

Package ‘refseqR’

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Type Package

Title Common Computational Operations Working with RefSeq Entries
(GenBank)

Version 1.1.4

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Description Fetches NCBI data (RefSeq <<https://www.ncbi.nlm.nih.gov/refseq/>> database) and provides an environment to extract information at the level of gene, mRNA or protein accessions.

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URL <https://github.com/jdieramon/refseqR>

BugReports <https://github.com/jdieramon/refseqR/issues>

Encoding UTF-8

Imports IRanges, rentrez, tibble, Biostrings

RoxygenNote 7.2.3

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Contents

refseqR	2
refseq_AAlen	2
refseq_AAlen_action	3
refseq_AAmol_wt	4
refseq_AAseq	5
refseq_CDScoords	5

refseq_CDSseq	6
refseq_description	7
refseq_fromGene	8
refseq_fromGene_action	9
refseq_GeneID	10
refseq_geneSymbol	11
refseq_geneSymbol_action	12
refseq_mRNAfeat	12
refseq_protein2RNA	13
refseq_RNA2protein	14

Index 16

refseqR	<i>refseqR: Common computational operations working with RefSeq</i>
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Description

refseqR is a framework of common computational operations working with RefSeq entries (GenBank)

Author(s)

Jose V. Die <jose.die@uco.es>

See Also

Useful links:

- <https://github.com/jdieramon/refseqR>
- Report bugs at <https://github.com/jdieramon/refseqR/issues>

refseq_AAlen	<i>Get the amino acid length from a protein accession</i>
--------------	---

Description

refseq_AAlen() Returns the amino acid length from a single protein accession.

Depending on the function, available accessions in refseqR include RefSeq models with the prefixes XM_ (mRNA), XR_ (non-coding RNA), and XP_ (protein), as well as subsequently curated RefSeq records with NM_, NR_, or NP_ accession prefixes.

Usage

```
refseq_AAlen(protein)
```

Arguments

protein A character string of the protein id.

Value

A numeric value representing the aa length of the protein.

Author(s)

Jose V. Die

See Also

[refseq_RNA2protein](#) to obtain the protein ids encoded by a set of transcript ids.

Examples

```
# Get the amino acid lengths from a set of protein accessions
protein = c("XP_004487758", "XP_004488550")
sapply(protein, function(x) refseq_AAlen(x), USE.NAMES = FALSE)
```

refseq_AAlen_action *Get the amino acid length from a protein accession*

Description

refseq_AA_len_action() Returns the amino acid length from a single protein accession.

Depending on the function, available accessions in refseqR include RefSeq models with the prefixes XM_ (mRNA), XR_ (non-coding RNA), and XP_ (protein), as well as subsequently curated RefSeq records with NM_, NR_, or NP_ accession prefixes.

Usage

```
refseq_AAlen_action(protein, retries)
```

Arguments

protein A character string of the protein id.

retries A numeric value to control the number of retry attempts to handle internet errors.

Value

A numeric value representing the aa length of the protein.

Author(s)

Jose V. Die

See Also

[refseq_RNA2protein](#) to obtain the protein ids encoded by a set of transcript ids.

refseq_AAmol_wt	<i>Extract the molecular weight from a protein accession</i>
-----------------	--

Description

refseq_AAmol_wt() Parses a protein accession output (RefSeq format) and extract the molecular weight (in Daltons).

Depending on the function, available accessions in refseqR include RefSeq models with the prefixes XM_ (mRNA), XR_ (non-coding RNA), and XP_ (protein), as well as subsequently curated RefSeq records with NM_, NR_, or NP_ accession prefixes.

Usage

```
refseq_AAmol_wt(protein)
```

Arguments

protein A character string of the protein id.

Details

First, get the character vector containing the fetched record. Then, this function parses the fetched record and returns the molecular weight.

Value

A numeric vector representing the molecular weight of the protein.

Author(s)

Jose V. Die

See Also

[refseq_RNA2protein](#) to obtain the protein ids encoded by a set of transcript ids.

Examples

```
# Get the molecular weight from a single protein accession
protein <- "XP_020244413"
refseq_AAmol_wt(protein)

# Get the molecular weight from from a set of protein accessions
protein = c("XP_004487758", "XP_004488550")
sapply(protein, function(x) refseq_AAmol_wt(x), USE.NAMES = TRUE)
```

refseq_AAseq	<i>Extract the amino acid sequence into a Biostrings object</i>
--------------	---

Description

refseq_AAseq() Parses a single/multiple protein accessions (RefSeq format) and extract the amino acid sequence(s) into a AAStringSet object.

Depending on the function, available accessions in refseqR include RefSeq models with the prefixes XM_ (mRNA), XR_ (non-coding RNA), and XP_ (protein), as well as subsequently curated RefSeq records with NM_, NR_, or NP_ accession prefixes.

Usage

```
refseq_AAseq(accession)
```

Arguments

accession A character string containing a single/multiple accession ids.

Value

An object of AAStringSet class.

Author(s)

Jose V. Die

Examples

```
accession = c("XP_004487758", "XP_004488550", "XP_004501961")
my_aa <- refseq_AAseq(accession)
# Now, the `AAStringSet` can be easily used to make a fasta file :
# writeXStringSet(x= my_aa, filepath = "aa_result")
```

refseq_CDScoords	<i>Extract the coding sequences (CDS) coordinates from a transcript accession</i>
------------------	---

Description

refseq_CDScoords() Parses a transcript accession (RefSeq format) and extract the CDS coordinates. The CDS coordinates refer to the mRNA molecule.

Depending on the function, available accessions in refseqR include RefSeq models with the prefixes XM_ (mRNA), XR_ (non-coding RNA), and XP_ (protein), as well as subsequently curated RefSeq records with NM_, NR_, or NP_ accession prefixes.

Usage

```
refseq_CDScoords(transcript)
```

Arguments

transcript A character string of the single/multiple transcript id.

Value

An IRanges object with the start and end position of the CDS of the putative mRNAs.

Author(s)

Jose V. Die

See Also

[refseq_CDSseq](#)

Examples

```
transcript = c("XM_004487701")
refseq_CDScoords(transcript)
```

```
transcript = c("XM_004487701", "XM_004488493")
refseq_CDScoords(transcript)
```

refseq_CDSseq

Extract the CDS nucleotide sequence into a Biostrings object

Description

refseq_CDSseq() Parses a single/multiple transcript accessions (RefSeq format) and extract the CDS nucleotide sequences into a DNASTringSet object.

Depending on the function, available accessions in refseqR include RefSeq models with the prefixes XM_ (mRNA), XR_ (non-coding RNA), and XP_ (protein), as well as subsequently curated RefSeq records with NM_, NR_, or NP_ accession prefixes.

Usage

```
refseq_CDSseq(transcript)
```

Arguments

transcript A character string of the single/multiple transcript id.

Value

An object of DNASTringSet class.

Author(s)

Jose V. Die

See Also

[refseq_CDScoords](#)

Examples

```
transcript <- c("XM_004487701", "XM_004488493", "XM_004501904")
my_cds <- refseq_CDSseq(transcript)
# Now, the `DNASTringSet` can easily used to make a fasta file :
# writeXStringSet(x= my_cds, filepath = "cds_result")
```

refseq_description *Get the sequence Description*

Description

refseq_description() Returns the sequence description from a single transcript, protein, or GeneID accession.

Depending on the function, available accessions in refseqR include RefSeq models with the prefixes transcript_ (mRNA), XR_ (non-coding RNA), and XP_ (protein), as well as subsequently curated RefSeq records with NM_, NR_, or NP_ accession prefixes.

Usage

```
refseq_description(id)
```

Arguments

id A character string of the transcript, protein, or GeneID accession.

Value

A character vector containing the sequence description corresponding to the specified sequence as id.

Author(s)

Jose V. Die

See Also

[refseq_protein2RNA](#) to obtain the transcript ids that encode a set of protein ids.

[refseq_RNA2protein](#) to obtain the protein ids encoded by a set of transcript ids.

Examples

```
# Get the sequence descriptions from a set of transcript accessions
transcript = c("XM_004487701")
sapply(transcript, function(x) refseq_description(x), USE.NAMES = FALSE)

# Get the sequence descriptions from a set of protein accessions
protein = c("XP_004487758")
sapply(protein, function(x) refseq_description(x), USE.NAMES = FALSE)

#' # Get the sequence descriptions from a set of Gene accessions
locs <- c("LOC101512347", "LOC101506901")
sapply(locs, function(x) refseq_description(x), USE.NAMES = FALSE)
```

refseq_fromGene	<i>Get the mRNA or protein accession</i>
-----------------	--

Description

refseq_fromGene() Returns the mRNA or protein accession from a single GeneID.

Usage

```
refseq_fromGene(GeneID, sequence)
```

Arguments

GeneID	A character string of the GeneID.
sequence	A character string of the mRNA or protein accession to fetch data from mRNA or protein databases, respectively.

Value

A character vector containing the mRNA or protein accession corresponding to the specified GeneID.

Author(s)

Jose V. Die

See Also

[refseq_protein2RNA](#) to obtain the transcript accessions that encode a set of protein accessions.

[refseq_RNA2protein](#) to obtain the protein accessions encoded by a set of transcript accessions.

Examples

```
# Get the XM accessions from a set of gene ids
locs <- c("LOC101512347")
sapply(locs, function(x) refseq_fromGene (x, sequence = "transcript"), USE.NAMES = FALSE)

# Get the XP accessions from a set of gene ids
locs <- c("LOC101512347")
sapply(locs, function(x) refseq_fromGene (x, sequence = "protein"), USE.NAMES = FALSE)
```

refseq_fromGene_action

Get the mRNA or protein accession

Description

refseq_fromGene_action() Returns the mRNA or protein accession from a single GeneID.

Usage

```
refseq_fromGene_action(GeneID, sequence, retries)
```

Arguments

GeneID	A character string of the GeneID.
sequence	A character string of the mRNA or protein accession to fetch data from mRNA or protein databases, respectively.
retries	A numeric value to control the number of retry attempts to handle 502 errors.

Value

A character vector containing the mRNA or protein accession corresponding to the specified GeneID.

Author(s)

Jose V. Die

`refseq_GeneID`*Get the GeneID*

Description

`refseq_GeneID()` Returns the GeneID from a single transcript or protein accession.

Depending on the function, available accessions in `refseqR` include RefSeq models with the prefixes `XM_` (mRNA), `XR_` (non-coding RNA), and `XP_` (protein), as well as subsequently curated RefSeq records with `NM_`, `NR_`, or `NP_` accession prefixes.

Usage

```
refseq_GeneID (accession, db, retries)
```

Arguments

<code>accession</code>	A character string of the transcript or protein accession.
<code>db</code>	A character string of the "nucore" or "protein" database.
<code>retries</code>	A numeric value to control the number of retry attempts to handle internet errors.

Value

A character vector containing the GeneID corresponding to the specified accession as `accession`.

Author(s)

Jose V. Die

See Also

[refseq_protein2RNA](#) to obtain the transcript accessions that encode a set of protein accessions.

[refseq_RNA2protein](#) to obtain the protein accessions encoded by a set of transcript accessions.

Examples

```
# Get the gene symbol from a set of transcript accessions
transcript = c("XM_004487701", "XM_004488493")
sapply(transcript, function(x) refseq_GeneID (x, db = "nucore", retries = 4), USE.NAMES = FALSE)

# Get the gene symbol from a set of protein accessions
protein = c("XP_004487758")
sapply(protein, function(x) refseq_GeneID (x, db = "protein", retries = 4), USE.NAMES = FALSE)
```

refseq_geneSymbol	<i>Get the gene symbol</i>
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Description

refseq_geneSymbol() Returns the gene symbol from a single Gene id. accession.

Usage

```
refseq_geneSymbol (id, db)
```

Arguments

id	A character string of the transcript or protein id.
db	A character string of the "nuccore" or "protein" database.

Value

A character vector containing the gene symbol corresponding to the specified accession as id.

Author(s)

Jose V. Die

See Also

[refseq_protein2RNA](#) to obtain the transcript ids that encode a set of protein ids.

[refseq_RNA2protein](#) to obtain the protein ids encoded by a set of transcript ids.

Examples

```
# Get the gene symbol from a set of transcript accessions
id = c("XM_004487701", "XM_004488493")
sapply(id, function(x) refseq_geneSymbol (x, db = "nuccore"), USE.NAMES = FALSE)

# Get the gene symbol from a set of XP accessions
id = c("XP_004487758")
sapply(id, function(x) refseq_geneSymbol (x, db = "protein"), USE.NAMES = FALSE)
```

 refseq_geneSymbol_action

Get the gene symbol

Description

refseq_geneSymbol_action() Returns the gene symbol from a single Gene id. accession.

Usage

```
refseq_geneSymbol_action (id, db, retries)
```

Arguments

id	A character string of the transcript or protein id.
db	A character string of the "nuccore" or "protein" database.
retries	A numeric value to control the number of retry attempts to handle internet errors.

Value

A character vector containing the gene symbol corresponding to the specified accession as id.

Author(s)

Jose V. Die

See Also

[refseq_protein2RNA](#) to obtain the XM ids that encode a set of XP ids.

[refseq_RNA2protein](#) to obtain the XP ids encoded by a set of XM ids.

 refseq_mRNAfeat

Get mRNA features

Description

refseq_mRNAfeat() Returns a number of features from a single/multiple mRNA accession(s).

Depending on the function, available accessions in refseqR include RefSeq models with the prefixes XM_ (mRNA), XR_ (non-coding RNA), and XP_ (protein), as well as subsequently curated RefSeq records with NM_, NR_, or NP_ accession prefixes.

Usage

```
refseq_mRNAfeat(transcript , feat)
```

Arguments

transcript	A character string of the transcript id.
feat	A character string of the selected features. Allowed features: 'caption', 'moltype', 'sourcedb', 'updatedate', 'slen', 'organism', 'title'.

Value

A tibble of summarized results including columns:

- caption, mRNA accession
- moltype, type of molecule
- sourcedb, database (GenBank)
- updatedate, date of updated record
- slen, molecule length (in bp)
- organism
- title, sequence description

Author(s)

Jose V. Die

See Also

[refseq_fromGene](#) to obtain the transcript or protein accession from a single GeneID accession.
[refseq_RNA2protein](#) to obtain the protein accessions encoded by a set of transcript ids.

Examples

```
# Get several molecular features from a set of mRNA accessions
transcript = c("XM_004487701", "XM_004488493", "XM_004501904")
feat = c("caption", "moltype", "sourcedb", "slen")
refseq_mRNAfeat(transcript ,feat)
```

refseq_protein2RNA *Get the transcript accession from the protein accession*

Description

refseq_protein2RNA() Returns the transcript accession from a single protein accession.

Depending on the function, available accessions in refseqR include RefSeq models with the prefixes XM_ (mRNA), XR_ (non-coding RNA), and XP_ (protein), as well as subsequently curated RefSeq records with NM_, NR_, or NP_ accession prefixes.

Usage

```
refseq_protein2RNA(protein)
```

Arguments

protein A character string of the protein id.

Value

A character vector containing the transcript ids that encode the protein.

Author(s)

Jose V. Die

See Also

[refseq_RNA2protein](#) to obtain the protein ids encoded by a set of transcript ids.

Examples

```
# Get the transcript id from a single protein accession
protein <- "XP_020244413"
refseq_protein2RNA(protein)

# Get the transcript ids from a set of protein accessions
protein = c("XP_004487758", "XP_004488550")
sapply(protein, function(x) refseq_protein2RNA(x), USE.NAMES = FALSE)
```

refseq_RNA2protein *Get the protein accession from the transcript accession*

Description

refseq_RNA2protein() Returns the protein accession from a single transcript accession.

Depending on the function, available accessions in refseqR include RefSeq models with the prefixes XM_ (mRNA), XR_ (non-coding RNA), and XP_ (protein), as well as subsequently curated RefSeq records with NM_, NR_, or NP_ accession prefixes.

Usage

```
refseq_RNA2protein(transcript)
```

Arguments

transcript A character string of the protein accession.

Value

A character vector containing the protein id encoded by the mRNA specified as transcript.

Author(s)

Jose V. Die

See Also

[refseq_protein2RNA](#) to obtain the transcript ids that encode a set of proteins ids.

Examples

```
# Get the protein id from a single transcript accession
transcript <- "XM_004487701"
refseq_RNA2protein(transcript)

# Get the protein ids from a set of transcript accessions
transcript = c("XM_004487701", "XM_004488493")
sapply(transcript, function(x) refseq_RNA2protein(x), USE.NAMES = FALSE)
```

Index

refseq_AAlen, [2](#)
refseq_AAlen_action, [3](#)
refseq_AAmol_wt, [4](#)
refseq_AAseq, [5](#)
refseq_CDScoords, [5](#), [7](#)
refseq_CDSseq, [6](#), [6](#)
refseq_description, [7](#)
refseq_fromGene, [8](#), [13](#)
refseq_fromGene_action, [9](#)
refseq_GeneID, [10](#)
refseq_geneSymbol, [11](#)
refseq_geneSymbol_action, [12](#)
refseq_mRNAfeat, [12](#)
refseq_protein2RNA, [8–12](#), [13](#), [15](#)
refseq_RNA2protein, [3](#), [4](#), [8–14](#), [14](#)
refseqR, [2](#)
refseqR-package (refseqR), [2](#)