame</code> containing the following columns:</p> <ul style="list-style-type: none"> <li>• <code>mod_id</code>: a integer value per modification and the link to the modification <code>data.frame</code>.</li> <li>• <code>ref_type</code>: a character or factor with a reference type, e.g. <code>PMID</code>. Is not checked for validity.</li> <li>• <code>ref</code>: a character or factor with a reference value, e.g. a specific pubmed id or an journal article. Is not checked for validity.</li> </ul> <p>(default: <code>references = NULL</code>)</p>                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <code>metadata</code>     | <p>An optional <code>data.frame</code> containing the following columns:</p> <ul style="list-style-type: none"> <li>• <code>name</code>: a character value used as name</li> <li>• <code>value</code>: a character value</li> </ul> <p>This dataframe will be returned by <code>metadata()</code> (default: <code>metadata = NULL</code>)</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <code>reassign.ids</code> | <p>TRUE or FALSE Controls how internal <code>mod_ids</code> should be assigned. If <code>reassign.ids</code> is FALSE (the default) and if the ids are supplied, then they are used as the internal ids, otherwise the internal ids are assigned in a way that is compatible with the order defined by ordering the modifications first by chromosome, then by strand, then by start, and finally by end.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |

## Value

a `EpiTxDb` object.

## See Also

- [makeEpiTxDbFromGRanges](#) for creating a `EpiTxDb` object from a `GRanges` object and it's metadata columns
- [makeEpiTxDbFromRMBase](#) for creating a `EpiTxDb` object from RMBase online resources
- [makeEpiTxDbFromtRNadb](#) for creating a `EpiTxDb` object from tRNadb online resources
- [shortName](#) and [ModRNAString](#) for information on `ModRNAString` objects.

**Examples**

```

mod <- data.frame(mod_id = 1L,
                  "mod_type" = "m1A",
                  "mod_name" = "m1A_1",
                  "mod_start" = 1L,
                  "mod_end" = 1L,
                  "mod_strand" = "+",
                  "sn_id" = 1L,
                  "sn_name" = "test")
rx <- data.frame(mod_id = 1L,
                 rx_genename = "test",
                 rx_rank = 1L,
                 rx_ensembl = "test",
                 rx_ensembltrans = "test",
                 rx_entrezid = "test")
spec <- data.frame(mod_id = 1L,
                   spec_type = "test",
                   spec_genename = "test",
                   spec_ensembl = "test",
                   spec_ensembltrans = "test",
                   spec_entrezid = "test")
ref <- data.frame(mod_id = 1L,
                  ref_type = "test",
                  ref = "test")
etdb <- makeEpiTxDb(mod, rx, spec, ref)

```

---

makeEpiTxDbFromGRanges

*Create a EpiTxDb object from a GRanges object*


---

**Description**

makeEpiTxDbFromGRanges extracts informations from a [GRanges](#) object. The following metadata columns can be used:

- mod\_id, mod\_type, mod\_name and tx\_ensembl. The first three are mandatory, whereas tx\_ensembl is optional.
- rx\_genename, rx\_rank, rx\_ensembl, rx\_ensembltrans and rx\_entrezid
- spec\_type, spec\_genename, spec\_ensembl, spec\_ensembltrans and spec\_entrezid
- ref\_type and ref

... and passed on the [makeEpiTxDb](#).

**Usage**

```
makeEpiTxDbFromGRanges(gr, metadata = NULL, reassign.ids = FALSE)
```

**Arguments**

|              |                                                                                                                                                                                                                                                                       |
|--------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| gr           | A <a href="#">GRanges</a> object, which contains at least the mandatory columns.                                                                                                                                                                                      |
| metadata     | A 2-column data.frame containing meta information to be included in the EpiTxDb object. This data.frame is just passed to <a href="#">makeEpiTxDb</a> . See <a href="#">makeEpiTxDb</a> for more information about the format of metadata. (default: metadata = NULL) |
| reassign.ids | = FALSE                                                                                                                                                                                                                                                               |

**Value**

a EpiTxDb object.

**Examples**

```
library(GenomicRanges)
gr <- GRanges(seqnames = "test",
              ranges = IRanges::IRanges(1,1),
              strand = "+",
              DataFrame(mod_id = 1L,
                        mod_type = "Am",
                        mod_name = "Am_1"))
etdb <- makeEpiTxDbFromGRanges(gr)
```

---

makeEpiTxDbFromRMBase *Create a EpiTxDb object from RMBase v2.0 online resources*

---

**Description**

makeEpiTxDbFromRMBase will make use of the RMBase v2.0 online resources.

**Usage**

EPITXDB\_RMBASE\_URL

downloadRMBaseFiles(organism, genome, modtype)

```
makeEpiTxDbFromRMBase(
  organism,
  genome,
  modtype,
  tx = NULL,
  sequences = NULL,
  metadata = NULL,
  reassign.ids = FALSE,
  verbose = FALSE
)
```

getRMBaseDataAsGRanges(files, verbose = FALSE)

```
makeEpiTxDbFromRMBaseFiles(
  files,
  tx = NULL,
  sequences = NULL,
  metadata = NULL,
  reassign.ids = FALSE,
  verbose = FALSE
)
```

listAvailableOrganismsFromRMBase()

```
listAvailableGenomesFromRMBase(organism)
```

```
listAvailableModFromRMBase(organism, genome)
```

### Arguments

|                        |                                                                                                                                                                                                                                                                                    |
|------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| organism               | A character value, which must match an organism descriptor on the RMBase download website.                                                                                                                                                                                         |
| genome                 | A character value, which must match a genome descriptor on the RMBase download website.                                                                                                                                                                                            |
| modtype                | A character value, which must match one or more modification descriptors on the RMBase download website.                                                                                                                                                                           |
| tx                     | A <a href="#">GRangesList</a> object which will be used to shift the genomic coordinates to transcript coordinates. This is optional, but highly recommended. (default: tx = NULL).                                                                                                |
| sequences              | A named <a href="#">DNAStringSet</a> or <a href="#">RNAStringSet</a> , which will be used to check whether the defined modifications are compatible with the original base. This uses <a href="#">removeIncompatibleModi</a> function from the <a href="#">Modstrings</a> package. |
| metadata, reassign.ids | See <a href="#">makeEpiTxDb</a>                                                                                                                                                                                                                                                    |
| verbose                | TRUE or FALSE: Should verbose message be printed?                                                                                                                                                                                                                                  |
| files                  | From organism, genome and modtype the available files will be downloaded using the <a href="#">BiocFileCache</a> interface and passed on to <a href="#">makeEpiTxDbFromRMBaseFiles</a> . However, individual files can be provided as well.                                        |

### Format

An object of class character of length 1.

### Value

a EpiTxDb object.

---

`makeEpiTxDbFromtRNAdb` *Create a EpiTxDb object from tRNAdb resources*

---

### Description

`makeEpiTxDbFromtRNAdb` will make use of the tRNAdb online resources and extract the modification information from the RNA database.

If a named [DNAStringSet](#) is provided as sequences, the result from the tRNAdb will be matched against the sequences. Valid matches will be used as transcript identifiers and returned after a check of modification compatibility with the provided sequence. By this process multiple copies of transcripts can be associated with a single modification.

`makeEpiTxDbFromtRNAdb` uses the functions provided by the [tRNAdbImport](#) package. `import.tRNAdb` will be used with `database = "RNA"` and the three different values for origin.

**Usage**

```

gettRNAdbDataAsGRanges(
  organism,
  sequences = NULL,
  dbURL = tRNAdbImport::TRNA_DB_URL
)

makeEpiTxDbFromtRNAdb(
  organism,
  sequences = NULL,
  metadata = NULL,
  dbURL = tRNAdbImport::TRNA_DB_URL
)

listAvailableOrganismsFromtRNAdb()

```

**Arguments**

|           |                                                                                                                   |
|-----------|-------------------------------------------------------------------------------------------------------------------|
| organism  | A character value for an organism available on the tRNAdb website.                                                |
| sequences | A named DNAStringSet or RNAStringSet, which will be used to associate a tRNAdb result with a specific transcript. |
| dbURL     | The URL to the tRNA db website.                                                                                   |
| metadata  | See <a href="#">makeEpiTxDb</a>                                                                                   |

**Value**

a EpiTxDb object.

**References**

Juehling F, Moerl M, Hartmann RK, Sprinzl M, Stadler PF, Puetz 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.

**Examples**

```

## Not run:
# getting just the annotation data
etdb <- makeEpiTxDbFromtRNAdb("Saccharomyces cerevisiae")

# For associating the result with transcripts, provide and additional
# named DNAStringSet object. Matching will be done against each sequence
# allowing 5 mismatches and indels. The final result will be checked for
# validity regarding the identity of the modifications
etdb <- makeEpiTxDbFromtRNAdb("Saccharomyces cerevisiae",
                             some_transcript_sequences)

## End(Not run)

```

---

modifications*Getting modification data from a EpiTxDb-object*

---

## Description

modifications and modificationsBy are functions to extract modification annotation from a [EpiTxDb](#) object.

modifiedSeqsByTranscript returns a [ModRNAStringSet](#) from a EpiTxDb object and compatible RNAStringSet object. This used the [combineIntoModstrings\(\)](#) function from the Modstrings package.

## Usage

```
modifications(  
  x,  
  columns = c("mod_id", "mod_type", "mod_name"),  
  filter = NULL,  
  use.names = FALSE,  
  ...  
)  
  
modificationsBy(  
  x,  
  by = c("seqnames", "mod_type", "reaction", "specifier", "specifier_type"),  
  ...  
)  
  
modifiedSeqsByTranscript(x, sequences, ...)  
  
## S4 method for signature 'EpiTxDb'  
modifications(  
  x,  
  columns = c("mod_id", "mod_type", "mod_name"),  
  filter = NULL,  
  use.names = FALSE  
)  
  
## S4 method for signature 'EpiTxDb'  
modificationsBy(  
  x,  
  by = c("seqnames", "modtype", "reaction", "specifier", "specifiertype")  
)  
  
## S4 method for signature 'EpiTxDb,DNAStringSet'  
modifiedSeqsByTranscript(x, sequences)
```

## Arguments

x                      a [EpiTxDb](#)

|           |                                                                                                                                                                                                                                                                                                                                                                                |
|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| columns   | Columns to include in the result. If the vector is named, those names are used for the corresponding column in the element metadata of the returned object. (default: <code>columns = c("mod_id", "mod_type", "mod_name")</code> )                                                                                                                                             |
| filter    | Either NULL or a named list of vectors to be used to restrict the output. Valid names for this list are: "mod_id", "mod_type", "mod_name", "sn_id", "sn_name", "rx_genename", "rx_ensembl", "rx_ensembltrans", "rx_entrezid", "spec_genename", "spec_type", "spec_ensembl", "spec_ensembltrans", "spec_entrezid", "ref_type" and "ref". (default: <code>filter = NULL</code> ) |
| use.names | TRUE or FALSE. If TRUE, the modification names are set as the names of the returned object. (default: <code>use.names = FALSE</code> )                                                                                                                                                                                                                                         |
| ...       | Not used.                                                                                                                                                                                                                                                                                                                                                                      |
| by        | By which information type should the result be split into? A character value from one of the following values: <ul style="list-style-type: none"> <li>• <code>seqnames</code></li> <li>• <code>mod_type</code></li> <li>• <code>reaction</code></li> <li>• <code>specifier</code></li> <li>• <code>specifier_type</code></li> </ul>                                            |
| sequences | A <code>RNAStringSet</code> , which can be used as input for <code>combineIntoModstrings()</code> . See <a href="#">?combineIntoModstrings</a> for additional details.                                                                                                                                                                                                         |

### Value

a `GRanges` object for modifications and a `GRangesList` for modificationsBy.

### Examples

```
etdb_file <- system.file("extdata", "EpiTxDb.Hs.hg38.snoRNadb.sqlite",
                        package="EpiTxDb")
etdb <- loadDb(etdb_file)
etdb
```

---

|                  |                                                                       |
|------------------|-----------------------------------------------------------------------|
| positionSequence | <i>Generate integer sequences from position information of Ranges</i> |
|------------------|-----------------------------------------------------------------------|

---

### Description

`positionSequence` generates sequences of integer values along the range information of `x`. This can be used for navigating specific positions on a range information.

### Usage

```
positionSequence(x, order = FALSE, decreasing = FALSE)

## S4 method for signature 'Ranges'
positionSequence(x, order = FALSE, decreasing = FALSE)

## S4 method for signature 'RangesList'
positionSequence(x, order = FALSE, decreasing = FALSE)

## S4 method for signature 'Ranges'
as.integer(x)
```

**Arguments**

|            |                                                                                                                                                                        |
|------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x          | a Ranges object, like a <a href="#">GRanges</a> or <a href="#">IRanges</a> , or a RangesList object, like a <a href="#">GRangesList</a> or <a href="#">IRangesList</a> |
| order      | TRUE or FALSE: Should the position be ordered? (default: order = FALSE)                                                                                                |
| decreasing | TRUE or FALSE: If order = TRUE Should the position be ordered in a decreasing order? (default: order = FALSE)                                                          |

**Value**

a integer vector if x is a [GRanges](#) object and a IntegerList if x is a [GRangesList](#)

**Examples**

```
library(GenomicRanges)
# Returns an integer vector
gr <- GRanges("chr1:1-5:+")
positionSequence(gr)
gr2 <- GRanges("chr1:1-5:-")
positionSequence(gr)
# returns an IntegerList
grl <- GRangesList("1" = gr, "2" = gr, "3" = gr2) # must be named
positionSequence(grl)
```

rescale

*Rescaling Ranges object***Description**

rescale() rescales IRanges, GRanges, IRangesList and GRangesList by using minima and maxima derived from to and from.

**Usage**

```
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'IRanges'
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'IRangesList'
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'GRanges'
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'GRangesList'
rescale(x, to = 1L, from = 1L)
```

**Arguments**

|          |                                                                                                                   |
|----------|-------------------------------------------------------------------------------------------------------------------|
| x        | a IRanges, GRanges, IRangesList and GRangesList object                                                            |
| to, from | an IRanges object, a character vector coercible to IRanges or a integer vector parallel to x or with length = 1L. |

**Value**

an object of the same type and dimensions as x

**Author(s)**

H. Pagès, F. Ernst

**See Also**

[IRanges](#) for details on character vectors coercible to IRanges.

**Examples**

```
x <- IRanges("5-10")
# widen the ranges
rescale(x, 100, 10)
# widen and shift
rescale(x, "31-60", "5-14")
```

---

select

*Using the "select" interface on EpiTxDb objects*

---

**Description**

As expected for a AnnotationDb object, the general accessors select, keys, columns and keytypes can be used to get information from a [EpiTxDb](#) object.

**Usage**

```
## S4 method for signature 'EpiTxDb'
select(x, keys, columns, keytype, ...)

## S4 method for signature 'EpiTxDb'
columns(x)

## S4 method for signature 'EpiTxDb'
keys(x, keytype, ...)

## S4 method for signature 'EpiTxDb'
keytypes(x)
```

**Arguments**

x                      a [EpiTxDb](#) object  
 keys, columns, keytype, ...  
     See [AnnotationDb](#) for more comprehensive description of the methods select, keys, columns and keytypes and their arguments.

**Value**

a data.frame object for select() and a character vecor for keytypes(), keys() and columns().

## Examples

```
etdb_file <- system.file("extdata", "EpiTxDb.Hs.hg38.snoRNAdb.sqlite",
                        package="EpiTxDb")
etdb <- loadDb(etdb_file)
etdb
```

---

shiftTranscriptToGenomic

*Shift GRanges coordinates based on another GRanges object*

---

## Description

shiftGenomicToTranscript shifts positions of a [GRanges](#) object based on coordinates of another [GRanges](#) object. The most common application is to shift genomic coordinates to transcript coordinates, which is reflected in the name. shiftTranscriptToGenomic implements the reverse operation.

Matches are determined by [findOverlaps](#) for shiftGenomicToTranscript and by [findMatches](#) for shiftTranscriptToGenomic using the seqnames of the subject and the names of tx.

## Usage

```
shiftTranscriptToGenomic(subject, tx)

shiftGenomicToTranscript(subject, tx)

## S4 method for signature 'GRanges,GRangesList'
shiftTranscriptToGenomic(subject, tx)

## S4 method for signature 'GRangesList,GRangesList'
shiftTranscriptToGenomic(subject, tx)

## S4 method for signature 'GRanges,GRangesList'
shiftGenomicToTranscript(subject, tx)

## S4 method for signature 'GRangesList,GRangesList'
shiftGenomicToTranscript(subject, tx)
```

## Arguments

|         |                                                                 |
|---------|-----------------------------------------------------------------|
| subject | a <a href="#">GRanges</a> or <a href="#">GRangesList</a> object |
| tx      | a named <a href="#">GRangesList</a> object.                     |

## Value

a [GRanges](#) or [GRangesList](#) object depending on the type of subject

**Examples**

```

library(GenomicRanges)
# Construct some example data
subject1 <- GRanges("chr1", IRanges(3, 6),
                    strand = "+")
subject2 <- GRanges("chr1", IRanges(c(17,23), width=3),
                    strand = c("+", "-"))
subject3 <- GRanges("chr2", IRanges(c(51, 54), c(53, 59)),
                    strand = "-")
subject <- GRangesList(a=subject1, b=subject2, c=subject3)
tx1 <- GRanges("chr1", IRanges(1, 40),
               strand="+")
tx2 <- GRanges("chr1", IRanges(10, 30),
               strand="+")
tx3 <- GRanges("chr2", IRanges(50, 60),
               strand="-")
tx <- GRangesList(a=tx1, b=tx2, c=tx3)

# shift to transcript coordinates. Since the third subject does not have
# a match in tx it is dropped with a warning
shifted_grl <- shiftGenomicToTranscript(subject,tx)

# ... and back
shifted_grl2 <- shiftTranscriptToGenomic(shifted_grl,tx)

# comparison of ranges work. However the seqlevels differ
ranges(shifted_grl2) == ranges(subject[[list(1,c(1,1),c(1,2))]])

```

# Index

- \* **datasets**
  - EpiTxDb-data, [4](#)
  - makeEpiTxDbFromRMBASE, [8](#)
- \* **internal**
  - EpiTxDb-package, [2](#)
  - .EpiTxDb (EpiTxDb-class), [3](#)
  - ?combineIntoModstrings, [12](#)
- AnnotationDb, [3](#), [14](#)
- as.integer, Ranges-method
  - (positionSequence), [12](#)
- as.list, EpiTxDb-method (EpiTxDb-class), [3](#)
- BiocFileCache, [9](#)
- columns (select), [14](#)
- columns, EpiTxDb-method (select), [14](#)
- combineIntoModstrings(), [11](#), [12](#)
- DNAStringSet, [9](#)
- downloadRMBASEFiles
  - (makeEpiTxDbFromRMBASE), [8](#)
- EpiTxDb, [5](#), [11](#), [14](#)
- EpiTxDb (EpiTxDb-class), [3](#)
- EpiTxDb-class, [3](#)
- EpiTxDb-data, [4](#)
- EpiTxDb-package, [2](#)
- EpiTxDb-package#, [4](#)
- EPITXDB\_RMBASE\_URL
  - (makeEpiTxDbFromRMBASE), [8](#)
- findMatches, [15](#)
- findOverlaps, [15](#)
- getRMBASEDataAsGRanges
  - (makeEpiTxDbFromRMBASE), [8](#)
- gettRNADBDataAsGRanges
  - (makeEpiTxDbFromtRNADB), [9](#)
- GRanges, [3](#), [6](#), [7](#), [12](#), [13](#), [15](#)
- GRangesList, [9](#), [12](#), [13](#), [15](#)
- import.tRNADB, [9](#)
- IRanges, [13](#), [14](#)
- IRangesList, [13](#)
- keys (select), [14](#)
- keys, EpiTxDb-method (select), [14](#)
- keytypes (select), [14](#)
- keytypes, EpiTxDb-method (select), [14](#)
- listAvailableGenomesFromRMBASE
  - (makeEpiTxDbFromRMBASE), [8](#)
- listAvailableModFromRMBASE
  - (makeEpiTxDbFromRMBASE), [8](#)
- listAvailableOrganismsFromRMBASE
  - (makeEpiTxDbFromRMBASE), [8](#)
- listAvailableOrganismsFromtRNADB
  - (makeEpiTxDbFromtRNADB), [9](#)
- makeEpiTxDb, [3](#), [5](#), [7](#), [9](#), [10](#)
- makeEpiTxDbFromGRanges, [3](#), [6](#), [7](#)
- makeEpiTxDbFromRMBASE, [3](#), [6](#), [8](#)
- makeEpiTxDbFromRMBASEFiles
  - (makeEpiTxDbFromRMBASE), [8](#)
- makeEpiTxDbFromtRNADB, [3](#), [6](#), [9](#)
- modifications, [3](#), [11](#)
- modifications, EpiTxDb-method
  - (modifications), [11](#)
- modificationsBy, [3](#)
- modificationsBy (modifications), [11](#)
- modificationsBy, EpiTxDb-method
  - (modifications), [11](#)
- modifiedSeqsByTranscript
  - (modifications), [11](#)
- modifiedSeqsByTranscript, EpiTxDb, DNAStringSet-method
  - (modifications), [11](#)
- ModRNAString, [6](#)
- ModRNAStringSet, [11](#)
- organism, EpiTxDb-method
  - (EpiTxDb-class), [3](#)
- positionSequence, [12](#)
- positionSequence, Ranges-method
  - (positionSequence), [12](#)
- positionSequence, RangesList-method
  - (positionSequence), [12](#)

`removeIncompatibleModifications()`, [9](#)  
`rescale`, [13](#)  
`rescale`, `GRanges`-method (`rescale`), [13](#)  
`rescale`, `GRangesList`-method (`rescale`), [13](#)  
`rescale`, `IRanges`-method (`rescale`), [13](#)  
`rescale`, `IRangesList`-method (`rescale`), [13](#)  
`rmbase_data` (`EpiTxDb`-data), [4](#)  
  
`select`, [3](#), [14](#)  
`select`, `EpiTxDb`-method (`select`), [14](#)  
`Seqinfo`, [3](#)  
`seqinfo`, `EpiTxDb`-method (`EpiTxDb`-class),  
[3](#)  
`seqlevels`, `EpiTxDb`-method  
    (`EpiTxDb`-class), [3](#)  
`shiftGenomicToTranscript`, [3](#)  
`shiftGenomicToTranscript`  
    (`shiftTranscriptToGenomic`), [15](#)  
`shiftGenomicToTranscript`, `GRanges`, `GRangesList`-method  
    (`shiftTranscriptToGenomic`), [15](#)  
`shiftGenomicToTranscript`, `GRangesList`, `GRangesList`-method  
    (`shiftTranscriptToGenomic`), [15](#)  
`shiftTranscriptToGenomic`, [3](#), [15](#)  
`shiftTranscriptToGenomic`, `GRanges`, `GRangesList`-method  
    (`shiftTranscriptToGenomic`), [15](#)  
`shiftTranscriptToGenomic`, `GRangesList`, `GRangesList`-method  
    (`shiftTranscriptToGenomic`), [15](#)  
`shortName`, [6](#)  
  
`tRNADBImport`, [9](#)