

Package ‘geneLenDataBase’

April 3, 2025

Title Lengths of mRNA transcripts for a number of genomes

Version 1.43.0

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Description Length of mRNA transcripts for a number of genomes and gene ID formats, largely based on UCSC table browser. Data objects are provided as individual pieces of information to be retrieved and loaded. A variety of different gene identifiers and genomes is supported to ensure wide applicability.

Depends R (>= 2.11.0)

Imports utils, rtracklayer, GenomicFeatures, txdbmaker

URL <https://github.com/federicomarini/geneLenDataBase>

BugReports <https://github.com/federicomarini/geneLenDataBase/issues>

License LGPL (>= 2)

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anoCar1.ensGene.LENGTH

*Transcript length data for the organism anoCar***Description**

anoCar1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(anoCar1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(anoCar1.ensGene.LENGTH)
head(anoCar1.ensGene.LENGTH)
```

anoCar1.genscan.LENGTH

*Transcript length data for the organism anoCar***Description**

anoCar1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(anoCar1, genscan)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(anoCar1.genscan.LENGTH)
head(anoCar1.genscan.LENGTH)
```

```
anoCar1.xenoRefGene.LENGTH
```

Transcript length data for the organism anoCar

Description

anoCar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(anoCar1, xenoRefGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(anoCar1.xenoRefGene.LENGTH)
head(anoCar1.xenoRefGene.LENGTH)
```

```
anoGam1.ensGene.LENGTH
```

Transcript length data for the organism anoGam

Description

anoGam1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(anoGam1, ensGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)

Examples

```
data(anoGam1.ensGene.LENGTH)
head(anoGam1.ensGene.LENGTH)
```

anoGam1.geneid.LENGTH *Transcript length data for the organism anoGam*

Description

anoGam1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(anoGam1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(anoGam1.geneid.LENGTH)
head(anoGam1.geneid.LENGTH)
```

anoGam1.genscan.LENGTH
Transcript length data for the organism anoGam

Description

anoGam1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(anoGam1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(anoGam1.genscan.LENGTH)
head(anoGam1.genscan.LENGTH)
```

apiMe11.genscan.LENGTH

Transcript length data for the organism apiMel

Description

apiMe11.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(apiMe11, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(apiMe11.genscan.LENGTH)
head(apiMe11.genscan.LENGTH)
```

apiMe12.ensGene.LENGTH

Transcript length data for the organism apiMel

Description

apiMe12.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(apiMe12, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(apiMe12.ensGene.LENGTH)
head(apiMe12.ensGene.LENGTH)
```

apiMel2.geneid.LENGTH *Transcript length data for the organism apiMel*

Description

apiMel2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(apiMel2, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(apiMel2.geneid.LENGTH)
head(apiMel2.geneid.LENGTH)
```

apiMel2.genscan.LENGTH
Transcript length data for the organism apiMel

Description

apiMel2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(apiMel2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(apiMel2.genscan.LENGTH)
head(apiMel2.genscan.LENGTH)
```

`aplCa11.xenoRefGene.LENGTH`*Transcript length data for the organism aplCa1*

Description

`aplCa11.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(aplCa11, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(aplCa11.xenoRefGene.LENGTH)
head(aplCa11.xenoRefGene.LENGTH)
```

`bosTau2.geneid.LENGTH` *Transcript length data for the organism bosTau*

Description

`bosTau2.geneid.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneid` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau2, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau2.geneid.LENGTH)
head(bosTau2.geneid.LENGTH)
```

`bosTau2.geneSymbol.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau2.geneSymbol.LENGTH)
head(bosTau2.geneSymbol.LENGTH)
```

`bosTau2.genscan.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau2.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau2.genscan.LENGTH)
head(bosTau2.genscan.LENGTH)
```

`bosTau2.refGene.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau2.refGene.LENGTH)
head(bosTau2.refGene.LENGTH)
```

`bosTau2.sgpGene.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau2.sgpGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `sgpGene` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau2, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau2.sgpGene.LENGTH)
head(bosTau2.sgpGene.LENGTH)
```

`bosTau3.ensGene.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau3.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau3, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau3.ensGene.LENGTH)
head(bosTau3.ensGene.LENGTH)
```

`bosTau3.geneid.LENGTH` *Transcript length data for the organism bosTau*

Description

`bosTau3.geneid.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneid` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau3, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau3.geneid.LENGTH)
head(bosTau3.geneid.LENGTH)
```

```
bosTau3.geneSymbol.LENGTH
```

Transcript length data for the organism bosTau

Description

bosTau3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(bosTau3, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau3.geneSymbol.LENGTH)
head(bosTau3.geneSymbol.LENGTH)
```

```
bosTau3.genscan.LENGTH
```

Transcript length data for the organism bosTau

Description

bosTau3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(bosTau3, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau3.genscan.LENGTH)
head(bosTau3.genscan.LENGTH)
```

`bosTau3.refGene.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau3.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau3, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau3.refGene.LENGTH)
head(bosTau3.refGene.LENGTH)
```

`bosTau3.sgpGene.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau3.sgpGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `sgpGene` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau3, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau3.sgpGene.LENGTH)
head(bosTau3.sgpGene.LENGTH)
```

`bosTau4.ensGene.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau4.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau4, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau4.ensGene.LENGTH)
head(bosTau4.ensGene.LENGTH)
```

`bosTau4.geneSymbol.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau4.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau4, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau4.geneSymbol.LENGTH)
head(bosTau4.geneSymbol.LENGTH)
```

`bosTau4.genscan.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau4.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau4, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau4.genscan.LENGTH)
head(bosTau4.genscan.LENGTH)
```

`bosTau4.nscanGene.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau4.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau4, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau4.nscanGene.LENGTH)
head(bosTau4.nscanGene.LENGTH)
```

`bosTau4.refGene.LENGTH`*Transcript length data for the organism bosTau*

Description

`bosTau4.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(bosTau4, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(bosTau4.refGene.LENGTH)
head(bosTau4.refGene.LENGTH)
```

`braFlo1.xenoRefGene.LENGTH`*Transcript length data for the organism braFlo*

Description

`braFlo1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(braFlo1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(braFlo1.xenoRefGene.LENGTH)
head(braFlo1.xenoRefGene.LENGTH)
```

```
caeJap1.xenoRefGene.LENGTH
```

Transcript length data for the organism caeJap

Description

caeJap1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(caeJap1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(caeJap1.xenoRefGene.LENGTH)
head(caeJap1.xenoRefGene.LENGTH)
```

```
caePb1.xenoRefGene.LENGTH
```

Transcript length data for the organism caePb

Description

caePb1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(caePb1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(caePb1.xenoRefGene.LENGTH)
head(caePb1.xenoRefGene.LENGTH)
```

```
caePb2.xenoRefGene.LENGTH
```

Transcript length data for the organism caePb

Description

caePb2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(caePb2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(caePb2.xenoRefGene.LENGTH)
head(caePb2.xenoRefGene.LENGTH)
```

```
caeRem2.xenoRefGene.LENGTH
```

Transcript length data for the organism caeRem

Description

caeRem2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(caeRem2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(caeRem2.xenoRefGene.LENGTH)
head(caeRem2.xenoRefGene.LENGTH)
```

```
caeRem3.xenoRefGene.LENGTH
```

Transcript length data for the organism caeRem

Description

caeRem3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(caeRem3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(caeRem3.xenoRefGene.LENGTH)
head(caeRem3.xenoRefGene.LENGTH)
```

```
calJac1.genscan.LENGTH
```

Transcript length data for the organism calJac

Description

calJac1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(calJac1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(calJac1.genscan.LENGTH)
head(calJac1.genscan.LENGTH)
```

`calJac1.nscanGene.LENGTH`*Transcript length data for the organism calJac*

Description

`calJac1.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(calJac1, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(calJac1.nscanGene.LENGTH)
head(calJac1.nscanGene.LENGTH)
```

`calJac1.xenoRefGene.LENGTH`*Transcript length data for the organism calJac*

Description

`calJac1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(calJac1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(calJac1.xenoRefGene.LENGTH)
head(calJac1.xenoRefGene.LENGTH)
```

`canFam1.ensGene.LENGTH`*Transcript length data for the organism canFam*

Description

canFam1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(canFam1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam1.ensGene.LENGTH)
head(canFam1.ensGene.LENGTH)
```

`canFam1.geneSymbol.LENGTH`*Transcript length data for the organism canFam*

Description

canFam1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(canFam1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam1.geneSymbol.LENGTH)
head(canFam1.geneSymbol.LENGTH)
```

`canFam1.genscan.LENGTH`*Transcript length data for the organism canFam*

Description

`canFam1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(canFam1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam1.genscan.LENGTH)
head(canFam1.genscan.LENGTH)
```

`canFam1.nscanGene.LENGTH`*Transcript length data for the organism canFam*

Description

`canFam1.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(canFam1, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam1.nscanGene.LENGTH)
head(canFam1.nscanGene.LENGTH)
```

`canFam1.refGene.LENGTH`*Transcript length data for the organism canFam*

Description

canFam1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(canFam1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam1.refGene.LENGTH)
head(canFam1.refGene.LENGTH)
```

`canFam1.xenoRefGene.LENGTH`*Transcript length data for the organism canFam*

Description

canFam1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(canFam1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam1.xenoRefGene.LENGTH)
head(canFam1.xenoRefGene.LENGTH)
```

`canFam2.ensGene.LENGTH`*Transcript length data for the organism canFam*

Description

`canFam2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(canFam2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam2.ensGene.LENGTH)
head(canFam2.ensGene.LENGTH)
```

`canFam2.geneSymbol.LENGTH`*Transcript length data for the organism canFam*

Description

`canFam2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(canFam2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam2.geneSymbol.LENGTH)
head(canFam2.geneSymbol.LENGTH)
```

`canFam2.genscan.LENGTH`*Transcript length data for the organism canFam*

Description

canFam2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(canFam2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam2.genscan.LENGTH)
head(canFam2.genscan.LENGTH)
```

`canFam2.nscanGene.LENGTH`*Transcript length data for the organism canFam*

Description

canFam2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(canFam2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam2.nscanGene.LENGTH)
head(canFam2.nscanGene.LENGTH)
```

`canFam2.refGene.LENGTH`*Transcript length data for the organism canFam*

Description

canFam2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(canFam2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam2.refGene.LENGTH)
head(canFam2.refGene.LENGTH)
```

`canFam2.xenoRefGene.LENGTH`*Transcript length data for the organism canFam*

Description

canFam2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(canFam2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(canFam2.xenoRefGene.LENGTH)
head(canFam2.xenoRefGene.LENGTH)
```

`cavPor3.ensGene.LENGTH`*Transcript length data for the organism cavPor*

Description

cavPor3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(cavPor3, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(cavPor3.ensGene.LENGTH)
head(cavPor3.ensGene.LENGTH)
```

`cavPor3.genscan.LENGTH`*Transcript length data for the organism cavPor*

Description

cavPor3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(cavPor3, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(cavPor3.genscan.LENGTH)
head(cavPor3.genscan.LENGTH)
```

`cavPor3.nscanGene.LENGTH`*Transcript length data for the organism cavPor*

Description

`cavPor3.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(cavPor3, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(cavPor3.nscanGene.LENGTH)
head(cavPor3.nscanGene.LENGTH)
```

`cavPor3.xenoRefGene.LENGTH`*Transcript length data for the organism cavPor*

Description

`cavPor3.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(cavPor3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(cavPor3.xenoRefGene.LENGTH)
head(cavPor3.xenoRefGene.LENGTH)
```

`cb1.xenoRefGene.LENGTH`*Transcript length data for the organism cb*

Description

cb1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(cb1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(cb1.xenoRefGene.LENGTH)
head(cb1.xenoRefGene.LENGTH)
```

`cb3.xenoRefGene.LENGTH`*Transcript length data for the organism cb*

Description

cb3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(cb3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(cb3.xenoRefGene.LENGTH)
head(cb3.xenoRefGene.LENGTH)
```

ce2.geneid.LENGTH *Transcript length data for the organism ce*

Description

ce2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(ce2, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ce2.geneid.LENGTH)
head(ce2.geneid.LENGTH)
```

ce2.geneSymbol.LENGTH *Transcript length data for the organism ce*

Description

ce2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(ce2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ce2.geneSymbol.LENGTH)
head(ce2.geneSymbol.LENGTH)
```

ce2.refGene.LENGTH *Transcript length data for the organism ce*

Description

ce2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(ce2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ce2.refGene.LENGTH)
head(ce2.refGene.LENGTH)
```

ce4.geneSymbol1.LENGTH *Transcript length data for the organism ce*

Description

ce4.geneSymbol1.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(ce4, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ce4.geneSymbol1.LENGTH)
head(ce4.geneSymbol1.LENGTH)
```

ce4.refGene.LENGTH *Transcript length data for the organism ce*

Description

ce4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(ce4, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ce4.refGene.LENGTH)
head(ce4.refGene.LENGTH)
```

ce4.xenoRefGene.LENGTH *Transcript length data for the organism ce*

Description

ce4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(ce4, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ce4.xenoRefGene.LENGTH)
head(ce4.xenoRefGene.LENGTH)
```

ce6.ensGene.LENGTH *Transcript length data for the organism ce*

Description

ce6.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(ce6, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ce6.ensGene.LENGTH)
head(ce6.ensGene.LENGTH)
```

ce6.geneSymbol1.LENGTH *Transcript length data for the organism ce*

Description

ce6.geneSymbol1.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(ce6, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ce6.geneSymbol1.LENGTH)
head(ce6.geneSymbol1.LENGTH)
```

ce6.refGene.LENGTH *Transcript length data for the organism ce*

Description

ce6.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(ce6, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ce6.refGene.LENGTH)
head(ce6.refGene.LENGTH)
```

ce6.xenoRefGene.LENGTH *Transcript length data for the organism ce*

Description

ce6.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(ce6, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ce6.xenoRefGene.LENGTH)
head(ce6.xenoRefGene.LENGTH)
```

ci1.geneSymbol.LENGTH *Transcript length data for the organism ci*

Description

ci1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(ci1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ci1.geneSymbol.LENGTH)
head(ci1.geneSymbol.LENGTH)
```

ci1.refGene.LENGTH *Transcript length data for the organism ci*

Description

ci1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(ci1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ci1.refGene.LENGTH)
head(ci1.refGene.LENGTH)
```

`ci1.xenoRefGene.LENGTH`*Transcript length data for the organism ci*

Description

`ci1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(ci1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ci1.xenoRefGene.LENGTH)
head(ci1.xenoRefGene.LENGTH)
```

`ci2.ensGene.LENGTH`*Transcript length data for the organism ci*

Description

`ci2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(ci2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ci2.ensGene.LENGTH)
head(ci2.ensGene.LENGTH)
```

ci2.geneSymbol.LENGTH *Transcript length data for the organism ci*

Description

ci2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(ci2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ci2.geneSymbol.LENGTH)
head(ci2.geneSymbol.LENGTH)
```

ci2.refGene.LENGTH *Transcript length data for the organism ci*

Description

ci2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(ci2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ci2.refGene.LENGTH)
head(ci2.refGene.LENGTH)
```

`ci2.xenoRefGene.LENGTH`*Transcript length data for the organism ci*

Description

`ci2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(ci2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ci2.xenoRefGene.LENGTH)
head(ci2.xenoRefGene.LENGTH)
```

`danRer3.ensGene.LENGTH`*Transcript length data for the organism danRer*

Description

`danRer3.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(danRer3, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer3.ensGene.LENGTH)
head(danRer3.ensGene.LENGTH)
```

`danRer3.geneSymbol.LENGTH`*Transcript length data for the organism danRer*

Description

`danRer3.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(danRer3, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer3.geneSymbol.LENGTH)
head(danRer3.geneSymbol.LENGTH)
```

`danRer3.refGene.LENGTH`*Transcript length data for the organism danRer*

Description

`danRer3.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(danRer3, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer3.refGene.LENGTH)
head(danRer3.refGene.LENGTH)
```

```
danRer4.ensGene.LENGTH
```

Transcript length data for the organism danRer

Description

danRer4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(danRer4, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer4.ensGene.LENGTH)
head(danRer4.ensGene.LENGTH)
```

```
danRer4.geneSymbol.LENGTH
```

Transcript length data for the organism danRer

Description

danRer4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(danRer4, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer4.geneSymbol.LENGTH)
head(danRer4.geneSymbol.LENGTH)
```

`danRer4.genscan.LENGTH`*Transcript length data for the organism danRer*

Description

`danRer4.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(danRer4, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer4.genscan.LENGTH)
head(danRer4.genscan.LENGTH)
```

`danRer4.nscanGene.LENGTH`*Transcript length data for the organism danRer*

Description

`danRer4.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(danRer4, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer4.nscanGene.LENGTH)
head(danRer4.nscanGene.LENGTH)
```

`danRer4.refGene.LENGTH`*Transcript length data for the organism danRer*

Description

`danRer4.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(danRer4, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer4.refGene.LENGTH)
head(danRer4.refGene.LENGTH)
```

`danRer5.ensGene.LENGTH`*Transcript length data for the organism danRer*

Description

`danRer5.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(danRer5, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer5.ensGene.LENGTH)
head(danRer5.ensGene.LENGTH)
```

```
danRer5.geneSymbol.LENGTH
```

Transcript length data for the organism danRer

Description

danRer5.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(danRer5, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer5.geneSymbol.LENGTH)
head(danRer5.geneSymbol.LENGTH)
```

```
danRer5.refGene.LENGTH
```

Transcript length data for the organism danRer

Description

danRer5.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(danRer5, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer5.refGene.LENGTH)
head(danRer5.refGene.LENGTH)
```

```
danRer5.vegaGene.LENGTH
```

Transcript length data for the organism danRer

Description

danRer5.vegaGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the vegaGene table.

The data file was made by calling `downloadLengthFromUCSC(danRer5, vegaGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer5.vegaGene.LENGTH)
head(danRer5.vegaGene.LENGTH)
```

```
danRer5.vegaPseudoGene.LENGTH
```

Transcript length data for the organism danRer

Description

danRer5.vegaPseudoGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the vegaPseudoGene table.

The data file was made by calling `downloadLengthFromUCSC(danRer5, vegaPseudoGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer5.vegaPseudoGene.LENGTH)
head(danRer5.vegaPseudoGene.LENGTH)
```

```
danRer6.ensGene.LENGTH
```

Transcript length data for the organism danRer

Description

danRer6.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(danRer6, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer6.ensGene.LENGTH)
head(danRer6.ensGene.LENGTH)
```

```
danRer6.geneSymbol.LENGTH
```

Transcript length data for the organism danRer

Description

danRer6.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(danRer6, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer6.geneSymbol.LENGTH)
head(danRer6.geneSymbol.LENGTH)
```

`danRer6.refGene.LENGTH`*Transcript length data for the organism danRer*

Description

`danRer6.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(danRer6, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer6.refGene.LENGTH)
head(danRer6.refGene.LENGTH)
```

`danRer6.xenoRefGene.LENGTH`*Transcript length data for the organism danRer*

Description

`danRer6.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(danRer6, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(danRer6.xenoRefGene.LENGTH)
head(danRer6.xenoRefGene.LENGTH)
```

dm1.geneSymbol.LENGTH *Transcript length data for the organism dm*

Description

dm1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(dm1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dm1.geneSymbol.LENGTH)
head(dm1.geneSymbol.LENGTH)
```

dm1.genscan.LENGTH *Transcript length data for the organism dm*

Description

dm1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(dm1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dm1.genscan.LENGTH)
head(dm1.genscan.LENGTH)
```

dm1.refGene.LENGTH *Transcript length data for the organism dm*

Description

dm1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(dm1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dm1.refGene.LENGTH)
head(dm1.refGene.LENGTH)
```

dm2.geneid.LENGTH *Transcript length data for the organism dm*

Description

dm2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(dm2, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dm2.geneid.LENGTH)
head(dm2.geneid.LENGTH)
```

dm2.geneSymbol.LENGTH *Transcript length data for the organism dm*

Description

dm2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(dm2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dm2.geneSymbol.LENGTH)
head(dm2.geneSymbol.LENGTH)
```

dm2.genscan.LENGTH *Transcript length data for the organism dm*

Description

dm2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(dm2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dm2.genscan.LENGTH)
head(dm2.genscan.LENGTH)
```

dm2.nscanGene.LENGTH *Transcript length data for the organism dm*

Description

dm2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(dm2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dm2.nscanGene.LENGTH)
head(dm2.nscanGene.LENGTH)
```

dm2.refGene.LENGTH *Transcript length data for the organism dm*

Description

dm2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(dm2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dm2.refGene.LENGTH)
head(dm2.refGene.LENGTH)
```

dm3.geneSymbol.LENGTH *Transcript length data for the organism dm*

Description

dm3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(dm3, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dm3.geneSymbol.LENGTH)
head(dm3.geneSymbol.LENGTH)
```

dm3.nscanPasaGene.LENGTH
Transcript length data for the organism dm

Description

dm3.nscanPasaGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanPasaGene table.

The data file was made by calling `downloadLengthFromUCSC(dm3, nscanPasaGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dm3.nscanPasaGene.LENGTH)
head(dm3.nscanPasaGene.LENGTH)
```

dm3.refGene.LENGTH *Transcript length data for the organism dm*

Description

dm3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(dm3, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dm3.refGene.LENGTH)
head(dm3.refGene.LENGTH)
```

downloadLengthFromUCSC
Download Transcript Length Data

Description

Attempts to download the length of each transcript for the genome and gene ID specified from the UCSC genome browser.

Usage

```
downloadLengthFromUCSC(genome, id)
```

Arguments

genome	A string identifying the genome that genes refer to. For a list of supported organisms see supportedGenomes .
id	A string identifying the gene identifier used by genes. For a list of supported gene identifiers see supportedGeneIDs .

Details

For each transcript, the UCSC genome browser is used to obtain the exon boundaries. The length of each transcript is then taken to be the sum of the lengths of all its exons. Each transcript is then associated with a gene.

The UCSC does not contain length information for all combinations of genome and gene ID listed by [supportedGeneIDs](#) and [supportedGenomes](#). If `downloadLengthFromUCSC` fails because your gene ID format is not supported for the genome you specified, a list of possible ID formats for the specified genome will be listed.

Value

A data.frame containing with three columns, the gene name, transcript identifier and the length of the transcript. Each row represents one transcript.

Note

For some genome / gene ID combinations, no gene ID will be provided by UCSC. In this case, the gene name column is set to NA. However, the transcript ID column will always be populated.

Author(s)

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See Also

[supportedGenomes](#), [supportedGeneIDs](#)

Examples

```
## Not run:
flat_length <- downloadLengthFromUCSC('hg19', 'ensGene')

## End(Not run)
```

dp2.genscan.LENGTH *Transcript length data for the organism dp*

Description

dp2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(dp2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dp2.genscan.LENGTH)
head(dp2.genscan.LENGTH)
```

```
dp2.xenoRefGene.LENGTH
```

Transcript length data for the organism dp

Description

dp2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(dp2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dp2.xenoRefGene.LENGTH)
head(dp2.xenoRefGene.LENGTH)
```

```
dp3.geneid.LENGTH
```

Transcript length data for the organism dp

Description

dp3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(dp3, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dp3.geneid.LENGTH)
head(dp3.geneid.LENGTH)
```

```
dp3.genscan.LENGTH      Transcript length data for the organism dp
```

Description

dp3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(dp3, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dp3.genscan.LENGTH)
head(dp3.genscan.LENGTH)
```

```
dp3.xenoRefGene.LENGTH      Transcript length data for the organism dp
```

Description

dp3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(dp3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(dp3.xenoRefGene.LENGTH)
head(dp3.xenoRefGene.LENGTH)
```

droAna1.geneid.LENGTH *Transcript length data for the organism droAna*

Description

droAna1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(droAna1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droAna1.geneid.LENGTH)
head(droAna1.geneid.LENGTH)
```

droAna1.genscan.LENGTH
Transcript length data for the organism droAna

Description

droAna1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(droAna1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droAna1.genscan.LENGTH)
head(droAna1.genscan.LENGTH)
```

`droAna1.xenoRefGene.LENGTH`*Transcript length data for the organism droAna*

Description

`droAna1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(droAna1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droAna1.xenoRefGene.LENGTH)
head(droAna1.xenoRefGene.LENGTH)
```

`droAna2.genscan.LENGTH`*Transcript length data for the organism droAna*

Description

`droAna2.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(droAna2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droAna2.genscan.LENGTH)
head(droAna2.genscan.LENGTH)
```

`droAna2.xenoRefGene.LENGTH`*Transcript length data for the organism droAna*

Description

`droAna2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(droAna2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droAna2.xenoRefGene.LENGTH)
head(droAna2.xenoRefGene.LENGTH)
```

`droEre1.genscan.LENGTH`*Transcript length data for the organism droEre*

Description

`droEre1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(droEre1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droEre1.genscan.LENGTH)
head(droEre1.genscan.LENGTH)
```

```
droEre1.xenoRefGene.LENGTH
```

Transcript length data for the organism droEre

Description

droEre1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(droEre1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droEre1.xenoRefGene.LENGTH)
head(droEre1.xenoRefGene.LENGTH)
```

```
droGri1.genscan.LENGTH
```

Transcript length data for the organism droGri

Description

droGri1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(droGri1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droGri1.genscan.LENGTH)
head(droGri1.genscan.LENGTH)
```

```
droGri1.xenoRefGene.LENGTH
```

Transcript length data for the organism droGri

Description

droGri1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(droGri1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droGri1.xenoRefGene.LENGTH)
head(droGri1.xenoRefGene.LENGTH)
```

```
droMoj1.geneid.LENGTH
```

Transcript length data for the organism droMoj

Description

droMoj1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(droMoj1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droMoj1.geneid.LENGTH)
head(droMoj1.geneid.LENGTH)
```

`droMoj1.genscan.LENGTH`*Transcript length data for the organism droMoj*

Description

droMoj1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(droMoj1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droMoj1.genscan.LENGTH)
head(droMoj1.genscan.LENGTH)
```

`droMoj1.xenoRefGene.LENGTH`*Transcript length data for the organism droMoj*

Description

droMoj1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(droMoj1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droMoj1.xenoRefGene.LENGTH)
head(droMoj1.xenoRefGene.LENGTH)
```

`droMoj2.genscan.LENGTH`*Transcript length data for the organism droMoj*

Description

droMoj2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(droMoj2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droMoj2.genscan.LENGTH)
head(droMoj2.genscan.LENGTH)
```

`droMoj2.xenoRefGene.LENGTH`*Transcript length data for the organism droMoj*

Description

droMoj2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(droMoj2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droMoj2.xenoRefGene.LENGTH)
head(droMoj2.xenoRefGene.LENGTH)
```

`droPer1.genscan.LENGTH`*Transcript length data for the organism droPer*

Description

`droPer1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(droPer1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droPer1.genscan.LENGTH)
head(droPer1.genscan.LENGTH)
```

`droPer1.xenoRefGene.LENGTH`*Transcript length data for the organism droPer*

Description

`droPer1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(droPer1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droPer1.xenoRefGene.LENGTH)
head(droPer1.xenoRefGene.LENGTH)
```

`droSec1.genscan.LENGTH`*Transcript length data for the organism droSec*

Description

`droSec1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(droSec1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droSec1.genscan.LENGTH)
head(droSec1.genscan.LENGTH)
```

`droSec1.xenoRefGene.LENGTH`*Transcript length data for the organism droSec*

Description

`droSec1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(droSec1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droSec1.xenoRefGene.LENGTH)
head(droSec1.xenoRefGene.LENGTH)
```

droSim1.geneid.LENGTH *Transcript length data for the organism droSim*

Description

droSim1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(droSim1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droSim1.geneid.LENGTH)
head(droSim1.geneid.LENGTH)
```

droSim1.genscan.LENGTH
Transcript length data for the organism droSim

Description

droSim1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(droSim1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droSim1.genscan.LENGTH)
head(droSim1.genscan.LENGTH)
```

`droSim1.xenoRefGene.LENGTH`*Transcript length data for the organism droSim*

Description

`droSim1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(droSim1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droSim1.xenoRefGene.LENGTH)
head(droSim1.xenoRefGene.LENGTH)
```

`droVir1.geneid.LENGTH` *Transcript length data for the organism droVir*

Description

`droVir1.geneid.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneid` table.

The data file was made by calling `downloadLengthFromUCSC(droVir1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droVir1.geneid.LENGTH)
head(droVir1.geneid.LENGTH)
```

`droVir1.genscan.LENGTH`*Transcript length data for the organism droVir*

Description

droVir1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(droVir1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droVir1.genscan.LENGTH)
head(droVir1.genscan.LENGTH)
```

`droVir1.xenoRefGene.LENGTH`*Transcript length data for the organism droVir*

Description

droVir1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(droVir1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droVir1.xenoRefGene.LENGTH)
head(droVir1.xenoRefGene.LENGTH)
```

```
droVir2.genscan.LENGTH
```

Transcript length data for the organism droVir

Description

droVir2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(droVir2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droVir2.genscan.LENGTH)
head(droVir2.genscan.LENGTH)
```

```
droVir2.xenoRefGene.LENGTH
```

Transcript length data for the organism droVir

Description

droVir2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(droVir2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droVir2.xenoRefGene.LENGTH)
head(droVir2.xenoRefGene.LENGTH)
```

droYak1.geneid.LENGTH *Transcript length data for the organism droYak*

Description

droYak1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(droYak1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droYak1.geneid.LENGTH)
head(droYak1.geneid.LENGTH)
```

droYak1.genscan.LENGTH
Transcript length data for the organism droYak

Description

droYak1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(droYak1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droYak1.genscan.LENGTH)
head(droYak1.genscan.LENGTH)
```

`droYak1.xenoRefGene.LENGTH`*Transcript length data for the organism droYak*

Description

`droYak1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(droYak1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droYak1.xenoRefGene.LENGTH)
head(droYak1.xenoRefGene.LENGTH)
```

`droYak2.genscan.LENGTH`*Transcript length data for the organism droYak*

Description

`droYak2.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(droYak2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droYak2.genscan.LENGTH)
head(droYak2.genscan.LENGTH)
```

`droYak2.xenoRefGene.LENGTH`*Transcript length data for the organism droYak*

Description

`droYak2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(droYak2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(droYak2.xenoRefGene.LENGTH)
head(droYak2.xenoRefGene.LENGTH)
```

`equCab1.geneid.LENGTH` *Transcript length data for the organism equCab*

Description

`equCab1.geneid.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneid` table.

The data file was made by calling `downloadLengthFromUCSC(equCab1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(equCab1.geneid.LENGTH)
head(equCab1.geneid.LENGTH)
```

```
equCab1.geneSymbol.LENGTH
```

Transcript length data for the organism equCab

Description

equCab1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(equCab1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(equCab1.geneSymbol.LENGTH)
head(equCab1.geneSymbol.LENGTH)
```

```
equCab1.nscanGene.LENGTH
```

Transcript length data for the organism equCab

Description

equCab1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(equCab1, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(equCab1.nscanGene.LENGTH)
head(equCab1.nscanGene.LENGTH)
```

`equCab1.refGene.LENGTH`*Transcript length data for the organism equCab*

Description

`equCab1.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(equCab1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(equCab1.refGene.LENGTH)
head(equCab1.refGene.LENGTH)
```

`equCab1.sgpGene.LENGTH`*Transcript length data for the organism equCab*

Description

`equCab1.sgpGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `sgpGene` table.

The data file was made by calling `downloadLengthFromUCSC(equCab1, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(equCab1.sgpGene.LENGTH)
head(equCab1.sgpGene.LENGTH)
```

```
equCab2.ensGene.LENGTH
```

Transcript length data for the organism equCab

Description

equCab2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(equCab2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(equCab2.ensGene.LENGTH)
head(equCab2.ensGene.LENGTH)
```

```
equCab2.geneSymbol.LENGTH
```

Transcript length data for the organism equCab

Description

equCab2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(equCab2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(equCab2.geneSymbol.LENGTH)
head(equCab2.geneSymbol.LENGTH)
```

`equCab2.nscanGene.LENGTH`*Transcript length data for the organism equCab*

Description

`equCab2.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(equCab2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(equCab2.nscanGene.LENGTH)
head(equCab2.nscanGene.LENGTH)
```

`equCab2.refGene.LENGTH`*Transcript length data for the organism equCab*

Description

`equCab2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(equCab2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(equCab2.refGene.LENGTH)
head(equCab2.refGene.LENGTH)
```

```
equCab2.xenoRefGene.LENGTH
```

Transcript length data for the organism equCab

Description

equCab2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(equCab2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(equCab2.xenoRefGene.LENGTH)
head(equCab2.xenoRefGene.LENGTH)
```

```
felCat3.ensGene.LENGTH
```

Transcript length data for the organism felCat

Description

felCat3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(felCat3, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(felCat3.ensGene.LENGTH)
head(felCat3.ensGene.LENGTH)
```

felCat3.geneid.LENGTH *Transcript length data for the organism felCat*

Description

felCat3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(felCat3, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(felCat3.geneid.LENGTH)
head(felCat3.geneid.LENGTH)
```

felCat3.geneSymbol.LENGTH
Transcript length data for the organism felCat

Description

felCat3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(felCat3, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(felCat3.geneSymbol.LENGTH)
head(felCat3.geneSymbol.LENGTH)
```

`felCat3.genscan.LENGTH`*Transcript length data for the organism felCat*

Description

felCat3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(felCat3, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(felCat3.genscan.LENGTH)
head(felCat3.genscan.LENGTH)
```

`felCat3.nscanGene.LENGTH`*Transcript length data for the organism felCat*

Description

felCat3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(felCat3, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(felCat3.nscanGene.LENGTH)
head(felCat3.nscanGene.LENGTH)
```

`felCat3.refGene.LENGTH`*Transcript length data for the organism felCat*

Description

felCat3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(felCat3, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(felCat3.refGene.LENGTH)
head(felCat3.refGene.LENGTH)
```

`felCat3.sgpGene.LENGTH`*Transcript length data for the organism felCat*

Description

felCat3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(felCat3, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(felCat3.sgpGene.LENGTH)
head(felCat3.sgpGene.LENGTH)
```

```
felCat3.xenoRefGene.LENGTH
```

Transcript length data for the organism felCat

Description

felCat3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(felCat3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(felCat3.xenoRefGene.LENGTH)
head(felCat3.xenoRefGene.LENGTH)
```

```
fr1.ensGene.LENGTH
```

Transcript length data for the organism fr

Description

fr1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(fr1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(fr1.ensGene.LENGTH)
head(fr1.ensGene.LENGTH)
```

fr1.genscan.LENGTH *Transcript length data for the organism fr*

Description

fr1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(fr1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(fr1.genscan.LENGTH)
head(fr1.genscan.LENGTH)
```

fr2.ensGene.LENGTH *Transcript length data for the organism fr*

Description

fr2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(fr2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(fr2.ensGene.LENGTH)
head(fr2.ensGene.LENGTH)
```

`galGal2.ensGene.LENGTH`*Transcript length data for the organism galGal*

Description

`galGal2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(galGal2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal2.ensGene.LENGTH)
head(galGal2.ensGene.LENGTH)
```

`galGal2.geneid.LENGTH` *Transcript length data for the organism galGal*

Description

`galGal2.geneid.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneid` table.

The data file was made by calling `downloadLengthFromUCSC(galGal2, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal2.geneid.LENGTH)
head(galGal2.geneid.LENGTH)
```

`galGal2.geneSymbol.LENGTH`*Transcript length data for the organism galGal*

Description

`galGal2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(galGal2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal2.geneSymbol.LENGTH)
head(galGal2.geneSymbol.LENGTH)
```

`galGal2.genscan.LENGTH`*Transcript length data for the organism galGal*

Description

`galGal2.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(galGal2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal2.genscan.LENGTH)
head(galGal2.genscan.LENGTH)
```

`galGal2.refGene.LENGTH`*Transcript length data for the organism galGal*

Description

galGal2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(galGal2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal2.refGene.LENGTH)
head(galGal2.refGene.LENGTH)
```

`galGal2.sgpGene.LENGTH`*Transcript length data for the organism galGal*

Description

galGal2.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(galGal2, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal2.sgpGene.LENGTH)
head(galGal2.sgpGene.LENGTH)
```

`galGal3.ensGene.LENGTH`*Transcript length data for the organism galGal*

Description

galGal3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(galGal3, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal3.ensGene.LENGTH)
head(galGal3.ensGene.LENGTH)
```

`galGal3.geneSymbol.LENGTH`*Transcript length data for the organism galGal*

Description

galGal3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(galGal3, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal3.geneSymbol.LENGTH)
head(galGal3.geneSymbol.LENGTH)
```

`galGal3.genscan.LENGTH`*Transcript length data for the organism galGal*

Description

`galGal3.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(galGal3, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal3.genscan.LENGTH)
head(galGal3.genscan.LENGTH)
```

`galGal3.nscanGene.LENGTH`*Transcript length data for the organism galGal*

Description

`galGal3.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(galGal3, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal3.nscanGene.LENGTH)
head(galGal3.nscanGene.LENGTH)
```

`galGal3.refGene.LENGTH`*Transcript length data for the organism galGal*

Description

galGal3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(galGal3, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal3.refGene.LENGTH)
head(galGal3.refGene.LENGTH)
```

`galGal3.xenoRefGene.LENGTH`*Transcript length data for the organism galGal*

Description

galGal3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(galGal3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(galGal3.xenoRefGene.LENGTH)
head(galGal3.xenoRefGene.LENGTH)
```

`gasAcu1.ensGene.LENGTH`*Transcript length data for the organism gasAcu*

Description

`gasAcu1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(gasAcu1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(gasAcu1.ensGene.LENGTH)
head(gasAcu1.ensGene.LENGTH)
```

`gasAcu1.nscanGene.LENGTH`*Transcript length data for the organism gasAcu*

Description

`gasAcu1.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(gasAcu1, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(gasAcu1.nscanGene.LENGTH)
head(gasAcu1.nscanGene.LENGTH)
```

geneLenDatabase-pkg *geneLenDatabase:*

Description

Lengths of mRNA transcripts for a number of genomes

Details

Length of mRNA transcripts for a number of genomes and gene ID formats, largely based on UCSC table browser. Data objects are provided as individual pieces of information to be retrieved and loaded. A variety of different gene identifiers and genomes is supported to ensure wide applicability.

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See Also

Useful links:

- <https://github.com/federicomarini/geneLenDataBase>
- Report bugs at <https://github.com/federicomarini/geneLenDataBase/issues>

hg16.acembly.LENGTH *Transcript length data for the organism hg*

Description

hg16.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the acembly table.

The data file was made by calling `downloadLengthFromUCSC(hg16, acembly)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg16.acembly.LENGTH)
head(hg16.acembly.LENGTH)
```

hg16.ensGene.LENGTH *Transcript length data for the organism hg*

Description

hg16.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(hg16, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg16.ensGene.LENGTH)
head(hg16.ensGene.LENGTH)
```

hg16.exoniphy.LENGTH *Transcript length data for the organism hg*

Description

hg16.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(hg16, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg16.exoniphy.LENGTH)
head(hg16.exoniphy.LENGTH)
```

hg16.geneid.LENGTH *Transcript length data for the organism hg*

Description

hg16.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(hg16, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg16.geneid.LENGTH)
head(hg16.geneid.LENGTH)
```

hg16.geneSymbol.LENGTH *Transcript length data for the organism hg*

Description

hg16.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(hg16, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg16.geneSymbol.LENGTH)
head(hg16.geneSymbol.LENGTH)
```

hg16.genscan.LENGTH *Transcript length data for the organism hg*

Description

hg16.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(hg16, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg16.genscan.LENGTH)
head(hg16.genscan.LENGTH)
```

hg16.knownGene.LENGTH *Transcript length data for the organism hg*

Description

hg16.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(hg16, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg16.knownGene.LENGTH)
head(hg16.knownGene.LENGTH)
```

hg16.refGene.LENGTH *Transcript length data for the organism hg*

Description

hg16.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(hg16, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg16.refGene.LENGTH)
head(hg16.refGene.LENGTH)
```

hg16.sgpGene.LENGTH *Transcript length data for the organism hg*

Description

hg16.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(hg16, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg16.sgpGene.LENGTH)
head(hg16.sgpGene.LENGTH)
```

hg17.acembly.LENGTH *Transcript length data for the organism hg*

Description

hg17.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the acembly table.

The data file was made by calling `downloadLengthFromUCSC(hg17, acembly)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.acembly.LENGTH)
head(hg17.acembly.LENGTH)
```

hg17.acescan.LENGTH *Transcript length data for the organism hg*

Description

hg17.acescan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the acescan table.

The data file was made by calling `downloadLengthFromUCSC(hg17, acescan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.acescan.LENGTH)
head(hg17.acescan.LENGTH)
```

hg17.ccdsGene.LENGTH *Transcript length data for the organism hg*

Description

hg17.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.ccdsGene.LENGTH)
head(hg17.ccdsGene.LENGTH)
```

hg17.ensGene.LENGTH *Transcript length data for the organism hg*

Description

hg17.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.ensGene.LENGTH)
head(hg17.ensGene.LENGTH)
```

hg17.exoniphy.LENGTH *Transcript length data for the organism hg*

Description

hg17.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(hg17, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.exoniphy.LENGTH)
head(hg17.exoniphy.LENGTH)
```

hg17.geneid.LENGTH *Transcript length data for the organism hg*

Description

hg17.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(hg17, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.geneid.LENGTH)
head(hg17.geneid.LENGTH)
```

`hg17.geneSymbol.LENGTH`*Transcript length data for the organism hg*

Description

hg17.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(hg17, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.geneSymbol.LENGTH)
head(hg17.geneSymbol.LENGTH)
```

`hg17.genscan.LENGTH`*Transcript length data for the organism hg*

Description

hg17.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(hg17, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.genscan.LENGTH)
head(hg17.genscan.LENGTH)
```

hg17.knownGene.LENGTH *Transcript length data for the organism hg*

Description

hg17.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.knownGene.LENGTH)
head(hg17.knownGene.LENGTH)
```

hg17.refGene.LENGTH *Transcript length data for the organism hg*

Description

hg17.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.refGene.LENGTH)
head(hg17.refGene.LENGTH)
```

hg17.sgpGene.LENGTH *Transcript length data for the organism hg*

Description

hg17.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.sgpGene.LENGTH)
head(hg17.sgpGene.LENGTH)
```

hg17.vegaGene.LENGTH *Transcript length data for the organism hg*

Description

hg17.vegaGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the vegaGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, vegaGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.vegaGene.LENGTH)
head(hg17.vegaGene.LENGTH)
```

`hg17.vegaPseudoGene.LENGTH`*Transcript length data for the organism hg*

Description

hg17.vegaPseudoGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the vegaPseudoGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, vegaPseudoGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.vegaPseudoGene.LENGTH)
head(hg17.vegaPseudoGene.LENGTH)
```

`hg17.xenoRefGene.LENGTH`*Transcript length data for the organism hg*

Description

hg17.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.xenoRefGene.LENGTH)
head(hg17.xenoRefGene.LENGTH)
```

hg18.acembly.LENGTH *Transcript length data for the organism hg*

Description

hg18.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the acembly table.

The data file was made by calling `downloadLengthFromUCSC(hg18, acembly)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.acembly.LENGTH)
head(hg18.acembly.LENGTH)
```

hg18.acescan.LENGTH *Transcript length data for the organism hg*

Description

hg18.acescan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the acescan table.

The data file was made by calling `downloadLengthFromUCSC(hg18, acescan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.acescan.LENGTH)
head(hg18.acescan.LENGTH)
```

hg18.ccdsGene.LENGTH *Transcript length data for the organism hg*

Description

hg18.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.ccdsGene.LENGTH)
head(hg18.ccdsGene.LENGTH)
```

hg18.ensGene.LENGTH *Transcript length data for the organism hg*

Description

hg18.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.ensGene.LENGTH)
head(hg18.ensGene.LENGTH)
```

hg18.exoniphy.LENGTH *Transcript length data for the organism hg*

Description

hg18.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(hg18, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.exoniphy.LENGTH)
head(hg18.exoniphy.LENGTH)
```

hg18.geneid.LENGTH *Transcript length data for the organism hg*

Description

hg18.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(hg18, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.geneid.LENGTH)
head(hg18.geneid.LENGTH)
```

`hg18.geneSymbol.LENGTH`*Transcript length data for the organism hg*

Description

hg18.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(hg18, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.geneSymbol.LENGTH)
head(hg18.geneSymbol.LENGTH)
```

`hg18.genscan.LENGTH`*Transcript length data for the organism hg*

Description

hg18.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(hg18, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.genscan.LENGTH)
head(hg18.genscan.LENGTH)
```

hg18.knownGene.LENGTH *Transcript length data for the organism hg*

Description

hg18.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.knownGene.LENGTH)
head(hg18.knownGene.LENGTH)
```

hg18.knownGeneOld3.LENGTH
Transcript length data for the organism hg

Description

hg18.knownGeneOld3.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGeneOld3 table.

The data file was made by calling `downloadLengthFromUCSC(hg18, knownGeneOld3)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.knownGeneOld3.LENGTH)
head(hg18.knownGeneOld3.LENGTH)
```

hg18.refGene.LENGTH *Transcript length data for the organism hg*

Description

hg18.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.refGene.LENGTH)
head(hg18.refGene.LENGTH)
```

hg18.sgpGene.LENGTH *Transcript length data for the organism hg*

Description

hg18.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.sgpGene.LENGTH)
head(hg18.sgpGene.LENGTH)
```

hg18.sibGene.LENGTH *Transcript length data for the organism hg*

Description

hg18.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sibGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, sibGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.sibGene.LENGTH)
head(hg18.sibGene.LENGTH)
```

hg18.xenoRefGene.LENGTH
Transcript length data for the organism hg

Description

hg18.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.xenoRefGene.LENGTH)
head(hg18.xenoRefGene.LENGTH)
```

hg19.ccdsGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.ccdsGene.LENGTH)
head(hg19.ccdsGene.LENGTH)
```

hg19.ensGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.ensGene.LENGTH)
head(hg19.ensGene.LENGTH)
```

hg19.exoniphy.LENGTH *Transcript length data for the organism hg*

Description

hg19.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(hg19, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.exoniphy.LENGTH)
head(hg19.exoniphy.LENGTH)
```

hg19.geneSymbol.LENGTH
Transcript length data for the organism hg

Description

hg19.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(hg19, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.geneSymbol.LENGTH)
head(hg19.geneSymbol.LENGTH)
```

hg19.knownGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.knownGene.LENGTH)
head(hg19.knownGene.LENGTH)
```

hg19.nscanGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.nscanGene.LENGTH)
head(hg19.nscanGene.LENGTH)
```

hg19.refGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.refGene.LENGTH)
head(hg19.refGene.LENGTH)
```

hg19.xenoRefGene.LENGTH
Transcript length data for the organism hg

Description

hg19.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.xenoRefGene.LENGTH)
head(hg19.xenoRefGene.LENGTH)
```

`loxAfr3.xenoRefGene.LENGTH`*Transcript length data for the organism loxAfr*

Description

`loxAfr3.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(loxAfr3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(loxAfr3.xenoRefGene.LENGTH)
head(loxAfr3.xenoRefGene.LENGTH)
```

`mm7.ensGene.LENGTH`*Transcript length data for the organism mm*

Description

`mm7.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm7, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.ensGene.LENGTH)
head(mm7.ensGene.LENGTH)
```

mm7.geneid.LENGTH *Transcript length data for the organism mm*

Description

mm7.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm7, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.geneid.LENGTH)
head(mm7.geneid.LENGTH)
```

mm7.geneSymbol.LENGTH *Transcript length data for the organism mm*

Description

mm7.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm7, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.geneSymbol.LENGTH)
head(mm7.geneSymbol.LENGTH)
```

mm7.genscan.LENGTH *Transcript length data for the organism mm*

Description

mm7.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm7, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.genscan.LENGTH)
head(mm7.genscan.LENGTH)
```

mm7.knownGene.LENGTH *Transcript length data for the organism mm*

Description

mm7.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.knownGene.LENGTH)
head(mm7.knownGene.LENGTH)
```

mm7.refGene.LENGTH *Transcript length data for the organism mm*

Description

mm7.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.refGene.LENGTH)
head(mm7.refGene.LENGTH)
```

mm7.sgpGene.LENGTH *Transcript length data for the organism mm*

Description

mm7.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.sgpGene.LENGTH)
head(mm7.sgpGene.LENGTH)
```

`mm7.xenoRefGene.LENGTH`*Transcript length data for the organism mm*

Description

`mm7.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm7, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.xenoRefGene.LENGTH)
head(mm7.xenoRefGene.LENGTH)
```

`mm8.ccdsGene.LENGTH`*Transcript length data for the organism mm*

Description

`mm8.ccdsGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ccdsGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm8, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.ccdsGene.LENGTH)
head(mm8.ccdsGene.LENGTH)
```

mm8.ensGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.ensGene.LENGTH)
head(mm8.ensGene.LENGTH)
```

mm8.geneid.LENGTH *Transcript length data for the organism mm*

Description

mm8.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm8, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.geneid.LENGTH)
head(mm8.geneid.LENGTH)
```

mm8.geneSymbol.LENGTH *Transcript length data for the organism mm*

Description

mm8.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm8, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.geneSymbol.LENGTH)
head(mm8.geneSymbol.LENGTH)
```

mm8.genscan.LENGTH *Transcript length data for the organism mm*

Description

mm8.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm8, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.genscan.LENGTH)
head(mm8.genscan.LENGTH)
```

mm8.knownGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.knownGene.LENGTH)
head(mm8.knownGene.LENGTH)
```

mm8.nscanGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.nscanGene.LENGTH)
head(mm8.nscanGene.LENGTH)
```

mm8.refGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.refGene.LENGTH)
head(mm8.refGene.LENGTH)
```

mm8.sgpGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.sgpGene.LENGTH)
head(mm8.sgpGene.LENGTH)
```

mm8.sibGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sibGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, sibGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.sibGene.LENGTH)
head(mm8.sibGene.LENGTH)
```

mm8.xenoRefGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.xenoRefGene.LENGTH)
head(mm8.xenoRefGene.LENGTH)
```

mm9.acembly.LENGTH *Transcript length data for the organism mm*

Description

mm9.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the acembly table.

The data file was made by calling `downloadLengthFromUCSC(mm9, acembly)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.acembly.LENGTH)
head(mm9.acembly.LENGTH)
```

mm9.ccdsGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.ccdsGene.LENGTH)
head(mm9.ccdsGene.LENGTH)
```

mm9.ensGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.ensGene.LENGTH)
head(mm9.ensGene.LENGTH)
```

mm9.exoniphy.LENGTH *Transcript length data for the organism mm*

Description

mm9.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(mm9, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.exoniphy.LENGTH)
head(mm9.exoniphy.LENGTH)
```

mm9.geneid.LENGTH *Transcript length data for the organism mm*

Description

mm9.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.geneid.LENGTH)
head(mm9.geneid.LENGTH)
```

mm9.geneSymbol.LENGTH *Transcript length data for the organism mm*

Description

mm9.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.geneSymbol.LENGTH)
head(mm9.geneSymbol.LENGTH)
```

mm9.genscan.LENGTH *Transcript length data for the organism mm*

Description

mm9.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm9, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.genscan.LENGTH)
head(mm9.genscan.LENGTH)
```

mm9.knownGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.knownGene.LENGTH)
head(mm9.knownGene.LENGTH)
```

mm9.nscanGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.nscanGene.LENGTH)
head(mm9.nscanGene.LENGTH)
```

mm9.refGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.refGene.LENGTH)
head(mm9.refGene.LENGTH)
```

mm9.sgpGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.sgpGene.LENGTH)
head(mm9.sgpGene.LENGTH)
```

mm9.xenoRefGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.xenoRefGene.LENGTH)
head(mm9.xenoRefGene.LENGTH)
```

`monDom1.genscan.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom1.genscan.LENGTH)
head(monDom1.genscan.LENGTH)
```

`monDom4.ensGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.ensGene.LENGTH)
head(monDom4.ensGene.LENGTH)
```

`monDom4.geneSymbol.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.geneSymbol.LENGTH)
head(monDom4.geneSymbol.LENGTH)
```

`monDom4.genscan.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.genscan.LENGTH)
head(monDom4.genscan.LENGTH)
```

`monDom4.nscanGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.nscanGene.LENGTH)
head(monDom4.nscanGene.LENGTH)
```

`monDom4.refGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.refGene.LENGTH)
head(monDom4.refGene.LENGTH)
```

`monDom4.xenoRefGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.xenoRefGene.LENGTH)
head(monDom4.xenoRefGene.LENGTH)
```

`monDom5.ensGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.ensGene.LENGTH)
head(monDom5.ensGene.LENGTH)
```

`monDom5.geneSymbol.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.geneSymbol.LENGTH)
head(monDom5.geneSymbol.LENGTH)
```

`monDom5.genscan.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.genscan.LENGTH)
head(monDom5.genscan.LENGTH)
```

`monDom5.nscanGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, nscanGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(monDom5.nscanGene.LENGTH)
head(monDom5.nscanGene.LENGTH)
```

`monDom5.refGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, refGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(monDom5.refGene.LENGTH)
head(monDom5.refGene.LENGTH)
```

```
monDom5.xenoRefGene.LENGTH
```

Transcript length data for the organism monDom

Description

monDom5.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.xenoRefGene.LENGTH)
head(monDom5.xenoRefGene.LENGTH)
```

```
ornAna1.ensGene.LENGTH
```

Transcript length data for the organism ornAna

Description

ornAna1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.ensGene.LENGTH)
head(ornAna1.ensGene.LENGTH)
```

`ornAna1.geneSymbol.LENGTH`*Transcript length data for the organism ornAna*

Description

`ornAna1.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.geneSymbol.LENGTH)
head(ornAna1.geneSymbol.LENGTH)
```

`ornAna1.refGene.LENGTH`*Transcript length data for the organism ornAna*

Description

`ornAna1.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.refGene.LENGTH)
head(ornAna1.refGene.LENGTH)
```

`ornAna1.xenoRefGene.LENGTH`*Transcript length data for the organism ornAna*

Description

`ornAna1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.xenoRefGene.LENGTH)
head(ornAna1.xenoRefGene.LENGTH)
```

`oryLat2.ensGene.LENGTH`*Transcript length data for the organism oryLat*

Description

`oryLat2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.ensGene.LENGTH)
head(oryLat2.ensGene.LENGTH)
```

```
oryLat2.geneSymbol.LENGTH
```

Transcript length data for the organism oryLat

Description

oryLat2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.geneSymbol.LENGTH)
head(oryLat2.geneSymbol.LENGTH)
```

```
oryLat2.refGene.LENGTH
```

Transcript length data for the organism oryLat

Description

oryLat2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.refGene.LENGTH)
head(oryLat2.refGene.LENGTH)
```

```
oryLat2.xenoRefGene.LENGTH
```

Transcript length data for the organism oryLat

Description

oryLat2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.xenoRefGene.LENGTH)
head(oryLat2.xenoRefGene.LENGTH)
```

```
panTro1.ensGene.LENGTH
```

Transcript length data for the organism panTro

Description

panTro1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.ensGene.LENGTH)
head(panTro1.ensGene.LENGTH)
```

panTro1.geneid.LENGTH *Transcript length data for the organism panTro*

Description

panTro1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.geneid.LENGTH)
head(panTro1.geneid.LENGTH)
```

panTro1.genscan.LENGTH
Transcript length data for the organism panTro

Description

panTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.genscan.LENGTH)
head(panTro1.genscan.LENGTH)
```

`panTro1.xenoRefGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.xenoRefGene.LENGTH)
head(panTro1.xenoRefGene.LENGTH)
```

`panTro2.ensGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.ensGene.LENGTH)
head(panTro2.ensGene.LENGTH)
```

`panTro2.geneSymbol.LENGTH`*Transcript length data for the organism panTro*

Description

`panTro2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.geneSymbol.LENGTH)
head(panTro2.geneSymbol.LENGTH)
```

`panTro2.genscan.LENGTH`*Transcript length data for the organism panTro*

Description

`panTro2.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.genscan.LENGTH)
head(panTro2.genscan.LENGTH)
```

`panTro2.nscanGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.nscanGene.LENGTH)
head(panTro2.nscanGene.LENGTH)
```

`panTro2.refGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.refGene.LENGTH)
head(panTro2.refGene.LENGTH)
```

`panTro2.xenoRefGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.xenoRefGene.LENGTH)
head(panTro2.xenoRefGene.LENGTH)
```

`petMar1.xenoRefGene.LENGTH`*Transcript length data for the organism petMar*

Description

petMar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(petMar1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(petMar1.xenoRefGene.LENGTH)
head(petMar1.xenoRefGene.LENGTH)
```

```
ponAbe2.ensGene.LENGTH
```

Transcript length data for the organism ponAbe

Description

ponAbe2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.ensGene.LENGTH)
head(ponAbe2.ensGene.LENGTH)
```

```
ponAbe2.geneSymbol.LENGTH
```

Transcript length data for the organism ponAbe

Description

ponAbe2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.geneSymbol.LENGTH)
head(ponAbe2.geneSymbol.LENGTH)
```

`ponAbe2.genscan.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.genscan.LENGTH)
head(ponAbe2.genscan.LENGTH)
```

`ponAbe2.nscanGene.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.nscanGene.LENGTH)
head(ponAbe2.nscanGene.LENGTH)
```

`ponAbe2.refGene.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.refGene.LENGTH)
head(ponAbe2.refGene.LENGTH)
```

`ponAbe2.xenoRefGene.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.xenoRefGene.LENGTH)
head(ponAbe2.xenoRefGene.LENGTH)
```

```
priPac1.xenoRefGene.LENGTH
```

Transcript length data for the organism priPac

Description

priPac1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(priPac1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(priPac1.xenoRefGene.LENGTH)
head(priPac1.xenoRefGene.LENGTH)
```

```
rheMac2.ensGene.LENGTH
```

Transcript length data for the organism rheMac

Description

rheMac2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.ensGene.LENGTH)
head(rheMac2.ensGene.LENGTH)
```

rheMac2.geneid.LENGTH Transcript length data for the organism rheMac

Description

`rheMac2.geneid.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneid` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.geneid.LENGTH)
head(rheMac2.geneid.LENGTH)
```

rheMac2.geneSymbol.LENGTH
Transcript length data for the organism rheMac

Description

`rheMac2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.geneSymbol.LENGTH)
head(rheMac2.geneSymbol.LENGTH)
```

`rheMac2.nscanGene.LENGTH`*Transcript length data for the organism rheMac*

Description

`rheMac2.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.nscanGene.LENGTH)
head(rheMac2.nscanGene.LENGTH)
```

`rheMac2.refGene.LENGTH`*Transcript length data for the organism rheMac*

Description

`rheMac2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.refGene.LENGTH)
head(rheMac2.refGene.LENGTH)
```

`rheMac2.sgpGene.LENGTH`*Transcript length data for the organism rheMac*

Description

`rheMac2.sgpGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `sgpGene` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.sgpGene.LENGTH)
head(rheMac2.sgpGene.LENGTH)
```

`rheMac2.xenoRefGene.LENGTH`*Transcript length data for the organism rheMac*

Description

`rheMac2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.xenoRefGene.LENGTH)
head(rheMac2.xenoRefGene.LENGTH)
```

rn3.ensGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.ensGene.LENGTH)
head(rn3.ensGene.LENGTH)
```

rn3.geneid.LENGTH *Transcript length data for the organism rn*

Description

rn3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.geneid.LENGTH)
head(rn3.geneid.LENGTH)
```

rn3.geneSymbol.LENGTH *Transcript length data for the organism rn*

Description

rn3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.geneSymbol.LENGTH)
head(rn3.geneSymbol.LENGTH)
```

rn3.genscan.LENGTH *Transcript length data for the organism rn*

Description

rn3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn3, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.genscan.LENGTH)
head(rn3.genscan.LENGTH)
```

rn3.knownGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.knownGene.LENGTH)
head(rn3.knownGene.LENGTH)
```

rn3.nscanGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.nscanGene.LENGTH)
head(rn3.nscanGene.LENGTH)
```

rn3.refGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.refGene.LENGTH)
head(rn3.refGene.LENGTH)
```

rn3.sgpGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.sgpGene.LENGTH)
head(rn3.sgpGene.LENGTH)
```

`rn3.xenoRefGene.LENGTH`*Transcript length data for the organism rn*

Description

rn3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.xenoRefGene.LENGTH)
head(rn3.xenoRefGene.LENGTH)
```

`rn4.ensGene.LENGTH`*Transcript length data for the organism rn*

Description

rn4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.ensGene.LENGTH)
head(rn4.ensGene.LENGTH)
```

rn4.geneid.LENGTH *Transcript length data for the organism rn*

Description

rn4.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.geneid.LENGTH)
head(rn4.geneid.LENGTH)
```

rn4.geneSymbol.LENGTH *Transcript length data for the organism rn*

Description

rn4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.geneSymbol.LENGTH)
head(rn4.geneSymbol.LENGTH)
```

rn4.genscan.LENGTH *Transcript length data for the organism rn*

Description

rn4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn4, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.genscan.LENGTH)
head(rn4.genscan.LENGTH)
```

rn4.knownGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.knownGene.LENGTH)
head(rn4.knownGene.LENGTH)
```

rn4.nscanGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.nscanGene.LENGTH)
head(rn4.nscanGene.LENGTH)
```

rn4.refGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.refGene.LENGTH)
head(rn4.refGene.LENGTH)
```

rn4.sgpGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.sgpGene.LENGTH)
head(rn4.sgpGene.LENGTH)
```

rn4.xenoRefGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.xenoRefGene.LENGTH)
head(rn4.xenoRefGene.LENGTH)
```

`sacCer1.ensGene.LENGTH`*Transcript length data for the organism sacCer*

Description

sacCer1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(sacCer1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(sacCer1.ensGene.LENGTH)
head(sacCer1.ensGene.LENGTH)
```

`sacCer2.ensGene.LENGTH`*Transcript length data for the organism sacCer*

Description

sacCer2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(sacCer2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(sacCer2.ensGene.LENGTH)
head(sacCer2.ensGene.LENGTH)
```

```
strPur1.geneSymbol.LENGTH
```

Transcript length data for the organism strPur

Description

strPur1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.geneSymbol.LENGTH)
head(strPur1.geneSymbol.LENGTH)
```

```
strPur1.genscan.LENGTH
```

Transcript length data for the organism strPur

Description

strPur1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.genscan.LENGTH)
head(strPur1.genscan.LENGTH)
```

```
strPur1.refGene.LENGTH
```

Transcript length data for the organism strPur

Description

strPur1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.refGene.LENGTH)
head(strPur1.refGene.LENGTH)
```

```
strPur1.xenoRefGene.LENGTH
```

Transcript length data for the organism strPur

Description

strPur1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.xenoRefGene.LENGTH)
head(strPur1.xenoRefGene.LENGTH)
```

```
strPur2.geneSymbol.LENGTH
```

Transcript length data for the organism strPur

Description

strPur2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.geneSymbol.LENGTH)
head(strPur2.geneSymbol.LENGTH)
```

```
strPur2.genscan.LENGTH
```

Transcript length data for the organism strPur

Description

strPur2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.genscan.LENGTH)
head(strPur2.genscan.LENGTH)
```

`strPur2.refGene.LENGTH`*Transcript length data for the organism strPur*

Description

strPur2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.refGene.LENGTH)
head(strPur2.refGene.LENGTH)
```

`strPur2.xenoRefGene.LENGTH`*Transcript length data for the organism strPur*

Description

strPur2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.xenoRefGene.LENGTH)
head(strPur2.xenoRefGene.LENGTH)
```

supportedGeneIDs	<i>Supported Gene IDs</i>
------------------	---------------------------

Description

Lists supported gene ID formats

Usage

```
supportedGeneIDs()
```

Details

Uses the supportedUCSCTables function from the GenomicFeatures package to obtain a list of gene ID formats available from the UCSC genome browser. The db column gives the gene ID formats which are provided to the id argument of various functions. The track and subtrack columns are the names of the UCSC track/subtrack from which information is fetched.

The GeneID column lists the "full name" of the gene ID format where available.

The final column, headed AvailableGenomes lists the genomes for which there is a local copy of the length information available for the gene ID format listed in the geneLenDataBase package.

Value

A data.frame containing supported gene ID formats.

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
supportedGeneIDs()
```

supportedGenomes	<i>Supported Genomes</i>
------------------	--------------------------

Description

Lists supported genomes

Usage

```
supportedGenomes()
```

Details

Uses the `ucscGenomes()` function from the `rtracklayer` package to obtain a list of genomes available from the UCSC genome browser. The `db` column lists genomes as they are provided to the genome argument of various functions.

The final column, headed `AvailableGeneIDs` lists the gene ID formats for which there is a local copy of the length information available for the genome listed in the `geneLenDataBase` package.

Value

A data.frame containing supported genomes.

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
supportedGenomes()
```

`taeGut1.ensGene.LENGTH`

Transcript length data for the organism taeGut

Description

`taeGut1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.ensGene.LENGTH)
head(taeGut1.ensGene.LENGTH)
```

```
taeGut1.geneSymbol.LENGTH
```

Transcript length data for the organism taeGut

Description

taeGut1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.geneSymbol.LENGTH)
head(taeGut1.geneSymbol.LENGTH)
```

```
taeGut1.genscan.LENGTH
```

Transcript length data for the organism taeGut

Description

taeGut1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.genscan.LENGTH)
head(taeGut1.genscan.LENGTH)
```

```
taeGut1.nscanGene.LENGTH
```

Transcript length data for the organism taeGut

Description

taeGut1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.nscanGene.LENGTH)
head(taeGut1.nscanGene.LENGTH)
```

```
taeGut1.refGene.LENGTH
```

Transcript length data for the organism taeGut

Description

taeGut1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.refGene.LENGTH)
head(taeGut1.refGene.LENGTH)
```

`taeGut1.xenoRefGene.LENGTH`*Transcript length data for the organism taeGut*

Description

`taeGut1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.xenoRefGene.LENGTH)
head(taeGut1.xenoRefGene.LENGTH)
```

`tetNig1.ensGene.LENGTH`*Transcript length data for the organism tetNig*

Description

`tetNig1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.ensGene.LENGTH)
head(tetNig1.ensGene.LENGTH)
```

tetNig1.geneid.LENGTH *Transcript length data for the organism tetNig*

Description

tetNig1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.geneid.LENGTH)
head(tetNig1.geneid.LENGTH)
```

tetNig1.genscan.LENGTH
Transcript length data for the organism tetNig

Description

tetNig1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.genscan.LENGTH)
head(tetNig1.genscan.LENGTH)
```

`tetNig1.nscanGene.LENGTH`*Transcript length data for the organism tetNig*

Description

`tetNig1.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.nscanGene.LENGTH)
head(tetNig1.nscanGene.LENGTH)
```

`tetNig2.ensGene.LENGTH`*Transcript length data for the organism tetNig*

Description

`tetNig2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(tetNig2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig2.ensGene.LENGTH)
head(tetNig2.ensGene.LENGTH)
```

`unfactor`*Purge factors*

Description

Removes all factors from a variable in a sensible way.

Usage

```
unfactor(var)
```

Arguments

`var` The variable from which you want the factors removed.

Details

As factors are their own type, to remove factors we must convert each level into another type. This is currently done using "typeless" behaviour: a factor is converted to a numeric vector if this can be done without inducing NAs, otherwise it is coerced using `as.character`. Currently supported types are: `factor`, `data.frame` and `list`.

Value

The variable with all factors converted to characters or numbers (see details).

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
# A named factor
x <- factor(sample(1:6, 100, replace=TRUE))
names(x) <- paste("Roll.No", 1:100, sep='.')
x
unfactor(x)

# A data.frame
x <- data.frame(player <- c("Alice", "Bob", "Mary", "Fred"),
                score <- factor(c(9, 7, 8, 9)), stringsAsFactors=TRUE)
x$player
x$score
y <- unfactor(x)
y$player
y$score
```

`xenTro1.genscan.LENGTH`*Transcript length data for the organism xenTro*

Description

`xenTro1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro1.genscan.LENGTH)
head(xenTro1.genscan.LENGTH)
```

`xenTro2.ensGene.LENGTH`*Transcript length data for the organism xenTro*

Description

`xenTro2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.ensGene.LENGTH)
head(xenTro2.ensGene.LENGTH)
```

```
xenTro2.geneSymbol.LENGTH
```

Transcript length data for the organism xenTro

Description

xenTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.geneSymbol.LENGTH)
head(xenTro2.geneSymbol.LENGTH)
```

```
xenTro2.genscan.LENGTH
```

Transcript length data for the organism xenTro

Description

xenTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.genscan.LENGTH)
head(xenTro2.genscan.LENGTH)
```

`xenTro2.refGene.LENGTH`*Transcript length data for the organism xenTro*

Description

xenTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.refGene.LENGTH)
head(xenTro2.refGene.LENGTH)
```

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